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Research Article

Molecular identification of *Pichia guilliermondii*, *Debaryomyces hansenii* and *Candida palmioleophila*

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Abstract

Traditional phenotypic methods and commercial kits based on carbohydrate assimilation patterns are unable to consistently distinguish among isolates of *Pichia guilliermondii*, *Debaryomyces hansenii* and *Candida palmioleophila.* As result, these species are often misidentified. In this work, we established a reliable method for the identification/differentiation of these species. Our assay was validated by DNA sequencing of the polymorphic region used in a real-time PCR assay driven by species-specific probes targeted to the fungal ITS 1 region. This assay provides a new tool for pathogen identification and for epidemiological, drug resistance and virulence studies of these organisms.

Key words: Candida palmioleophila, *Debaryomyces hansenii*, differential identification, *Pichia guilliermondii*, real-time PCR.

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Introduction

The precise identification of some fungal species is often very difficult when using only biochemical or phenotypic methods (Dooley *et al.*, 1994; Fenn *et al.*, 1994). However, the advent of DNA-based methods largely overcame the limitations of traditional methods and studies using molecular approaches revealed a greater diversity in fungi (Odds *et al.*, 1998; Chen *et al.*, 2000).

Some closely related species are often misidentified because of the great similarity in their biochemical and morphological characteristics. Desnos-Ollivier *et al.* (2008) reported the misidentification of *Pichia guilliermondii* (teleomorph *Candida guilliermondii*), *Debaryomyces hansenii* (teleomorph *Candida famata*) and *Candida palmioleophila.* Their results showed that only 23 of 36 isolates identified as *P. guilliermondii* and three of 26 identified as *D. hansenii* were confirmed by sequencing the ITS1-5.8S-ITS2 and D1/D2 regions of the ribosomal cistron. Other species such as *Candida albicans* (Odds *et al.*, 1998; Jabra-Rizk *et al.*, 2000; Tietz *et al.*, 2001) and *Candida parapsilosis* (Lasker *et al.*, 2006) show the same problem.

In our laboratory, we have had problems differentiating (1) *P. guilliermondii*, *C. palmioleophila* and *D. hansenii*, (2) *Candida krusei* and *Candida inconspicua*, and (3) *Candida pelliculosa* and *Candida subpelliculosa* when using the commercial kit API® 20 C AUX (Biomérieux, France) (Table S1). The Vitek Yeast Biochemical Card and the ID 32C, two widely used methods for yeast identification, were tested by different groups (Dooley *et al.*, 1994; Lo *et al.*, 2001; Burton *et al.*, 2010) and their findings confirmed the problem of incorrect or inconsistent identification. Lo *et al.* (2001) suggested that the laboratory routine should include at least two methods for yeast identification.

Misidentification of the fungal species can compromise epidemiological or antibiotic susceptibility studies and over- or underestimate the species abundance. Precise identification is therefore necessary and molecular approaches can provide the tools for a fast method. In this study, we developed a real-time PCR method that can differentiate/identify *P. guilliermondii*, *D. hansenii* and *C. palmioleophila*, and sequencing the ITS 1 region of these species confirmed our results.

Materials and Methods

Total DNA was extracted as described by Philippsen *et al.* (1991). DNA was quantified with a Qubit® fluorometer and a Quant-iT PicoGreen® dsDNA BR assay kit (Invitrogen, Life Technologies, Eugene, OR, USA) according to the manufacturers recommendations.

A Go® Taq Flexi DNA Polymerase kit (Promega, Madison, WI, USA) was used to amplify the ITS 1 region

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with ITS1/ITS2 primers (White and Lee, 1990) and a TopoTA Cloning® kit (Invitrogen) was used for the constructions. The sequences were obtained using a Big Dye® Terminator v3.1 Cycle Sequencing kit followed by automatic sequencing in an ABI 3100 (Applied Biosystems, Life Technologies, Foster City, CA, USA).

The sequences obtained from the three American Tissue Culture Collection (ATCC) species, *D. hansenii* ATCC 36239, *C. famata* ATCC 62894 and *P. guilliermondii* ATCC 6260, were compared by the BLASTN program (Zhang *et al.*, 2000) against the GenBank non-redundant database (nr), EMBL, DDBJ and PDB nucleotide collections. The sequences obtained were aligned with ClustalW software (Larkin *et al.*, 2007) and then used to create a consensus sequence for each species and to choose target regions (data not shown). The primers and TaqMan® Minor Groove Binder (MGB) probes were designed using the software Primer Express v. 2.0 and default parameters (Applied Biosystems).

A real-time PCR was done using the TaqMan® Universal PCR Master Mix (Applied Biosystems) in the following singleplex reaction mixture: 10 ng of sample DNA, 1X TaqMan® Universal PCR Master Mix, 200 nM of each primer, 300 nM of TaqMan® MGB probe (Table 1) and water to a total volume of 25 μL. All reactions were done in duplicate. The cycling conditions were set in an ABI 7300 real-time PCR cycler fitted with SDS software v. 1.2.3 (Applied Biosystems) as follows: 10 min at 95 °C followed by 35 cycles of 95 °C for 30 s and 60 °C for 1 min.

The efficiency of multiplex reactions was tested by mixing all of the probes together in the same concentrations as shown above.

Results and Discussion

The sequences obtained from the ATCC strains (data not shown) were matched in a search against the (nr) nucleotide bank using the BLAST program (the alignment files are provided in Supplementary Material Figure S2) in order to choose the potential target region for genotyping by real-time PCR (Figure 1).

Comparison of the two methods of identification (API 20C AUX and ribotyping by sequencing) revealed the difficulty in differentiating *P. guilliermondii* and *D. hansenii*, in the correct identification of *C. parapsilosis* versus *D. hansenii* (Burton *et al.*, 2010 and Table S1) and the impossibility of differentiating *C. krusei* and *C. insconspicua*.

Initially, three polymorphic domains (ITS 1, ITS 2 and D1/D2) of the ribosomal cistron from these species were aligned using ClustalW (Larkin *et al.*, 2007). Of these three regions, only the ITS 1 region provided suitable discrimination (Figure 1). This region is ideal because it is flanked by two conserved domains: the end of 18S rRNA and the beginning of 5.8S rRNA. The amplicon is short (about 300 bp) and the sequence is variable among different species but conserved among strains of the same species.

Figure 2 shows the amplification plot of the real-time PCR genotyping done using species-specific probes. The region indicated as NTC (no template control) confirmed the specificity of each probe since only in the presence of the specific target was there amplification. To confirm this finding, we analyzed the real-time PCR products in a 2% agarose gel stained with ethidium bromide and detected the expected amplicons (data not shown).

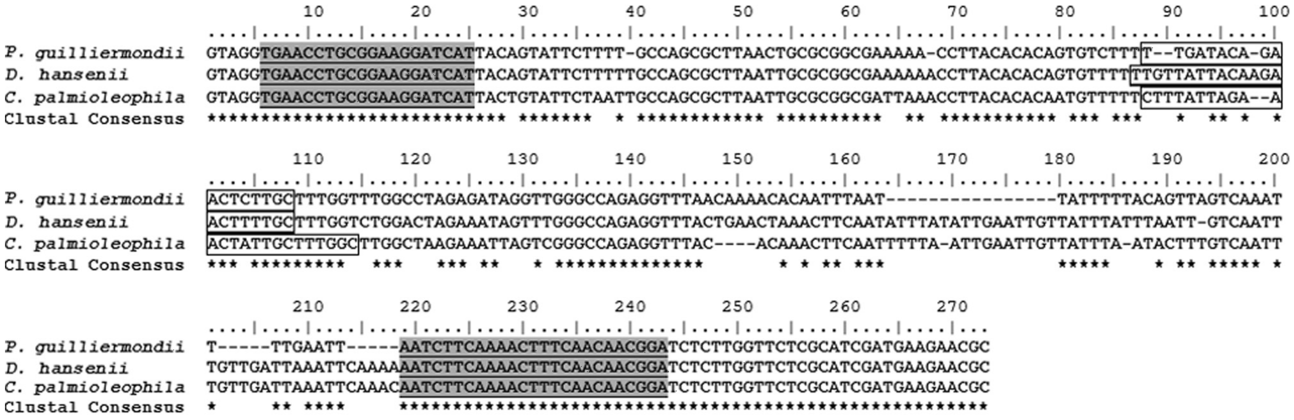
The multiplex reaction worked as well as the singleplex test (Figure S1) and can be used for fungus identification, thereby reducing the costs of the assay.

The close relationship between *C. palmioleophila* and *D. hansenii* has previously been shown by a phylogenetic analysis using data from the D1/D2 and ITS regions (Desnos-Ollivier *et al.*, 2008). In our study, the strain *C. famata* ATCC 62894, used as a positive control, was identified as *C. palmioleophila* by sequence analysis of the D1/D2 region of rRNA (Table S1) and by the real-time PCR assay described here (Figure 2).

In conclusion, the three species examined here are difficult to identify using standard laboratory tests. Ribosomal RNA sequencing is the gold standard for identification but is generally expensive and time consuming. The real-time PCR assay described here is a very effective, rapid, low-cost alternative. The method can unambiguously identify isolates and confirm the identification of strains analyzed by traditional methods, with the advantage of measuring species abundance if necessary.

Table 1 - Sequences of primers and probes used in this work. In the probes, the reporter dye is indicated in bold and the "No fluorescent quencher (NFQ)" region is underlined. The probe sequence is inserted between these two regions.

Primers/probes	Sequence	Tm (ºC)
ITS1 Fw	TGAACCTGCGGAAGGATCAT	59
ITS2 Rev	TCCGTTGTTGAAAGTTTTGAAGATT	59
TaqMan® MGB probes		
D. hansenii	**VIC**TTGTTATTACAAGAACTTTTGC<u>MGBNFQ</u>	70
P. guilliermondii	**6FAM**TTGATACAGAACTCTTGCTTTG<u>MGBNFQ</u>	70
C. palmioleophila	**NED**CTTTATTAGAAACTATTGCTTTGGC<u>MGBNFQ</u>	70



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                            10        20        30        40        50        60        70        80        90       100
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
P. guilliermondii   GTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTT-GCCAGCGCTTAACTGCGCGGCGAAAAA-CCTTACACACAGTGTCTTTT--TGATACA-GA
D. hansenii         GTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCGCGGCGAAAAAACCTTACACACAGTGTTTTTTGTTATTACAAGA
C. palmioleophila   GTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCGCGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGA--A
Clustal Consensus   **************************** *******  * ************ **********  ** *********** *** ***   *  ** *  *

                           110       120       130       140       150       160       170       180       190       200
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
P. guilliermondii   ACTCTTGCTTTGGTTTGGCCTAGAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAAT----------------TATTTTTACAGTTAGTCAAAT
D. hansenii         ACTTTTGCTTTGGTCTGGACTAGAAATAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTGAATTGTTATTTATTTAATT-GTCAATT
C. palmioleophila   ACTATTGCTTTGGCTTGGCTAAGAAATTAGTCGGGCCAGAGGTTTAC----ACAAACTTCAATTTTTA-ATTGAATTGTTATTTA-ATACTTTGTCAATT
Clustal Consensus   *** *********  ***   *** **   * **************       * * ** ***                *****    * ** ***** *

                           210       220       230       240       250       260       270
                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|...
P. guilliermondii   T-----TTGAATT-----AATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGC
D. hansenii         TGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGC
C. palmioleophila   TGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGC
Clustal Consensus   *     ** ****     *******************************************************
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Figure 1 - Sequence alignment of the polymorphic ITS 1 region. The ITS 1 regions of the three species were aligned using ClustalW. The numbers above the sequences represent base positions, the gray boxes are the targets of forward and reverse primers and the clear boxes indicate the probe targets.

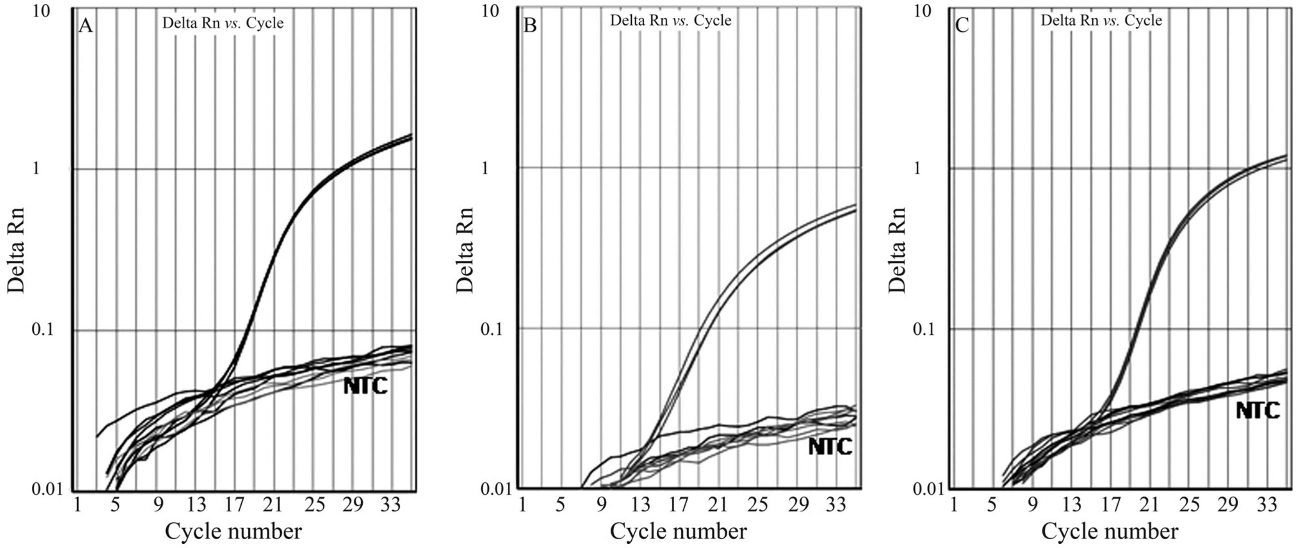

Figure 2 - Plots showing real-time PCR amplification of singleplex assays monitored with fluorescent TaqMan® MGB probes. Delta Rn versus Cycle amplification plots were obtained using probes for (A) *P. guilliermondii*, (B) *C. palmioleophila* and (C) *D. hansenii* templates. The NTC (no template control) curves show no detection in the absence of templates and in the presence of non-specific targets, *i.e.*, *C. palmioleophila* and *D. hansenii* in (A), *P. guilliermondii* and *D. hansenii* in (B) and *P. guilliermondii* and *C. palmioleophila* in (C).

Acknowledgments

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References

Burton MJ, Shah P and Swiatlo E (2010) Misidentification of *Candida parapsilosis* as *C. famata* in a clinical case of vertebral osteomyelitis. Am J Med Sci 341:71-73.

Chen YC, Eisner JD, Kattar MM, Rassoulian-Barrett SL, LaFe K, Yarfitz SL, Limaye AP and Cookson BT (2000) Identification of medically important yeast using PCR-based detection of DNA sequence polymorphism in the internal transcribed spacer 2 region of the rRNA genes. J Clin Microbiol 38:2302-2310.

Desnos-Ollivier M, Ragon M, Robert V, Raoux D, Gantier JC and Domer F (2008) *Debaryomyces hansenii* (*Candida famata*), a rare human fungal pathogen often misidentified as *Pichia guilliermondii* (*Candida guilliermondii*). J Clin Microbiol 46:3237-3242.

Dooley DP, Miriam BL and Jeffrey BS (1994) Misidentification of clinical yeast isolates by using the Vitek Yeast Biochemical Card. J Clin Microbiol 32:2889-2892.

Fenn JP, Segal H, Barland B, Denton D, Whisenant J, Chun H, Christofferson K, Hamilton L and Carroll K (1994) Comparison of updated Vitek Yeast biochemical card and API 20C Yeast identification systems. J Clin Microbiol 32:1184-1187.

Jabra-Rizk MA, Falkler Jr WA, Merz WG, Baqui AAMA, Kelley JI and Meiller TF (2000) Retrospective identification and characterization of *Candida dubliniensis* isolates among *Candida albicans* clinical laboratory isolates from human immunodeficiency virus (HIV)-infected and non-HIV-infected individuals. J Clin Microbiol 38:2423-2426.

Larkin MA, Blackshields G, Brown NP, Chenna R, McGettigan PA, McWilliam H, Valentin F, Wallace IM, Wilm A, Lopez R, *et al.* (2007) Clustal W and Clustal X ver. 20. Bioinformatics 23:2947-2948.

Lasker BA, Butler G and Lott TJL (2006) Molecular genotyping of *Candida parapsilosis* group I clinical isolates by analysis of polymorphic microsatellite markers. J Clin Microbiol 44:750-759.

Lo HJ, Ho YA and Ho M (2001) Factors accounting for misidentification of *Candida* species. J Microbiol Infect 34:171-177.

Odds FC, Nuffel LV and Dams G (1998) Prevalence of *Candida dubliniensis* isolates in a yeast stock collection. J Clin Microbiol 36:2869-2873.

Philippsen P, Stotz A and Scherf C (1991) DNA of *Saccharomyces cerevisiae*. Methods Enzymol 194:169-171.

Tietz HJ, Hopp M, Schmalreck A, Sterry W and Czaika V (2001) *Candida africana* sp. nov. a new human pathogen or a variant of *Candida albicans*? Mycoses 44:437-445.

White TB and Lee S (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ and White TJ (eds) PCR Protocols. A Guide to Methods and Applications. Academic Press, San Diego, pp 315-322.

Zhang Z, Schwartz S, Wagner L and Miller W (2000) A greedy algorithm for aligning DNA sequences: J Comput Biol 7:203-214.

Supplementary Material

The following online material is available for this article:

Table S1 - Comparison of results obtained DNA sequencing.

Figure S1 - Real-time PCR amplification of multiplex assays.

Figure S2 - BLAST alignments for *C. palmioleophila*; *D. hansenii* and *P. guilliermondii*.

This material is available as part of the online article from http://www.scielo.br/gmb.

Associate Editor: Célia Maria de Almeida Soares

Table S1. Comparison between results with the API 20C AUX commercial kit and DNA sequence identification of some species.

Nº	Strain	API 20 CAUX			Sequencing
		Species	%	T	
1.	UNESP 4B	*C. famata* *C. guilliermondii*	62,6 37,2	0,65 0,55	*C. parapsilosis*
2.	UNESP 4C	*C. guilliermondii* *C. famata*	84,3 15,6	1,0 0,94	*C. guilliermondii*
3.	LGMG 4B	*C. guilliermondii* *C. famata*	60,3 39,6	0,83 0,86	*C. guilliermondii*
4.	LGMG 4E	*C. guilliermondii* *C. famata*	60,3 39,6	0,83 0,86	*C. guilliermondii*
5.	UNESP 1A	*C. guilliermondii* *C. famata*	60,3 39,6	0,83 0,86	*C. guilliermondii*
6.	UNESP 1B	*C. guilliermondii* *C. famata*	84,3 15,6	1,0 0,94	*C. guilliermondii*
7.	UNESP 1C	*C. guilliermondii* *C. famata*	84,3 15,6	1,0 0,94	*C. guilliermondii*
8.	UNESP 1D	*C. guilliermondii* *C. famata*	84,3 15,6	1,0 0,94	*C. guilliermondii*
9.	UNESP 4A	*C. guilliermondii* *C. famata*	84,3 15,3	1,0 0,94	*C. guilliermondii*
10.	UNESP 6A	*C. guilliermondii* *C. famata*	60,3 39,6	0,83 0,86	*C. guilliermondii*
11.	UNESP 6B	*C. guilliermondii* *C. famata*	60,3 39,6	0,83 0,86	*C. guilliermondii*
12.	UNESP 6C	*C. guilliermondii* *C. famata*	60,3 39,6	0,83 0,86	*C. guilliermondii*
13.	UNESP 7A	*C. guilliermondii* *C. famata*	60,3 39,6	0,83 0,86	*C. guilliermondii*
14.	USP H585	*C. guilliermondii* *C. famata*	84,3 15,3	1,0 0,94	*C. guilliermondii*
15.	SK 043	*C. guilliermondii* *C. famata*	84,3 15,6	1,0 0,94	*C. guilliermondii*
16.	SK 063	*C. guilliermondii* *C. famata*	60,3 39,6	0,83 0,86	*C. guilliermondii*
17.	45 Cont A	*C. guilliermondii* *C. famata*	60,3 39,6	0,83 0,86	*C. guilliermondii*
18.	USP H1020	*C. guilliermondii* *C. famata*	60,3 39,6	0,83 0,86	*C. guilliermondii*
19.	LGMG3A	*C. krusei/ inconspicua*	98,9	0,91	*C. krusei*
20.	LGMG3B	*C. krusei/ inconspicua*	98,9	0,91	*C. krusei*
21.	LGMG3D	*C. krusei/ inconspicua*	98,9	0,91	*C. krusei*
22.	LGMG 5G	*C. krusei/ inconspicua*	98,9	0,91	*C. krusei*
23.	SK 088	*C. krusei /inconspicua*	96,2	1,00	*C. krusei*
24.	11ANBN A	*C. krusei/ inconspicua*	98,9	0,91	*C. krusei*
25.	11ANBN B	*C. krusei/ inconspicua*	98,9	0,91	*C. krusei*
26.	LGMG 8A	*C. pelliculosa*	79,1	0,69	*C. subpeliculosa*
27.	LGMG 8B	*C. pelliculosa*	79,1	0,69	*C. subpeliculosa*
28.	ATCC 62894	*C. guilliermondii* *C. famata*	60,3 39,6	0,83 0,86	*C. palmioleophila*

% - Designates the similarity between the unknown and the standard sample used when the test was assembled
T - Confiability index; maximum value is 1.

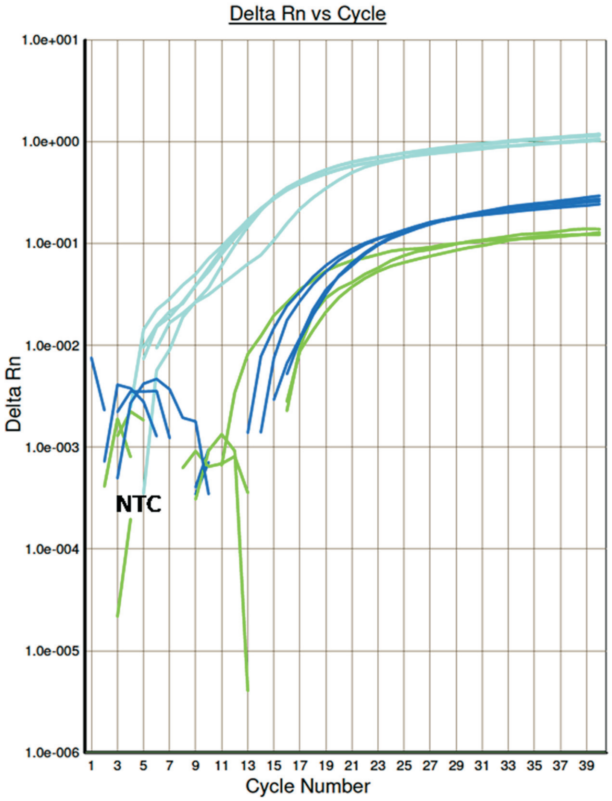

Figure S1 - Plot showing real-time PCR amplification of multiplex assays monitored with fluorescent TaqMan® MGB probes. Delta Rn versus Cycle amplification plot of *P. guilliermondii*, *D. hansenii* and *C. palmioleophila* templates. Light blue – *P. guilliermondii*, light green – *C. palmioleophila* and dark blue – *D. hansenii*. The NTC (no template control) curves shows no detection in the absence of templates.

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BLASTN 2.2.23+
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and
Webb Miller (2000), "A greedy algorithm for aligning DNA
sequences", J Comput Biol 2000; 7(1-2):203-14.



RID: 2DDJM8AX014



Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
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           12,090,198 sequences; 31,882,540,517 total letters
Query= gi|171918730|gb|EU568917.1| Candida palmioleophila 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence; and
28S ribosomal RNA gene, partial sequence
Length=632



                                                                   Score     E
Sequences producing significant alignments:                       (Bits)  Value

gb|EU569035.1|  Candida palmioleophila isolate CNRMA 200500813...  1168    0.0
gb|EU569033.1|  Candida palmioleophila isolate CNRMA 200500825...  1168    0.0
gb|EU569031.1|  Candida palmioleophila isolate CNRMA 200500840...  1168    0.0
gb|EU568917.1|  Candida palmioleophila 18S ribosomal RNA gene,...  1168    0.0
emb|FM875849.1|  Uncultured fungus ITS1, 5.8S rRNA gene and IT...  1157    0.0
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gb|FJ609219.1|  Candida palmioleophila strain IHEM 22283 18S r...  1018    0.0
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dbj|AB016582.1|  Candida palmioleophila 5.8S rRNA gene, strain...   966    0.0
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dbj|AB513336.1|  Pichia sp. MT-LUC0012 genes for 18S rRNA, ITS...   898    0.0
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gb|EU343826.1|  Candida ergastensis strain MUCL 30034 18S ribo...   824    0.0
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emb|FM178351.1|  Candida glaebosa 18S rRNA gene (partial), ITS...   815    0.0
gb|HM032737.1|  Debaryomyces hansenii strain NJ147 18S ribosom...   813    0.0
gb|GQ458041.1|  Debaryomyces hansenii strain ATCC 60978 18S ri...   813    0.0
gb|GQ458019.1|  Debaryomyces hansenii strain MA09-J 18S riboso...   813    0.0
gb|GQ376084.1|  Debaryomyces hansenii var. hansenii isolate UO...   813    0.0
dbj|AB220030.1|  Debaryomyces hansenii var. hansenii genes for...   813    0.0
gb|EU569039.1|  Debaryomyces hansenii isolate CNRMA 200600362 ...   813    0.0
gb|EF432798.1|  Pueraria montana var. lobata from China: Jiang...   813    0.0
gb|EF432797.1|  Pueraria montana var. lobata from China: Jiang...   813    0.0
gb|AF210327.1|AF210327  Debaryomyces hansenii var. hansenii CB...   813    0.0
gb|GQ913348.1|  Debaryomyces hansenii strain W4682 18S ribosom...   811    0.0
dbj|AB220032.1|  Candida psychrophila genes for 18S rRNA, ITS1...   809    0.0
gb|AY040667.1|  Candida psychrophila internal transcribed spac...   809    0.0
gb|FJ172253.1|  Candida sinolaborantium strain ATCC MYA-4337 1...   808    0.0
gb|EF198011.1|  Debaryomyces pseudopolymorphus strain WC43-3 1...   808    0.0
gb|EF222225.1|  Debaryomyces hansenii strain gao1hou2 18S ribo...   804    0.0
gb|EU149790.1|  Debaryomyces hansenii strain CBS 10629 18S rib...   802    0.0
gb|EF194843.1|  Debaryomyces hansenii voucher MCCC2E00222 18S ...   802    0.0
gb|EF197815.1|  Debaryomyces hansenii strain GAO2 18S ribosoma...   802    0.0
gb|EF643596.1|  Debaryomyces hansenii strain LN-5 18S ribosoma...   800    0.0
gb|EF643588.1|  Debaryomyces hansenii strain LN-2 18S ribosoma...   800    0.0
dbj|AB220029.1|  Debaryomyces nepalensis genes for 18S rRNA, I...   798    0.0
dbj|AB220028.1|  Debaryomyces nepalensis genes for 18S rRNA, I...   798    0.0
gb|EF192232.1|  Debaryomyces hansenii strain shi2wei 18S ribos...   798    0.0
gb|EF192224.1|  Debaryomyces hansenii 18S ribosomal RNA gene, ...   798    0.0
gb|EF193070.1|  Debaryomyces hansenii voucher MCCC2E00282 18S ...   798    0.0
gb|EF222227.1|  Debaryomyces hansenii strain gaoyandie zhongch...   797    0.0
emb|AJ606466.1|  Candida coipomoensis 18S rRNA gene (partial),...   797    0.0
gb|EU343832.1|  Candida glaebosa strain MUCL 29834 18S ribosom...   795    0.0
gb|EU149791.1|  Debaryomyces hansenii strain CBS 10751 18S rib...   791    0.0
gb|EF193068.1|  Debaryomyces hansenii voucher MCCC2E00280 18S ...   791    0.0
gb|DQ668354.1|  Debaryomyces hansenii isolate Sy-8 18S ribosom...   789    0.0
gb|AY964676.1|  Candida sinolaborantium strain BG04-2-20-1-1-C...   789    0.0
gb|AY964675.1|  Candida sinolaborantium strain BG04-2-20-1-1-1...   789    0.0
gb|AY964674.1|  Candida sinolaborantium strain CBS 9940 18S ri...   789    0.0
gb|AY964679.1|  Candida temnochilae strain CBS 9939 18S riboso...   787    0.0
gb|AY964678.1|  Candida temnochilae strain CBS 9938 18S riboso...   787    0.0
gb|AY964677.1|  Candida temnochilae strain BG01-7-25-009A-3-1 ...   787    0.0
gb|DQ317356.1|  Saccharomycetaceae sp. BC41 18S ribosomal RNA ...   785    0.0
gb|EF192225.1|  Debaryomyces hansenii 18S ribosomal RNA gene, ...   784    0.0
gb|AY845351.1|  Candida lignicola 18S ribosomal RNA gene, part...   784    0.0
gb|EF643593.1|  Debaryomyces hansenii strain LN-3 18S ribosoma...   782    0.0
gb|EF543259.1|  Debaryomyces hansenii strain hcx-1 18S ribosom...   782    0.0
gb|EF190234.1|  Debaryomyces hansenii strain NA-1 18S ribosoma...   782    0.0
gb|DQ534410.1|  Debaryomyces hansenii strain SWJ-10b 18S ribos...   782    0.0
gb|GQ376085.1|  Debaryomyces hansenii var. hansenii isolate UO...   780    0.0
gb|EF197943.1|  Debaryomyces hansenii strain HK67-4 18S riboso...   780    0.0
gb|EF190231.1|  Debaryomyces hansenii strain wwl-2 18S ribosom...   778    0.0
gb|EF192227.1|  Debaryomyces hansenii strain w-14-1 18S riboso...   778    0.0
gb|FJ153162.1|  Candida sp. SG6L02 18S ribosomal RNA gene, par...   776    0.0
gb|EF197950.1|  Debaryomyces hansenii strain HK32-1 18S riboso...   776    0.0
gb|EF197946.1|  Debaryomyces hansenii strain HK67-5 18S riboso...   776    0.0
gb|EF197944.1|  Debaryomyces hansenii strain WC56-1 18S riboso...   776    0.0

ALIGNMENTS
>gb|EU569035.1| Candida palmioleophila isolate CNRMA 200500813 18S ribosomal
RNA gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
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Length=632

 Score = 1168 bits (632),  Expect = 0.0
 Identities = 632/632 (100%), Gaps = 0/632 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
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Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120

Query  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTATTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTATTT  180

Query  181  AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATC  240

Query  241  TCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGA  300

Query  301  TTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCAT  360

Query  361  GCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTA  420

Query  421  GTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGAAGTGCATTCAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGAAGTGCATTCAG  480

Query  481  GAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGG  540

Query  541  TGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACC  600

Query  601  CGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||
Sbjct  601  CGCTGAACTTAAGCATATCAATAAGCGGAGGA  632


>gb|EU569033.1| Candida palmioleophila isolate CNRMA 200500825 18S ribosomal
RNA gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=632

 Score = 1168 bits (632),  Expect = 0.0
 Identities = 632/632 (100%), Gaps = 0/632 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
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Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120
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Sbjct  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120

Query  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTATTT  180
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Sbjct  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTATTT  180

Query  181  AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATC  240
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Sbjct  181  AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATC  240

Query  241  TCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGA  300
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Sbjct  241  TCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGA  300

Query  301  TTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCAT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCAT  360

Query  361  GCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTA  420

Query  421  GTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGAAGTGCATTCAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGAAGTGCATTCAG  480

Query  481  GAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGG  540

Query  541  TGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACC  600
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Sbjct  541  TGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACC  600

Query  601  CGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
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Sbjct  601  CGCTGAACTTAAGCATATCAATAAGCGGAGGA  632


>gb|EU569031.1| Candida palmioleophila isolate CNRMA 200500840 18S ribosomal
RNA gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=632

 Score = 1168 bits (632),  Expect = 0.0
 Identities = 632/632 (100%), Gaps = 0/632 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
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Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120
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Sbjct  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120

Query  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTATTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTATTT  180
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Query  181  AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATC  240
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Sbjct  181  AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATC  240

Query  241  TCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGA  300
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Sbjct  241  TCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGA  300

Query  301  TTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCAT  360
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Sbjct  301  TTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCAT  360

Query  361  GCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTA  420

Query  421  GTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGAAGTGCATTCAG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGAAGTGCATTCAG  480

Query  481  GAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGG  540

Query  541  TGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  TGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACC  600

Query  601  CGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
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Sbjct  601  CGCTGAACTTAAGCATATCAATAAGCGGAGGA  632


>gb|EU568917.1| Candida palmioleophila 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene,
and internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence
Length=632

 Score = 1168 bits (632),  Expect = 0.0
 Identities = 632/632 (100%), Gaps = 0/632 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
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Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120
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Sbjct  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120

Query  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTATTT  180
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Sbjct  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTATTT  180

Query  181  AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATC  240
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Sbjct  181  AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATC  240

Query  241  TCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGA  300

Query  301  TTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCAT  360
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Sbjct  301   TTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCAT  360

Query  361   GCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTA  420

Query  421   GTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGAAGTGCATTCAG  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   GTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGAAGTGCATTCAG  480

Query  481   GAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGG  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGG  540

Query  541   TGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACC  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   TGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACC  600

Query  601   CGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
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Sbjct  601   CGCTGAACTTAAGCATATCAATAAGCGGAGGA  632


>emb|FM875849.1| Uncultured fungus ITS1, 5.8S rRNA gene and ITS2 region, clone
f11
Length=670

 Score = 1157 bits (626),  Expect = 0.0
 Identities = 630/632 (99%), Gaps = 0/632 (0%)
 Strand=Plus/Minus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
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Sbjct  632   TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  573

Query  61    CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  572   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAGCTATTGCTTTGGCTTGGC  513

Query  121   TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTATTT  180
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Sbjct  512   TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTATTT  453

Query  181   AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATC  240
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Sbjct  452   AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATC  393

Query  241   TCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGA  300
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Sbjct  392   TCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGA  333

Query  301   TTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCAT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  332   TTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCAT  273

Query  361   GCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTA  420
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Sbjct  272   GCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTA  213

Query  421   GTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGAAGTGCATTCAG  480
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  212   GTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGATGCTGAGAAGTGCATTCAG  153
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Query  481  GAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGG  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  152  GAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGG  93

Query  541  TGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACC  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  92   TGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACC  33

Query  601  CGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
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Sbjct  32   CGCTGAACTTAAGCATATCAATAAGCGGAGGA  1


>gb|EU604759.1| Candida sp. C22 internal transcribed spacer 1, partial sequence;
5.8S ribosomal RNA gene and internal transcribed spacer
2, complete sequence; and 28S ribosomal RNA gene, partial sequence
Length=593

 Score = 1086 bits (588),  Expect = 0.0
 Identities = 591/592 (99%), Gaps = 1/592 (0%)
 Strand=Plus/Plus

Query  42   TTGCCAGCGCTTAATTGCGCGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAA  101
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TTGCCAGCGCTTAATTGCGCGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAA  60

Query  102  ACTATTGCTTTGGCTTGGCTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATT  161
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACTATTGCTTTGGCTTGGCTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATT  120

Query  162  TTTAATTGAATTGTTATTTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCA  221
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  TTTAATTGAATTGTTATTTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCA  180

Query  222  AAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGAT  281
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGAT  240

Query  282  AAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCT  341
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCT  300

Query  342  CTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTG  401
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTG  360

Query  402  GTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGA  461
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  GTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGA  420

Query  462  CGCTGAGAAGTGCATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATT  521
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  CGCTGAGAAGTGCATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATT  480

Query  522  CTTGGTTGTGAATTTTTGGTGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCT  581
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CTTGGTTGTGAATTTTTGGTGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCT  540

Query  582  CAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGC-GGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  541  CAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCCGGAGGA  592


>gb|FJ609219.1| Candida palmioleophila strain IHEM 22283 18S ribosomal RNA gene,
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partial sequence; and internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence
Length=551

 Score = 1018 bits (551),  Expect = 0.0
 Identities = 551/551 (100%), Gaps = 0/551 (0%)
 Strand=Plus/Plus

Query  23   GATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCGCGGCGATTAAACCTTACACACA  82
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCGCGGCGATTAAACCTTACACACA  60

Query  83   ATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGCTAAGAAATTAGTCGGGCCAGAG  142
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGCTAAGAAATTAGTCGGGCCAGAG  120

Query  143  GTTTACACAAACTTCAATTTTTAATTGAATTGTTATTTAATACTTTGTCAATTTGTTGAT  202
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTTTACACAAACTTCAATTTTTAATTGAATTGTTATTTAATACTTTGTCAATTTGTTGAT  180

Query  203  TAAATTCAAACAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAA  262
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TAAATTCAAACAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAA  240

Query  263  GAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTT  322
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTT  300

Query  323  TGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTC  382
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  TGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTC  360

Query  383  TCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGA  442
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGA  420

Query  443  AATTTATTGGCATGAGTGACGCTGAGAAGTGCATTCAGGAAATATCAATGTATTAGGTTT  502
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AATTTATTGGCATGAGTGACGCTGAGAAGTGCATTCAGGAAATATCAATGTATTAGGTTT  480

Query  503  ATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGGTGTTAGGCTTTGCCTTAAAAAA  562
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGGTGTTAGGCTTTGCCTTAAAAAA  540

Query  563  CAACAAACAAG  573
            |||||||||||
Sbjct  541  CAACAAACAAG  551


>emb|FN868154.1| Candida sp. CBS 11774 genomic DNA containing 18S rRNA gene, ITS1,
5.8S rRNA gene, ITS2, 28S rRNA gene, strain CBS11774
Length=1154

 Score = 1000 bits (541),  Expect = 0.0
 Identities = 580/599 (96%), Gaps = 2/599 (0%)
 Strand=Plus/Plus

Query  34   TATTCTAATTGCCAGCGCTTAATTGCGCGGCGATTAAACCTTACACACAATGTTTTTCTT  93
            ||||||||||||| |||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  1    TATTCTAATTGCCTGCGCTTAATTGCGCGGCGATTAAACCTTACACACTATGTTTTTCTT  60

Query  94   TATTAGAAACTATTGCTTTGGCTTGGCTAAGAAATTAGTCGGGCCAGAGGTTTACACAAA  153
            |||||||||||||| |||||| ||||||||||||||||| |||||||||||||  | |||
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Sbjct  61    TATTAGAAACTATTACTTTGGTTTGGCTAAGAAATTAGTTGGGCCAGAGGTTT--ATAAA  118

Query  154   CTTCAATTTTAATTGAATTGTTATTTAATACTTTGTCAATTTGTTGATTAAATTCAAAC  213
             |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  119   CTTCAATTTTAATTGAATTGTTATTTAAAACTTTGTCAATTTGTTGATTAAATTCAAAC  178

Query  214   AATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGA  273
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  179   AATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGA  238

Query  274   AATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACAT  333
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239   AATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACAT  298

Query  334   TGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCT  393
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  299   TGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTCCTCTCTCAAACCCT  358

Query  394   TGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGC  453
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  359   CGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGC  418

Query  454   ATGAGTGACGCTGAGAAGTGCATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGT  513
             |||||||| ||| | ||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  419   ATGAGTGATGCTAAAAAGTGCATTCAGGAACTATCAATGTATTAGGTTTATCCAACTCGT  478

Query  514   TGACAATTCTTGGTTGTGAATTTTTGGTGTTAGGCTTTGCCTTAAAAAACAACAAACAAG  573
             ||||||| |||| |||||||||||| |||||||||||||||||| |||||||||||||||
Sbjct  479   TGACAATCCTTGATTGTGAATTTTTAGTGTTAGGCTTTGCCTTATAAAACAACAAACAAG  538

Query  574   TTTGACCTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  539   TTTGACCTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  597


>dbj|AB016583.1| Candida palmioleophila 5.8S rRNA gene, strain JCM 5218, complete
sequence
Length=538

 Score =  966 bits (523),  Expect = 0.0
 Identities = 538/544 (98%), Gaps = 6/544 (1%)
 Strand=Plus/Plus

Query  31    CTGTATTCTAATTGCCAGCGCTTAATTGCGCGGCGATTAAACCTTACACACAATGTTTTT  90
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CTGTATTCTAATTGCCAGCGCTTAATTGCGCGGCGATTAAACCTTACACACAATGTTTTT  60

Query  91    CTTTATTAGAAACTATTGCTTTGGCTTGGCTAAGAAATTAGTCGGGCCAGAGGTTTACAC  150
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CTTTATTAGAAACTATTGCTTTGGCTTGGCTAAGAAATTAGTCGGGCCAGAGGTTTACAC  120

Query  151   AAACTTCAATTTTAATTGAATTGTTATTTAATACTTTGTCAATTTGTTGATTAAATTCA  210
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   AAACTTCAATTTTAATTGAATTGTTATTTAATACTTTGTCAATTTGTTGATTAAATTCA  180

Query  211   AACAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAG  270
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AACAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAG  240

Query  271   CGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCA  330
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   CGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCA  300

Query  331   CATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAAC  390
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAAC  360

Query  391  CCTTGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATT  450
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCTTGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATT  420

Query  451  GGCATGAGTGACGCTGAGAAGTGCATTCAGGAAATATCAATGTATTAGGTTTATCCAACT  510
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GGCATGAGTGACGCTGAGAAGTGCATTCAGGAAATATCAATGTATTAGGTTTATCCAACT  480

Query  511  CGTTGACAATTCTTGGTTGTGAATTTTTGGTGTTAGGCTTTGCCTTAAAAAACAACAAAC  570
            ||||||||||||||||||||||||||| | |||||| ||| |||| |||||||| |||||
Sbjct  481  CGTTGACAATTCTTGGTTGTGAATTTT-G-TGTTAG-CTT-GCCT-AAAAAACA-CAAAC  534

Query  571  AAGT  574
            ||||
Sbjct  535  AAGT  538


>dbj|AB016582.1| Candida palmioleophila 5.8S rRNA gene, strain JCM 6896, complete
sequence
Length=538

 Score =  966 bits (523),  Expect = 0.0
 Identities = 538/544 (98%), Gaps = 6/544 (1%)
 Strand=Plus/Plus

Query  31   CTGTATTCTAATTGCCAGCGCTTAATTGCGCGGCGATTAAACCTTACACACAATGTTTTT  90
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CTGTATTCTAATTGCCAGCGCTTAATTGCGCGGCGATTAAACCTTACACACAATGTTTTT  60

Query  91   CTTTATTAGAAACTATTGCTTTGGCTTGGCTAAGAAATTAGTCGGGCCAGAGGTTTACAC  150
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTTTATTAGAAACTATTGCTTTGGCTTGGCTAAGAAATTAGTCGGGCCAGAGGTTTACAC  120

Query  151  AAACTTCAATTTTTAATTGAATTGTTATTTAATACTTTGTCAATTTGTTGATTAAATTCA  210
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AAACTTCAATTTTTAATTGAATTGTTATTTAATACTTTGTCAATTTGTTGATTAAATTCA  180

Query  211  AACAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAG  270
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  AACAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAG  240

Query  271  CGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCA  330
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCA  300

Query  331  CATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAAC  390
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAAC  360

Query  391  CCTTGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATT  450
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCTTGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATT  420

Query  451  GGCATGAGTGACGCTGAGAAGTGCATTCAGGAAATATCAATGTATTAGGTTTATCCAACT  510
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GGCATGAGTGACGCTGAGAAGTGCATTCAGGAAATATCAATGTATTAGGTTTATCCAACT  480

Query  511  CGTTGACAATTCTTGGTTGTGAATTTTTGGTGTTAGGCTTTGCCTTAAAAAACAACAAAC  570
            ||||||||||||||||||||||||||| | |||||| ||| |||| |||||||| |||||
Sbjct  481  CGTTGACAATTCTTGGTTGTGAATTTT-G-TGTTAG-CTT-GCCT-AAAAAACA-CAAAC  534
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Query  571  AAGT  574
            ||||
Sbjct  535  AAGT  538


>gb|FJ873416.1| Candida sp. GA1S01 internal transcribed spacer 1, partial sequence;
5.8S ribosomal RNA gene and internal transcribed spacer
2, complete sequence; and 26S ribosomal RNA gene, partial
sequence
Length=553

 Score =  946 bits (512),  Expect = 0.0
 Identities = 543/557 (97%), Gaps = 5/557 (0%)
 Strand=Plus/Plus

Query  48   GCGCTTAATTGCGCGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATT  107
            |||||| |||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  1    GCGCTT-ATTGCGCGGCGATTAAACCTTATACACAATGTTTTTCTTTATTAGAAACTATT  59

Query  108  GCTTTGGCTTGGCTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAAT  167
             |||||| ||||||||||||||||| |||||||||||||  | |||||||||||||||||
Sbjct  60   ACTTTGGTTTGGCTAAGAAATTAGTTGGGCCAGAGGTTT--ATAAACTTCAATTTTTAAT  117

Query  168  TGAATTGTTATTTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  118  TGAATTGTTATTTAATTCTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  177

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  178  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  237

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  238  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  297

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            |||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  298  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  356

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  357  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGATGCTA  416

Query  467  AGAAGTGCATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGG  526
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  417  AGAAGTGCATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGG  476

Query  527  TTGTGAATTTTTGGTGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAAT  586
            |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  477  TTGTGAATTTTTAGTGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAAT  536

Query  587  CAGGTAGGATTACCCGC  603
            |||||||||||||||||
Sbjct  537  CAGGTAGGATTACCCGC  553


>gb|DQ409166.1| Pichia segobiensis strain CECT 10210 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 26S ribosomal RNA gene, partial sequence
Length=628

 Score =  904 bits (489),  Expect = 0.0
 Identities = 590/637 (92%), Gaps = 14/637 (2%)
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 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| |||||
Sbjct  61   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGGTTTGGC  119

Query  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-TT  179
            | |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| ||
Sbjct  120  TCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATTT  176

Query  180  TAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGAT  239
            || || ||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  177  TATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGAT  235

Query  240  CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAG  299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAG  295

Query  300  ATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCA  359
            |||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||
Sbjct  296  ATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCA  355

Query  360  TGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTT  419
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  356  TGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCTT  415

Query  420  AGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT-  477
            |||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  416  AGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TGA  473

Query  478  CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTT  536
            ||| || || |||||||||||||||||||||||||||||| | |||| ||  ||||||||
Sbjct  474  CAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATTT  531

Query  537  TTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGA  595
            ||||| | | |||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  532  TTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGA  591

Query  596  TTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||||||||||||||||||||||||
Sbjct  592  TTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  628


>emb|AJ606464.1| Candida shehatae var. shehatae 18S rRNA gene (partial), 5.8S
rRNA gene, 26S rRNA (partial) gene, ITS1 and ITS2, strain CBS
5813
Length=783

 Score =  904 bits (489),  Expect = 0.0
 Identities = 594/642 (92%), Gaps = 17/642 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  62

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  63   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  120
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Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTT-TAATTGAATTGTTA-  177
            || |||||| ||| |||||||||||| || |||||||||||||| | ||||||||||||
Sbjct  121  CTTAGAAATAAGTTGGGCCAGAGGTTAAC-CAAACTTCAATTTTATTATTGAATTGTTAT  179

Query  178  TTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACG  236
            ||||  || ||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  180  TTTATTTAATTTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAACG  239

Query  237  GATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTG  296
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240  GATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTG  299

Query  297  CAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGG  356
            ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  300  CAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAGAGG  359

Query  357  GCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACT  416
            |||||||||||||||||||||||||||||||| |||| ||||||||||||||||||||||
Sbjct  360  GCATGCCTGTTTGAGCGTCATTTCTCTCTCAAGCCCTCGGGTTTGGTATTGAGTGATACT  419

Query  417  CTTAGTC-GAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-G-ACGCTGAGA-AGT  472
            ||||||| || ||||||||||||||||||  ||| ||||||||| | ||  | ||| |||
Sbjct  420  CTTAGTCAGA-CTAGGCGTTTGCTTGAAAAGTATCGGCATGAGTAGTAC--T-AGATAGT  475

Query  473  GCATTCAGGAAATATCAATGTATTAGGTTTATCCAACTC-GTTGACAATTCTTGGTTGTG  531
            || ||||||| || ||||||||||||||||||||||||| ||||| |||||||||| |||
Sbjct  476  GCTTTCAGGATATTTCAATGTATTAGGTTTATCCAACTCCGTTGAGAATTCTTGGTAGTG  535

Query  532  AATTTTTGGTGTTA-GGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGG  590
            ||||||| || | | |||| ||||||| ||||||||||||||||||||||||||||||||
Sbjct  536  AATTTTTAGTATCATGGCTCTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGG  595

Query  591  TAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||
Sbjct  596  TAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  637


>dbj|AB513338.1| Pichia sp. MT-LUC0016 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2,
26S rRNA, partial and complete sequence
Length=653

 Score =  898 bits (486),  Expect = 0.0
 Identities = 589/637 (92%), Gaps = 14/637 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  26   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  85

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| |||||
Sbjct  86   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGGTTTGGC  144

Query  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-TT  179
            | |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| ||
Sbjct  145  TCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATTT  201

Query  180  TAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGAT  239
            || || ||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  202  TATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGAT  260

Query  240  CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAG  299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261  CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAG  320
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Query  300  ATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCA  359
            |||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||
Sbjct  321  ATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCA  380

Query  360  TGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTT  419
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  381  TGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCTT  440

Query  420  AGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT-  477
            ||| |||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  441  AGTTGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TGA  498

Query  478  CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTT  536
            ||| || || |||||||||||||||||||||||||||||| | |||| ||  ||||||||
Sbjct  499  CAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATTT  556

Query  537  TTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGA  595
            ||||| | | |||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  557  TTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGA  616

Query  596  TTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||||||||||||||||||||||||
Sbjct  617  TTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  653


>dbj|AB513336.1| Pichia sp. MT-LUC0012 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2,
26S rRNA, partial and complete sequence
Length=653

 Score =  898 bits (486),  Expect = 0.0
 Identities = 589/637 (92%), Gaps = 14/637 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  26   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  85

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| |||||
Sbjct  86   CGGCGAAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGGTTTGGC  144

Query  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-TT  179
            | |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| ||
Sbjct  145  TCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATTT  201

Query  180  TAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGAT  239
            || || ||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  202  TATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGAT  260

Query  240  CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAG  299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261  CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAG  320

Query  300  ATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCA  359
            |||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||
Sbjct  321  ATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCA  380

Query  360  TGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTT  419
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  381  TGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCTT  440

Query  420  AGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT-  477
            ||| |||||||||||||||||||||  |||||||| |||||   || | | ||| | |
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Sbjct  441  AGTTGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TGA  498

Query  478  CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTT  536
            ||| || || |||||||||||||||||||||||||||||| | |||| ||  ||||||||
Sbjct  499  CAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATTT  556

Query  537  TTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGA  595
            ||||| | | |||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  557  TTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGA  616

Query  596  TTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||||||||||||||||||||||||
Sbjct  617  TTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  653


>dbj|AB513335.1| Pichia sp. MT-LUC0009 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2,
26S rRNA, partial and complete sequence
Length=653

 Score =  898 bits (486),  Expect = 0.0
 Identities = 590/638 (92%), Gaps = 16/638 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  26   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  85

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  86   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  143

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| |
Sbjct  144  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATT  200

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  201  TTATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA  259

Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  319

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  320  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  379

Query  359  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  380  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  439

Query  419  TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
            ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  440  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  497

Query  478  -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
             ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  498  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGATACTTCT-GGCGGTGAATT  555

Query  536  TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
            |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  556  TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  615

Query  595  ATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
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            ||||||||||||||||||||||||||||||||||||||
Sbjct  616  ATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  653


>dbj|AB513334.1| Pichia sp. MT-LUC0008 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2,
26S rRNA, partial and complete sequence
Length=653

 Score =  898 bits (486),  Expect = 0.0
 Identities = 589/637 (92%), Gaps = 14/637 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  26   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  85

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| |||||
Sbjct  86   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGGTTTGGC  144

Query  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-TT  179
            | |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| ||
Sbjct  145  TCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATTT  201

Query  180  TAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGAT  239
            || || ||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  202  TATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGAT  260

Query  240  CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAG  299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261  CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAG  320

Query  300  ATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCA  359
            |||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||
Sbjct  321  ATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCA  380

Query  360  TGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTT  419
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  381  TGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCTT  440

Query  420  AGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT-  477
            |||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  441  AGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TGA  498

Query  478  CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTT  536
            ||| || || |||||||||||||||||||||||||||||| | |||| ||  ||||||||
Sbjct  499  CAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATTT  556

Query  537  TTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGA  595
            ||||| | |  ||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  557  TTGGTATATTTGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGA  616

Query  596  TTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||||||||||||||||||||||||
Sbjct  617  TTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  653


>dbj|AB513333.1| Pichia sp. MT-LUC0007 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2,
26S rRNA, partial and complete sequence
Length=653

 Score =  898 bits (486),  Expect = 0.0
 Identities = 589/637 (92%), Gaps = 14/637 (2%)
 Strand=Plus/Plus
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Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  26   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  85

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGC  120
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| |||||
Sbjct  86   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGGTTTGGC  144

Query  121  TAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-TT  179
            | |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| ||
Sbjct  145  TCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATTT  201

Query  180  TAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGAT  239
            || || ||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  202  TATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGAT  260

Query  240  CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAG  299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261  CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAG  320

Query  300  ATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCA  359
            |||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||
Sbjct  321  ATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCA  380

Query  360  TGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTT  419
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  381  TGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCTT  440

Query  420  AGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT-  477
            |||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  441  AGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TGA  498

Query  478  CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTT  536
            ||| || || |||||||||||||||||||||||||||||| | |||| ||  ||||||||
Sbjct  499  CAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATTT  556

Query  537  TTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGA  595
            ||||| | |  ||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  557  TTGGTATATTTGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGA  616

Query  596  TTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||||||||||||||||||||||||
Sbjct  617  TTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  653


>gb|CP000497.1| Pichia stipitis CBS 6054 chromosome 3, complete sequence
Length=1841851

 Features flanking this part of subject sequence:
   606 bp at 5' side: predicted protein
   4526 bp at 3' side: Unknown protein

 Score =  898 bits (486),  Expect = 0.0
 Identities = 590/638 (92%), Gaps = 16/638 (2%)
 Strand=Plus/Minus

Query  1        TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
                ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  1709780  TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG
1709721

Query  61       CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
                ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
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Sbjct  1709720  CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG
1709663

Query  120      CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
                || |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| |
Sbjct  1709662  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATT
1709606

Query  179      TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
                ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  1709605  TTATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA
1709547

Query  239      TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1709546  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA
1709487

Query  299      GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
                ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  1709486  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC
1709427

Query  359      ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
                ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  1709426  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT
1709367

Query  419      TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
                ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | | 
Sbjct  1709366  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG
1709309

Query  478      -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
                 ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  1709308  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT
1709251

Query  536      TTTGGTGT-TAGGCTTTGCCTTAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
                |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  1709250  TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG
1709191

Query  595      ATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
                ||||||||||||||||||||||||||||||||||||||
Sbjct  1709190  ATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  1709153


>gb|DQ409167.1| Pichia stipitis strain CECT 1922 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 26S ribosomal RNA gene, partial sequence
Length=628

 Score =  898 bits (486),  Expect = 0.0
 Identities = 590/638 (92%), Gaps = 16/638 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
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Sbjct  61   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  118

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| |
Sbjct  119  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATT  175

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  176  TTATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA  234

Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  235  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  294

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  295  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  354

Query  359  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  355  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  414

Query  419  TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
            ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | | 
Sbjct  415  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  472

Query  478  -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
             ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  473  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT  530

Query  536  TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
            |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  531  TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  590

Query  595  ATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||
Sbjct  591  ATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  628


>dbj|AB513332.1| Pichia sp. MT-LUC0006 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2,
26S rRNA, partial and complete sequence
Length=654

 Score =  893 bits (483),  Expect = 0.0
 Identities = 589/638 (92%), Gaps = 15/638 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  26   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  85

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  86   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  143

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| |
Sbjct  144  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATT  200

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  201  TTATTATTTTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAACGGA  260

Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  320

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  321  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  380

Query  359  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  381  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  440

Query  419  TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
            ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  441  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  498

Query  478  -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
             ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  499  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT  556

Query  536  TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
            |||||| | |  ||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  557  TTTGGTATATTTGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  616

Query  595  ATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||
Sbjct  617  ATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  654


>gb|AY227905.1| Candida sp. BG02-4-1-3-1 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene
and internal transcribed spacer 2, complete sequence; and 26S
ribosomal RNA gene, partial sequence
Length=611

 Score =  863 bits (467),  Expect = 0.0
 Identities = 571/619 (92%), Gaps = 16/619 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  62

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  63   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  120

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| |
Sbjct  121  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATT  177

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  178  TTATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA  236

Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  296

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  297  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  356

Query  359  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
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Sbjct  357  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  416

Query  419  TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
            ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  417  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  474

Query  478  -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
             ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  475  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT  532

Query  536  TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
            |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  533  TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  592

Query  595  ATTACCCGCTGAACTTAAG  613
            |||||||||||||||||||
Sbjct  593  ATTACCCGCTGAACTTAAG  611


>gb|AY227904.1| Candida sp. BG02-2-11-6-5 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene
and internal transcribed spacer 2, complete sequence; and
26S ribosomal RNA gene, partial sequence
Length=611

 Score =  863 bits (467),  Expect = 0.0
 Identities = 571/619 (92%), Gaps = 16/619 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  62

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  63   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  120

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| |
Sbjct  121  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATT  177

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  178  TTATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA  236

Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  296

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  297  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  356

Query  359  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  357  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  416

Query  419  TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
            ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  417  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  474

Query  478  -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
             ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  475  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT  532
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Query  536  TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
            |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  533  TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  592

Query  595  ATTACCCGCTGAACTTAAG  613
            |||||||||||||||||||
Sbjct  593  ATTACCCGCTGAACTTAAG  611


>gb|AY227903.1| Candida sp. BG02-7-16-1 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene
and internal transcribed spacer 2, complete sequence; and 26S
ribosomal RNA gene, partial sequence
Length=611

 Score =  863 bits (467),  Expect = 0.0
 Identities = 571/619 (92%), Gaps = 16/619 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  62

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  63   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  120

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| |
Sbjct  121  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATT  177

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  178  TTATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA  236

Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  296

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  297  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  356

Query  359  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  357  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  416

Query  419  TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
            ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  417  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  474

Query  478  -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
             ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  475  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT  532

Query  536  TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
            |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  533  TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  592

Query  595  ATTACCCGCTGAACTTAAG  613
            |||||||||||||||||||
Sbjct  593  ATTACCCGCTGAACTTAAG  611
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>gb|AY227902.1| Pichia sp. KS-42-W2 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene and
internal transcribed spacer 2, complete sequence; and 26S ribosomal
RNA gene, partial sequence
Length=611

 Score =  863 bits (467),  Expect = 0.0
 Identities = 571/619 (92%), Gaps = 16/619 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  62

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  63   CGGCGAAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  120

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| |
Sbjct  121  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATT  177

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  178  TTATTATTTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA  236

Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  296

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  297  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  356

Query  359  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  357  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  416

Query  419  TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
            ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | | 
Sbjct  417  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  474

Query  478  -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
             ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  475  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT  532

Query  536  TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
            |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  533  TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  592

Query  595  ATTACCCGCTGAACTTAAG  613
            |||||||||||||||||||
Sbjct  593  ATTACCCGCTGAACTTAAG  611


>gb|AY227901.1| Candida sp. BG01-5-4-2-1 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene
and internal transcribed spacer 2, complete sequence; and 26S
ribosomal RNA gene, partial sequence
Length=611

 Score =  863 bits (467),  Expect = 0.0
 Identities = 571/619 (92%), Gaps = 16/619 (2%)
```

```
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  62

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  63   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  120

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| |
Sbjct  121  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATT  177

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  178  TTATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA  236

Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  296

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  297  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  356

Query  359  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  357  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  416

Query  419  TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
            ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  417  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  474

Query  478  -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
             ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  475  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT  532

Query  536  TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
            |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  533  TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  592

Query  595  ATTACCCGCTGAACTTAAG  613
            |||||||||||||||||||
Sbjct  593  ATTACCCGCTGAACTTAAG  611


>gb|AY227900.1| Candida sp. GA012-1-1 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene and
internal transcribed spacer 2, complete sequence; and 26S
ribosomal RNA gene, partial sequence
Length=611

 Score =  863 bits (467),  Expect = 0.0
 Identities = 571/619 (92%), Gaps = 16/619 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  62

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  63   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  120
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Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| |
Sbjct  121  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATT  177

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  178  TTATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA  236

Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  296

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  297  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  356

Query  359  ATGCCTGTTTGAGCGTCATTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
            |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  357  ATGCCTGTTTGAGCGTCATTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  416

Query  419  TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
            ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  417  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  474

Query  478  -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
             ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  475  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT  532

Query  536  TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
            |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  533  TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  592

Query  595  ATTACCCGCTGAACTTAAG  613
            |||||||||||||||||||
Sbjct  593  ATTACCCGCTGAACTTAAG  611


>gb|AY227907.1| Candida sp. BG02-7-14-003-2-1 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
gene and internal transcribed spacer 2, complete sequence;
and 26S ribosomal RNA gene, partial sequence
Length=611

 Score =  857 bits (464),  Expect = 0.0
 Identities = 570/619 (92%), Gaps = 16/619 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  62

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  63   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  120

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| |||||||||||||||  ||||||||| |||| |||||||||||| |
Sbjct  121  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-TAAACTTCAA-TTTT-ATTGAATTGTTATT  177

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  178  TTATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA  236
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Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  296

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  297  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  356

Query  359  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  357  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  416

Query  419  TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
            ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  417  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  474

Query  478  -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
             ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  475  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT  532

Query  536  TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
            |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  533  TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  592

Query  595  ATTACCCGCTGAACTTAAG  613
            |||||||||||||||||||
Sbjct  593  ATTACCCGCTGAACTTAAG  611


>gb|AY227906.1| Candida sp. BG02-7-14-003-1-1 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
gene and internal transcribed spacer 2, complete sequence;
and 26S ribosomal RNA gene, partial sequence
Length=611

 Score =  857 bits (464),  Expect = 0.0
 Identities = 570/619 (92%), Gaps = 16/619 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  62

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  63   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  120

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| |||||||||||||||  ||||||||| |||| |||||||||||| |
Sbjct  121  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-TAAACTTCAA-TTTT-ATTGAATTGTTATT  177

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  178  TTATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA  236

Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  296

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  297  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  356

Query  359  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
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             ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  357   ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  416

Query  419   TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
             ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  417   TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  474

Query  478   -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
              ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  475   ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT  532

Query  536   TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
             |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  533   TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  592

Query  595   ATTACCCGCTGAACTTAAG  613
             |||||||||||||||||||
Sbjct  593   ATTACCCGCTGAACTTAAG  611


>gb|GU256745.1| Pichia stipitis strain ATCC 62970 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 26S ribosomal RNA gene, partial sequence
Length=601

 Score =  848 bits (459),  Expect = 0.0
 Identities = 563/611 (92%), Gaps = 16/611 (2%)
 Strand=Plus/Plus

Query  15    TGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCGCGGCGATTAAACCT  74
             ||||||||||||||||| |||||||  |||||||||||||| ||||||||||  ||||||
Sbjct  1     TGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCGCGGCGAAAAAACCT  60

Query  75    TACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGGCTAAGAAATTAGTC  133
             |||||||| || |||||||||||||||||||||||||||| | ||||| |||||| |||
Sbjct  61    TACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGGCTCAGAAATGAGTT  118

Query  134   GGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-TTTAATACTTTGTCA  192
             ||||||||||||||| |||||||||| |||| |||||||||||| |||| || |||||||
Sbjct  119   GGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATTTTATTAATTTGTCA  175

Query  193   ATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCG  252
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  176   ATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCG  234

Query  253   CATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATC  312
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  235   CATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATC  294

Query  313   ATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGC  372
             ||||||||||||||||||||||||||||| |||||||||| |||||||||||||||||||
Sbjct  295   ATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCATGCCTGTTTGAGC  354

Query  373   GTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGC  432
             ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  355   GTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGC  414

Query  433   GTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT-CAGGAA-ATATCA  489
             ||||||||||||  |||||||| |||||   || | | ||| | |  ||| || || |||
Sbjct  415   GTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TGACAG-AATATTTCA  471

Query  490   ATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGGTGT-TAGGC  548
             ||||||||||||||||||||||||||| | |||| ||  ||||||||||||| | | |||
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Sbjct  472  ATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATTTTTGGTATATTGGC  530

Query  549  TTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACCCGCTGAAC  608
            ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  531  TTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACCCGCTGAAC  590

Query  609  TTAAGCATATC  619
            |||||||||||
Sbjct  591  TTAAGCATATC  601


>emb|FM178314.1| Candida coipomoensis 18S rRNA gene (partial), ITS1, 5.8S rRNA
gene, ITS2 and 28S rRNA gene (partial), strain WM 07.91
Length=640

 Score =  848 bits (459),  Expect = 0.0
 Identities = 584/641 (91%), Gaps = 21/641 (3%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATT-CTAATTGCCAGCGCTTAATTGC  59
            ||||||||||||||||||||||||||||||| |||||  |  || || ||||||||||||
Sbjct  11   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTAGT-TTTACCTGCGCTTAATTGC  69

Query  60   GCGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGG  119
            ||||  |  ||| |||||||||| ||||||||||||||||||||| ||||||||| ||||
Sbjct  70   GCGGTAAACAAATCTTACACACAGTGTTTTTCTTTATTAGAAACTTTTGCTTTGGTTTGG  129

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTG-TTAT  178
            || |||||| ||| |||||||||||||  |  ||||||||||||||||||||||| ||||
Sbjct  130  CTTAGAAATAAGTTGGGCCAGAGGTTT--A-TAACTTCAATTTTTAATTGAATTGTTTAT  186

Query  179  TTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGG  237
            |||  ||  ||||||||||||||||||| |||||| ||||||||||||||||||||||||
Sbjct  187  TTATTTA-ATTGTCAATTTGTTGATTAATTTCAAA-AATCTTCAAAACTTTCAACAACGG  244

Query  238  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  245  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  304

Query  298  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGG  357
            |||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||
Sbjct  305  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGG  364

Query  358  CATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTGAGTGATACT  416
            |||||||||||||||||||||||||||||||||| || ||||||||| ||||||||||||
Sbjct  365  CATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTTTTGAGTGATACT  423

Query  417  CTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-G-ACGCTGAGA-AGTG  473
            ||||||||||||||||||||||||||||  |||||||| |||| | ||  | | | ||||
Sbjct  424  CTTAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTAGTAC--TAA-ATAGTG  480

Query  474  CATTCAGGAA-ATAT-CAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTG  531
            | |||||||| || | ||||||||||||||||||||||||||||| |||||  | | |||
Sbjct  481  CTTTCAGGAACATTTTCAATGTATTAGGTTTATCCAACTCGTTGAGAATTCCCGCTAGTG  540

Query  532  AATTTTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGG  590
            |||||||||| | | |||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  541  AATTTTTGGTATAT-GGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGG  599

Query  591  TAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGG  631
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  600  TAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGG  640
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>gb|AY325112.1| Candida sp. BG03-3-25-1-5 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene,
and internal transcribed spacer 2, complete sequence; and
26S ribosomal RNA gene, partial sequence
Length=602

 Score =  846 bits (458),  Expect = 0.0
 Identities = 562/610 (92%), Gaps = 16/610 (2%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  62

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  63   CGGCGAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  120

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| |
Sbjct  121  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATT  177

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  178  TTATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA  236

Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  296

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  297  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  356

Query  359  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  357  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  416

Query  419  TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
            ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | | 
Sbjct  417  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  474

Query  478  -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
             ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  475  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT  532

Query  536  TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
            |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  533  TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  592

Query  595  ATTACCCGCT  604
            ||||||||||
Sbjct  593  ATTACCCGCT  602


>gb|AY325111.1| Candida sp. BG03-3-25-1-3 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene,
and internal transcribed spacer 2, complete sequence; and
26S ribosomal RNA gene, partial sequence
Length=602

 Score =  846 bits (458),  Expect = 0.0
 Identities = 562/610 (92%), Gaps = 16/610 (2%)
 Strand=Plus/Plus
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Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCG  62

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-TGG  119
            ||||||  |||||||||||||| || |||||||||||||||||||||||||||| | |||
Sbjct  63   CGGCGAAAAAAACCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGG-TCTGG  120

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-T  178
            || |||||| ||| ||||||||||||||| |||||||||| |||| |||||||||||| |
Sbjct  121  CTCAGAAATGAGTTGGGCCAGAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTTATT  177

Query  179  TTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGA  238
            ||| || ||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct  178  TTATTAATTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGGA  236

Query  239  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  TCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCA  296

Query  299  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGC  358
            ||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  297  GATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGC  356

Query  359  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACTCT  418
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  357  ATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCT  416

Query  419  TAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCATT  477
            ||||||||||||||||||||||||||  |||||||| |||||   || | | ||| | |
Sbjct  417  TAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAA-ATAGTAC-TG  474

Query  478  -CAGGAA-ATATCAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATT  535
             ||| || || |||||||||||||||||||||||||||||| | |||| ||  |||||||
Sbjct  475  ACAG-AATATTTCAATGTATTAGGTTTATCCAACTCGTTGAGACTTCT-GGCGGTGAATT  532

Query  536  TTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  594
            |||||| | | |||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  533  TTTGGTATATTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGG  592

Query  595  ATTACCCGCT  604
            ||||||||||
Sbjct  593  ATTACCCGCT  602


>emb|FM178352.1| Candida ergastensis 18S rRNA gene (partial), ITS1, 5.8S rRNA
gene, ITS2 and 28S rRNA gene (partial), strain WM 07.29
Length=644

 Score =  845 bits (457),  Expect = 0.0
 Identities = 589/647 (91%), Gaps = 31/647 (4%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATT-CTAATTGCCAGCGCTTAATTGC  59
            |||||||||||||||||||||||||||||| ||||||  |  || || ||||||||||||
Sbjct  11   TCCGTAGGTGAACCTGCGGAAGGATCATTATTGTATTAGT-TTTACCTGCGCTTAATTGC  69

Query  60   GCGG-CGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-T  117
            ||||  ||  ||| |||||||||| |||||||||||||| |||||||||||||||| | |
Sbjct  70   GCGGTAGA-CAAA-CTTACACACAGTGTTTTTCTTTATT-GAAACTATTGCTTTGG-TCT  125

Query  118  GGCTAAGAAATTAGTC-GGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTG-T  175
            | || |||||| || | |||||||||||||  | |||||||||||||||||||||||| |
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Sbjct  126  GACTTAGAAATAAG-CTGGGCCAGAGGTTT--A-AAACTTCAATTTTTAATTGAATTGTT  181

Query  176  TATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAA  234
            ||||||  ||  |||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  182  TATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAA  239

Query  235  CGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAAT  294
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240  CGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAAT  299

Query  295  TGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGA  354
            ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |
Sbjct  300  TGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAA  359

Query  355  GGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTGAGTGAT  413
            ||||||||||||||||||||||||||||||||||||| || |||||||||||||||||||
Sbjct  360  GGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTGAGTGAT  418

Query  414  ACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-G-ACGCTGAGA-A  470
            |||||||||||||||||||||||||||||||  ||| ||||||||| | ||  ||| | |
Sbjct  419  ACTCTTAGTCGAACTAGGCGTTTGCTTGAAAAGTATCGGCATGAGTCGTAC--TGA-ATA  475

Query  471  GTGCATTCAGGAA-ATAT-CAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTT  528
            |||| || ||||| || | ||||||||||||||||||||||||||||| |||||||  ||
Sbjct  476  GTGCTTTTAGGAACATTTTCAATGTATTAGGTTTATCCAACTCGTTGAGAATTCTTA-TT  534

Query  529  -GTGAATTTTTGGTGT-TA-GGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAA  585
             ||||||||||||| | |  |||||||||||| |||||||||||||||||||||||||||
Sbjct  535  AGTGAATTTTTGGTATATTTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAA  594

Query  586  TCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  595  TCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  641


>dbj|AB513337.1| Candida sp. MT-LUC0013 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2,
26S rRNA, partial and complete sequence
Length=652

 Score =  843 bits (456),  Expect = 0.0
 Identities = 581/638 (91%), Gaps = 21/638 (3%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATT-CTAATTGCCAGCGCTTAATTGC  59
            ||||||||||||||||||||||||||||||| |||||  |  || || ||||||||||||
Sbjct  26   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTAGT-TTTACCTGCGCTTAATTGC  84

Query  60   GCGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGG  119
            ||||  |  ||| |||||||||| ||||||||||||||||||||| ||||||||| ||||
Sbjct  85   GCGGTAAACAAATCTTACACACAGTGTTTTTCTTTATTAGAAACTTTTGCTTTGGTTTGG  144

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTG-TTAT  178
            || |||||| ||| |||||||||||||  |  ||||||||||||||||||||||| ||||
Sbjct  145  CTTAGAAATAAGTTGGGCCAGAGGTTT--A-TAACTTCAATTTTTAATTGAATTGTTTAT  201

Query  179  TTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGG  237
            |||  ||  ||||||||||||||||||| |||||| ||||||||||||||||||||||||
Sbjct  202  TTATTTA-ATTGTCAATTTGTTGATTAATTTCAAA-AATCTTCAAAACTTTCAACAACGG  259

Query  238  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  319

Query  298  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGG  357
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            |||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||
Sbjct  320  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGG  379

Query  358  CATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTGAGTGATACT  416
            |||||||||||||||||||||||||||||||||| || ||||||||| ||||||||||||
Sbjct  380  CATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTTTTGAGTGATACT  438

Query  417  CTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-G-ACGCTGAGA-AGTG  473
            ||||||||||||||||||||||||||||  |||||||| |||| | ||  | | | ||||
Sbjct  439  CTTAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTAGTAC--TAA-ATAGTG  495

Query  474  CATTCAGGAA-ATAT-CAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTG  531
            | |||||||| || | ||||||||||||||||||||||||||||| |||||  | | |||
Sbjct  496  CTTTCAGGAACATTTTCAATGTATTAGGTTTATCCAACTCGTTGAGAATTCCCGCTAGTG  555

Query  532  AATTTTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGG  590
            |||||||||| | | |||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  556  AATTTTTGGTATAT-GGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGG  614

Query  591  TAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGG  628
            ||||||||||||||||||||||||||||||||||||||
Sbjct  615  TAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGG  652


>gb|EF627975.1| Candida lignicola strain NBRC 102564 internal transcribed spacer
1, partial sequence; 5.8S ribosomal RNA gene, complete sequence;
and internal transcribed spacer 2, partial sequence
Length=665

 Score =  841 bits (455),  Expect = 0.0
 Identities = 580/636 (91%), Gaps = 26/636 (4%)
 Strand=Plus/Plus

Query  9    TGAACCTGCGGAAGGATCATTACTGTATTCTA--ATTGCCAGCGCTTAATTGCGCGGCG-  65
            |||||||||||||||||||||||||| || ||   || ||||||||||||||||||| |
Sbjct  43   TGAACCTGCGGAAGGATCATTACTGT-TT-TAGTTTTACCAGCGCTTAATTGCGCGGTGA  100

Query  66   ATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGCTAAGA  125
            |  ||| |||||||||| || |||||||||||||||||||||||||||| |||||| |||
Sbjct  101  ACAAAATCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGGTTTGGCTTAGA  159

Query  126  AATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTG-TTATTTAATA  184
            ||| ||| ||| |||||||||  |  ||||||||||||||||||||||| ||||||| ||
Sbjct  160  AATAAGTTGGG-CAGAGGTTT--A-TAACTTCAATTTTTAATTGAATTGTTTATTTATTA  215

Query  185  CTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATCTCTT  244
              ||||||||||||||||||| |||||| |||||||||||||||||||||||||||||||
Sbjct  216  -ATTGTCAATTTGTTGATTAATTTCAAA-AATCTTCAAAACTTTCAACAACGGATCTCTT  273

Query  245  GGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTT  304
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  274  GGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTT  333

Query  305  CGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCT  364
            ||||||||||||||||||||||||||||||||||||| |||||||||| |||||||||||
Sbjct  334  CGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCATGCCT  393

Query  365  GTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTGAGTGATACTCTTAGTC  423
            ||||||||||||||||||||||||||| || |||||||||||||||||||||||||||||
Sbjct  394  GTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTGAGTGATACTCTTAGTC  452

Query  424  GAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-G-ACGCTGAGA-AGTGCATTCAG  480
            |||||||||||||||||||||  |||||||| |||| | ||  | | | ||||| |||||
Sbjct  453  GAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTAGTAC--TAA-ATAGTGCTTTCAG  509
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Query  481  GAA-ATAT-CAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTT  538
            ||| || | ||||||||||||||||||||||||||||| | |||||| | ||||||||||
Sbjct  510  GAACATTTTCAATGTATTAGGTTTATCCAACTCGTTGAGATTTCTTGCTAGTGAATTTTT  569

Query  539  GGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATT  597
            ||| | | |||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  570  GGTATAT-GGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATT  628

Query  598  ACCCGCTGAACTTAAGCATATCAATAAGC-GGAGGA  632
            ||||||||||||||||||||||| ||||| ||||||
Sbjct  629  ACCCGCTGAACTTAAGCATATCATTAAGCCGGAGGA  664


>gb|EU343874.1| Candida coipomoensis strain MUCL 29818 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=627

 Score =  830 bits (449),  Expect = 0.0
 Identities = 574/631 (90%), Gaps = 21/631 (3%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATT-CTAATTGCCAGCGCTTAATTGC  59
            ||||||||||||||||||||||||||||||| |||||  |  || || ||||||||||||
Sbjct  8    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTAGT-TTTACCTGCGCTTAATTGC  66

Query  60   GCGGCGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGG  119
            ||||  |  ||| |||||||||| ||||||||||||||||||||| ||||||||| ||||
Sbjct  67   GCGGTAAACAAATCTTACACACAGTGTTTTTCTTTATTAGAAACTTTTGCTTTGGTTTGG  126

Query  120  CTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTG-TTAT  178
            || |||||| ||| |||||||||||||  |  ||||||||||||||||||||||| ||||
Sbjct  127  CTTAGAAATAAGTTGGGCCAGAGGTTT--A-TAACTTCAATTTTTAATTGAATTGTTTAT  183

Query  179  TTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGG  237
            |||  ||  ||||||||||||||||||| |||||| ||||||||||||||||||||||||
Sbjct  184  TTATTTA-ATTGTCAATTTGTTGATTAATTTCAAA-AATCTTCAAAACTTTCAACAACGG  241

Query  238  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  242  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  301

Query  298  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGG  357
            |||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||
Sbjct  302  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGG  361

Query  358  CATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTGAGTGATACT  416
            |||||||||||||||||||||||||||||||||| || ||||||||| ||||||||||||
Sbjct  362  CATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTTTTGAGTGATACT  420

Query  417  CTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-G-ACGCTGAGA-AGTG  473
            ||||||||||||||||||||||||||||  |||||||| |||| | ||  | | | ||||
Sbjct  421  CTTAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTAGTAC--TAA-ATAGTG  477

Query  474  CATTCAGGAA-ATAT-CAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTG  531
            | |||||||| || | ||||||||||||||||||||||||||||| |||||  | | |||
Sbjct  478  CTTTCAGGAACATTTTCAATGTATTAGGTTTATCCAACTCGTTGAGAATTCCCGCTAGTG  537

Query  532  AATTTTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGG  590
            |||||||||| | | |||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  538  AATTTTTGGTATAT-GGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGG  596
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Query  591  TAGGATTACCCGCTGAACTTAAGCATATCAA  621
            |||||||||||||||||||||||||||||||
Sbjct  597  TAGGATTACCCGCTGAACTTAAGCATATCAA  627


>gb|EU343826.1| Candida ergastensis strain MUCL 30034 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=627

 Score =  824 bits (446),  Expect = 0.0
 Identities = 578/636 (90%), Gaps = 31/636 (4%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATT-CTAATTGCCAGCGCTTAATTGC  59
            |||||||||||||||||||||||||||||| ||||||  |  || || ||||||||||||
Sbjct  8    TCCGTAGGTGAACCTGCGGAAGGATCATTATTGTATTAGT-TTTACCTGCGCTTAATTGC  66

Query  60   GCGG-CGATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCT-T  117
            ||||  ||  ||| |||||||||| |||||||||||||| |||||||||||||||| | |
Sbjct  67   GCGGTAGA-CAAA-CTTACACACAGTGTTTTTCTTTATT-GAAACTATTGCTTTGG-TCT  122

Query  118  GGCTAAGAAATTAGTC-GGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTG-T  175
            | || |||||| || | |||||||||||||  | |||||||||||||||||||||||| |
Sbjct  123  GACTTAGAAATAAG-CTGGGCCAGAGGTTT--A-AAACTTCAATTTTTAATTGAATTGTT  178

Query  176  TATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAA  234
            ||||||  ||  |||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  179  TATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAA  236

Query  235  CGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAAT  294
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  237  CGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAAT  296

Query  295  TGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGA  354
            ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |
Sbjct  297  TGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAA  356

Query  355  GGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTGAGTGAT  413
            ||||||||||||||||||||||||||||||||||||| || |||||||||||||||||||
Sbjct  357  GGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTGAGTGAT  415

Query  414  ACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-G-ACGCTGAGA-A  470
            |||||||||||||||||||||||||||||||  ||| ||||||||| | ||  ||| | |
Sbjct  416  ACTCTTAGTCGAACTAGGCGTTTGCTTGAAAAGTATCGGCATGAGTCGTAC--TGA-ATA  472

Query  471  GTGCATTCAGGAA-ATAT-CAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTT  528
            |||| || ||||| || | ||||||||||||||||||||||||||||| |||||||  ||
Sbjct  473  GTGCTTTTAGGAACATTTTCAATGTATTAGGTTTATCCAACTCGTTGAGAATTCTTA-TT  531

Query  529  -GTGAATTTTTGGTGT-TA-GGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAA  585
             ||||||||||||| | |  |||||||||||| |||||||||||||||||||||||||||
Sbjct  532  AGTGAATTTTTGGTATATTTGGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAA  591

Query  586  TCAGGTAGGATTACCCGCTGAACTTAAGCATATCAA  621
            |||||||||| |||||||||||||||||||||||||
Sbjct  592  TCAGGTAGGACTACCCGCTGAACTTAAGCATATCAA  627


>gb|GQ458025.1| Debaryomyces hansenii strain MA09-AK 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
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Length=2991

 Score =  819 bits (443),  Expect = 0.0
 Identities = 588/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
             ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1753  TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  1812

Query  61    CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
             ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  1813  CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  1870

Query  117   TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
             ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  1871  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  1928

Query  170   AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
             ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  1929  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  1987

Query  229   CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1988  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  2047

Query  289   ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2048  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  2107

Query  349   TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
             ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  2108  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  2166

Query  408   AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
             |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  2167  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  2225

Query  468   GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  2226  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  2280

Query  525   GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
               | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  2281  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  2339

Query  581   TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2340  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  2391


>dbj|AB220031.1| Debaryomyces fabryi genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2,
26S rRNA, partial sequence, strain: IFM 54260
Length=648

 Score =  819 bits (443),  Expect = 0.0
 Identities = 588/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  10   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  69

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
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            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  70   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  127

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  128  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  185

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  186  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  244

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  245  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  304

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  305  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  364

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  365  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  423

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  424  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  482

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  483  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  537

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  538  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  596

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  597  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  648


>gb|EU149789.1| Debaryomyces hansenii strain CBS 10686 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=639

 Score =  819 bits (443),  Expect = 0.0
 Identities = 588/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  61   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  118

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  119  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  176

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
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Sbjct  177  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  235

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  295

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  355

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  356  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  414

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  415  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  473

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  474  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  528

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  529  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  587

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  588  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  639


>gb|EU569041.1| Debaryomyces hansenii isolate CNRMA 200600935 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=639

 Score =  819 bits (443),  Expect = 0.0
 Identities = 588/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  61   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  118

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  119  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  176

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  177  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  235

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  295

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  355
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Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  356  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  414

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  415  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  473

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  474  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  528

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  529  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  587

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  588  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  639


>gb|EU569037.1| Debaryomyces hansenii isolate CNRMA 200500815 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=639

 Score =  819 bits (443),  Expect = 0.0
 Identities = 588/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  61   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  118

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  119  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  176

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  177  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  235

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  295

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  355

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  356  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  414

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  415  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  473
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Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  474  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  528

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  529  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  587

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  588  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  639


>gb|EU568915.1| Debaryomyces hansenii 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene, and
internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence
Length=639

 Score =  819 bits (443),  Expect = 0.0
 Identities = 588/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  61   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  118

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  119  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  176

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  177  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  235

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  295

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  355

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  356  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  414

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  415  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  473

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  474  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  528

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  529  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  587

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  588  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  639


>gb|EF196809.1| Debaryomyces hansenii voucher MCCC2E00323 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=667

 Score =  819 bits (443),  Expect = 0.0
 Identities = 588/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Minus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  640  TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  581

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  580  CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  523

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  522  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  465

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  464  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  406

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  405  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  346

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  345  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  286

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  285  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  227

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  226  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  168

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  167  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  113

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  112  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  54

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  53   TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  2


>gb|AF210326.1|AF210326 Debaryomyces hansenii var. fabryi CBS789 internal
transcribed
spacer 1, 5.8S ribosomal RNA gene, and internal transcribed
spacer 2, complete sequence
Length=639
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 Score =  819 bits (443),  Expect = 0.0
 Identities = 588/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  61   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  118

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  119  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  176

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  177  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  235

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  295

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  355

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  356  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  414

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  415  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  473

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  474  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  528

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  529  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  587

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  588  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  639


>gb|GU213439.1| Saccharomycetes sp. HZ10 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene,
and internal transcribed spacer 2, complete sequence; and
28S ribosomal RNA gene, partial sequence
Length=640

 Score =  817 bits (442),  Expect = 0.0
 Identities = 586/650 (90%), Gaps = 31/650 (4%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  62
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Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  ||||||||||||| |||||||| | ||||||  | |||||||||||||| |
Sbjct  63   CGGCGAAAAAACCTTACACACTATGTTTTT-TGTTATTACAAGAACTATTGCTTTGG-TC  120

Query  117  TGGCT-AAGAAATTAG--TCGGGCCAGAGGTTTACAC-AAACTTCAATTTTTA-ATTGAA  171
            || ||  ||||| |||  | |||||||||||||| || ||||||||| ||||| ||||||
Sbjct  121  TGTCTCTAGAAA-TAGATTTGGGCCAGAGGTTTA-ACTAAACTTCAA-TTTTATATTGAA  177

Query  172  TTGTTATTTAA--TACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTC  229
            ||||| | |||  ||  ||||||||||||||||||| |||||| ||||||||||||||||
Sbjct  178  TTGTT-TCTAATTTA-ATTGTCAATTTGTTGATTAATTTCAAAAAATCTTCAAAACTTTC  235

Query  230  AACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATA  289
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  AACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATA  295

Query  290  TGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATT  349
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  TGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATT  355

Query  350  CCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAG  409
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  356  CCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAG  415

Query  410  TGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-G-ACGCTGA  467
            |||||||||||||||||||||||||||||||||||| ||| ||||||||| | ||  |||
Sbjct  416  TGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATCGGCATGAGTAGTAC--TGA  473

Query  468  GA-AGTGCATTCAGGAAATAT-CAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTG  525
             | ||| | |||| ||  | | ||||||||||||||||||||||||||||| | |  ||
Sbjct  474  -ATAGTAC-TTCAAGACTTTTTCAATGTATTAGGTTTATCCAACTCGTTGA-A-TGGTTT  529

Query  526  -GTTGTGAATTTTTGGTGTTA--GGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTC  582
             || || ||||||| || |||  ||||  |||||| || |||||||||||||||||||||
Sbjct  530  AGTAGTAAATTTTTAGTATTATTGGCTCGGCCTTACAATACAACAAACAAGTTTGACCTC  589

Query  583  AAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  590  AAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  639


>emb|FM178351.1| Candida glaebosa 18S rRNA gene (partial), ITS1, 5.8S rRNA gene,
ITS2 and 28S rRNA gene (partial), strain WM 07.36
Length=637

 Score =  815 bits (441),  Expect = 0.0
 Identities = 582/644 (90%), Gaps = 33/644 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| ||||||| |||||| |||||||||||||
Sbjct  13   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCT-ATTGCCTGCGCTTAATTGCG  71

Query  61   CGGCGATTAAACCTTACACACAATGT-TTTTCTTTATTA-GAAACTATTGCTTTGGCTTG  118
            |||||| ||||||||  |||||| || |||| ||||||| | ||||||| |||||| |||
Sbjct  72   CGGCGA-TAAACCTT--ACACAACGTGTTTT-TTTATTATG-AACTATTACTTTGGTTTG  126

Query  119  GCTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-  177
            |||||||||||||| | |||||||| | |   ||||||||| |||| ||||||||||||
Sbjct  127  GCTAAGAAATTAGTTGAGCCAGAGG-TGATTTAAACTTCAA-TTTT-ATTGAATTGTTAT  183

Query  178  TTTAATACT-TTGTCAATTTGTTGATTAAATTC-AAACAATCTTCAAAACTTTCAACAAC  235
            ||||||  | ||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  184  TTTAAT-TTATTGTCAATTTGTTGATTAAATTCAAAACAATCTTCAAAACTTTCAACAAC  242
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Query  236  GGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATT  295
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  243  GGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATT  302

Query  296  GCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAG  355
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  303  GCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCACCCTCTGGTATTCCAGAG  362

Query  356  GGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATAC  415
            || ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  363  GGTATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCTTTGGGTTTGGTATTGAGTGATAC  422

Query  416  TCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-GACGCTGAGA-AGTG  473
            |||||||||||||||||||||||||||||| |||||||| |||| |  | ||| | ||||
Sbjct  423  TCTTAGTCGAACTAGGCGTTTGCTTGAAATATATTGGCACGAGTAGT-GTTGA-ACAGTG  480

Query  474  CAT-TCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAAT-TCTT-GGTTGT  530
              | || | ||  ||||||||||||||||||||||||||||||| |   | || ||| ||
Sbjct  481  T-TGTCTG-AAC-ATCAATGTATTAGGTTTATCCAACTCGTTGA-AGCGT-TTAGGTCGT  535

Query  531  GAAT-TT-TTGGTGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCA  588
             | | || ||  | | ||||||||||||| |||||| |||||||||||||||||||||||
Sbjct  536  -ACTATTCTTCAT-T-AGGCTTTGCCTTATAAAACA-CAAACAAGTTTGACCTCAAATCA  591

Query  589  GGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  592  GGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  635


>gb|HM032737.1| Debaryomyces hansenii strain NJ147 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=637

 Score =  813 bits (440),  Expect = 0.0
 Identities = 585/649 (90%), Gaps = 33/649 (5%)
 Strand=Plus/Plus

Query  4    GTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCGCGG  63
            |||||||||||||||||||||||||||| |||||||  ||||||||||||||||||||||
Sbjct  1    GTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCGCGG  60

Query  64   CGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-TGG  119
            |||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | |||
Sbjct  61   CGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TCTGG  118

Query  120  -CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTGAAT  172
             || ||||| ||| | |||||||||||||||   || |||||||||| |||| |||||||
Sbjct  119  ACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTGAAT  176

Query  173  TGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAA  231
            |||||||||  ||  |||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  177  TGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAA  235

Query  232  CAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATG  291
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  CAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATG  295

Query  292  AATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCC  351
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  AATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCC  355
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Query  352  AGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTGAGT  410
            |||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Sbjct  356  AGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTGAGT  414

Query  411  GATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-  469
            ||||||||||||||||||||||||||||||||||| ||||||||||||||   ||| ||
Sbjct  415  GATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-GAT  473

Query  470  AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTTGGT  527
            ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||  |
Sbjct  474  AGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TTAAT  528

Query  528  TGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCA  583
             || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||||||
Sbjct  529  GGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACCTCA  587

Query  584  AATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  588  AATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  636


>gb|GQ458041.1| Debaryomyces hansenii strain ATCC 60978 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=2961

 Score =  813 bits (440),  Expect = 0.0
 Identities = 587/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
             ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1729  TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  1788

Query  61    CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
             ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  1789  CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  1846

Query  117   TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
             ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  1847  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  1904

Query  170   AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
             ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  1905  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  1963

Query  229   CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1964  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  2023

Query  289   ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2024  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  2083

Query  349   TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
             ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  2084  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  2142

Query  408   AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
             ||||||||||||||| |||||||||||||||||||||| ||||||||||||||   |||
Sbjct  2143  AGTGATACTCTTAGTTGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  2201

Query  468   GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
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             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  2202  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  2256

Query  525   GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
               | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  2257  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  2315

Query  581   TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2316  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  2367


>gb|GQ458019.1| Debaryomyces hansenii strain MA09-J 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=2969

 Score =  813 bits (440),  Expect = 0.0
 Identities = 587/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
             ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1737  TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  1796

Query  61    CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
             ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  1797  CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  1854

Query  117   TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
             ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  1855  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  1912

Query  170   AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
             ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  1913  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  1971

Query  229   CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1972  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  2031

Query  289   ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2032  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  2091

Query  349   TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
             ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  2092  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  2150

Query  408   AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
             ||||||||||||||| |||||||||||||||||||||| ||||||||||||||   |||
Sbjct  2151  AGTGATACTCTTAGTTGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  2209

Query  468   GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  2210  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  2264

Query  525   GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
               | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  2265  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  2323

Query  581   TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  2324  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  2375


>gb|GQ376084.1| Debaryomyces hansenii var. hansenii isolate UOA/HCPF 5104 18S
ribosomal RNA gene, partial sequence; internal transcribed
spacer 1, 5.8S ribosomal RNA gene, and internal transcribed
spacer 2, complete sequence; and 28S ribosomal RNA gene, partial
sequence
Length=663

 Score =  813 bits (440),  Expect = 0.0
 Identities = 587/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  25   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  84

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  85   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  142

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  143  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  200

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  201  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  259

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  319

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  379

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  380  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  438

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            ||||||||||||||| |||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  439  AGTGATACTCTTAGTTGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  497

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  498  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  552

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  553  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  611

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  612  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  663


>dbj|AB220030.1| Debaryomyces hansenii var. hansenii genes for 18S rRNA, ITS1,
5.8S rRNA, ITS2, 26S rRNA, partial sequence, strain: IFM 54259
Length=648

 Score =  813 bits (440),  Expect = 0.0
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 Identities = 587/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  10   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  69

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  70   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  127

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  128  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  185

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  186  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  244

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  245  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  304

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  305  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  364

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  365  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  423

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            ||||||||||||||| |||||||||||||||||||||| ||||||||||||||   |||
Sbjct  424  AGTGATACTCTTAGTTGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  482

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  483  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  537

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  538  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  596

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  597  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  648


>gb|EU569039.1| Debaryomyces hansenii isolate CNRMA 200600362 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=639

 Score =  813 bits (440),  Expect = 0.0
 Identities = 587/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
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Sbjct  61   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  118

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  119  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  176

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  177  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  235

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  295

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  355

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  356  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  414

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            ||||||||||||||| |||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  415  AGTGATACTCTTAGTTGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  473

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  474  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  528

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  529  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  587

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  588  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  639


>gb|EF432798.1| Pueraria montana var. lobata from China: Jiangxi 18S ribosomal
RNA gene, partial sequence; internal transcribed spacer 1,
5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence; and 28S ribosomal RNA gene, partial sequence
Length=657

 Score =  813 bits (440),  Expect = 0.0
 Identities = 587/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  19   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  78

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  79   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  136

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  137  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  194

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  195  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  253
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Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  254  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  313

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  314  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  373

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  374  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  432

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  433  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  491

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  492  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  546

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  547  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  605

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  606  TCAAATCAGGTAGGATTACCCGCTGAACGTAAGCATATCAATAAGCGGAGGA  657


>gb|EF432797.1| Pueraria montana var. lobata from China: Jiangxi 18S ribosomal
RNA gene, partial sequence; internal transcribed spacer 1,
5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence; and 28S ribosomal RNA gene, partial sequence
Length=657

 Score =  813 bits (440),  Expect = 0.0
 Identities = 587/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  19   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  78

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||| ||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  79   CGGCGAAAAAACCTTATACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  136

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  137  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  194

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  195  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  253

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  254  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  313

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  314  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  373
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Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  374  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  432

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  433  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  491

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  492  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  546

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  547  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  605

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  606  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  657


>gb|AF210327.1|AF210327 Debaryomyces hansenii var. hansenii CBS767 internal 
transcribed 
spacer 1, 5.8S ribosomal RNA gene, and internal transcribed 
spacer 2, complete sequence
Length=639

 Score =  813 bits (440),  Expect = 0.0
 Identities = 587/652 (90%), Gaps = 33/652 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  61   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  118

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  119  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  176

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  177  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  235

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  295

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  355

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  356  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  414

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            ||||||||||||||| |||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  415  AGTGATACTCTTAGTTGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  473

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
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            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  474  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  528

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  529  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  587

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  588  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  639


>gb|GQ913348.1| Debaryomyces hansenii strain W4682 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=618

 Score =  811 bits (439),  Expect = 0.0
 Identities = 579/641 (90%), Gaps = 32/641 (4%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| ||||||| |||||| |||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCT-ATTGCCTGCGCTTAATTGCG  59

Query  61   CGGCGATTAAACCTTACACACAATGT-TTTTCTTTATT-AGAAACTATTGCTTTGGCT-T  117
            |||||| ||||||||  |||||| || |||| ||||||  | ||||||| |||||| | |
Sbjct  60   CGGCGA-TAAACCTT--ACACAACGTGTTTT-TTTATTCTG-AACTATTACTTTGG-TCT  113

Query  118  GGCTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA  177
            ||||||||||||||| |||||||||| | |   ||||||||| |||| ||||||||||||
Sbjct  114  GGCTAAGAAATTAGTTGGGCCAGAGG-TGATTTAAACTTCAA-TTTT-ATTGAATTGTTA  170

Query  178  -TTTAATACTTTGTCAATTTGTTGATTAAATTC-AAACAATCTTCAAAACTTTCAACAAC  235
             ||||||  |||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  171  TTTTAAT-TTTTGTCAATTTGTTGATTAAATTCAAAACAATCTTCAAAACTTTCAACAAC  229

Query  236  GGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATT  295
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  230  GGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATT  289

Query  296  GCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAG  355
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  290  GCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCACCCTCTGGTATTCCAGAG  349

Query  356  GGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATAC  415
            || ||||||||||||||||||||||||||||||||||  |||||||||||||||||||||
Sbjct  350  GGTATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCCCGGGTTTGGTATTGAGTGATAC  409

Query  416  TCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-GACGCTGAGA-AGTG  473
            |||||||||||||||||||||||||||||| |||||||| |||| |  | ||| | ||||
Sbjct  410  TCTTAGTCGAACTAGGCGTTTGCTTGAAATATATTGGCACGAGTAGT-GTTGA-ACAGTG  467

Query  474  CAT-TCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTTGGTTGTG  531
              | || | ||  ||||||||||||||||||||||||||||||| | |   | ||| | |
Sbjct  468  T-TGTCTG-AAC-ATCAATGTATTAGGTTTATCCAACTCGTTGATACAGG-T-GGT-GCG  521

Query  532  AATTTTTGGTGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGT  591
            | || ||  | | ||||||||||||| |||||| ||||||||||||||||||||||||||
Sbjct  522  A-TTCTTCAT-T-AGGCTTTGCCTTATAAAACA-CAAACAAGTTTGACCTCAAATCAGGT  577

Query  592  AGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||||||||||||||||||||||||||||
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Sbjct  578  AGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  618


>dbj|AB220032.1| Candida psychrophila genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2,
26S rRNA, partial sequence, strain: IFM 54261
Length=649

 Score =  809 bits (438),  Expect = 0.0
 Identities = 587/653 (89%), Gaps = 34/653 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  10   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  69

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  70   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  127

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  128  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  185

Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  186  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  244

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  245  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  304

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  305  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  364

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            |||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  365  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  423

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  424  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  483

Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  484  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  537

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  538  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  596

Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  597  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  649


>gb|AY040667.1| Candida psychrophila internal transcribed spacer 1, partial
sequence;
5.8S ribosomal RNA gene, complete sequence; and internal
transcribed spacer 2, partial sequence
Length=640

 Score =  809 bits (438),  Expect = 0.0
 Identities = 587/653 (89%), Gaps = 34/653 (5%)
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 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  61   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  118

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  119  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  176

Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  177  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  235

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  295

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  355

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            |||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  356  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  414

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  415  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  474

Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  475  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  528

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  529  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  587

Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  588  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  640


>gb|FJ172253.1| Candida sinolaborantium strain ATCC MYA-4337 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 26S ribosomal RNA gene, partial sequence
Length=619

 Score =  808 bits (437),  Expect = 0.0
 Identities = 573/632 (90%), Gaps = 36/632 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  11   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCT-TTTGCCAGCGCTTAATTGCG  69

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTAGAAACTATTGCTTTGGCTTGG  119
            ||||||  |||||||||||||||||||||| | || ||  |||| |||||||||||||||
Sbjct  70   CGGCGA-AAAACCTTACACACAATGTTTTT-TGTT-TT--AAACCATTGCTTTGGCTTGG  124
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Query  120  -CTAAGAAATTA-GTCGGGCCAGAGGTTTAC-AC-AAACTTCAATTTTTAATTGAATTGT  175
             || ||||| || || ||| ||||||||||| || |||||||||||||| ||||||||||
Sbjct  125  CCT-AGAAA-TAGGTTGGGTCAGAGGTTTACAACTAAACTTCAATTTTT-ATTGAATTGT  181

Query  176  TATTT-AA-TACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACA  233
            | ||| || || ||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  182  T-TTTAAATTA-TTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACA  238

Query  234  ACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAA  293
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239  ACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAA  298

Query  294  TTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAG  353
            |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  299  TTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAA  358

Query  354  AGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGAT  413
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  359  AGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGAT  418

Query  414  ACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTG-ACGCTGAGA-AG  471
            ||||||||||| |||||||||||||||||||  |||||||||||||| ||  || || ||
Sbjct  419  ACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATTGGCATGAGTGTAC--TG-GATAG  475

Query  472  TGCATTCAGGAAATAT-CAATGTATTAGGTTTATCCAACTCGTTGACA--ATTCTTGGTT  528
            | | ||| | |  ||| ||||||||||||||||||||||||||||| |  || |  |||
Sbjct  476  TACGTTCTG-AT-TATTCAATGTATTAGGTTTATCCAACTCGTTGA-AGGAT-CA-GGT-  529

Query  529  GTGAATTTTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATC  587
            || ||||| |||||| | ||||  |||||| ||  |||||||||||||||||||||||||
Sbjct  530  GTAAATTTCTGGTGTATTGGCTCGGCCTTACAA--CAACAAACAAGTTTGACCTCAAATC  587

Query  588  AGGTAGGATTACCCGCTGAACTTAAGCATATC  619
            ||||||||||||||||||||||||||||||||
Sbjct  588  AGGTAGGATTACCCGCTGAACTTAAGCATATC  619


>gb|EF198011.1| Debaryomyces pseudopolymorphus strain WC43-3 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=644

 Score =  808 bits (437),  Expect = 0.0
 Identities = 577/639 (90%), Gaps = 31/639 (4%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  17   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  76

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  ||||||||||||| |||||||| | ||||||  | |||||||||||||| |
Sbjct  77   CGGCGAAAAAAACCTTACACACTATGTTTTT-TGTTATTACAAGAACTATTGCTTTGG-TC  134

Query  117  TGGCT-AAGAAATTAG--TCGGGCCAGAGGTTTACAC-AAACTTCAATTTTTA-ATTGAA  171
            || ||  ||||| |||  | |||||||||||||| || ||||||||| ||||| ||||||
Sbjct  135  TGTCTCTAGAAA-TAGATTTGGGCCAGAGGTTTA-ACTAAACTTCAA-TTTTATATTGAA  191

Query  172  TTGTTATTTAA--TACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTC  229
            ||||| |||||  ||  ||||||||||||||||||| |||||| ||||||||||||||||
Sbjct  192  TTGTT-TTTAATTTA-ATTGTCAATTTGTTGATTAATTTCAAAAAATCTTCAAAACTTTC  249
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Query  230  AACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATA  289
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250  AACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATA  309

Query  290  TGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATT  349
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  310  TGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATT  369

Query  350  CCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAG  409
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  370  CCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAG  429

Query  410  TGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-G-ACGCTGA  467
            |||||||||||||||||||||||||||||||||||| ||| ||||||||| | ||  |||
Sbjct  430  TGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATCGGCATGAGTAGTAC--TGA  487

Query  468  GA-AGTGCATTCAGGAAATAT-CAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTG  525
             | ||||| |||| ||  | | ||||||||||||||||||||||||||||| | |  ||
Sbjct  488  -ATAGTGC-TTCAAGACTTTTTCAATGTATTAGGTTTATCCAACTCGTTGA-A-TGGTTT  543

Query  526  -GTTGTGAATTTTTGGTGTTA--GGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTC  582
             || || ||||||| || |||  ||||  |||||| || |||||||||||||||||||||
Sbjct  544  AGTAGTAAATTTTTAGTATTATTGGCTCGGCCTTACAACACAACAAACAAGTTTGACCTC  603

Query  583  AAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAA  621
            ||||||||||||| |||||||||||||||||||||||||
Sbjct  604  AAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAA  642


>gb|EF222225.1| Debaryomyces hansenii strain gao1hou2 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=658

 Score =  804 bits (435),  Expect = 0.0
 Identities = 580/644 (90%), Gaps = 33/644 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  28   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  87

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  88   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  145

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  146  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  203

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  204  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  262

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  263  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  322

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  323  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  382

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
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            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  383  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  441

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  442  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  500

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  501  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  555

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  556  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  614

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAA  624
            ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  615  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAA  658


>gb|EU149790.1| Debaryomyces hansenii strain CBS 10629 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=630

 Score =  802 bits (434),  Expect = 0.0
 Identities = 579/643 (90%), Gaps = 33/643 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  61   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  118

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  119  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  176

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  177  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  235

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  295

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  355

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  356  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  414

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  415  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  473

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
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Sbjct  474  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  528

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  529  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  587

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATA  623
            |||||||||||||||||||||||||||||||||||||||||||
Sbjct  588  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATA  630


>gb|EF194843.1| Debaryomyces hansenii voucher MCCC2E00222 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=669

 Score =  802 bits (434),  Expect = 0.0
 Identities = 586/653 (89%), Gaps = 36/653 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  28   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  87

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  88   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  145

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  146  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  203

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  204  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  262

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  263  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  322

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  323  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  382

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  383  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  441

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  442  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  500

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  501  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  555

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  556  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  614

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAG-CGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||| ||| ||| |||
Sbjct  615  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAA-AAGGCGG-GGA  665
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>gb|EF197815.1| Debaryomyces hansenii strain GAO2 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=657

 Score =  802 bits (434),  Expect = 0.0
 Identities = 579/643 (90%), Gaps = 33/643 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  28   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  87

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  88   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  145

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  146  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  203

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  204  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  262

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  263  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  322

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  323  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  382

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  383  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  441

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  442  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  500

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  501  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  555

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  556  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  614

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATA  623
            |||||||||||||||||||||||||||||||||||||||||||
Sbjct  615  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATA  657


>gb|EF643596.1| Debaryomyces hansenii strain LN-5 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=669

 Score =  800 bits (433),  Expect = 0.0
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```
 Identities = 578/642 (90%), Gaps = 33/642 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  29   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  88

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  89   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  146

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  147  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  204

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  205  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  263

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  264  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  323

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  324  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  383

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  384  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  442

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  443  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  501

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  502  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  556

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  557  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  615

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAAT  622
            ||||||||||||||||||||||||||||||||||||||||||
Sbjct  616  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAAT  657


>gb|EF643588.1| Debaryomyces hansenii strain LN-2 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=674

 Score =  800 bits (433),  Expect = 0.0
 Identities = 583/649 (89%), Gaps = 35/649 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  29   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  88

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
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Sbjct  89   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  146

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  147  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  204

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  205  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  263

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  264  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  323

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  324  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  383

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  384  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  442

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  443  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  501

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  502  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  556

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  557  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  615

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAA-GCGG  628
            |||||||||||||||||||||||||||||||||||||||| ||| ||||
Sbjct  616  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCA-TAAAGCGG  663


>dbj|AB220029.1| Debaryomyces nepalensis genes for 18S rRNA, ITS1, 5.8S rRNA,
ITS2, 26S rRNA, partial sequence, strain: IFM 54258
Length=649

 Score =  798 bits (432),  Expect = 0.0
 Identities = 585/653 (89%), Gaps = 34/653 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  10   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  69

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  70   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTCTTGCTTTGG-TC  127

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  128  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  185

Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  186  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  244

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  245  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  304

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  305  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTA  364

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            ||||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  365  TTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  423

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  424  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  483

Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  484  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  537

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  538  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  596

Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  597  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  649


>dbj|AB220028.1| Debaryomyces nepalensis genes for 18S rRNA, ITS1, 5.8S rRNA,
ITS2, 26S rRNA, partial sequence, strain: IFM 54257
Length=649

 Score =  798 bits (432),  Expect = 0.0
 Identities = 585/653 (89%), Gaps = 34/653 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  10   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  69

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  70   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTCTTGCTTTGG-TC  127

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  128  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  185

Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  186  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  244

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  245  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  304

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  305  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTA  364

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            ||||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  365  TTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  423
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Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  424  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  483

Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  484  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  537

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  538  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  596

Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  597  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  649


>gb|EF192232.1| Debaryomyces hansenii strain shi2wei 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=646

 Score =  798 bits (432),  Expect = 0.0
 Identities = 577/641 (90%), Gaps = 33/641 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  18   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  77

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  78   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  135

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  136  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  193

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  194  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  252

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  253  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  312

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  313  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  372

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  373  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  431

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  432  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  490

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  491  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  545

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
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              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  546   AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  604

Query  581   TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAA  621
             |||||||||||||||||||||||||||||||||||||||||
Sbjct  605   TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAA  645


>gb|EF192224.1| Debaryomyces hansenii 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene, and
internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence
Length=657

 Score =  798 bits (432),  Expect = 0.0
 Identities = 579/644 (89%), Gaps = 34/644 (5%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
             ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  28    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  87

Query  61    CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
             ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  88    CGGCGAAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  145

Query  117   TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
             ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  146   TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  203

Query  170   AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
             ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  204   AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  262

Query  229   CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  263   CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  322

Query  289   ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  323   ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  382

Query  349   TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
             ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  383   TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  441

Query  408   AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
             |||||||||||||||||||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  442   AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  500

Query  468   GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  501   GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  555

Query  525   GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
               | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  556   AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  614

Query  581   TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAA  624
             |||||||||||||||||||||||||||||||||||||||| |||
Sbjct  615   TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCA-TAA  657


>gb|EF193070.1| Debaryomyces hansenii voucher MCCC2E00282 18S ribosomal RNA gene,
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partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=673

 Score =  798 bits (432),  Expect = 0.0
 Identities = 577/641 (90%), Gaps = 33/641 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  32   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  91

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  92   CGGCGAAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  149

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  150  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  207

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  208  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  266

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  326

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  386

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  387  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  445

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  446  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  504

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  505  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  559

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  560  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  618

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAA  621
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  619  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAA  659


>gb|EF222227.1| Debaryomyces hansenii strain gaoyandie zhongchang 18S ribosomal
RNA gene, partial sequence; internal transcribed spacer 1,
5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence; and 28S ribosomal RNA gene, partial sequence
Length=656

 Score =  797 bits (431),  Expect = 0.0
 Identities = 576/640 (90%), Gaps = 33/640 (5%)
 Strand=Plus/Plus
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Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  28   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  87

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  88   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  145

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  146  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  203

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  204  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  262

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  263  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  322

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  323  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  382

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  383  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  441

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  442  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  500

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  501  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  555

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  556  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  614

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCA  620
            ||||||||||||||||||||||||||||||||||||||||
Sbjct  615  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCA  654


>emb|AJ606466.1| Candida coipomoensis 18S rRNA gene (partial), 5.8S rRNA gene,
26S rRNA gene (partial), ITS1 and ITS2, strain CBS 8178
Length=609

 Score =  797 bits (431),  Expect = 0.0
 Identities = 556/613 (90%), Gaps = 21/613 (3%)
 Strand=Plus/Plus

Query  15   TGCGGAAGGATCATTACTGTATT-CTAATTGCCAGCGCTTAATTGCGCGGCGATTAAACC  73
            ||||||||||||||||| |||||  |  || || ||||||||||||||||  |  ||| |
Sbjct  1    TGCGGAAGGATCATTACAGTATTAGT-TTTACCTGCGCTTAATTGCGCGGTAAACAAATC  59

Query  74   TTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTTGGCTAAGAAATTAGTC  133
            ||||||||| ||||||||||||||||||||| ||||||||| |||||| |||||| |||
Sbjct  60   TTACACACAGTGTTTTTCTTTATTAGAAACTTTTGCTTTGGTTTGGCTTAGAAATAAGTT  119

Query  134  GGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTG-TTATTTA-ATACTTTGTC  191
            |||||||||||||  |  ||||||||||||||||||||||| |||||||  ||  |||||
Sbjct  120  GGGCCAGAGGTTT--A-TAACTTCAATTTTTAATTGAATTGTTTATTTATTTA-ATTGTC  175
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Query  192  AATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTC  251
            |||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  176  AATTTGTTGATTAATTTCAAA-AATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTC  234

Query  252  GCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAAT  311
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  235  GCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAAT  294

Query  312  CATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAG  371
            |||||||||||||||||||||||||||||| |||||||||| ||||||||||||||||||
Sbjct  295  CATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCATGCCTGTTTGAG  354

Query  372  CGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAG  430
            |||||||||||||||||||| || ||||||||| ||||||||||||||||||||||||||
Sbjct  355  CGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTTTTGAGTGATACTCTTAGTCGAACTAG  413

Query  431  GCGTTTGCTTGAAATTTATTGGCATGAGT-G-ACGCTGAGA-AGTGCATTCAGGAA-ATA  486
            ||||||||||||||  |||||||| |||| | ||  | | | ||||| |||||||| ||
Sbjct  414  GCGTTTGCTTGAAAAGTATTGGCACGAGTAGTAC--TAA-ATAGTGCTTTCAGGAACATT  470

Query  487  T-CAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTGTGAATTTTTGGTGT-T  544
            | ||||||||||||||||||||||||||||| |||||  | | ||||||||||||| | |
Sbjct  471  TTCAATGTATTAGGTTTATCCAACTCGTTGAGAATTCCCGCTAGTGAATTTTTGGTATAT  530

Query  545  AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACCCGCT  604
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  531  -GGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACCCGCT  589

Query  605  GAACTTAAGCATA  617
            |||||||||||||
Sbjct  590  GAACTTAAGCATA  602


>gb|EU343832.1| Candida glaebosa strain MUCL 29834 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=619

 Score =  795 bits (430),  Expect = 0.0
 Identities = 571/633 (90%), Gaps = 33/633 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| ||||||| |||||| |||||||||||||
Sbjct  8    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCT-ATTGCCTGCGCTTAATTGCG  66

Query  61   CGGCGATTAAACCTTACACACAATGT-TTTTCTTTATTA-GAAACTATTGCTTTGGCTTG  118
            |||||| ||||||||  |||||| || |||| ||||||| | ||||||| |||||| |||
Sbjct  67   CGGCGA-TAAACCTT--ACACAACGTGTTTT-TTTATTATG-AACTATTACTTTGGTTTG  121

Query  119  GCTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTA-  177
            |||||||||||||| | |||||||| | |   ||||||||| |||| ||||||||||||
Sbjct  122  GCTAAGAAATTAGTTGAGCCAGAGG-TGATTTAAACTTCAA-TTTT-ATTGAATTGTTAT  178

Query  178  TTTAATACT-TTGTCAATTTGTTGATTAAATTC-AAACAATCTTCAAAACTTTCAACAAC  235
            ||||||  | ||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  179  TTTAAT-TTATTGTCAATTTGTTGATTAAATTCAAAACAATCTTCAAAACTTTCAACAAC  237

Query  236  GGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATT  295
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  238  GGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATT  297
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Query  296  GCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAG  355
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  298  GCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCACCCTCTGGTATTCCAGAG  357

Query  356  GGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATAC  415
            || ||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  358  GGTATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCTTTGGGTTTGGTATTGAGTGATAC  417

Query  416  TCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-GACGCTGAGA-AGTG  473
            |||||||||||||||||||||||||||||| |||||||| |||| |  | ||| | ||||
Sbjct  418  TCTTAGTCGAACTAGGCGTTTGCTTGAAATATATTGGCACGAGTAGT-GTTGA-ACAGTG  475

Query  474  CAT-TCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACAAT-TCTT-GGTTGT  530
              | || | ||  ||||||||||||||||||||||||||||||| |   | || ||| ||
Sbjct  476  T-TGTCTG-AAC-ATCAATGTATTAGGTTTATCCAACTCGTTGA-AGCGT-TTAGGTCGT  530

Query  531  GAAT-TT-TTGGTGTTAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCA  588
             | | || ||  | | ||||||||||||| |||||| |||||||||||||||||||||||
Sbjct  531  -ACTATTCTTCAT-T-AGGCTTTGCCTTATAAAACA-CAAACAAGTTTGACCTCAAATCA  586

Query  589  GGTAGGATTACCCGCTGAACTTAAGCATATCAA  621
            |||||||||||||||||||||||||||||||||
Sbjct  587  GGTAGGATTACCCGCTGAACTTAAGCATATCAA  619


>gb|EU149791.1| Debaryomyces hansenii strain CBS 10751 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=624

 Score =  791 bits (428),  Expect = 0.0
 Identities = 573/637 (89%), Gaps = 33/637 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  61   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  118

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  119  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  176

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  177  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  235

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  295

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  355

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  356  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  414

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
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            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  415  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  473

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  474  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  528

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  529  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  587

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATA  617
            |||||||||||||||||||||||||||||||||||||
Sbjct  588  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATA  624


>gb|EF193068.1| Debaryomyces hansenii voucher MCCC2E00280 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=645

 Score =  791 bits (428),  Expect = 0.0
 Identities = 573/637 (89%), Gaps = 33/637 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  18   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  77

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  78   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  135

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  136  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  193

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  194  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  252

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  253  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  312

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  313  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  372

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  373  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  431

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  432  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  490

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  491  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  545

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
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Sbjct  546  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  604

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATA  617
            |||||||||||||||||||||||||||||||||||||
Sbjct  605  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATA  641


>gb|DQ668354.1| Debaryomyces hansenii isolate Sy-8 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=633

 Score =  789 bits (427),  Expect = 0.0
 Identities = 572/636 (89%), Gaps = 33/636 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  9    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  68

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  69   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  126

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  127  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  184

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  185  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  243

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  244  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  303

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  304  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  363

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  364  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  422

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  423  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  481

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  482  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  536

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  537  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  595

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCAT  616
            ||||||||||||||||||||||||||||||||||||
Sbjct  596  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCAT  631


>gb|AY964676.1| Candida sinolaborantium strain BG04-2-20-1-1-C1 18S ribosomal
RNA gene, partial sequence; internal transcribed spacer 1,
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5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence; and 26S ribosomal RNA gene, partial sequence
Length=604

 Score =  789 bits (427),  Expect = 0.0
 Identities = 566/626 (90%), Gaps = 37/626 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCT-TTTGCCAGCGCTTAATTGCG  61

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTAGAAACTATTGCTTTGGCTTGG  119
            ||||||  |||||||||||||||||||||| | || ||  |||| |||||||||||||||
Sbjct  62   CGGCGA-AAAACCTTACACACAATGTTTTT-TGTT-TT--AAACCATTGCTTTGGCTTGG  116

Query  120  -CTAAGAAATTA-GTCGGGCCAGAGGTTTAC-AC-AAACTTCAATTTTTAATTGAATTGT  175
             || ||||| || || ||| ||||||||||| || |||||||||||||| ||||||||||
Sbjct  117  CCT-AGAAA-TAGGTTGGGTCAGAGGTTTACAACTAAACTTCAATTTTT-ATTGAATTGT  173

Query  176  TATTT-AA-TACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACA  233
            | ||| || || ||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  174  T-TTTAAATTA-TTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACA  230

Query  234  ACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAA  293
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  231  ACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAA  290

Query  294  TTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAG  353
            |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  291  TTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAA  350

Query  354  AGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGAT  413
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  351  AGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCTTTGGGTTTGGTATTGAGTGAT  410

Query  414  ACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTG-ACGCTGAGA-AG  471
            ||||||||||| |||||||||||||||||||  |||||||||||||| ||  || || ||
Sbjct  411  ACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATTGGCATGAGTGTAC--TG-GATAG  467

Query  472  TGCATTCAGGAAATAT-CAATGTATTAGGTTTATCCAACTCGTTGACA--ATTCTTGGTT  528
            | | ||| | |  ||| ||||||||||||||||||||||||||||| |  || |  |||
Sbjct  468  TACGTTCTG-AT-TATTCAATGTATTAGGTTTATCCAACTCGTTGA-AGGAT-CA-GGT-  521

Query  529  GTGAATTTTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATC  587
            || ||||| |||||| | ||||  |||||| ||  ||||||||||||| |||||||||||
Sbjct  522  GTAAATTTCTGGTGTATTGGCTCGGCCTTACAA--CAACAAACAAGTT-GACCTCAAATC  578

Query  588  AGGTAGGATTACCCGCTGAACTTAAG  613
            ||||||||||||||||||||||||||
Sbjct  579  AGGTAGGATTACCCGCTGAACTTAAG  604


>gb|AY964675.1| Candida sinolaborantium strain BG04-2-20-1-1-1 18S ribosomal
RNA gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 26S ribosomal RNA gene, partial sequence
Length=604

 Score =  789 bits (427),  Expect = 0.0
 Identities = 566/626 (90%), Gaps = 37/626 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
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            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCT-TTTGCCAGCGCTTAATTGCG  61

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTAGAAACTATTGCTTTGGCTTGG  119
            ||||||  |||||||||||||||||||||| | || ||  |||| |||||||||||||||
Sbjct  62   CGGCGA-AAAACCTTACACACAATGTTTTT-TGTT-TT--AAACCATTGCTTTGGCTTGG  116

Query  120  -CTAAGAAATTA-GTCGGGCCAGAGGTTTAC-AC-AAACTTCAATTTTTAATTGAATTGT  175
             || ||||| || || ||| ||||||||||| || |||||||||||||| ||||||||||
Sbjct  117  CCT-AGAAA-TAGGTTGGGTCAGAGGTTTACAACTAAACTTCAATTTTT-ATTGAATTGT  173

Query  176  TATTT-AA-TACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACA  233
            | ||| || || ||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  174  T-TTTAAATTA-TTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACA  230

Query  234  ACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAA  293
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  231  ACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAA  290

Query  294  TTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAG  353
            |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  291  TTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAA  350

Query  354  AGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGAT  413
            |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  351  AGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCTTTGGGTTTGGTATTGAGTGAT  410

Query  414  ACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTG-ACGCTGAGA-AG  471
            ||||||||||| |||||||||||||||||||  |||||||||||||| ||  || || ||
Sbjct  411  ACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATTGGCATGAGTGTAC--TG-GATAG  467

Query  472  TGCATTCAGGAAATAT-CAATGTATTAGGTTTATCCAACTCGTTGACA--ATTCTTGGTT  528
            | | ||| | |  ||| ||||||||||||||||||||||||||||| |  || |  |||
Sbjct  468  TACGTTCTG-AT-TATTCAATGTATTAGGTTTATCCAACTCGTTGA-AGGAT-CA-GGT-  521

Query  529  GTGAATTTTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATC  587
            || ||||| |||||| | ||||  |||||| ||  ||||||||||||| |||||||||||
Sbjct  522  GTAAATTTCTGGTGTATTGGCTCGGCCTTACAA--CAACAAACAAGTT-GACCTCAAATC  578

Query  588  AGGTAGGATTACCCGCTGAACTTAAG  613
            ||||||||||||||||||||||||||
Sbjct  579  AGGTAGGATTACCCGCTGAACTTAAG  604


>gb|AY964674.1| Candida sinolaborantium strain CBS 9940 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 26S ribosomal RNA gene, partial sequence
Length=604

 Score =  789 bits (427),  Expect = 0.0
 Identities = 566/626 (90%), Gaps = 37/626 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCT-TTTGCCAGCGCTTAATTGCG  61

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTAGAAACTATTGCTTTGGCTTGG  119
            ||||||  |||||||||||||||||||||| | || ||  |||| |||||||||||||||
Sbjct  62   CGGCGA-AAAACCTTACACACAATGTTTTT-TGTT-TT--AAACCATTGCTTTGGCTTGG  116

Query  120  -CTAAGAAATTA-GTCGGGCCAGAGGTTTAC-AC-AAACTTCAATTTTTAATTGAATTGT  175
             || ||||| || || ||| ||||||||||| || |||||||||||||| ||||||||||
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Sbjct  117  CCT-AGAAA-TAGGTTGGGTCAGAGGTTTACAACTAAACTTCAATTTTT-ATTGAATTGT  173

Query  176  TATTT-AA-TACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACA  233
            | ||| || || ||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  174  T-TTTAAATTA-TTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACA  230

Query  234  ACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAA  293
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  231  ACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAA  290

Query  294  TTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAG  353
            |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  291  TTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAA  350

Query  354  AGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGAT  413
            |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  351  AGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGAT  410

Query  414  ACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTG-ACGCTGAGA-AG  471
            ||||||||||| |||||||||||||||||||  |||||||||||||| ||  || || ||
Sbjct  411  ACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATTGGCATGAGTGTAC--TG-GATAG  467

Query  472  TGCATTCAGGAAATAT-CAATGTATTAGGTTTATCCAACTCGTTGACA--ATTCTTGGTT  528
            | | ||| | |  ||| ||||||||||||||||||||||||||||| |  || |  |||
Sbjct  468  TACGTTCTG-AT-TATTCAATGTATTAGGTTTATCCAACTCGTTGA-AGGAT-CA-GGT-  521

Query  529  GTGAATTTTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATC  587
            || ||||| |||||| | ||||  |||||| ||  ||||||||||||| |||||||||||
Sbjct  522  GTAAATTTCTGGTGTATTGGCTCGGCCTTACAA--CAACAAACAAGTT-GACCTCAAATC  578

Query  588  AGGTAGGATTACCCGCTGAACTTAAG  613
            ||||||||||||||||||||||||||
Sbjct  579  AGGTAGGATTACCCGCTGAACTTAAG  604


>gb|AY964679.1| Candida temnochilae strain CBS 9939 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 26S ribosomal RNA gene, partial sequence
Length=602

 Score =  787 bits (426),  Expect = 0.0
 Identities = 562/622 (90%), Gaps = 31/622 (4%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||| ||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCT-TTTGCCAGCGCTTAACTGCG  61

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTAGAAACTATTGCTTTGGCTTGG  119
            ||||||  |||||||||||||| ||||||| | || ||| |||| |||||||||||||||
Sbjct  62   CGGCGA-AAAACCTTACACACAGTGTTTTT-TGTT-TTA-AAACCATTGCTTTGGCTTGG  117

Query  120  CTAAGAAATTA-GTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTAT  178
            || ||||| || || |||||| ||||||||  ||||||||| |||| ||||||||||| |
Sbjct  118  CTTAGAAA-TAGGTTGGGCCAAAGGTTTAC-TAAACTTCAA-TTTT-ATTGAATTGTT-T  172

Query  179  TT-AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGG  237
            || ||||  |||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  173  TTAAATA-ATTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGG  230

Query  238  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  231  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  290
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Query  298  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCT-GGTATTCCAGAGG  356
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||| ||
Sbjct  291  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCC-CTTGGTATTCCAGGGG  349

Query  357  GCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTGGTATTGAGTGATACT  416
            ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  350  GCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCTTTGGGTTTGGTATTGAGTGATACT  409

Query  417  CTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGCA  475
            ||||||||||||||||||||||||||||  ||||||||||||||  |||| || ||| |
Sbjct  410  CTTAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCATGAGTGT-GCTG-GATAGTACG  467

Query  476  TTCAGGAAATAT-CAATGTATTAGGTTTATCCAACTCGTTGA-CAATTCTTGGTTGTGAA  533
            ||| | |  ||| ||||||||||||||||||||||||||||| |  | |  ||| || ||
Sbjct  468  TTCTG-AT-TATTCAATGTATTAGGTTTATCCAACTCGTTGAACGGT-CA-GGT-GTAAA  522

Query  534  TTTTTGGT-GT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGT  591
            ||| |||| || | ||||  |||||| ||  |||||||||||||||||||||||||||||
Sbjct  523  TTTCTGGTAGTATTGGCTCGGCCTTATAA--CAACAAACAAGTTTGACCTCAAATCAGGT  580

Query  592  AGGATTACCCGCTGAACTTAAG  613
            ||||||||||||||||||||||
Sbjct  581  AGGATTACCCGCTGAACTTAAG  602


>gb|AY964678.1| Candida temnochilae strain CBS 9938 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 26S ribosomal RNA gene, partial sequence
Length=602

 Score =  787 bits (426),  Expect = 0.0
 Identities = 563/623 (90%), Gaps = 33/623 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCT-TTTGCCAGCGCTTAATTGCG  61

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTAGAAACTATTGCTTTGGCTTGG  119
            ||||||  |||||||||||||| ||||||| | || ||| ||||||||||||||||||||
Sbjct  62   CGGCGA-AAAACCTTACACACAGTGTTTTT-TGTT-TTA-AAACTATTGCTTTGGCTTGG  117

Query  120  CTAAGAAATTA-GTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTAT  178
            || ||||| || || |||||| |||||||| |||||||||| |||| ||||||||||| |
Sbjct  118  CTTAGAAA-TAGGTTGGGCCAAAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTT-T  172

Query  179  TT-AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGG  237
            || |||  ||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  173  TTAAAT-GTTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGG  230

Query  238  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  231  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  290

Query  298  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCT-GGTATTCCAGAGG  356
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||| ||
Sbjct  291  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCC-CTTGGTATTCCAGGGG  349

Query  357  GCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-CTTGGGTTTGGTATTGAGTGATAC  415
            ||||||||||||||||||||||||||||||||||| |  |||||||||||||||||||||
Sbjct  350  GCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCTCA-GGGTTTGGTATTGAGTGATAC  408
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Query  416  TCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGC  474
            ||||||||| |||||||||||||||||||  ||||||||||||||  |||| || ||| |
Sbjct  409  TCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATTGGCATGAGTGT-GCTG-GATAGTAC  466

Query  475  ATTCAGGAAATAT-CAATGTATTAGGTTTATCCAACTCGTTGA-CAATTCTTGGTTGTGA  532
             ||| | |  ||| ||||||||||||||||||||||||||||| |  | |  ||| || |
Sbjct  467  GTTCTG-AT-TATTCAATGTATTAGGTTTATCCAACTCGTTGAACGGT-CG-GGT-GTAA  521

Query  533  ATTTTTGGT-GT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGG  590
            |||| |||| || | ||||  |||||| ||  ||||||||||||||||||||||||||||
Sbjct  522  ATTTCTGGTAGTATTGGCTCGGCCTTACAA--CAACAAACAAGTTTGACCTCAAATCAGG  579

Query  591  TAGGATTACCCGCTGAACTTAAG  613
            |||||||||||||||||||||||
Sbjct  580  TAGGATTACCCGCTGAACTTAAG  602


>gb|AY964677.1| Candida temnochilae strain BG01-7-25-009A-3-1 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 26S ribosomal RNA gene, partial sequence
Length=602

 Score =  787 bits (426),  Expect = 0.0
 Identities = 563/623 (90%), Gaps = 33/623 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCT-TTTGCCAGCGCTTAATTGCG  61

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTAGAAACTATTGCTTTGGCTTGG  119
            ||||||  |||||||||||||| ||||||| | || ||| ||||||||||||||||||||
Sbjct  62   CGGCGA-AAAACCTTACACACAGTGTTTTT-TGTT-TTA-AAACTATTGCTTTGGCTTGG  117

Query  120  CTAAGAAATTA-GTCGGGCCAGAGGTTTACACAAACTTCAATTTTTAATTGAATTGTTAT  178
            || ||||| || || |||||| |||||||| |||||||||| |||| ||||||||||| |
Sbjct  118  CTTAGAAA-TAGGTTGGGCCAAAGGTTTAC-CAAACTTCAA-TTTT-ATTGAATTGTT-T  172

Query  179  TT-AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGG  237
            || |||  ||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  173  TTAAAT-GTTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAAAACTTTCAACAACGG  230

Query  238  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  231  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  290

Query  298  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCT-GGTATTCCAGAGG  356
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||| ||
Sbjct  291  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCC-CTTGGTATTCCAGGGG  349

Query  357  GCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-CTTGGGTTTGGTATTGAGTGATAC  415
            ||||||||||||||||||||||||||||||||||| |  |||||||||||||||||||||
Sbjct  350  GCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCTCA-GGGTTTGGTATTGAGTGATAC  408

Query  416  TCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGC  474
            ||||||||| |||||||||||||||||||  ||||||||||||||  |||| || ||| |
Sbjct  409  TCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATTGGCATGAGTGT-GCTG-GATAGTAC  466

Query  475  ATTCAGGAAATAT-CAATGTATTAGGTTTATCCAACTCGTTGA-CAATTCTTGGTTGTGA  532
             ||| | |  ||| ||||||||||||||||||||||||||||| |  | |  ||| || |
Sbjct  467  GTTCTG-AT-TATTCAATGTATTAGGTTTATCCAACTCGTTGAACGGT-CG-GGT-GTAA  521

Query  533  ATTTTTGGT-GT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGG  590
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            |||| |||| || | ||||  |||||| ||  ||||||||||||||||||||||||||||
Sbjct  522  ATTTCTGGTAGTATTGGCTCGGCCTTACAA--CAACAAACAAGTTTGACCTCAAATCAGG  579

Query  591  TAGGATTACCCGCTGAACTTAAG  613
            |||||||||||||||||||||||
Sbjct  580  TAGGATTACCCGCTGAACTTAAG  602


>gb|DQ317356.1| Saccharomycetaceae sp. BC41 18S ribosomal RNA gene, partial
sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene,
and internal transcribed spacer 2, complete sequence; and
28S ribosomal RNA gene, partial sequence
Length=652

 Score =  785 bits (425),  Expect = 0.0
 Identities = 570/634 (89%), Gaps = 33/634 (5%)
 Strand=Plus/Plus

Query  19   GAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCGCGGCGATTAAACCTTACA  78
            ||||||||||||| |||||||  |||||||||||||||||||||||||  ||||||||||
Sbjct  1    GAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCGCGGCGAAAAAACCTTACA  60

Query  79   CACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-TGG-CTAAGAAATTAG-T  132
            |||| ||||||| | ||||||  | |||| ||||||||| | ||| || ||||| ||| |
Sbjct  61   CACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TCTGGACT-AGAAA-TAGTT  116

Query  133  CGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTGAATTGTTATTTA-ATACT  186
             |||||||||||||||   || |||||||||| |||| ||||||||||||||||  ||
Sbjct  117  TGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTGAATTGTTATTTATTTA-A  175

Query  187  TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGGATCTCTTGG  246
            |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Sbjct  176  TTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAACGGATCTCTTGG  235

Query  247  TTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCG  306
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  TTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCG  295

Query  307  TGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGT  366
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  TGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGT  355

Query  367  TTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTGAGTGATACTCTTAGTCGA  425
            ||||||||||||||||||||||||| || |||||||||||||||||||||||||||||||
Sbjct  356  TTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTGAGTGATACTCTTAGTCGA  414

Query  426  ACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGC-ATTCAGGAA  483
            |||||||||||||||||||| ||||||||||||||   ||| || ||||| ||  | ||
Sbjct  415  ACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-GATAGTGCTAT--ATGAC  471

Query  484  ATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTTGGTTGTGA-ATTTTT-GG  540
             | |||||||||||||||||||||||||||||| | | | ||  | || | |||| | ||
Sbjct  472  TT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TTAATGGT-ATATTTCTCGG  527

Query  541  TGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAGGTAGGATTA  598
            | ||  |||||  |||||| || | |||||||||||||||||||||||||||||||||||
Sbjct  528  TATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACCTCAAATCAGGTAGGATTA  587

Query  599  CCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||
Sbjct  588  CCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  621
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>gb|EF192225.1| Debaryomyces hansenii 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene, and
internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence
Length=659

 Score =  784 bits (424),  Expect = 0.0
 Identities = 571/636 (89%), Gaps = 33/636 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||| ||||||
Sbjct  33   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTGATTGCG  92

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| | 
Sbjct  93   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  150

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  151  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  208

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  209  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  267

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  268  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  327

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  328  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  387

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  388  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  446

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            |||||||||||||||||||||||||||||||||||||| ||||||||||||||   ||| 
Sbjct  447  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  505

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  506  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  560

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||||||||
Sbjct  561  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACC  619

Query  581  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCAT  616
            ||||||||||||||||||||||||||||||||||||
Sbjct  620  TCAAATCAGGTAGGATTACCCGCTGAACTTAAGCAT  655


>gb|AY845351.1| Candida lignicola 18S ribosomal RNA gene, partial sequence
Length=2337

 Score =  784 bits (424),  Expect = 0.0
 Identities = 547/602 (90%), Gaps = 26/602 (4%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTA--ATTGCCAGCGCTTAATTG  58
             |||||||||||||||||||||||||||||||||| || ||   || ||||||||||||||
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Sbjct  1750  TCCGTAGGTGAACCTGCGGAAGGATCATTACTGT-TT-TAGTTTTACCAGCGCTTAATTG  1807

Query  59    CGCGGCG-ATTAAACCTTACACACAATGTTTTTCTTTATTAGAAACTATTGCTTTGGCTT  117
             ||||| | |  ||| |||||||||| || |||||||||||||||||||||||||||| ||
Sbjct  1808  CGCGGTGAACAAAATCTTACACACAGTG-TTTTCTTTATTAGAAACTATTGCTTTGGTTT  1866

Query  118   GGCTAAGAAATTAGTCGGGCCAGAGGTTTACACAAACTTCAA-TTTTTAATTGAATTG-T  175
             |||| |||||| ||| |||||||||||||  |  |||||||| ||||||||||||||| |
Sbjct  1867  GGCTTAGAAATAAGTTGGGCCAGAGGTTT--A-TAACTTCAATTTTTTAATTGAATTGTT  1923

Query  176   TATTTAATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAAC  235
             |||||| ||  ||||||||||||||||||| |||||| ||||||||||||||||||||||
Sbjct  1924  TATTTATTA-ATTGTCAATTTGTTGATTAATTTCAAA-AATCTTCAAAACTTTCAACAAC  1981

Query  236   GGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATT  295
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1982  GGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATT  2041

Query  296   GCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAG  355
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||
Sbjct  2042  GCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAG  2101

Query  356   GGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTGAGTGATA  414
             |||||||||||||||||||||||||||||||||||| || ||||||||||||||||||||
Sbjct  2102  GGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTGAGTGATA  2160

Query  415   CTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGT-G-ACGCTGAGA-AG  471
             ||||||||||||||||||||||||||||||  |||||||| |||| | ||  | | | ||
Sbjct  2161  CTCTTAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTAGTAC--TAA-ATAG  2217

Query  472   TGCATTCAGGAA-ATAT-CAATGTATTAGGTTTATCCAACTCGTTGACAATTCTTGGTTG  529
             ||| |||||||| || | ||||||||||||||||||||||||||||| | |||||| | |
Sbjct  2218  TGCTTTCAGGAACATTTTCAATGTATTAGGTTTATCCAACTCGTTGAGATTTCTTGCTAG  2277

Query  530   TGAATTTTTGGTGT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCA  588
             |||||||||||| | | |||||||||||| ||||||||||||||||| ||||||||||||
Sbjct  2278  TGAATTTTTGGTATAT-GGCTTTGCCTTACAAAACAACAAACAAGTT-GACCTCAAATCA  2335

Query  589   GG  590
             ||
Sbjct  2336  GG  2337


>gb|EF643593.1| Debaryomyces hansenii strain LN-3 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=671

 Score =  782 bits (423),  Expect = 0.0
 Identities = 576/644 (89%), Gaps = 34/644 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  29   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  88

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  89   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTCTTGCTTTGG-TC  146

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  147  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  204
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Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  205  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  263

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  264  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  323

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  324  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTA  383

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            ||||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  384  TTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  442

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  443  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  502

Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  503  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  556

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  557  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  615

Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATA  623
            |||||||||||||||| |||||||||||||||||||||||||||
Sbjct  616  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATA  659


>gb|EF543259.1| Debaryomyces hansenii strain hcx-1 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=659

 Score =  782 bits (423),  Expect = 0.0
 Identities = 576/644 (89%), Gaps = 34/644 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  29   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  88

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  89   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTCTTGCTTTGG-TC  146

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  147  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  204

Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  205  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  263

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  264  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  323
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Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  324  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTA  383

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            ||||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  384  TTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  442

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  443  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  502

Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  503  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  556

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  557  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  615

Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATA  623
            |||||||||||||||| |||||||||||||||||||||||||||
Sbjct  616  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAATA  659


>gb|EF190234.1| Debaryomyces hansenii strain NA-1 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=672

 Score =  782 bits (423),  Expect = 0.0
 Identities = 584/655 (89%), Gaps = 37/655 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  31   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  90

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  91   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTCTTGCTTTGG-TC  148

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  149  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  206

Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  207  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  265

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  266  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  325

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  326  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTA  385

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            ||||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  386  TTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  444

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
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            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  445  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  504

Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  505  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  558

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  559  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  617

Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGC-GG-AGGA  632
            |||||||||||||||| |||||||||||||||||||||||| ||||| || ||||
Sbjct  618  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCA-TAAGCCGGGAGGA  671


>gb|DQ534410.1| Debaryomyces hansenii strain SWJ-10b 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=629

 Score =  782 bits (423),  Expect = 0.0
 Identities = 576/643 (89%), Gaps = 38/643 (5%)
 Strand=Plus/Plus

Query  10   GAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCGCGGCGATTA  69
            |||||||||||||||||||||| |||||||  |||||||||| ||||||||||||||  |
Sbjct  3    GAACCTGCGGAAGGATCATTACAGTATTCT-TTTGCCAGCGC-TAATTGCGCGGCGA--A  58

Query  70   AACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-TGG-CTAAG  124
            ||||||||||||| ||||||| | ||||||  | |||| ||||||||| | ||| || ||
Sbjct  59   AACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TCTGGACT-AG  115

Query  125  AAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTGAATTGTTAT  178
            ||| ||| | |||||||||||||||   || |||||||||| |||| |||||||||||||
Sbjct  116  AAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTGAATTGTTAT  174

Query  179  TTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTTCAACAACGG  237
            |||  ||  |||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  175  TTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAACGG  233

Query  238  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  297
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  234  ATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGC  293

Query  298  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGG  357
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  294  AGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGG  353

Query  358  CATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTGAGTGATACT  416
            |||||||||||||||||||||||||||||||||| || ||||||||||||||||||||||
Sbjct  354  CATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTGAGTGATACT  412

Query  417  CTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGAGA-AGTGC-  474
            |||||| |||||||||||||||||||||| ||||||||||||||   ||| || |||||
Sbjct  413  CTTAGTTGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-GATAGTGCT  471

Query  475  ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTTGGTTGTGA-  532
            ||  | ||  | |||||||||||||||||||||||||||||| | | | ||  | || |
Sbjct  472  AT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TTAATGGT-AT  525

Query  533  ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACCTCAAATCAG  589
            |||| | ||| ||  |||||  |||||| || | ||||||||||||||||||||||||||
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Sbjct  526  ATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACCTCAAATCAG  585

Query  590  GTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            |||||||||||||||||||||||||||||||||| ||||||||
Sbjct  586  GTAGGATTACCCGCTGAACTTAAGCATATCAATA-GCGGAGGA  627


>gb|GQ376085.1| Debaryomyces hansenii var. hansenii isolate UOA/HCPF 10197B 18S
ribosomal RNA gene, partial sequence; internal transcribed
spacer 1, 5.8S ribosomal RNA gene, and internal transcribed
spacer 2, complete sequence; and 28S ribosomal RNA gene, partial
sequence
Length=639

 Score =  780 bits (422),  Expect = 0.0
 Identities = 584/655 (89%), Gaps = 39/655 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  60

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  61   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTTTTGCTTTGG-TC  118

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  119  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTG  176

Query  170  AATTGTTATTTA-ATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTTT  228
            ||||||||||||  ||  |||||||||||||||||||||||||| |||||||||||||||
Sbjct  177  AATTGTTATTTATTTA-ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTT  235

Query  229  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  288
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  236  CAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAAT  295

Query  289  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  348
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  296  ATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTAT  355

Query  349  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATTG  407
            ||||||||||||||||||||||||||||||||||||||||||| || |||||||||||||
Sbjct  356  TCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATTG  414

Query  408  AGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTGA  467
            ||||||||||||||| |||||||||||||||||||||| ||||||||||||||   |||
Sbjct  415  AGTGATACTCTTAGTTGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG-  473

Query  468  GA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCTT  524
            || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | ||
Sbjct  474  GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-TT  528

Query  525  GGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGACC  580
              | || | |||| | ||| ||  |||||  |||||| || | |||||||||||| ||||
Sbjct  529  AATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTT-GACC  586

Query  581  TCAAATCAGGTAGGA-T--TACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||| | ||| |  |||||||||||||||||||||||||||||||||||||
Sbjct  587  TCAAATCAG-T-GGAATACTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  639


>gb|EF197943.1| Debaryomyces hansenii strain HK67-4 18S ribosomal RNA gene, partial
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sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=669

 Score =  780 bits (422),  Expect = 0.0
 Identities = 583/654 (89%), Gaps = 37/654 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  28   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  87

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  88   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTCTTGCTTTGG-TC  145

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  146  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  203

Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  204  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  262

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  263  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  322

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  323  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTA  382

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            ||||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  383  TTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  441

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  442  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  501

Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  502  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  555

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  556  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  614

Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAG-C-GGAGG  631
            |||||||||||||||| ||||||||||||||||||||||||| ||| | |||||
Sbjct  615  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAA-AAGGCCGGAGG  667


>gb|EF190231.1| Debaryomyces hansenii strain wwl-2 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=672

 Score =  778 bits (421),  Expect = 0.0
 Identities = 574/642 (89%), Gaps = 34/642 (5%)
 Strand=Plus/Plus
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Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  30   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  89

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  90   CGGCGAAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTCTTGCTTTGG-TC  147

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  148  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  205

Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  206  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  264

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  265  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  324

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  325  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTA  384

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            ||||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  385  TTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  443

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  444  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  503

Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  504  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  557

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  558  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  616

Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAA  621
            |||||||||||||||| |||||||||||||||||||||||||
Sbjct  617  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAA  658


>gb|EF192227.1| Debaryomyces hansenii strain w-14-1 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=642

 Score =  778 bits (421),  Expect = 0.0
 Identities = 574/642 (89%), Gaps = 34/642 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  12   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  71

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  72   CGGCGAAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTCTTGCTTTGG-TC  129

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
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            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  130  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  187

Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  188  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  246

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  247  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  306

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  307  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTA  366

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            ||||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  367  TTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  425

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  426  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  485

Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  486  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  539

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  540  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  598

Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAA  621
            |||||||||||||||| |||||||||||||||||||||||||
Sbjct  599  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCAA  640


>gb|FJ153162.1| Candida sp. SG6L02 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene, and
internal transcribed spacer 2, complete sequence; and 28S ribosomal
RNA gene, partial sequence
Length=579

 Score =  776 bits (420),  Expect = 0.0
 Identities = 542/596 (90%), Gaps = 28/596 (4%)
 Strand=Plus/Plus

Query  48   GCGCTTAATTGCGCGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTAGAAACTAT  106
            |||||||||||||||||||  |||||||||||||| ||||||| | || ||| |||| ||
Sbjct  1    GCGCTTAATTGCGCGGCGA-AAAACCTTACACACAGTGTTTTT-TGTT-TTACAAACCAT  57

Query  107  TGCTTTGGCTTGGCTAAGAAATTA-GTCGGGCCAGAGGTTTACAC-AAACTTCAAT-TTT  163
            ||||||||||||||| ||||| || || |||||| |||||||||| |||||||||| |||
Sbjct  58   TGCTTTGGCTTGGCTTAGAAA-TAGGTTGGGCCAAAGGTTTACACTAAACTTCAATATTT  116

Query  164  TAATTGAATTGTTATTT-AATACTTTGTCAATTTGTTGATTAAATTCAAACAATCTTCAA  222
            | ||||||||||| ||| |||| ||||||||||||||||||||||||||| |||||||||
Sbjct  117  T-ATTGAATTGTT-TTTAAATATTTTGTCAATTTGTTGATTAAATTCAAA-AATCTTCAA  173

Query  223  AACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATA  282
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  174  AACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATA  233

Query  283  AGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTC  342
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
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Sbjct  234  AGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCC-C  292

Query  343  T-GGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTG  401
            | |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  293  TTGGTATTCCAGGGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTTGGGTTTG  352

Query  402  GTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGA  461
            ||||||||||||||||||||||| |||||||||||||||||||  ||||||||||||||
Sbjct  353  GTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATTGGCATGAGTGT  412

Query  462  CGCTGAGA-AGTGCATTCAGGAAATAT-CAATGTATTAGGTTTATCCAACTCGTTGA-CA  518
             |||| || ||| | ||| | |  ||| ||||||||||||||||||||||||||||| |
Sbjct  413  -GCTG-GATAGTACGTTCTG-AT-TATTCAATGTATTAGGTTTATCCAACTCGTTGAACG  468

Query  519  ATTCTTGGTTGTGAATTTTTGGT-GT-TAGGCTTTGCCTTAAAAAACAACAAACAAGTTT  576
             | |  ||| || ||||| |||| || | ||||  |||||| ||  ||||||||||||||
Sbjct  469  GT-CA-GGT-GTAAATTTCTGGTAGTATTGGCTCGGCCTTACAA--CAACAAACAAGTTT  523

Query  577  GACCTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  632
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  524  GACCTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  579


>gb|EF197950.1| Debaryomyces hansenii strain HK32-1 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=660

 Score =  776 bits (420),  Expect = 0.0
 Identities = 573/641 (89%), Gaps = 34/641 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  31   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  90

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  91   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTCTTGCTTTGG-TC  148

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  149  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  206

Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  207  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  265

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  266  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  325

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  326  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTA  385

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            ||||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  386  TTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  444

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  445  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  504
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Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  505  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  558

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  559  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  617

Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCA  620
            |||||||||||||||| ||||||||||||||||||||||||
Sbjct  618  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCA  658


>gb|EF197946.1| Debaryomyces hansenii strain HK67-5 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=653

 Score =  776 bits (420),  Expect = 0.0
 Identities = 573/641 (89%), Gaps = 34/641 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  13   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  72

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  73   CGGCGAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTCTTGCTTTGG-TC  130

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  131  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  188

Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  189  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  247

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  307

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  308  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTA  367

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            ||||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  368  TTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  426

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  427  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  486

Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  487  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  540

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  541  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  599
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Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCA  620
            |||||||||||||||| ||||||||||||||||||||||||
Sbjct  600  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCA  640


>gb|EF197944.1| Debaryomyces hansenii strain WC56-1 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=657

 Score =  776 bits (420),  Expect = 0.0
 Identities = 573/641 (89%), Gaps = 34/641 (5%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACTGTATTCTAATTGCCAGCGCTTAATTGCG  60
            ||||||||||||||||||||||||||||||| |||||||  |||||||||||||||||||
Sbjct  28   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCG  87

Query  61   CGGCGATTAAACCTTACACACAATGTTTTTCT-TTATTA-GA-AACTATTGCTTTGGCT-  116
            ||||||  |||||||||||||| ||||||| | ||||||  | |||| ||||||||| |
Sbjct  88   CGGCGAAAAAAACCTTACACACAGTGTTTTT-TGTTATTACAAGAACTCTTGCTTTGG-TC  145

Query  117  TGG-CTAAGAAATTAG-TCGGGCCAGAGGTTTAC---AC-AAACTTCAATTTTTA-ATTG  169
            ||| || ||||| ||| | |||||||||||||||   || |||||||||| |||| ||||
Sbjct  146  TGGACT-AGAAA-TAGTTTGGGCCAGAGGTTTACTAAACTAAACTTCAATATTTATATTG  203

Query  170  AATTGTTATTTAATACT--TTGTCAATTTGTTGATTAAATTCAAACAATCTTCAAAACTT  227
            ||||||||||| ||  |  |||||||||||||||||||||||||| ||||||||||||||
Sbjct  204  AATTGTTATTT-ATTTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTT  262

Query  228  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  287
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  263  TCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAA  322

Query  288  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTA  347
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  323  TATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTA  382

Query  348  TTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTT-GGGTTTGGTATT  406
            ||||| |||||||||||||||||||||||||||||||||||||| || ||||||||||||
Sbjct  383  TTCCAAAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACC-TTCGGGTTTGGTATT  441

Query  407  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATTTATTGGCATGAGTGACGCTG  466
            ||||||||||||||||||||||||||||||||||||||| ||||||||||||||   |||
Sbjct  442  GAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTG  501

Query  467  AGA-AGTGC-ATTCAGGAAATATCAATGTATTAGGTTTATCCAACTCGTTGACA-ATTCT  523
             || ||||| ||  | ||  | |||||||||||||||||||||||||||||| | | | |
Sbjct  502  -GATAGTGCTAT--ATGACTT-TCAATGTATTAGGTTTATCCAACTCGTTGA-ATAGT-T  555

Query  524  TGGTTGTGA-ATTTTT-GGTGTT--AGGCTTTGCCTTAAAAAACAACAAACAAGTTTGAC  579
            |  | || | |||| | ||| ||  |||||  |||||| || | ||||||||||||||||
Sbjct  556  TAATGGT-ATATTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGAC  614

Query  580  CTCAAATCAGGTAGGATTACCCGCTGAACTTAAGCATATCA  620
            |||||||||||||||| ||||||||||||||||||||||||
Sbjct  615  CTCAAATCAGGTAGGACTACCCGCTGAACTTAAGCATATCA  655



  Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
    Posted date:  Jun 26, 2010  5:44 PM
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  Number of letters in database: 1,817,769,445
  Number of sequences in database:  12,090,198

Lambda     K      H
    1.33    0.621     1.12
Gapped
Lambda     K      H
    1.28    0.460    0.850
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 12090198
Number of Hits to DB: 2155225
Number of extensions: 11315
Number of successful extensions: 11315
Number of sequences better than 10: 8423
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 11065
Number of HSP's successfully gapped: 11064
Length of query: 632
Length of database: 31882540517
Length adjustment: 32
Effective length of query: 600
Effective length of database: 31495654181
Effective search space: 18897392508600
Effective search space used: 18897392508600
A: 0
X1: 14 (26.9 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 14 (27.0 bits)
S2: 22 (41.7 bits)
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BLASTN 2.2.23+
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and
Webb Miller (2000), "A greedy algorithm for aligning DNA
sequences", J Comput Biol 2000; 7(1-2):203-14.


RID: 2DEPU2RJ016


Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
           12,090,198 sequences; 31,882,540,517 total letters
Query= gi|259018353|gb|GQ458041.1| Debaryomyces hansenii strain ATCC 60978
18S ribosomal RNA gene, partial sequence; internal transcribed spacer
1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,
complete sequence; and 28S ribosomal RNA gene, partial sequence
Length=2961


                                                                   Score     E
Sequences producing significant alignments:                       (Bits)  Value

gb|GQ458041.1|  Debaryomyces hansenii strain ATCC 60978 18S ri...  5465    0.0
gb|GQ458025.1|  Debaryomyces hansenii strain MA09-AK 18S ribos...  5446    0.0
gb|GQ458019.1|  Debaryomyces hansenii strain MA09-J 18S riboso...  5421    0.0
gb|CP000497.1|  Pichia stipitis CBS 6054 chromosome 3, complet...  4776    0.0
dbj|AB285026.1|  Candida sp. BCMU BX03 genes for 18S rRNA, ITS...  4119    0.0
gb|AY845351.1|  Candida lignicola 18S ribosomal RNA gene, part...  3419    0.0
dbj|AB013590.1|  Debaryomyces hansenii var. hansenii 18S rRNA ...  3230    0.0
dbj|AB013568.1|  Debaryomyces hansenii var. hansenii 18S rRNA ...  3230    0.0
dbj|AB013567.1|  Debaryomyces hansenii var. fabryi 18S rRNA ge...  3225    0.0
emb|X58053.1|  D.hansenii gene for 18S ribosomal RNA               3217    0.0
dbj|AB013587.1|  Pichia guilliermondii 18S rRNA gene, strain J...  3203    0.0
dbj|AB013566.1|  Candida fukuyamaensis 18S rRNA gene, strain J...  3203    0.0
dbj|AB013517.1|  Candida xestobii 18S rRNA gene, strain JCM 95...  3203    0.0
dbj|AB013528.1|  Candida psychrophila 18S rRNA gene, strain JC...  3201    0.0
emb|X62649.1|  D.hansenii 17S rDNA                                 3192    0.0
dbj|AB070854.1|  Debaryomyces hansenii gene for 18S rRNA, part...  3188    0.0
dbj|AB106349.1|  Debaryomyces hansenii var. hansenii gene for ...  3188    0.0
dbj|AB013525.1|  Candida fermenticarens 18S rRNA gene, strain ...  3186    0.0
gb|AY520288.1|  Candida sp. BG02-6-6-2-1 18S ribosomal RNA gen...  3182    0.0
gb|AY518523.1|  Candida athensensis strain BG02-7-13-014-3-1 1...  3181    0.0
dbj|AB013513.1|  Pichia farinosa 18S rRNA gene, strain JCM 889...  3177    0.0
dbj|AB022440.1|  Debaryomyces sp. MBIC4210 gene for 18S rRNA, ...  3171    0.0
gb|AY518520.1|  Candida smithsonii strain BG02-7-13-007B-1-2 1...  3168    0.0
gb|AY242150.1|  Candida sp. BG99-8-11-1-4-1 18S ribosomal RNA ...  3164    0.0
gb|AY518522.1|  Candida athensensis strain BG02-5-23-003I-4 18...  3162    0.0
dbj|AB013546.1|  Candida laureliae 18S rRNA gene, strain JCM 8...  3162    0.0
emb|X83821.1|  Debaryomyces udenii 18S rRNA gene (NCYC 2394)       3162    0.0
gb|EF194890.1|  Pichia guilliermondii strain HJM 18S ribosomal...  3157    0.0
gb|DQ534400.1|  Debaryomyces hansenii strain WHCX-1 18S riboso...  3157    0.0
dbj|AB054277.1|  Debaryomyces prosopidis gene for 18S rRNA, pa...  3157    0.0
dbj|AB054269.1|  Debaryomyces hansenii var. fabryi gene for 18...  3157    0.0
dbj|AB013555.1|  Candida krissii 18S rRNA gene, strain JCM 945...  3157    0.0
dbj|AB013553.1|  Candida ralunensis 18S rRNA gene, strain JCM ...  3157    0.0
dbj|AB013537.1|  Candida schatavii 18S rRNA gene, strain JCM 1...  3157    0.0
dbj|AB013532.1|  Candida boleticola 18S rRNA gene, strain JCM ...  3157    0.0
dbj|AB013509.1|  Candida zeylanoides 18S rRNA gene, strain JCM...  3157    0.0
gb|DQ534402.1|  Debaryomyces hansenii strain hcx-1 18S ribosom...  3153    0.0
dbj|AB054261.1|  Debaryomyces maramus gene for 18S rRNA, parti...  3153    0.0
gb|AF440017.1|  Debaryomyces mycophilus 18S ribosomal RNA gene...  3151    0.0
dbj|AB054272.1|  Debaryomyces coudertii gene for 18S rRNA, par...  3151    0.0
dbj|AB013562.1|  Candida beechii 18S rRNA gene, strain JCM 180...  3151    0.0
dbj|AB054270.1|  Debaryomyces hansenii var. hansenii gene for ...  3147    0.0
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gb|AY520262.1|  Candida sp. BG02-7-14-001H-1-1 18S ribosomal R...  3145    0.0
dbj|AB054271.1|  Debaryomyces nepalensis gene for 18S rRNA, pa...  3142    0.0
gb|AY553853.1|  Candida fermentati strain NRRL Y-17903 18S rib...  3142    0.0
gb|EF428134.1|  Debaryomyces hansenii strain shiziwei2 18S rib...  3140    0.0
dbj|AB013581.1|  Candida santamariae var. membranifaciens 18S ...  3140    0.0
dbj|AB013536.1|  Candida santamariae var. santamariae 18S rRNA...  3138    0.0
dbj|AB013534.1|  Candida oleophila 18S rRNA gene, strain JCM 1...  3138    0.0
emb|FN690502.1|  Uncultured fungus partial 18S rRNA gene, clon...  3136    0.0
dbj|AB054259.1|  Debaryomyces robertsiae gene for 18S rRNA, pa...  3136    0.0
dbj|AB070856.1|  Marine yeast Y5318 gene for 18S rRNA, partial...  3136    0.0
dbj|AB106351.1|  Debaryomyces hansenii gene for 18S rRNA, part...  3136    0.0
emb|AJ508273.1|  Debaryomyces hansenii partial 18S rRNA gene, ...  3134    0.0
dbj|AB054268.1|  Debaryomyces udenii gene for 18S rRNA, partia...  3133    0.0
emb|X83819.1|  Debaryomyces castellii 18S rRNA gene (NCYC 604)     3133    0.0
dbj|AB054266.1|  Debaryomyces yamadae gene for 18S rRNA, parti...  3131    0.0
gb|AY520192.1|  Candida sp. BG02-7-14-001I-1-1 18S ribosomal R...  3131    0.0
dbj|AB054274.1|  Debaryomyces vanrijiae gene for 18S rRNA, par...  3127    0.0
dbj|AB105434.1|  Pichia guilliermondii gene for 18S rRNA, part...  3127    0.0
gb|AY520212.1|  Candida sp. BG02-6-15-010A-3 18S ribosomal RNA...  3125    0.0
dbj|AB013542.1|  Candida sophiae-reginae 18S rRNA gene, strain...  3123    0.0
dbj|AB013535.1|  Candida multigemmis 18S rRNA gene, strain JCM...  3120    0.0
dbj|AB013519.1|  Candida glucosophila 18S rRNA gene, strain JC...  3120    0.0
dbj|AB054267.1|  Debaryomyces vanrijiae var. yarrowii gene for...  3118    0.0
gb|AY242152.1|  Candida athensensis strain BG99-8-11-1-C1 18S ...  3118    0.0
dbj|AB013579.1|  Candida quercitrusa 18S rRNA gene, strain JCM...  3118    0.0
dbj|AB013541.1|  Candida natalensis 18S rRNA gene, strain JCM ...  3118    0.0
gb|DQ534404.1|  Debaryomyces hansenii strain JHSa 18S ribosoma...  3114    0.0
gb|AY520250.1|  Candida sp. BG02-5-27-4-5-1 18S ribosomal RNA ...  3114    0.0
dbj|AB054263.1|  Debaryomyces occidentalis var. persoonii gene...  3112    0.0
dbj|AB054276.1|  Debaryomyces castellii gene for 18S rRNA, par...  3109    0.0
gb|AY520269.1|  Candida sp. BG02-5-27-4-2-1 18S ribosomal RNA ...  3109    0.0
gb|AY520264.1|  Candida sp. BG02-7-18-022A-1-1 18S ribosomal R...  3109    0.0
gb|EF532297.1|  Pichia guilliermondii strain gao1zhong2 18S ri...  3107    0.0
gb|EF061756.1|  Debaryomyces hansenii strain G7a1 18S ribosoma...  3107    0.0
gb|DQ534403.1|  Pichia guilliermondii strain JHSd 18S ribosoma...  3105    0.0
dbj|AB054282.1|  Pichia guilliermondii gene for 18S rRNA, part...  3105    0.0
dbj|AB000950.1|  Taphrina farlowii gene for 18S rRNA, complete...  3105    0.0
gb|EU784644.1|  Pichia guilliermondii strain CXF-1 18S ribosom...  3103    0.0
dbj|AB013573.1|  Candida fragi 18S rRNA gene, strain JCM 1791,...  3101    0.0
emb|FN690501.1|  Uncultured fungus partial 18S rRNA gene, clon...  3097    0.0
dbj|AB054275.1|  Debaryomyces polymorphus gene for 18S rRNA, p...  3097    0.0
dbj|AB054273.1|  Debaryomyces pseudopolymorphus gene for 18S r...  3097    0.0
dbj|AB054265.1|  Debaryomyces polymorphus var. africanus gene ...  3097    0.0
gb|AY520271.1|  Candida sp. BG02-5-27-1-2-C 18S ribosomal RNA ...  3097    0.0
dbj|AB054262.1|  Debaryomyces occidentalis gene for 18S rRNA, ...  3096    0.0
gb|GU570441.1|  Candida sp. NN-2010a 18S ribosomal RNA gene, p...  3092    0.0
emb|AJ508276.1|  Pichia caribbica partial 18S rRNA gene, strai...  3092    0.0
gb|AY227715.1|  Candida xestobii strain ATCC 24001 18S ribosom...  3090    0.0
gb|AY242159.1|  Candida sp. BG01-7-21-003B-1-1 18S ribosomal R...  3090    0.0
dbj|AB054258.1|  Debaryomyces etchellsii gene for 18S rRNA, pa...  3086    0.0
gb|AY227020.1|  Pichia guilliermondii strain CCO 8 18S ribosom...  3086    0.0
gb|AY520226.1|  Candida sp. BG02-5-23-003D-5 18S ribosomal RNA...  3086    0.0
emb|AJ508269.1|  Pichia caribbica partial 18S rRNA gene, strai...  3086    0.0
gb|AY242197.1|  Candida sp. BG01-7-21-009A-1-1 18S ribosomal R...  3083    0.0
emb|AJ508270.1|  Candida carpophila partial 18S rRNA gene, str...  3083    0.0
emb|AM261069.1|  Debaryomyces sp. MTCC 7061 18S rRNA gene, str...  3079    0.0
gb|DQ499512.1|  Candida sp. ny4e 18S ribosomal RNA gene, parti...  3077    0.0
gb|DQ438179.1|  Candida sp. N12C 18S ribosomal RNA gene, parti...  3077    0.0

ALIGNMENTS
>gb|GQ458041.1| Debaryomyces hansenii strain ATCC 60978 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
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Length=2961

 Score = 5465 bits (2959),  Expect = 0.0
 Identities = 2961/2961 (100%), Gaps = 0/2961 (0%)
 Strand=Plus/Plus

Query  1     TCGCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAA  60
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Sbjct  1     TCGCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAA  60

Query  61    TCAGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGC  120
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Sbjct  61    TCAGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGC  120

Query  121   TAATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAA  180
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Sbjct  121   TAATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAA  180

Query  181   TGCTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTG  240
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Sbjct  181   TGCTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTG  240

Query  241   GCGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCA  300
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Sbjct  241   GCGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCA  300

Query  301   TGGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGG  360
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Sbjct  301   TGGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGG  360

Query  361   CTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTA  420
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Sbjct  361   CTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTA  420

Query  421   GTGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGT  480
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Sbjct  421   GTGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGT  480

Query  481   AAATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  540
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Sbjct  481   AAATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  540

Query  541   AGCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGC  600
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Sbjct  541   AGCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGC  600

Query  601   TTGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGC  660
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Sbjct  601   TTGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGC  660

Query  661   TAACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGT  720
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Sbjct  661   TAACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGT  720

Query  721   GTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGG  780
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Sbjct  721   GTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGG  780

Query  781   TTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCA  840
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Sbjct  781   TTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCA  840

Query  841   GTATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCA  900
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Sbjct  841    GTATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCA  900

Query  901    TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
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Sbjct  901    TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960

Query  961    ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
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Sbjct  961    ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1020

Query  1021   ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1021   ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080

Query  1081   AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
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Sbjct  1081   AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140

Query  1141   TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
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Sbjct  1141   TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200

Query  1201   GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1201   GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260

Query  1261   TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1261   TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320

Query  1321   CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
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Sbjct  1321   CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380

Query  1381   AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
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Sbjct  1381   AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440

Query  1441   ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
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Sbjct  1441   ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500

Query  1501   ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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Sbjct  1501   ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560

Query  1561   TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
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Sbjct  1561   TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620

Query  1621   GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
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Sbjct  1621   GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680

Query  1681   GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
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Sbjct  1681   GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740

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Sbjct  1741   CCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCGCGGCGAAAAAAC  1800

Query  1801   CTTACACACAGTGTTTTTTGTTATTACAAGAACTTTTGCTTTGGTCTGGACTAGAAATAG  1860
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Sbjct  1801  CTTACACACAGTGTTTTTTGTTATTACAAGAACTTTTGCTTTGGTCTGGACTAGAAATAG  1860

Query  1861  TTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTGAATTGTTATTTATTTA  1920
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Query  1921  ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAACGGATCTCTTG  1980
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Sbjct  1921  ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAACGGATCTCTTG  1980

Query  1981  GTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTC  2040
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Sbjct  1981  GTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTC  2040

Query  2041  GTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTG  2100
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Sbjct  2041  GTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTG  2100

Query  2101  TTTGAGCGTCATTTCTCTCTCAAACCTTCGGGTTTGGTATTGAGTGATACTCTTAGTTGA  2160
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Sbjct  2101  TTTGAGCGTCATTTCTCTCTCAAACCTTCGGGTTTGGTATTGAGTGATACTCTTAGTTGA  2160

Query  2161  ACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTGGATAGTGCTATATGACTTT  2220
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Sbjct  2161  ACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTGGATAGTGCTATATGACTTT  2220

Query  2221  CAATGTATTAGGTTTATCCAACTCGTTGAATAGTTTAATGGTATATTTCTCGGTATTCTA  2280
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Sbjct  2221  CAATGTATTAGGTTTATCCAACTCGTTGAATAGTTTAATGGTATATTTCTCGGTATTCTA  2280

Query  2281  GGCTCGGCCTTACAATATAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACCCGCTG  2340
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Sbjct  2281  GGCTCGGCCTTACAATATAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACCCGCTG  2340

Query  2341  AACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTTAGTAACGGC  2400
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Query  2401  GAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCACCTTCGGTGTCCGAGTTGTAATT  2460
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Sbjct  2401  GAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCACCTTCGGTGTCCGAGTTGTAATT  2460

Query  2461  TGAAGAAGGTAACTTTGGAGTTGGCTCTTGTCTATGTTCCTTGGAACAGGACGTCACAGA  2520
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Sbjct  2461  TGAAGAAGGTAACTTTGGAGTTGGCTCTTGTCTATGTTCCTTGGAACAGGACGTCACAGA  2520

Query  2521  GGGTGAGAATCCCGTGCGATGAGATGCCCAATTCTATGTAAAGTGCTTTCGAAGAGTCGA  2580
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Sbjct  2521  GGGTGAGAATCCCGTGCGATGAGATGCCCAATTCTATGTAAAGTGCTTTCGAAGAGTCGA  2580

Query  2581  GTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCG  2640
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Sbjct  2581  GTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCG  2640

Query  2641  AGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGT  2700
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Sbjct  2641  AGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGT  2700

Query  2701  GAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGAGATCAGACTTGGTATTTTGCGA  2760
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Sbjct  2701  GAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGAGATCAGACTTGGTATTTTGCGA  2760

Query  2761  TCCTTTCCTTCTTGGTTGGGTTCCTCGCAGCTTACTGGGCCAGCATCGGTTTGGATGGTA  2820
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Sbjct  2761  TCCTTTCCTTCTTGGTTGGGTTCCTCGCAGCTTACTGGGCCAGCATCGGTTTGGATGGTA  2820

Query  2821  GGATAATGACTAAGGAATGTGGCTCTACTTCGGTGGAGTGTTATAGCCTTGGTTGATACT  2880
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Sbjct  2821  GGATAATGACTAAGGAATGTGGCTCTACTTCGGTGGAGTGTTATAGCCTTGGTTGATACT  2880

Query  2881  GCCTGTCTAGACCGAGGACTGCGTCTTTTGACTAGGATGTTGGCATAATGATCTTAANCC  2940
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Sbjct  2881  GCCTGTCTAGACCGAGGACTGCGTCTTTTGACTAGGATGTTGGCATAATGATCTTAANCC  2940

Query  2941  ACCCGTCTGAAACACGGACCA  2961
             |||||||||||||||||||||
Sbjct  2941  ACCCGTCTGAAACACGGACCA  2961


>gb|GQ458025.1| Debaryomyces hansenii strain MA09-AK 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=2991

 Score = 5446 bits (2949),  Expect = 0.0
 Identities = 2958/2961 (99%), Gaps = 2/2961 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  25    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  84

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAA-CCGTGGTAATTCTAGAGCT  121
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  85    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCCGTGGTAATTCTAGAGCT  144

Query  122   AATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAAT  181
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  145   AATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAAT  204

Query  182   GCTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  205   GCTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  264

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  265   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  324

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  325   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  384

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  385   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  444

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  445   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  504

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  505   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  564

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  565   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  624
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Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
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Sbjct  625   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  684

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  685   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  744

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  745   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  804

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  805   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  864

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  865   TATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCAT  924

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  925   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  984

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  985   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1044

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1045  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1104

Query  1082  GGCTGAAACTTAAAGGAATTGAC-GGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  1105  GGCTGAAACTTAAAGGAATTGACGGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1164

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1165  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1224

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1225  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1284

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1285  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1344

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1345  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1404

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1405  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1464

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1465  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1524

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1525  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1584
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Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1585  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1644

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1645  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1704

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1705  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1764

Query  1741  CCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCGCGGCGAAAAAAC  1800
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1765  CCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCGCGGCGAAAAAAC  1824

Query  1801  CTTACACACAGTGTTTTTTGTTATTACAAGAACTTTTGCTTTGGTCTGGACTAGAAATAG  1860
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1825  CTTACACACAGTGTTTTTTGTTATTACAAGAACTTTTGCTTTGGTCTGGACTAGAAATAG  1884

Query  1861  TTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTGAATTGTTATTTATTTA  1920
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1885  TTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTGAATTGTTATTTATTTA  1944

Query  1921  ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAACGGATCTCTTG  1980
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1945  ATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAACGGATCTCTTG  2004

Query  1981  GTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTC  2040
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2005  GTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTC  2064

Query  2041  GTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTG  2100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2065  GTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTG  2124

Query  2101  TTTGAGCGTCATTTCTCTCTCAAACCTTCGGGTTTGGTATTGAGTGATACTCTTAGTTGA  2160
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  2125  TTTGAGCGTCATTTCTCTCTCAAACCTTCGGGTTTGGTATTGAGTGATACTCTTAGTCGA  2184

Query  2161  ACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTGGATAGTGCTATATGACTTT  2220
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2185  ACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTGGATAGTGCTATATGACTTT  2244

Query  2221  CAATGTATTAGGTTTATCCAACTCGTTGAATAGTTTAATGGTATATTTCTCGGTATTCTA  2280
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2245  CAATGTATTAGGTTTATCCAACTCGTTGAATAGTTTAATGGTATATTTCTCGGTATTCTA  2304

Query  2281  GGCTCGGCCTTACAATATAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACCCGCTG  2340
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2305  GGCTCGGCCTTACAATATAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACCCGCTG  2364

Query  2341  AACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTTAGTAACGGC  2400
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2365  AACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTTAGTAACGGC  2424

Query  2401  GAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCACCTTCGGTGTCCGAGTTGTAATT  2460
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2425  GAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCACCTTCGGTGTCCGAGTTGTAATT  2484

Query  2461  TGAAGAAGGTAACTTTGGAGTTGGCTCTTGTCTATGTTCCTTGGAACAGGACGTCACAGA  2520
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2485  TGAAGAAGGTAACTTTGGAGTTGGCTCTTGTCTATGTTCCTTGGAACAGGACGTCACAGA  2544
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Query  2521  GGGTGAGAATCCCGTGCGATGAGATGCCCAATTCTATGTAAAGTGCTTTCGAAGAGTCGA  2580
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2545  GGGTGAGAATCCCGTGCGATGAGATGCCCAATTCTATGTAAAGTGCTTTCGAAGAGTCGA  2604

Query  2581  GTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCG  2640
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2605  GTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCG  2664

Query  2641  AGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGT  2700
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2665  AGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTTTGAAAAGAGAGT  2724

Query  2701  GAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGAGATCAGACTTGGTATTTTGCGA  2760
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2725  GAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGAGATCAGACTTGGTATTTTGCGA  2784

Query  2761  TCCTTTCCTTCTTGGTTGGGTTCCTCGCAGCTTACTGGGCCAGCATCGGTTTGGATGGTA  2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2785  TCCTTTCCTTCTTGGTTGGGTTCCTCGCAGCTTACTGGGCCAGCATCGGTTTGGATGGTA  2844

Query  2821  GGATAATGACTAAGGAATGTGGCTCTACTTCGGTGGAGTGTTATAGCCTTGGTTGATACT  2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2845  GGATAATGACTAAGGAATGTGGCTCTACTTCGGTGGAGTGTTATAGCCTTGGTTGATACT  2904

Query  2881  GCCTGTCTAGACCGAGGACTGCGTCTTTTGACTAGGATGTTGGCATAATGATCTTAANCC  2940
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2905  GCCTGTCTAGACCGAGGACTGCGTCTTTTGACTAGGATGTTGGCATAATGATCTTAANCC  2964

Query  2941  ACCCGTCTGAAACACGGACCA  2961
             |||||||||||||||||||||
Sbjct  2965  ACCCGTCTGAAACACGGACCA  2985


>gb|GQ458019.1| Debaryomyces hansenii strain MA09-J 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=2969

 Score = 5421 bits (2935),  Expect = 0.0
 Identities = 2952/2961 (99%), Gaps = 5/2961 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  12    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  71

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  72    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  131

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  132   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  191

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  192   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  251

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  252   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  311
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Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  312   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  371

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  372   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  431

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  432   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  491

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             |||||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  492   ATACCTTAANNAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  551

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  552   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  611

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  612   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  671

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  672   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  731

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  732   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  791

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  792   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  851

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  852   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  911

Query  903   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  912   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  971

Query  963   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGAC  1022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  972   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGAC  1031

Query  1023  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1032  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1091

Query  1083  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1142
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  1092  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAG-CTGCGGCTTAATT  1150

Query  1143  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1151  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1210

Query  1203  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1211  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1270
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Query  1263  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1271  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1330

Query  1323  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1331  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1390

Query  1383  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1442
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1391  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1450

Query  1443  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1502
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1451  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1510

Query  1503  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1562
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1511  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1570

Query  1563  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1622
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1571  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1630

Query  1623  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1682
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1631  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1690

Query  1683  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACC  1742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1691  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACC  1750

Query  1743  TGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCGCGGCGAAAAAACCT  1802
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Sbjct  1751  TGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCGCGGCGAAAAAACCT  1810

Query  1803  TACACACAGTGTTTTTTGTTATTACAAGAACTTTTGCTTTGGTCTGGACTAGAAATAGTT  1862
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Sbjct  1811  TACACACAGTGTTTTTTGTTATTACAAGAACTTTTGCTTTGGTCTGGACTAGAAATAGTT  1870

Query  1863  TGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTGAATTGTTATTTATTTAAT  1922
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Sbjct  1871  TGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTGAATTGTTATTTATTTAAT  1930

Query  1923  TGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAACGGATCTCTTGGT  1982
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Sbjct  1931  TGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAACGGATCTCTTGGT  1990

Query  1983  TCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGT  2042
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Sbjct  1991  TCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGT  2050

Query  2043  GAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTT  2102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2051  GAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTT  2110

Query  2103  TGAGCGTCATTTCTCTCTCAAACCTTCGGGTTTGGTATTGAGTGATACTCTTAGTTGAAC  2162
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2111  TGAGCGTCATTTCTCTCTCAAACCTTCGGGTTTGGTATTGAGTGATACTCTTAGTTGAAC  2170

Query  2163  TAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTGGATAGTGCTATATGACTTTCA  2222
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Sbjct  2171  TAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTGGATAGTGCTATATGACTTTCA  2230
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Query  2223  ATGTATTAGGTTTATCCAACTCGTTGAATAGTTTAATGGTATATTTCTCGGTATTCTAGG  2282
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Sbjct  2231  ATGTATTAGGTTTATCCAACTCGTTGAATAGTTTAATGGTATATTTCTCGGTATTCTAGG  2290

Query  2283  CTCGGCCTTACAATATAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACCCGCTGAA  2342
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Sbjct  2291  CTCGGCCTTACAATATAACAAACAAGTTTGACCTCAAATCAGGTAGGATTACCCGCTGAA  2350

Query  2343  CTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTTAGTAACGGCGA  2402
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Sbjct  2351  CTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTTAGTAACGGCGA  2410

Query  2403  GTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCACCTTCGGTGTCCGAGTTGTAATTTG  2462
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Query  2463  AAGAAGGTAACTTTGGAGTTGGCTCTTGTCTATGTTCCTTGGAACAGGACGTCACAGAGG  2522
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Sbjct  2471  AAGAAGGTAACTTTGGAGTTGGCTCTTGTCTATGTTCCTTGGAACAGGACGTCACAGAGG  2530

Query  2523  GTGAGAATCCCGTGCGATGAGATGCCCAATTCTATGTAAAGTGCTTTCGAAGAGTCGAGT  2582
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Sbjct  2531  GTGAGAATCCCGTGCGATGAGATGCCCAATTCTATGTAAAGTGCTTTCGAAGAGTCGAGT  2590

Query  2583  TGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAG  2642
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Sbjct  2591  TGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGCTAAATATTGGCGAG  2650

Query  2643  AGACCGATAGCGAACAAGTACAGTGATGG-AAAGATGAAAAGAACTTTGAAAAGAGAGTG  2701
             ||||||||||||||||||||||||||||| |||||||||||||||||||||| |||||||
Sbjct  2651  AGACCGATAGCGAACAAGTACAGTGATGGNAAAGATGAAAAGAACTTTGAAA-GAGAGTG  2709

Query  2702  AAAAAGTACGTGAAATTGTTGAAAGGGAA-GGGCTTGAGATCAGACTTGGTATTTTGCGA  2760
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Sbjct  2710  AAAAAGTACGTGAAATTGTTGAAAGGGAANGGGCTTGAGATCAGACTTGGTATTTTGCGA  2769

Query  2761  TCCTTTCCTTCTTGGTTGGGTTCCTCGCAGCTTACTGGGCCAGCATCGGTTTGGATGGTA  2820
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2770  TCCTTTCCTTCTTGGTTGGGTTCCTCGCAGCTTACTGGGCCAGCATCGGTTTGGATGGTA  2829

Query  2821  GGATAATGACTAAGGAATGTGGCTCTACTTCGGTGGAGTGTTATAGCCTTGGTTGATACT  2880
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2830  GGATAATGACTAAGGAATGTGGCTCTACTTCGGTGGAGTGTTATAGCCTTGGTTGATACT  2889

Query  2881  GCCTGTCTAGACCGAGGACTGCGTCTTTTGACTAGGATGTTGGCATAATGATCTTAANCC  2940
             |||||||||||||||||||||||||||| ||||||||||||||||||| |||||||| ||
Sbjct  2890  GCCTGTCTAGACCGAGGACTGCGTCTTTNGACTAGGATGTTGGCATAANGATCTTAA-CC  2948

Query  2941  ACCCGTCTGAAACACGGACCA  2961
             |||||||||||||||||||||
Sbjct  2949  ACCCGTCTGAAACACGGACCA  2969


>gb|CP000497.1| Pichia stipitis CBS 6054 chromosome 3, complete sequence
Length=1841851

 Features flanking this part of subject sequence:
   14 bp at 5' side: predicted protein
   2803 bp at 3' side: Unknown protein

 Score = 4776 bits (2586),  Expect = 0.0
 Identities = 2855/2977 (95%), Gaps = 52/2977 (1%)
 Strand=Plus/Minus
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Query  3        GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1711503  GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC
1711444

Query  63       AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
                |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  1711443  AGTTATCGTTTATTTGATAGTACC-TTACTACTTGGATAACCGTGGTAATTCTAGAGCTA
1711385

Query  123      ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
                ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1711384  ATACATGCTTAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG
1711325

Query  183      CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
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Sbjct  1711324  C-CTTCGG-GCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCCGGC
1711267

Query  243      GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
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Sbjct  1711266  GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG
1711207

Query  303      GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1711206  GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT
1711147

Query  363      ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
                |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  1711146  ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGATACGGGGAGGTAGT
1711087

Query  423      GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
                ||||||||||||||||| |||||||||||||||||| |||||||||||||||||||||||
Sbjct  1711086  GACAATAAATAACGATATAGGGCCCTTTCGGGTCTTATAATTGGAATGAGTACAATGTAA
1711027

Query  483      ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1711026  ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG
1710967

Query  543      CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
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Sbjct  1710966  CTCCAAAAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT
1710907

Query  603      GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
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Sbjct  1710906  GGTTAGCCGGTCCACCTTTTTGGTGTGTACTGGACCTAACCGAGCCTTTCCTTCTGGCTA
1710847

Query  663      ACCTTTC-GCCCTTGT-GGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGT  720
                ||| |||  || || | || | ||||||||||||||||||||||||||||||||||||||
Sbjct  1710846  ACC-TTCTTCCTTTTTGGGAG-TTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGT
1710789

Query  721      GTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGG  780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1710788  GTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGG
1710729
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Query  781       TTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCA  840
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Sbjct  1710728   TTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGAACGGTCGGGGGCATCA
1710669

Query  841       GTATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGC  899
                 ||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Sbjct  1710668   GTATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGC
1710610

Query  900       ATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGA  959
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1710609   ATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGA
1710550

Query  960       TACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCttttttt  1019
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Sbjct  1710549   TACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTT
1710490

Query  1020      GACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGC  1079
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Sbjct  1710489   GACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGC
1710430

Query  1080      AAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTA  1139
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Sbjct  1710429   AAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTA
1710370

Query  1140      ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1199
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1710369   ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG
1710310

Query  1200      AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1259
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Sbjct  1710309   AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT
1710250

Query  1260      GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1319
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Sbjct  1710249   GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTA
1710190

Query  1320      GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1379
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Sbjct  1710189   GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA
1710130

Query  1380      TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1439
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Sbjct  1710129   TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC
1710070

Query  1440      AACGAGTATTA-ACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGG  1498
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Sbjct  1710069   AGCGAGT-TTATACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGG
1710011

Query  1499      GGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCA  1558
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Sbjct  1710010  GGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCA
1709951

Query  1559     GCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAA  1618
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Sbjct  1709950  GCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAA
1709891

Query  1619     TGGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAA  1678
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Sbjct  1709890  TGGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACTGAG
1709831

Query  1679     AAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTG  1738
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Sbjct  1709830  AAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTG
1709771

Query  1739     AACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCGCGGCGAAAAA  1798
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Sbjct  1709770  AACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAACTGCGCGGCGAAAAA
1709711

Query  1799     ACCTTACACACAGTGTTTTTTGTTATTACAAGAACTTTTGCTTTGGTCTGGACT-AGAAA  1857
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Sbjct  1709710  ACCTTACACACAGTGTTTTCT-TTATTAGAA-A-CTATTGCTTTGGTCTGG-CTCAGAAA
1709655

Query  1858     T-AGTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATATTGAATTGTTATTT-  1915
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Sbjct  1709654  TGAGTT-GGGCCAGAGGTTTAC----C-AAACTTCAAT-TTTAT-T-GAATTGTTATTTT
1709604

Query  1916     ATTTAATT-GTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAACGGAT  1974
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Sbjct  1709603  ATT-AATTTGTCAATTTGTTGATTAAATTCAAAAA-TCTTCAAAACTTTCAACAACGGAT
1709546

Query  1975     CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAG  2034
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Sbjct  1709545  CTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAG
1709486

Query  2035     ATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCA  2094
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Sbjct  1709485  ATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAGGGCA
1709426

Query  2095     TGCCTGTTTGAGCGTCATTTCTCTCTCAAACCTTCGGGTTTGGTATTGAGTGATACTCTT  2154
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Sbjct  1709425  TGCCTGTTTGAGCGTCATTTCTCTCTCAAACCCTCGGGTTTGGTATTGAGTGATACTCTT
1709366

Query  2155     AGTTGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTGGATAGTGCT-ATA  2213
                ||| ||||||||||||||||||||| ||||||||| ||||||||||  ||||| || | |
Sbjct  1709365  AGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTGGTACTAAATAGTACTGACA
1709306

Query  2214     TGACT-TT-CAATGTATTAGGTTTATCCAACTCGTTGAATAGTT-TAATGGT-ATATTTC  2269
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Sbjct  1709305  -GAATATTTCAATGTATTAGGTTTATCCAACTCGTTGAG-ACTTCTGGCGGTGA-ATTTT
1709249

Query  2270     TCGGTAT-TCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACCTCAAATCAGGTAG  2328
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Sbjct  1709248  T-GGTATAT-T-GGCTTTGCCTTACAAAACAACAAACAAGTTTGACCTCAAATCAGGTAG
1709192

Query  2329     GATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGC  2388
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Sbjct  1709191  GATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGC
1709132

Query  2389     CTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCACCTTCGGTGTC  2448
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Sbjct  1709131  CTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCACCTTCGGTGTC
1709072

Query  2449     CGAGTTGTAATTTGAAGAAGGTAACTTTGGAGTTGGCTCTTGTCTATGTTCCTTGGAACA  2508
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Sbjct  1709071  CGAGTTGTAATTTGAAGAAGGTAACTTTGGAGTCAGCTCTTGTCTATGTTCCTTGGAACA
1709012

Query  2509     GGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGCCCAATTCTATGTAAAGTGCTT  2568
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Sbjct  1709011  GGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGTCTGATTCTATGTAAAGTGCTT
1708952

Query  2569     TCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGC  2628
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Sbjct  1708951  TCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCATCTAAAGC
1708892

Query  2629     TAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAAAAGAACTT  2688
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1708832

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Sbjct  1708831  TGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGTTTGAGATCAGACTT
1708772

Query  2749     GGTATTTTGCGATC-CTTTCCTTCTTGGTTGGGTTCCTCG-CAGCTTACTGGGCCAGCAT  2806
                |||||||||  ||  ||| | |||  ||| |||  ||||  ||| |||||||||||||||
Sbjct  1708771  GGTATTTTGT-ATGTCTTGCTTTCG-GGTGGGG--CCTCTACAGTTTACTGGGCCAGCAT
1708716

Query  2807     CGGTTTGGATGGTAGGATAATGAC-TAAGGAATGTGGCTCTACTTCGGTGGAGTGTTATA  2865
                ||||||||| |||||||||||||| |  |||||||||| | |||||||||| ||||||||
Sbjct  1708715  CGGTTTGGACGGTAGGATAATGACATT-GGAATGTGGCACCACTTCGGTGGTGTGTTATA
1708657

Query  2866     GCCTTGGTTGATACTGCCTGTCTAGACCGAGGACTGCGTCTTTTGACTAGGATGTTGGCA  2925
                | ||| ||||||||||||||||||||||||||||||||||||| |||||||||| |||||
Sbjct  1708656  GACTTTGTTGATACTGCCTGTCTAGACCGAGGACTGCGTCTTT-GACTAGGATGCTGGCA
1708598

Query  2926     TAATGATCTTAANCCACCCGTCT-GAAACACGGACCA  2961
                |||||||||||| || ||||||| |||||||||||||
Sbjct  1708597  TAATGATCTTAAACCGCCCGTCTTGAAACACGGACCA  1708561


>dbj|AB285026.1| Candida sp. BCMU BX03 genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2,
26S rRNA, partial and complete sequence
Length=3227

 Score = 4119 bits (2230),  Expect = 0.0
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 Identities = 2751/2986 (92%), Gaps = 103/2986 (3%)
 Strand=Plus/Plus

Query  19     TATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTG  78
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  1      TATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTACTTG  60

Query  79     ATAGTACCTTTACTACTTGG--ATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAA  136
              ||||| ||||||||||| ||  |||||||||||||  ||||||||||||| |||||| ||
Sbjct  61     ATAGTGCCTTTACTACTCGGTTATAACCGTGGTAAAACTAGAGCTAATACGTGCTAACAA  120

Query  137    TCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCT-TTTCGGAGC-T  194
               |||||||||||||||||| |||||||||||||||||||||||||||| |||  |||| |
Sbjct  121    CCCCGACTGTTTGGAAGGGGTGTATTTATTAGATAAAAAATCAATGCTCTTT--GAGCTT  178

Query  195    CTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTC  254
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  179    C-TTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTC  237

Query  255    AAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGT  314
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  238    AAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTGCAACGGGT  297

Query  315    AACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAG  374
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  298    AACGGGGAATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAG  357

Query  375    GAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAA  434
              |||||||||||||||||||||||||||||||| | |||||||||||||||||||||||||
Sbjct  358    GAAGGCAGCAGGCGCGCAAATTACCCAATCCCAATACGGGGAGGTAGTGACAATAAATAA  417

Query  435    CGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGA  494
              |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  418    CGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATTTAAATACCTTAACGA  477

Query  495    GGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGT  554
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  478    GGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAAGAGCGT  537

Query  555    ATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGTTGGCCGGTC  614
              || | |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  538    ATGTAAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGTTGGCCGGTC  597

Query  615    CGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCTTTCGCCCT  674
              ||||  | ||||||||||||||  |||||||||||||||| |||||||| |  | | |||
Sbjct  598    CGCC--TATGGCGAGTACTGGATTCAACCGAGCCTTTCCTCCTGGCTAA-C--TAGTCCT  652

Query  675    TGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCC  734
              |  || |  | ||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  653    T-CGG-GGCTAGCGAACCAGGACTTTTACTTTGAGAAAATTAGAGTGTTCAAAGCAGGCA  710

Query  735    TTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGG  794
              || ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  711    TTAGCTTGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGG  770

Query  795    TTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCA  854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  771    TTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAATTGTCA  830

Query  855    GAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACG  913
              ||||||||||||||||| |||  |||||||||||||||||||||||||||||||||||||
Sbjct  831    GAGGTGAAATTCTTGGATTTA-TTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACG  889

Query  914    TTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCT  973
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  890   TTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCT  949

Query  974   TAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGACGCACTCGGCAC  1033
             ||||||||||||||||||||||||||||||||||||| ||||||||| ||||||||||||
Sbjct  950   TAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTCCTTTTTTTGGCGCACTCGGCAC  1009

Query  1034  CTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTA  1093
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  1010  CTTACGAGAAATCAAAGTTTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTA  1069

Query  1094  AAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACAC  1153
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1070  AAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACAC  1129

Query  1154  GGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGAT  1213
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1130  GGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGAT  1189

Query  1214  TTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGC  1273
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1190  TTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGC  1249

Query  1274  GATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCAC  1333
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1250  GATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCAC  1309

Query  1334  TTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGA  1393
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1310  TTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGA  1369

Query  1394  TGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAACGAGTAT-TAAC  1452
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||| || |
Sbjct  1370  TGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAGCGAGTATCTA-C  1428

Query  1453  CTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGT  1512
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1429  CTTGGCCGAGAGGCCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGT  1488

Query  1513  AATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTA  1572
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1489  AATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTA  1548

Query  1573  CGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGC  1632
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1549  CGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGC  1608

Query  1633  CTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACT  1692
             || |||||||||||||||||||||| |||||||||||| ||| |||||| ||| ||||||
Sbjct  1609  CTTCGGATTGGTTTAAAGAAGGGGGTAACTCCATCTTGTAACTGAAAAGTTGGACAAACT  1668

Query  1693  TGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA  1752
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1669  TGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACCTGCGGAAGGA  1728

Query  1753  TCATTACAGTATTCTTTT---------TGCCAGCGCTTAATTGCGCGGCGAAA------A  1797
             |||||||||| |  ||||         |||| |||||||| |||||||||         |
Sbjct  1729  TCATTACAGT-TAGTTTTCGGCACCGCTGCCTGCGCTTAACTGCGCGGCGGGGCGCCGGA  1787

Query  1798  -AACCTTACACACAGTGTTTTTTGTTATTACAAGAACTTTTGCTTTGGTCT-GGACTAGA  1855
              |||||||||||| |||||||| ||| || |  ||||  ||||||||| || || || ||
Sbjct  1788  CAACCTTACACACTGTGTTTTT-GTTTTT-CT-GAACACTTGCTTTGG-CTTGG-CTTGA  1842

Query  1856  AATAGTTTGGGCCAGAGGTTTACTGAACTAAAC-TTCAATATTTATATTGAATTGTTATT  1914
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               | ||  |||||| ||  | ||  | |  ||| ||||| |||||| ||||||| || ||
Sbjct  1843  T-T-GTC-GGGCCAAAGACT-AC--A-CGCAACCTTCAAAATTTATTTTGAATTTTT-TT  1894

Query  1915  TATTTAA-TT-GTCAATTT-GTT-GATTAAATTCAAAAA-A-TCTTCAAAACTTTCAACA  1968
             |||| |  || |||||||| ||| |||||| |||||||| | ||||||||||||||||||
Sbjct  1895  TATT-ACGTTTGTCAATTTTGTTTGATTAATTTCAAAAATAATCTTCAAAACTTTCAACA  1953

Query  1969  ACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAA  2028
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1954  ACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAA  2013

Query  2029  TTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAG  2088
             ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||| |
Sbjct  2014  TTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCTCTCTGGTATTCCGG  2073

Query  2089  AGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCTTCGGGTTTGGTATTGAGTGAT  2148
             || ||||||||||||||||||||||||||||||| ||| |||||  ||||||||||||||
Sbjct  2074  AGAGCATGCCTGTTTGAGCGTCATTTCTCTCTCACACCCTCGGGCGTGGTATTGAGTGAT  2133

Query  2149  ACTCTTAGTTGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTGGATAGTG  2208
             ||||||||| | ||||||||||||||||||| |||  |||| ||||| |||||||||||
Sbjct  2134  ACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTAACGGCAGGAGTG-TACTGGATAGTA  2192

Query  2209  CTATA-TGACT-TT-CAATGTATTAGGTTTATCCAACTCGTTGAATAGTTTAATG--GTA  2263
             | | | ||  | || ||||||||||||||||||||||||||||||  |      |  |||
Sbjct  2193  CGA-ACTGGTTATTTCAATGTATTAGGTTTATCCAACTCGTTGAAGCGCCGGG-GCAGTA  2250

Query  2264  TATTTCTCGGTATTCTA-GGCTCGGCCTTACAATATAACAAACA-A-GTTTGACCTCAAA  2320
              |||||| ||| |   | ||||||||| ||||| | | |||||| | |||||||||||||
Sbjct  2251  AATTTCT-GGT-TGA-ACGGCTCGGCCCTACAACA-A-CAAACATAAGTTTGACCTCAAA  2305

Query  2321  TCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACA  2380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2306  TCAGGTAGGATTACCCGCTGAACTTAAGCATATCAATAAGCGGAGGAAAAGAAACCAACA  2365

Query  2381  GGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAAAAGCTCAAATTTGAAATCTGGCACCT  2440
             ||||||||||||||| |||||||||||||||||| ||||||||||||||||||||| |||
Sbjct  2366  GGGATTGCCTTAGTAGCGGCGAGTGAAGCGGCAATAGCTCAAATTTGAAATCTGGCGCCT  2425

Query  2441  TCGGTGTCCGAGTTGTAATTTGAAGAAGGTAACTTTGGAGTTGGCTCTTGTCTATGTTCC  2500
             |||| |||||||||||||||||||||||||| ||||||  ||||||||||||||||||||
Sbjct  2426  TCGGCGTCCGAGTTGTAATTTGAAGAAGGTATCTTTGGTTTTGGCTCTTGTCTATGTTCC  2485

Query  2501  TTGGAACAGGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGCCCAATTCTATGTA  2560
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  2486  TTGGAACAGGACGTCACAGAGGGTGAGAATCCCGTGCGATGAGATGCCCAATTCCATGTA  2545

Query  2561  AAGTGCTTTCGAAGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCA  2620
             |||| | ||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2546  AAGTTCCTTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAGTGGGTGGTAAATTCCA  2605

Query  2621  TCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACAGTGATGGAAAGATGAA  2680
             ||||||||||||||||||||||||||||||||||||||||||| |||| |||||||||||
Sbjct  2606  TCTAAAGCTAAATATTGGCGAGAGACCGATAGCGAACAAGTACTGTGAAGGAAAGATGAA  2665

Query  2681  AAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGAGA  2740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2666  AAGAACTTTGAAAAGAGAGTGAAAAAGTACGTGAAATTGTTGAAAGGGAAGGGCTTGAGA  2725

Query  2741  TCAGACTTGGTATTTTGCGATCCTTTCCTTCTTGGTTGGGTTCCTCGCAGCTTACTGGGC  2800
             |||||||||| ||||| | | |    | | |  | | ||         ||||| | ||||
Sbjct  2726  TCAGACTTGGAATTTTCC-A-CG---C-T-C--G-T-GG---------AGCTTTCCGGGC  2765

Query  2801  CAGCATCGGTTTGGATGGTAGGATAAT-GACTAAGGAATGTGGCTCTACTTCGGTGGAGT  2859
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             ||||||| |||||| ||| |||||||| | |   |||| || || || |||||| | |||
Sbjct  2766  CAGCATCAGTTTGGGTGGCAGGATAATTG-CGCGGGAAAGTAGCACTGCTTCGG-G-AGT  2822

Query  2860  GT-T-ATAGCCTTG-GTTGATACTGCCTGTCTAGACCGAGGACTGCGTCTTTTGACTAGG  2916
             || | ||||||| | || ||||||||||| |||||| ||||||||||||||| |||||||
Sbjct  2823  GTATTATAGCCT-GCGTCGATACTGCCTGCCTAGACTGAGGACTGCGTCTTT-GACTAGG  2880

Query  2917  ATGTTGGCATAATGATCTTAANCCACCCGTCT-GAAACACGGACCA  2961
             ||| ||||||||||||||||| || ||||||| |||||||||||||
Sbjct  2881  ATGCTGGCATAATGATCTTAAGCCGCCCGTCTTGAAACACGGACCA  2926


>gb|AY845351.1| Candida lignicola 18S ribosomal RNA gene, partial sequence
Length=2337

 Score = 3419 bits (1851),  Expect = 0.0
 Identities = 2188/2342 (93%), Gaps = 58/2342 (2%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  35    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  94

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  95    AGTTATCGTTTATTTGATCGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  154

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||| |||||||| ||  || ||||||||||||||||||||||||||||||||||
Sbjct  155   ATACATGCTTAAAATCCCAAC--TTCGGAAGGGATGTATTTATTAGATAAAAAATCAATG  212

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  213   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCCGG  270

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  271   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  330

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  331   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  390

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  391   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGATACGGGGAGGTAG  450

Query  422   TGACAATAAATAACGATACAGGGCCCTTT-CGGGTCTTGTAATTGGAATGAGTACAATGT  480
             |||||||||||||||||  | || |||||   |||| | |||||||||||||||||||||
Sbjct  451   TGACAATAAATAACGATGTATGG-CCTTTATAGGTCATATAATTGGAATGAGTACAATGT  509

Query  481   AAATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  510   AAATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  569

Query  541   AGCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGC  600
             |||||||| |||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  570   AGCTCCAAAAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGC  629

Query  601   TTGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGC  660
             |||||| |||||||| ||||||||| | ||||| |||| |||||||||||||||||||||
Sbjct  630   TTGGTTAGCCGGTCCACCTTTTTGGTGTGTACT-GACCTAACCGAGCCTTTCCTTCTGGC  688

Query  661   TAACCTTTCGCCCT-TGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAG  719
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              ||||| |||  |||  | || | |||||||||||||||||||||||||||||||||||||
Sbjct  689    TAACC-TTC-TCCTCCG-GGAG-TTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAG  744

Query  720    TGTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATG  779
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  745    TGTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATG  804

Query  780    GTTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATC  839
              |||||||||||||||||||||||||||||||||||||||||||||| || | |||| ||
Sbjct  805    GTTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGATGGACAGGGGAATT  864

Query  840    AGTATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAG  898
              |||||||| | ||||||||||||||||||||| |||  ||||||||||||||||||||||
Sbjct  865    AGTATTCAATAGTCAGAGGTGAAATTCTTGGATTTA-TTGAAGACTAACTACTGCGAAAG  923

Query  899    CATTTGCCAAGGACGTTTTCAT--TAATCAAGAACGAAAGTTAGGGGATCGAAGATGATC  956
              ||||| || ||| |    || |  ||||||||||||||||||||||||||||||||||||
Sbjct  924    CATTTTCC-AGG-CACACTCCTGCTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATC  981

Query  957    AGATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttt  1016
              |||||||||||||||||||||||||||||||||||||||||||||||| |  |||| |||
Sbjct  982    AGATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGCGGCGTTCATTT  1041

Query  1017   tttGACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGT  1076
                |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1042   AGTGACGCGCTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGT  1101

Query  1077   CGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGC  1136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1102   CGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGC  1161

Query  1137   TTAATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATT  1196
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1162   TTAATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATT  1221

Query  1197   GAGAGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGA  1256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1222   GAGAGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGA  1281

Query  1257   TTTGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCT  1316
              ||||||||||||||||||||||||||||||||||||||||  ||||||| || || |||
Sbjct  1282   TTTGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTT-TAAATAGCGCCGCGAGCC  1340

Query  1317   TT-TGCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAG  1375
              || ||||||    | | |||||||| |||||||| || || |||||||||||||||||||
Sbjct  1341   TTGTGCTGGCGC-G-CGCTTCTTAGGGGGACTATTGACTTGAAGTCGATGGAAGTTTGAG  1398

Query  1376   GCAATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGG  1435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1399   GCAATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGG  1458

Query  1436   AGCCAACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGC  1495
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Sbjct  1459   AGCCAGCGAGT-TGA-CCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGC  1516

Query  1496   TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCA  1555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1517   TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCA  1576

Query  1556   TCAGCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATT  1615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1577   TCAGCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATT  1636

Query  1616   GAATGGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACC  1675
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Sbjct  1637  GAATGGCTTAGTGAGGCCTCCGGATTGGTTTAAAGTAGGAGGCAACTCCAACTTGGAACT  1696

Query  1676  GAAAAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
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Sbjct  1697  GAAAAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1756

Query  1736  GTGAACCTGCGGAAGGATCATTACAGTATTCTTTTTGCCAGCGCTTAATTGCGCGGCGAA  1795
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Sbjct  1757  GTGAACCTGCGGAAGGATCATTACTGTTTTAGTTTTACCAGCGCTTAATTGCGCGGTGAA  1816

Query  1796  -AAAACCTTACACACAGTGTTTTTTGTTATTACAAGAACTTTTGCTTTGGTCTGGACT-A  1853
              |||| ||||||||||||||||| | |||||| || | || |||||||||| ||| || |
Sbjct  1817  CAAAATCTTACACACAGTGTTTTCT-TTATTAGAA-A-CTATTGCTTTGGTTTGG-CTTA  1872

Query  1854  GAAATA-GTTTGGGCCAGAGGTTTACTGAACTAAACTTCAATATTTATA-TTGAATTGTT  1911
             |||||| ||| |||||||||||||| | ||||    | |||| ||| || ||||||||||
Sbjct  1873  GAAATAAGTT-GGGCCAGAGGTTTA-T-AACT----T-CAATTTTT-TAATTGAATTGTT  1923

Query  1912  -ATTTATTTAATTGTCAATTTGTTGATTAAATTCAAAAAATCTTCAAAACTTTCAACAAC  1970
              ||||||| ||||||||||||||||||||| |||||||| ||||||||||||||||||||
Sbjct  1924  TATTTATT-AATTGTCAATTTGTTGATTAATTTCAAAAA-TCTTCAAAACTTTCAACAAC  1981

Query  1971  GGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATT  2030
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Sbjct  1982  GGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATATGAATT  2041

Query  2031  GCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTCTGGTATTCCAGAG  2090
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| ||
Sbjct  2042  GCAGATTTTCGTGAATCATCGAATCTTTGAACGCACATTGCGCCCTTTGGTATTCCAAAG  2101

Query  2091  GGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCTTCGGGTTTGGTATTGAGTGATAC  2150
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Sbjct  2102  GGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCTTCGGGTTTGGTATTGAGTGATAC  2161

Query  2151  TCTTAGTTGAACTAGGCGTTTGCTTGAAATGTATTGGCATGAGTGGTACTGGATAGTGCT  2210
             ||||||| ||||||||||||||||||||| ||||||||| |||| |||||  ||||||||
Sbjct  2162  TCTTAGTCGAACTAGGCGTTTGCTTGAAAAGTATTGGCACGAGTAGTACTAAATAGTGCT  2221

Query  2211  AT-ATGA-C-TTT-CAATGTATTAGGTTTATCCAACTCGTTGAATAGTTTAATGGTA-T-  2264
              | | || | ||| |||||||||||||||||||||||||||||  | |||  || || |
Sbjct  2222  TTCAGGAACATTTTCAATGTATTAGGTTTATCCAACTCGTTGAG-A-TTTCTTGCTAGTG  2279

Query  2265  A-TTTCTCGGTATTCTAGGCTCGGCCTTACAATATAACAAACAAGTTTGACCTCAAATCA  2323
             | ||| | |||||  | ||||  ||||||||| | |||||||||||| ||||||||||||
Sbjct  2280  AATTTTT-GGTATA-T-GGCTTTGCCTTACAAAACAACAAACAAGTT-GACCTCAAATCA  2335

Query  2324  GG  2325
             ||
Sbjct  2336  GG  2337


>dbj|AB013590.1| Debaryomyces hansenii var. hansenii 18S rRNA gene, strain JCM
1990, partial sequence
Length=1784

 Score = 3230 bits (1749),  Expect = 0.0
 Identities = 1754/1756 (99%), Gaps = 1/1756 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89
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Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  209

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  210   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  269

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  270   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  329

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  330   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  389

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  390   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  449

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  450   GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  508

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  509   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  568

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  569   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  628

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  629   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  688

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  689   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  748

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  749   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  808

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  809   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  868

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  902
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  869   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTAACTGAAGACTAACTACTGCGAAAGCATT  928

Query  903   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  929   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  988

Query  963   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGAC  1022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  989   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGAC  1048
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Query  1023  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1082
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Sbjct  1049  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1108

Query  1083  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1142
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Sbjct  1109  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1168

Query  1143  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1202
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Sbjct  1169  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1228

Query  1203  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1262
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Sbjct  1229  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1288

Query  1263  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1322
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Sbjct  1289  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1348

Query  1323  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1349  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1408

Query  1383  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1442
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Sbjct  1409  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1468

Query  1443  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1502
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Sbjct  1469  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1528

Query  1503  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1562
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1529  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1588

Query  1563  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1622
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Sbjct  1589  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1648

Query  1623  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1682
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Sbjct  1649  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1708

Query  1683  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACC  1742
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Sbjct  1709  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACC  1768

Query  1743  TGCGGAAGGATCATTA  1758
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Sbjct  1769  TGCGGAAGGATCATTA  1784


>dbj|AB013568.1| Debaryomyces hansenii var. hansenii 18S rRNA gene, strain JCM
1521, partial sequence
Length=1784

 Score = 3230 bits (1749),  Expect = 0.0
 Identities = 1754/1756 (99%), Gaps = 1/1756 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89
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Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
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Sbjct  150   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  209

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
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Sbjct  210   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  269

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  270   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  329

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  330   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  389

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  390   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  449

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
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Sbjct  450   GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  508

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
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Sbjct  509   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  568

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
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Sbjct  569   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  628

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  629   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  688

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  689   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  748

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  749   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  808

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  809   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  868

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  902
             |||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Sbjct  869   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTAACTGAAGACTAACTACTGCGAAAGCATT  928

Query  903   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  929   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  988

Query  963   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGAC  1022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  989   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGAC  1048
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Query  1023  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1082
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Sbjct  1049  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1108

Query  1083  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1109  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1168

Query  1143  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1169  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1228

Query  1203  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1229  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1288

Query  1263  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1289  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1348

Query  1323  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1349  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1408

Query  1383  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1442
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1409  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1468

Query  1443  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1502
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1469  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1528

Query  1503  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1562
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1529  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1588

Query  1563  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1622
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1589  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1648

Query  1623  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1682
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1649  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1708

Query  1683  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACC  1742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1709  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACC  1768

Query  1743  TGCGGAAGGATCATTA  1758
             ||||||||||||||||
Sbjct  1769  TGCGGAAGGATCATTA  1784


>dbj|AB013567.1| Debaryomyces hansenii var. fabryi 18S rRNA gene, strain JCM 2166,
partial sequence
Length=1784

 Score = 3225 bits (1746),  Expect = 0.0
 Identities = 1754/1757 (99%), Gaps = 3/1757 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  209

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  210   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  269

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  270   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  329

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  330   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  389

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  390   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  449

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  450   GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  508

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  509   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  568

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  569   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  628

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  629   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  688

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  689   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  748

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  749   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  808

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  809   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  868

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  869   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  927

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  928   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  987

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  988   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1047

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1048  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1107

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1108  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1167

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1168  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1227

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1228  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1287

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1288  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1347

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1348  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1407

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1408  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1467

Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1468  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1527

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1528  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1587

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1588  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1647

Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1648  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1707

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAAC  1741
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1708  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAAC  1767

Query  1742  CTGCGGAAGGATCATTA  1758
             |||||||||||||||||
Sbjct  1768  CTGCGGAAGGATCATTA  1784


>emb|X58053.1| D.hansenii gene for 18S ribosomal RNA
Length=1800

 Score = 3217 bits (1742),  Expect = 0.0
 Identities = 1751/1755 (99%), Gaps = 2/1755 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  48    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  107

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  108   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  167

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  168   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  227

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  228   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  287

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  288   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  347

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  348   GTTTCAACGGGTAACGGGGAATAAGGGTTGGATTCCGGAGAGGGAGCCTGAGAAACGGCT  407

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  408   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  467

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  468   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  527

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
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Sbjct  528   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  587

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  588   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  647

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  648   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  707

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  708   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  767

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  768   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  827

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  828   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  887

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  888   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  947

Query  903   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  948   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  1007

Query  963   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGAC  1022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1008  CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGAC  1067

Query  1023  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1068  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1127

Query  1083  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1142
             || ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  1128  GCCGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCG-CTTAATT  1186

Query  1143  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1187  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1246

Query  1203  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1247  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1306

Query  1263  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1307  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1366

Query  1323  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1367  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1426

Query  1383  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1442
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1427  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1486

Query  1443  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1502
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1487  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1546

Query  1503  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1562
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1547  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1606

Query  1563  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1622
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1607  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1666

Query  1623  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1682
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  1667  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTC-ATCTTGGAACCGAAAAGC  1725

Query  1683  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACC  1742
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1726  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAACC  1785

Query  1743  TGCGGAAGGATCATT  1757
             |||||||||||||||
Sbjct  1786  TGCGGAAGGATCATT  1800


>dbj|AB013587.1| Pichia guilliermondii 18S rRNA gene, strain JCM 1539, partial
sequence
Length=1784

 Score = 3203 bits (1734),  Expect = 0.0
 Identities = 1751/1758 (99%), Gaps = 5/1758 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  209

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  210   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  267

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  268   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  327

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  328   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  387

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Sbjct  388   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  447

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
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Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
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Sbjct  508   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  567

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
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Sbjct  568   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  627

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
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Sbjct  628   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  687

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
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Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
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Sbjct  748   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  807

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
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Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
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Sbjct  927   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  986

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
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Sbjct  1107  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1166

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Sbjct  1167  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1226

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
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Sbjct  1707  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1766

Query  1741  CCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||
Sbjct  1767  CCTGCGGAAGGATCATTA  1784


>dbj|AB013566.1| Candida fukuyamaensis 18S rRNA gene, strain JCM 9396, partial
sequence
Length=1784

 Score = 3203 bits (1734),  Expect = 0.0
 Identities = 1751/1758 (99%), Gaps = 5/1758 (0%)
 Strand=Plus/Plus
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Query  3    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30   GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

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Sbjct  150  ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  209

Query  183  CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
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Sbjct  210  CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  267

Query  242  CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
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Query  302  GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
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Sbjct  328  GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  387

Query  362  TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
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Query  422  TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
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Query  482  AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
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Query  602  TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
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Sbjct  628  TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  687

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Sbjct  868  TATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCA  926

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Sbjct  927  TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  986
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Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
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Sbjct  987   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1046

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Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
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Sbjct  1107  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1166

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Sbjct  1167  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1226

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Query  1741  CCTGCGGAAGGATCATTA  1758
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Sbjct  1767  CCTGCGGAAGGATCATTA  1784


>dbj|AB013517.1| Candida xestobii 18S rRNA gene, strain JCM 9569, partial sequence
Length=1784

 Score = 3203 bits (1734),  Expect = 0.0
 Identities = 1751/1758 (99%), Gaps = 5/1758 (0%)
 Strand=Plus/Plus
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Query  3      GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
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Sbjct  30     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
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Query  302    GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
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Sbjct  328    GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  387

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Sbjct  448    TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  507

Query  482    AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
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Sbjct  508    AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  567

Query  542    GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
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Sbjct  628    TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  687

Query  662    AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
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Query  782    TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
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Sbjct  808    TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  867

Query  842    TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
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Sbjct  868    TATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCA  926

Query  901    TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
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Sbjct  927    TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  986
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Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  987   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1046

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Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
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Sbjct  1167  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1226

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1227  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1286

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1287  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1346

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1347  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1406

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1407  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1466

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1467  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1526

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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Sbjct  1527  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1586

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
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Sbjct  1587  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1646

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1647  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1706

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1707  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1766

Query  1741  CCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||
Sbjct  1767  CCTGCGGAAGGATCATTA  1784


>dbj|AB013528.1| Candida psychrophila 18S rRNA gene, strain JCM 2388, partial
sequence
Length=1782

 Score = 3201 bits (1733),  Expect = 0.0
 Identities = 1750/1757 (99%), Gaps = 5/1757 (0%)
 Strand=Plus/Plus
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Query  3    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30   GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123  ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
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Sbjct  150  ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  209

Query  183  CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  210  CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  269

Query  243  GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  270  GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  329

Query  303  GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
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Sbjct  330  GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  389

Query  363  ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
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Sbjct  390  ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  449

Query  423  GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
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Sbjct  450  GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  508

Query  483  ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  509  ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  568

Query  543  CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  569  CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  628

Query  603  GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
            |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  629  GGTTGGCCGGTCCG-CTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  687

Query  663  ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  688  ACCTTTCGGCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  747

Query  723  TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  748  TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  807

Query  783  CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  808  CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  867

Query  843  ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
            ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  868  ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  926

Query  902  TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  927  TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  986
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Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  987   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1046

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1047  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1106

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1107  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1166

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1167  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1226

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1227  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1286

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1287  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1346

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1347  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1406

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1407  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1466

Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
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Sbjct  1467  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1526

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
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Sbjct  1527  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1586

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1587  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1646

Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
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Sbjct  1647  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1706

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAAC  1741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  1707  TTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TGAAC  1765

Query  1742  CTGCGGAAGGATCATTA  1758
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Sbjct  1766  CTGCGGAAGGATCATTA  1782


>emb|X62649.1| D.hansenii 17S rDNA
Length=1810

 Score = 3192 bits (1728),  Expect = 0.0
 Identities = 1748/1756 (99%), Gaps = 7/1756 (0%)
 Strand=Plus/Plus
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Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  54    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  113

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  114   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  173

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  174   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  233

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  234   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  293

Query  243   GA-TGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
              | |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  294   -AGTGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  352

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  353   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  412

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
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Sbjct  413   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  472

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  473   TGACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  531

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  532   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  591

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
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Sbjct  592   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  651

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
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Sbjct  652   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  711

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
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Sbjct  712   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  771

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
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Sbjct  772   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  831

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGA-CGGTCGGGGGCATCA  840
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Sbjct  832   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACCGGTCGGGGGCATCA  891

Query  841   GTATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCA  900
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  892   GTATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAG-A  950

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  951   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  1010
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Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTC-ttttttt  1019
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Sbjct  1011  ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTT  1070

Query  1020  GACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGC  1079
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Sbjct  1071  GACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGC  1130

Query  1080  AAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTA  1139
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Sbjct  1131  AAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGC-GCTTA  1189

Query  1140  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1199
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Sbjct  1190  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1249

Query  1200  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1250  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1309

Query  1260  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1310  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1369

Query  1320  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1370  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1429

Query  1380  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1439
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Sbjct  1430  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1489

Query  1440  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1499
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Sbjct  1490  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1549

Query  1500  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1559
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Sbjct  1550  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1609

Query  1560  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1619
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Sbjct  1610  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1669

Query  1620  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1679
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Query  1680  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGA  1739
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Sbjct  1730  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGA  1789

Query  1740  ACCTGCGGAAGGATCA  1755
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Sbjct  1790  ACCTGCAGAAGGATCA  1805


>dbj|AB070854.1| Debaryomyces hansenii gene for 18S rRNA, partial sequence
Length=1752

 Score = 3188 bits (1726),  Expect = 0.0
 Identities = 1726/1726 (100%), Gaps = 0/1726 (0%)
 Strand=Plus/Plus
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Query  3    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  27   GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  86

Query  63   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  87   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  146

Query  123  ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  147  ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  206

Query  183  CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
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Sbjct  207  CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  266

Query  243  GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267  GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  326

Query  303  GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327  GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  386

Query  363  ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
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Sbjct  387  ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  446

Query  423  GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  447  GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  506

Query  483  ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
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Sbjct  507  ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  566

Query  543  CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  567  CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  626

Query  603  GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
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Sbjct  627  GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  686

Query  663  ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  687  ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  746

Query  723  TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
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Sbjct  747  TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  806

Query  783  CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
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Sbjct  807  CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  866

Query  843  ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  902
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  867  ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  926

Query  903  TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  962
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  927  TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  986
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Query  963   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGAC  1022
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Sbjct  987   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGAC  1046

Query  1023  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1047  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1106

Query  1083  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1107  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1166

Query  1143  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1167  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1226

Query  1203  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1262
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Sbjct  1227  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1286

Query  1263  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1322
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Sbjct  1287  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1346

Query  1323  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1382
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Sbjct  1347  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1406

Query  1383  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1442
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Sbjct  1407  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1466

Query  1443  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1502
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Sbjct  1467  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1526

Query  1503  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1562
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Query  1563  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1622
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Sbjct  1587  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1646

Query  1623  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1682
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Sbjct  1647  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1706

Query  1683  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1728
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Sbjct  1707  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1752


>dbj|AB106349.1| Debaryomyces hansenii var. hansenii gene for 18S rRNA, partial
sequence
Length=1752

 Score = 3188 bits (1726),  Expect = 0.0
 Identities = 1726/1726 (100%), Gaps = 0/1726 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  27    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  86

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  87    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  146

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  147   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  206

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  207   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  266

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  326

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  386

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  446

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  447   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  506

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  566

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  567   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  626

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
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Sbjct  627   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  686

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  687   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  746

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
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Sbjct  747   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  806

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
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Sbjct  807   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  866

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  867   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  926

Query  903   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  927   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  986

Query  963   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGAC  1022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  987   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGAC  1046

Query  1023  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1082
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Sbjct  1047  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1106

Query  1083  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1142
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Sbjct  1107  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1166

Query  1143  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1167  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1226

Query  1203  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1262
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Sbjct  1227  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1286

Query  1263  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1322
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Sbjct  1287  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1346

Query  1323  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1382
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Sbjct  1347  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1406

Query  1383  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1442
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Sbjct  1407  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1466

Query  1443  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1502
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Sbjct  1467  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1526

Query  1503  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1562
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Query  1563  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1622
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Sbjct  1587  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1646

Query  1623  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1682
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Sbjct  1647  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1706

Query  1683  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1728
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>dbj|AB013525.1| Candida fermenticarens 18S rRNA gene, strain JCM 9589, partial
sequence
Length=1783

 Score = 3186 bits (1725),  Expect = 0.0
 Identities = 1747/1757 (99%), Gaps = 4/1757 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
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Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
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Sbjct  90     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123    ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  150    ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  209

Query  183    CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  210    CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  269

Query  243    GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
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Sbjct  270    GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  329

Query  303    GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  330    GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  389

Query  363    ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  390    ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  449

Query  423    GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  450    GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  509

Query  483    ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
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Sbjct  510    ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  569

Query  543    CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
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Sbjct  570    CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCTT  629

Query  603    GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
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Sbjct  630    GGTTGGCCGGTCCGCCTTTT-GGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  688

Query  663    ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
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Sbjct  689    ACCATGCACCCTTGTGGTGTATGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  748

Query  723    TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  749    TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  808

Query  783    CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
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Sbjct  809    CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  868

Query  843    ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
              ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  869    ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  927

Query  902    TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  928    TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  987

Query  962    CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  988    CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1047

Query  1022   CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
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Sbjct  1048  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1107

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1108  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1167

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1168  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1227

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1228  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1287

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1288  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTGGC  1347

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1348  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1407

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1408  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1467

Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1468  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1527

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1528  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1587

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1588  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1647

Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1648  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1707

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAAC  1741
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  1708  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TGAAC  1766

Query  1742  CTGCGGAAGGATCATTA  1758
             |||||||||||||||||
Sbjct  1767  CTGCGGAAGGATCATTA  1783


>gb|AY520288.1| Candida sp. BG02-6-6-2-1 18S ribosomal RNA gene, partial sequence
Length=1741

 Score = 3182 bits (1723),  Expect = 0.0
 Identities = 1730/1733 (99%), Gaps = 2/1733 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70       AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123      ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130      ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  189

Query  183      CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190      CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  249

Query  243      GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250      GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  309

Query  303      GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  310      GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  369

Query  363      ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  370      ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  429

Query  423      GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  430      GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  489

Query  483      ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  490      ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  549

Query  543      CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  550      CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  609

Query  603      GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  610      GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  669

Query  663      ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
                ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  670      ACCTTTCGCCCTTGTGGTGATTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  729

Query  723      TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  730      TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  789

Query  783      CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  790      CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  849

Query  843      ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
                ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  850      ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  908

Query  902      TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  909      TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  968

Query  962      CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  969      CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1028

Query  1022     CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1029  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1088

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1089  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1148

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1149  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1208

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1209  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1268

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1269  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1328

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1329  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1388

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1389  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1448

Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1449  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1508

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1509  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1568

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1569  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1628

Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1629  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1688

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1734
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1689  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1741


>gb|AY518523.1| Candida athensensis strain BG02-7-13-014-3-1 18S ribosomal RNA
gene, partial sequence
Length=1761

 Score = 3181 bits (1722),  Expect = 0.0
 Identities = 1745/1755 (99%), Gaps = 5/1755 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129
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Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  189

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  247

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  307

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  308   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  367

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  368   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  427

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  428   TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  487

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  488   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  547

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  548   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  607

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  608   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  667

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  668   AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  727

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  787

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  847

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             ||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Sbjct  848   TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  906

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  966

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCttttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1026

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1086
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Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1146

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1206

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1266

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1326

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1386

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1387  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1446

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1447  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1506

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1507  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1566

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1567  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1626

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1627  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1686

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1687  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1746

Query  1741  CCTGCGGAAGGATCA  1755
             |||||||||||||||
Sbjct  1747  CCTGCGGAAGGATCA  1761


>dbj|AB013513.1| Pichia farinosa 18S rRNA gene, strain JCM 8895, partial sequence
Length=1785

 Score = 3177 bits (1720),  Expect = 0.0
 Identities = 1746/1758 (99%), Gaps = 4/1758 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149
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Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  209

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             || ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  210   CTCTTCGGAGCTTTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  269

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  270   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  329

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  330   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  389

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  390   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  449

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  450   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  509

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  510   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  569

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  570   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  629

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  630   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  689

Query  663   ACC-TTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
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Sbjct  690   ACCATTT-GCCCCTGTGGTGGATGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  748

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
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Sbjct  749   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  808

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  809   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  868

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
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Sbjct  869   TATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCA  927

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  928   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  987

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  988   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1047

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1048  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1107
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Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
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Sbjct  1108  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1167

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1168  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1227

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1228  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1287

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1288  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1347

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1348  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1407

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1408  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1467

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1468  GCGAGTTTTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1527

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1528  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1587

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1588  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1647

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1648  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1707

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1708  GTTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1767

Query  1741  CCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||
Sbjct  1768  CCTGCGGAAGGATCATTA  1785


>dbj|AB022440.1| Debaryomyces sp. MBIC4210 gene for 18S rRNA, partial sequence
Length=1738

 Score = 3171 bits (1717),  Expect = 0.0
 Identities = 1717/1717 (100%), Gaps = 0/1717 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  81

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  82    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  141
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Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  142   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  201

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  202   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  261

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  321

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  381

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  441

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  442   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  501

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  502   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  561

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  562   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  621

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  622   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  681

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  682   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  741

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  742   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  801

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  802   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  861

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  862   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  921

Query  903   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  922   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  981

Query  963   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGAC  1022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  982   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGAC  1041

Query  1023  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1042  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1101
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Query  1083  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1102  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1161

Query  1143  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1162  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1221

Query  1203  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1222  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1281

Query  1263  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1282  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1341

Query  1323  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1342  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1401

Query  1383  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1442
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1402  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1461

Query  1443  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1502
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1462  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1521

Query  1503  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1562
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1522  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1581

Query  1563  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1622
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1582  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1641

Query  1623  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1682
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Sbjct  1642  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1701

Query  1683  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGT  1719
             |||||||||||||||||||||||||||||||||||||
Sbjct  1702  TGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGT  1738


>gb|AY518520.1| Candida smithsonii strain BG02-7-13-007B-1-2 18S ribosomal RNA
gene, partial sequence
Length=1754

 Score = 3168 bits (1715),  Expect = 0.0
 Identities = 1738/1748 (99%), Gaps = 5/1748 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  189
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Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  247

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
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Sbjct  248   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  307

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  308   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  367

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  368   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  427

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
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Sbjct  428   TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  487

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  488   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  547

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
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Sbjct  548   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  607

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  608   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  667

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  668   AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  727

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
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Sbjct  728   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  787

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  847

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             ||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Sbjct  848   TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  906

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  966

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1026

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1086

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1146
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Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1206

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1266

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1326

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1386

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1387  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1446

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1447  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1506

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1507  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1566

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1567  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1626

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1627  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1686

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1687  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1746

Query  1741  CCTGCGGA  1748
             ||||||||
Sbjct  1747  CCTGCGGA  1754


>gb|AY242150.1| Candida sp. BG99-8-11-1-4-1 18S ribosomal RNA gene, partial
sequence
Length=1731

 Score = 3164 bits (1713),  Expect = 0.0
 Identities = 1720/1723 (99%), Gaps = 2/1723 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  130   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  189

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  249

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  250   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  309

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  310   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  369

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  370   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  429

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  430   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  489

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  490   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  549

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  550   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  609

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  610   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  669

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  670   ACCTTTCGCCCTTGTGGTGTTTGTCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  729

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  730   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  789

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  790   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  849

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  850   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  908

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  909   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  968

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  969   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1028

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1029  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1088

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1089  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1148

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1149  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1208

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1209  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1268

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1269  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1328

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1329  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1388

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1389  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1448

Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1449  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1508

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1509  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1568

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1569  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1628

Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1629  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1688

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAA  1724
              |||||||||||||||||||||||||||||||||||||||||||
Sbjct  1689  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAA  1731


>gb|AY518522.1| Candida athensensis strain BG02-5-23-003I-4 18S ribosomal RNA
gene, partial sequence
Length=1751

 Score = 3162 bits (1712),  Expect = 0.0
 Identities = 1735/1745 (99%), Gaps = 5/1745 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  189

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
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             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  247

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  307

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  308   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  367

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  368   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  427

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  428   TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  487

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  488   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  547

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  548   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  607

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  608   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  667

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  668   AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  727

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  787

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  847

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             ||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Sbjct  848   TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  906

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  966

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1026

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1086

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1146

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147   TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1206

Query  1201   GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207   GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1266

Query  1261   TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267   TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1326

Query  1321   CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327   CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1386

Query  1381   AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1387   AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1446

Query  1441   ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1447   GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1506

Query  1501   ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1507   ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1566

Query  1561   TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1567   TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1626

Query  1621   GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1627   GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1686

Query  1681   GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1687   GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1746

Query  1741   CCTGC  1745
              |||||
Sbjct  1747   CCTGC  1751


>dbj|AB013546.1| Candida laureliae 18S rRNA gene, strain JCM 8917, partial sequence
Length=1782

 Score = 3162 bits (1712),  Expect = 0.0
 Identities = 1744/1758 (99%), Gaps = 7/1758 (0%)
 Strand=Plus/Plus

Query  3      GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123    ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
              |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150    ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183    CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
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Sbjct  209   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  268

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  269   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  328

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  329   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  388

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  389   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  448

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  449   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  508

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  509   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  568

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  569   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  628

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  629   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  687

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  688   ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  747

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  748   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  807

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  808   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  867

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  868   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  926

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  927   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  986

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  987   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1046

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1047  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1106

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1107  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1166

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1167  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1226

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1227  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1286

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1287  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1346

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1347  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1406

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1407  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1466

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||| | ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1467  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1525

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1526  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1585

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1586  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1645

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1646  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1705

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  1706  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TGAA  1764

Query  1741  CCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||
Sbjct  1765  CCTGCGGAAGGATCATTA  1782


>emb|X83821.1| Debaryomyces udenii 18S rRNA gene (NCYC 2394)
Length=1804

 Score = 3162 bits (1712),  Expect = 0.0
 Identities = 1742/1761 (98%), Gaps = 5/1761 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             |||||||||||||||||||||||  |   ||||||||  ||||| |||||||||||||||
Sbjct  46    GCCATGCATGTCTAAGTATAAGCNNTNNNTACAGTGANNCTGCGNATGGCTCATTAAATC  105

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  106   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  165

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  225

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
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Sbjct  226   CTCTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  285

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  286   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  345

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  346   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  405

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  406   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  465

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  466   GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  524

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  525   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  584

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             |||||||||||||||||||||||||||||||||||||||||| |||||||||||||| ||
Sbjct  585   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGNAGTTGAACCTTGGGTTT  644

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  645   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  704

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  705   ACCTCTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  764

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  765   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  824

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Sbjct  825   CTATTTTGTTGGTTTCTAGGNNCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  884

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  885   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  943

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  944   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  1003

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1004  CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1063

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1064  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1123

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1124  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1183

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
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Sbjct  1184  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1243

Query  1202  CTCTTTCTTGATTTTGTGGGT-GGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  1244  CTCTTTCTTGATTTTGTGGGTCGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1303

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1304  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1363

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGG-CAA  1379
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  1364  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCCAA  1423

Query  1380  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1424  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1483

Query  1440  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1484  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1543

Query  1500  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1544  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1603

Query  1560  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1604  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1663

Query  1620  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1664  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1723

Query  1680  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGA  1739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1724  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGA  1783

Query  1740  ACCTGCGGAAGGATCATTACA  1760
             |||||||||||||||||||||
Sbjct  1784  ACCTGCGGAAGGATCATTACA  1804


>gb|EF194890.1| Pichia guilliermondii strain HJM 18S ribosomal RNA gene, partial
sequence
Length=1773

 Score = 3157 bits (1709),  Expect = 0.0
 Identities = 1736/1748 (99%), Gaps = 5/1748 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  29    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  88

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  89    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  148

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  149   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208
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Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  266

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  326

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  386

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  446

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  447   TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  506

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  566

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  567   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  626

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  627   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  686

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  687   AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  746

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  747   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  806

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  807   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  866

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             ||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Sbjct  867   TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  925

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  926   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  985

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  986   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1045

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1046  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1105

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1106  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1165
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Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1166  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1225

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1226  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1285

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1286  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1345

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1346  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1405

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  1406  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGGCGGAGCCA  1465

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1466  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1525

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  1526  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAGGCGCAAGTCATCAGC  1585

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1586  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1645

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1646  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1705

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1706  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1765

Query  1741  CCTGCGGA  1748
             ||||||||
Sbjct  1766  CCTGCGGA  1773


>gb|DQ534400.1| Debaryomyces hansenii strain WHCX-1 18S ribosomal RNA gene, partial
sequence
Length=1740

 Score = 3157 bits (1709),  Expect = 0.0
 Identities = 1719/1723 (99%), Gaps = 4/1723 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  20    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  79

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  80    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  139

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  140   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  199
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Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  200   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  259

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  319

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  379

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  439

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  499

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  559

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  619

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  620   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  679

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  680   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  739

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  799

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  800   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  859

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  860   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  918

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  919   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  978

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  979   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1038

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1039  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1098

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1099  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1158
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Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1159  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1218

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1219  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1278

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1279  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1338

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1339  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1398

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1399  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1458

Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1459  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1518

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1519  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1578

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1579  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1638

Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1639  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1698

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAA  1724
             ||||||||||||||||||| ||||||||||||||||| |||||
Sbjct  1699  CTGGTCAAACTTGGTCATT-AGAGGAAGTAAAAGTCG-AACAA  1739


>dbj|AB054277.1| Debaryomyces prosopidis gene for 18S rRNA, partial sequence,
strain:JCM 9913
Length=1753

 Score = 3157 bits (1709),  Expect = 0.0
 Identities = 1726/1735 (99%), Gaps = 4/1735 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  201   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  440

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  500

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  560

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  620

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  621   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  680

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  681   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  740

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  800

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  801   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  860

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  861   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  919

Query  902   TT-GCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  920   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  979

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  980   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1039

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  1040  ACGCACTCGGCACCTTACGGGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1099

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             |||||||||||||||||||||||||||||||||||||||||||||| | |||||||||||
Sbjct  1100  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTAA  1158

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1159  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1218

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1219  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1278

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
              ||||||||||   |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1279  TCTGCTTAATNNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1338

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1339  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1398

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1399  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1458

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1459  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1518

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1519  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1578

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1579  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1638

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1639  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1698

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1699  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1753


>dbj|AB054269.1| Debaryomyces hansenii var. fabryi gene for 18S rRNA, partial
sequence, stain:JCM 2104
Length=1753

 Score = 3157 bits (1709),  Expect = 0.0
 Identities = 1726/1735 (99%), Gaps = 4/1735 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
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Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
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Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
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Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
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Sbjct  201   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
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Sbjct  261    GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303    GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321    GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363    ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
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Sbjct  381    ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  440

Query  423    GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
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Sbjct  441    GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  500

Query  483    ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501    ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  560

Query  543    CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561    CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  620

Query  603    GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  621    GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  680

Query  663    ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  681    ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  740

Query  723    TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741    TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  800

Query  783    CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  801    CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  860

Query  843    ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
              ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  861    ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  919

Query  902    TT-GCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  920    TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  979

Query  961    ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  980    ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1039

Query  1021   ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
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Sbjct  1040   ACGCACTCGGCACCTTACGGGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1099

Query  1081   AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
              |||||||||||||||||||||||||||||||||||||||||||||| | |||||||||||
Sbjct  1100   AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTAA  1158

Query  1141   TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1159   TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1218

Query  1201   GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
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Sbjct  1219  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1278

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||   |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1279  TCTGCTTAATNNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1338

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1339  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1398

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1399  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1458

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
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Sbjct  1459  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1518

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1519  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1578

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
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Sbjct  1579  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1638

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1639  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1698

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1699  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1753


>dbj|AB013555.1| Candida krissii 18S rRNA gene, strain JCM 9454, partial sequence
Length=1782

 Score = 3157 bits (1709),  Expect = 0.0
 Identities = 1743/1758 (99%), Gaps = 7/1758 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   CTCTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  268

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
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Sbjct  269   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  328

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
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Sbjct  329   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  388

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  389   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  448

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  449   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  508

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
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Sbjct  509   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  568

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  569   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  628

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  629   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  687

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  688   ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  747

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  748   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  807

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  808   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  867

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  868   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  926

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  927   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  986

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  987   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1046

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1047  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1106

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1107  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1166

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1167  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1226

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1227  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1286

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
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Sbjct  1287  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1346

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1347  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1406

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1407  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1466

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
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Sbjct  1467  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1525

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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Sbjct  1526  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1585

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
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Sbjct  1586  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1645

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1646  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1705

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
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Sbjct  1706  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TGAA  1764

Query  1741  CCTGCGGAAGGATCATTA  1758
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Sbjct  1765  CCTGCGGAAGGATCATTA  1782


>dbj|AB013553.1| Candida ralunensis 18S rRNA gene, strain JCM 8923, partial
sequence
Length=1781

 Score = 3157 bits (1709),  Expect = 0.0
 Identities = 1743/1758 (99%), Gaps = 8/1758 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
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Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
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Sbjct  209   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  268

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  269   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  328
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Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  329   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  388

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
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Sbjct  389   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  448

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  449   GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  507

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
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Sbjct  508   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  567

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
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Sbjct  568   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  627

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
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Sbjct  628   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  686

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
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Sbjct  687   ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  746

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  747   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  806

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
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Sbjct  807   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  866

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  867   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  925

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  926   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  985

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  986   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1045

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
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Sbjct  1046  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1105

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
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Sbjct  1106  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1165

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1166  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1225

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1226  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1285
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Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1286  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1345

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1346  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1405

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1406  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1465

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
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Sbjct  1466  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1524

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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Sbjct  1525  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1584

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1585  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1644

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1645  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1704

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  1705  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TGAA  1763

Query  1741  CCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||
Sbjct  1764  CCTGCGGAAGGATCATTA  1781


>dbj|AB013537.1| Candida schatavii 18S rRNA gene, strain JCM 1778, partial sequence
Length=1781

 Score = 3157 bits (1709),  Expect = 0.0
 Identities = 1743/1758 (99%), Gaps = 8/1758 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  268

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  269   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  328
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Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  329   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  388

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  389   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  448

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  449   GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  507

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  508   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  567

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  568   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  627

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  628   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  686

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  687   ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  746

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  747   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  806

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  807   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  866

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  867   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  925

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  926   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  985

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  986   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1045

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
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Sbjct  1046  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1105

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
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Sbjct  1106  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1165

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1166  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1225

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1226  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1285
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Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1286  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1345

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
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Sbjct  1346  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1405

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
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Sbjct  1406  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1465

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
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Sbjct  1466  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1524

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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Sbjct  1525  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1584

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
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Sbjct  1585  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1644

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
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Sbjct  1645  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1704

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
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Sbjct  1705  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TGAA  1763

Query  1741  CCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||
Sbjct  1764  CCTGCGGAAGGATCATTA  1781


>dbj|AB013532.1| Candida boleticola 18S rRNA gene, strain JCM 1500, partial
sequence
Length=1781

 Score = 3157 bits (1709),  Expect = 0.0
 Identities = 1743/1758 (99%), Gaps = 8/1758 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  268

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  269   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  328
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Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  329   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  388

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  389   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  448

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  449   GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  507

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
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Sbjct  508   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  567

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
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Sbjct  568   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  627

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
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Sbjct  628   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  686

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
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Sbjct  687   ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  746

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
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Sbjct  747   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  806

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
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Sbjct  807   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  866

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  867   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  925

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  926   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  985

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  986   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1045

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
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Sbjct  1046  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1105

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
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Sbjct  1106  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1165

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1166  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1225

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1226  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1285
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Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1286  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1345

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1346  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1405

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCTACACTGACGGAGCCAA  1441
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1406  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCTACACTGACGGAGCCAG  1465

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
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Sbjct  1466  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1524

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1525  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1584

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1585  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1644

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
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Sbjct  1645  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1704

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  1705  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TGAA  1763

Query  1741  CCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||
Sbjct  1764  CCTGCGGAAGGATCATTA  1781


>dbj|AB013509.1| Candida zeylanoides 18S rRNA gene, strain JCM 1627, partial
sequence
Length=1782

 Score = 3157 bits (1709),  Expect = 0.0
 Identities = 1743/1758 (99%), Gaps = 7/1758 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   CTCTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  268

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  269   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  328

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  329   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  388

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  389   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  448

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  449   GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  507

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  508   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  567

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  568   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  627

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  628   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  686

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  687   ACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  746

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  747   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  806

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  807   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  866

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  867   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  925

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  926   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  985

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  986   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1045

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1046  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1105

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1106  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1165

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1166  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1225

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1226  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1285

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1286  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1345

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1346  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1405

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1406  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1465

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||| | ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1466  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1524

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1525  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1584

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1585  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1644

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1645  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1704

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1705  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1764

Query  1741  CCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||
Sbjct  1765  CCTGCGGAAGGATCATTA  1782


>gb|DQ534402.1| Debaryomyces hansenii strain hcx-1 18S ribosomal RNA gene, partial
sequence
Length=1738

 Score = 3153 bits (1707),  Expect = 0.0
 Identities = 1717/1721 (99%), Gaps = 4/1721 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  15    GCC-TGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  73

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  74    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  133

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  193

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  194   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  253

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  254   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  313

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  314   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  373

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  374   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  433

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  434   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  493

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  494   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  553

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  554   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  613

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  614   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  673

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  674   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  733

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  734   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  793

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  794   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  853

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  854   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  912

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  913   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  972

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  973   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1032

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1033  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1092

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1093  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1152

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1153  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1212

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1213   CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1272

Query  1262   CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1273   CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1332

Query  1322   TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1333   TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1392

Query  1382   ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1393   ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1452

Query  1442   CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1453   CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1512

Query  1502   TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1513   TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1572

Query  1562   TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1573   TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1632

Query  1622   CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1633   CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1692

Query  1682   CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAAC  1722
              ||||||||||||||||||||||||||||||||||||| |||
Sbjct  1693   CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCG-AAC  1732


>dbj|AB054261.1| Debaryomyces maramus gene for 18S rRNA, partial sequence,
strain:JCM
1528
Length=1752

 Score = 3153 bits (1707),  Expect = 0.0
 Identities = 1725/1734 (99%), Gaps = 3/1734 (0%)
 Strand=Plus/Plus

Query  3      GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123    ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141    ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183    CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201    CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243    GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261    GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320
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Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  440

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  500

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  560

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  561   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGTTT  620

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  621   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  680

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  681   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  740

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  800

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  801   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  860

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| | | ||||||||||||||||||||||||
Sbjct  861   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTATC-GAAGACTAACTACTGCGAAAGCAT  919

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  920   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  979

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  980   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1039

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  1040  CGCACTCGGCACCTTACGGGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1099

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  1100  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGC-TGCGGCTTAAT  1158

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1159  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1218

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1219  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1278
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Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1279  CTGCTTAATTNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1338

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1339  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1398

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1399  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1458

Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1459  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1518

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  1519  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTTATCAGCT  1578

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1579  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1638

Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1639  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1698

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1699  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1752


>gb|AF440017.1| Debaryomyces mycophilus 18S ribosomal RNA gene, partial sequence
Length=1769

 Score = 3151 bits (1706),  Expect = 0.0
 Identities = 1733/1745 (99%), Gaps = 5/1745 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  27    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  86

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  87    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  146

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  147   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAACG  206

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  207   CTCTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  266

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  326

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  386
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Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  446

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  447   GACAATAAATAACGATACAGGGCCCTTTTGGGTCTTGTAATTGGAATGAGTACAATGTAA  506

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  566

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  567   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  626

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  627   GGTTGGCCGGTCCGCCTTTTTGGCGAGCACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  686

Query  663   ACCT-TTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             |||| || |||||||||||| | |||||||||||||||||||||||||||||||||||||
Sbjct  687   ACCTATT-GCCCTTGTGGTGGTAGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  745

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  746   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  805

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  806   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  865

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             |||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||
Sbjct  866   TATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCA  924

Query  901   -TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGA  959
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  925   TTTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGA  984

Query  960   TACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCttttttt  1019
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  985   TACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTT  1044

Query  1020  GACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGC  1079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1045  GACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGC  1104

Query  1080  AAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTA  1139
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1105  AAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTA  1164

Query  1140  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1165  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1224

Query  1200  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1225  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1284

Query  1260  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1285  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1344
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Query  1320  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1345  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1404

Query  1380  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1405  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1464

Query  1440  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1499
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1465  AGCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1524

Query  1500  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1525  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1584

Query  1560  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1585  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1644

Query  1620  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1645  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1704

Query  1680  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGA  1739
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1705  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGA  1764

Query  1740  ACCTG  1744
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Sbjct  1765  ACCTG  1769


>dbj|AB054272.1| Debaryomyces coudertii gene for 18S rRNA, partial sequence,
strain:JCM
2387
Length=1750

 Score = 3151 bits (1706),  Expect = 0.0
 Identities = 1725/1734 (99%), Gaps = 5/1734 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
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Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  440

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  441   GACAATAAATAACGATACAGGGCCC-TTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  499

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  559

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  619

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  620   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  679

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  680   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  739

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TCAAAGCAGGCC-TTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  798

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  799   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  858

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  859   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  917

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  918   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  977

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  978   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1037

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  1038  CGCACTCGGCACCTTACGGGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1097

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Sbjct  1098  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTAAT  1156

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1157  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1216

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1217  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1276

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
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             ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1277  CTGCTTAATTNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1336

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1337  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1396

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1397  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1456

Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1457  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1516

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1517  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1576

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1577  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1636

Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1637  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1696

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1697  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1750


>dbj|AB013562.1| Candida beechii 18S rRNA gene, strain JCM 1802, partial sequence
Length=1781

 Score = 3151 bits (1706),  Expect = 0.0
 Identities = 1742/1758 (99%), Gaps = 8/1758 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             | |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   C-TTTC-GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  266

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  326

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  386

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  446

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  447   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  506

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  566

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  567   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAGCTCGTAGTTGAACCTTGGGTTT  626

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  627   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  685

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  686   ACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  745

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  746   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  805

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  806   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  865

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  866   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  924

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  925   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  984

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  985   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1044

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1045  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1104

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1105  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1164

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1165  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1224

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1225  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1284

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1285  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1344

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1345  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1404

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1405  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1464

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||| | ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1465  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1523

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1524  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1583

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1584  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1643

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1644  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1703

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1704  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1763

Query  1741  CCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||
Sbjct  1764  CCTGCGGAAGGATCATTA  1781


>dbj|AB054270.1| Debaryomyces hansenii var. hansenii gene for 18S rRNA, partial
sequence, strain:JCM 1990
Length=1752

 Score = 3147 bits (1704),  Expect = 0.0
 Identities = 1725/1735 (99%), Gaps = 5/1735 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380
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Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  440

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  441   GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  499

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  559

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  619

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  620   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  679

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  680   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  739

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  799

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  800   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  859

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA-  900
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||| 
Sbjct  860   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  918

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  919   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  978

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  979   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1038

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||| |||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  1039  ACGGACTCGGCACCTTACGGGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1098

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             |||||||||||||||||||||||||||||||||||||||||||||| | |||||||||||
Sbjct  1099  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTAA  1157

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1158  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1217

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1218  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1277

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             |||||||||||  |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1278  TCTGCTTAATTNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1337
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Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1338  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1397

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1398  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1457

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1458  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1517

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1518  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1577

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1578  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1637

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1638  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1697

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1698  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1752


>gb|AY520262.1| Candida sp. BG02-7-14-001H-1-1 18S ribosomal RNA gene, partial
sequence
Length=1750

 Score = 3145 bits (1703),  Expect = 0.0
 Identities = 1732/1745 (99%), Gaps = 6/1745 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  130   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  188

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  248

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  308

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  309   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  368

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  369   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  428
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Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  429   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  488

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  489   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  548

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  549   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  608

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  609   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  667

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  668   ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  727

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  787

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  847

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  848   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  906

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  966

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1026

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1086

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1146

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1206

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1266

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1326

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1386
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Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1387  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1446

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||| | ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1447  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1505

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1506  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1565

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1566  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1625

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1626  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1685

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1686  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1745

Query  1741  CCTGC  1745
             |||||
Sbjct  1746  CCTGC  1750


>dbj|AB054271.1| Debaryomyces nepalensis gene for 18S rRNA, partial sequence,
strain:JCM 2095
Length=1752

 Score = 3142 bits (1701),  Expect = 0.0
 Identities = 1725/1736 (99%), Gaps = 7/1736 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
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Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACA-GGGGAGGTAGT  439

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  499

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  559

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  619

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  620   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  679

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  680   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  739

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TCAAAGCAGGCC-TTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  798

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  799   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  858

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA-  900
             ||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||
Sbjct  859   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  917

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  918   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  977

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  978   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1037

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||| ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  1038  ACGGACTCGGCACCTTACGGGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1097

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGT-GGAGCCTGCGGCTTA  1139
             |||||||||||||||||||||||||||||||||||||||||||| ||| |||||||||||
Sbjct  1098  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGGA-CCTGCGGCTTA  1156

Query  1140  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1157  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1216

Query  1200  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1217  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1276

Query  1260  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1319
             ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1277  GTCTGCTTAATTNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1336

Query  1320  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1337  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1396

Query  1380  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1397  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1456

Query  1440  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1457  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1516

Query  1500  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1517  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1576

Query  1560  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1577  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1636

Query  1620  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1637  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1696

Query  1680  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1697  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1752


>gb|AY553853.1| Candida fermentati strain NRRL Y-17903 18S ribosomal RNA gene,
partial sequence
Length=1740

 Score = 3142 bits (1701),  Expect = 0.0
 Identities = 1724/1734 (99%), Gaps = 5/1734 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  189

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  247

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  307

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  308   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  367

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  368   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  427

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
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Sbjct  428   TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  487

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  488   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  547

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  548   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  607

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  608   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  667

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  668   AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  727

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  787

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  847

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             ||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Sbjct  848   TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  906

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  966

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1026

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1086

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1146

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1206

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1266

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1326

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1386

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
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Sbjct  1387  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1446

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1447  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1506

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1507  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1566

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1567  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1626

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1627  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1686

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1734
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1687  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1740


>gb|EF428134.1| Debaryomyces hansenii strain shiziwei2 18S ribosomal RNA gene,
partial sequence
Length=1708

 Score = 3140 bits (1700),  Expect = 0.0
 Identities = 1706/1709 (99%), Gaps = 2/1709 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  60

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  120

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  180

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  240

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  300

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  360

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  420

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  480
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Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  540

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  600

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  660

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  720

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   TCAAAGCAGGCCYTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  780

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  840

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  841   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  899

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  900   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  959

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  960   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1019

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1020  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1079

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1080  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1139

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1140  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1199

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1200  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1259

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1260  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1319

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1320  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1379

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1380  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1439
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Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1440  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1499

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1500  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1559

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1560  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1619

Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1620  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1679

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGT  1710
             |||||||||||||||||||||||||||||
Sbjct  1680  CTGGTCAAACTTGGTCATTTAGAGGAAGT  1708


>dbj|AB013581.1| Candida santamariae var. membranifaciens 18S rRNA gene, strain
JCM 9844, partial sequence
Length=1781

 Score = 3140 bits (1700),  Expect = 0.0
 Identities = 1740/1758 (98%), Gaps = 8/1758 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             | |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   C-TTTC-GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  266

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  326

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  386

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  446

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  447   GACAATAAATAACGATACAGGGGCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  506

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  566
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Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
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Sbjct  567   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGTTT  626

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||| |||| ||||||||||||||||||||||| ||||||||||||||||
Sbjct  627   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAACCTTTCCTTCTGGCTA  685

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  686   ACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  745

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  746   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  805

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  806   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  865

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  866   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  924

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  925   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  984

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  985   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1044

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1045  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1104

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1105  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1164

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1165  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1224

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1225  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1284

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1285  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1344

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1345  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1404

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1405  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1464

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||| | ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1465  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1523
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Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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Sbjct  1524  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1583

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1584  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1643

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1644  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1703

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1704  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1763

Query  1741  CCTGCGGAAGGATCATTA  1758
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Sbjct  1764  CCTGCGGAAGGATCATTA  1781


>dbj|AB013536.1| Candida santamariae var. santamariae 18S rRNA gene, strain JCM
1816, partial sequence
Length=1780

 Score = 3138 bits (1699),  Expect = 0.0
 Identities = 1740/1758 (98%), Gaps = 9/1758 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             | |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   C-TTTC-GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  266

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  326

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  386

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  446

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  447   GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  505

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
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Sbjct  506   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  565

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  566   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGTTT  625

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||| |||| ||||||||||||||||||||||| ||||||||||||||||
Sbjct  626   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAACCTTTCCTTCTGGCTA  684

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  685   ACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  744

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  745   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  804

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  805   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  864

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  865   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  923

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  924   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  983

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  984   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1043

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1044  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1103

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1104  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1163

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1164  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1223

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1224  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1283

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1284  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1343

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1344  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1403

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1404  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1463

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||| | ||||||||||||||||||||||| ||||||||||||||||||||||||||||
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Sbjct  1464  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1522

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1523  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1582

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1583  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1642

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1643  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1702

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1703  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1762

Query  1741  CCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||
Sbjct  1763  CCTGCGGAAGGATCATTA  1780


>dbj|AB013534.1| Candida oleophila 18S rRNA gene, strain JCM 1620, partial sequence
Length=1780

 Score = 3138 bits (1699),  Expect = 0.0
 Identities = 1741/1759 (98%), Gaps = 11/1759 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  266

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  326

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  386

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  446

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  447   TGACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  505

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
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Sbjct  506   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  565

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  566   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  625

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||| |||| |||||||||||||||||||||||||||||||||||||||
Sbjct  626   TGGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  684

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  685   AACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  744

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  745   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  804

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  805   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  864

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             |||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||
Sbjct  865   TATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCA  923

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  924   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  983

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  984   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1043

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1044  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1103

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1104  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1163

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1164  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1223

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1224  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1283

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1284  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1343

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1344  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1403

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1404  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1463

Query  1441  ACGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1499
              ||||| | ||||||||||||||||||||||| |||||||||||||||||||||||||||
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Sbjct  1464  GCGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGG  1522

Query  1500  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1523  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1582

Query  1560  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1583  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1642

Query  1620  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1679
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1643  GGCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1702

Query  1680  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGA  1739
             |||| ||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  1703  AGCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TGA  1761

Query  1740  ACCTGCGGAAGGATCATTA  1758
             |||||||||||||||||||
Sbjct  1762  ACCTGCGGAAGGATCATTA  1780


>emb|FN690502.1| Uncultured fungus partial 18S rRNA gene, clone 3c-D10
Length=1699

 Score = 3136 bits (1698),  Expect = 0.0
 Identities = 1698/1698 (100%), Gaps = 0/1698 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  2     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  61

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  62    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  121

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  122   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  181

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  182   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  241

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  242   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  301

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  302   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  361

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  362   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  421

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  422   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  481

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  482   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  541

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  542   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  601

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  602   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  661

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
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Sbjct  662   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  721

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  722   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  781

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  782   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  841

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  902
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  842   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATT  901

Query  903   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  962
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  902   TGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATAC  961

Query  963   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGAC  1022
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  962   CGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGAC  1021

Query  1023  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1082
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1022  GCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAG  1081

Query  1083  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1142
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1082  GCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATT  1141

Query  1143  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1142  TGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGC  1201

Query  1203  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1262
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1202  TCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTC  1261

Query  1263  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1322
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1262  TGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCT  1321

Query  1323  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1382
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1322  GGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAA  1381

Query  1383  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1442
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1382  CAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAAC  1441

Query  1443  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1502
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1442  GAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGAT  1501

Query  1503  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1562
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1502  AGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTT  1561

Query  1563  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1622
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1562  GCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGC  1621

Query  1623  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1682
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1622  TTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGC  1681

Query  1683  TGGTCAAACTTGGTCATT  1700
             ||||||||||||||||||
Sbjct  1682  TGGTCAAACTTGGTCATT  1699


>dbj|AB054259.1| Debaryomyces robertsiae gene for 18S rRNA, partial sequence,
strain:CBS 2934
Length=1751

 Score = 3136 bits (1698),  Expect = 0.0
 Identities = 1723/1735 (99%), Gaps = 6/1735 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
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Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
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Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
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Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  258

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  259   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  318

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  319   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  378

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  379   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  438

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  439   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  498

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  499   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  558

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
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Sbjct  559   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  618

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  619   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  678

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             ||||| |||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  679   AACCTCTCGCCCTTGTGGCGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  738

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  739   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  798

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  799   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  858

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCA  900
             |||||||||||||||||||||||||||||||| || ||||||||||||||||||||||||
Sbjct  859   TATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCA  917

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  918   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  977

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  978   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1037

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
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Sbjct  1038  ACGGACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1097

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
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Sbjct  1098  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTAA  1156

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1157  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1216

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1217  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1276

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1277  TCTGCTTAATTGNNATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1336

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1337  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1396

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
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Sbjct  1397  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1456

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
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Sbjct  1457  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1516

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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Sbjct  1517  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1576

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1577  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1636

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1637  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1696

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
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Sbjct  1697  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1751


>dbj|AB070856.1| Marine yeast Y5318 gene for 18S rRNA, partial sequence
Length=1751

 Score = 3136 bits (1698),  Expect = 0.0
 Identities = 1719/1728 (99%), Gaps = 5/1728 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  27    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  86

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  87    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  146

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
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Sbjct  147   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  206

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  207   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  264

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  265   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  324

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  325   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  384

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  385   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  444

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  445   TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  504

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  505   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  564

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
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Sbjct  565   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  624

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
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Sbjct  625   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  684

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
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Sbjct  685   AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  744

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
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Sbjct  745   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  804

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
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Sbjct  805   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  864

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
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Sbjct  865   TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  923

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  924   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  983

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  984   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1043

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
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Sbjct  1044  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1103

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1104  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1163

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
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Sbjct  1164  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1223

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
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Sbjct  1224  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1283

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1284  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1343

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
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Sbjct  1344  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1403

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
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Sbjct  1404  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1463

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
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Sbjct  1464  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1523

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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Sbjct  1524  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1583

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
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Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1644  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1703

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1728
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Sbjct  1704  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1751


>dbj|AB106351.1| Debaryomyces hansenii gene for 18S rRNA, partial sequence
Length=1751

 Score = 3136 bits (1698),  Expect = 0.0
 Identities = 1719/1728 (99%), Gaps = 5/1728 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  27    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  86

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  87    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  146

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  147   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  206

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  207   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  264

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
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Sbjct  265   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  324

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
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Sbjct  325   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  384

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  385   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  444

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
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Sbjct  445   TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  504

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
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Sbjct  505   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  564

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
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Sbjct  565   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  624

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  625   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  684

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
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             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  685   AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  744

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  745   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  804

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  805   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  864

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             ||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Sbjct  865   TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  923

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  924   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  983

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  984   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1043

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1044  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1103

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1104  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1163

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1164  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1223

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1224  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1283

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1284  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1343

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1344  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1403

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1404  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1463

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1464  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1523

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1524  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1583

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1584  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1643

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1644  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1703

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1728
             ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1704  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1751


>emb|AJ508273.1| Debaryomyces hansenii partial 18S rRNA gene, strain CBS 789T
Length=1710

 Score = 3134 bits (1697),  Expect = 0.0
 Identities = 1707/1712 (99%), Gaps = 3/1712 (0%)
 Strand=Plus/Plus

Query  18    GTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTT  77
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTT  60

Query  78    GATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAAT  137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAAT  120

Query  138   CCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCTTTTCGGAGCTCTT  197
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCTTTTCGGAGCTCTT  180

Query  198   TGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAAA  257
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAAA  240

Query  258   TTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAAC  317
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAAC  300

Query  318   GGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAA  377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAA  360

Query  378   GGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACGA  437
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACGA  420

Query  438   TACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGGA  497
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGGA  480

Query  498   ACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATA  557
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   ACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATA  540

Query  558   TTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGTTGGCCGGTCCGC  617
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   TTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGTTGGCCGGTCCGC  600

Query  618   CTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCTTTCGCCCTTGT  677
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   CTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCTTTCGCCCTTGT  660

Query  678   GGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTTT  737
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   GGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTTT  720

Query  738   GCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTTT  797
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721     GCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTTT  780

Query  798     CTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGAG  857
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781     CTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGAG  840

Query  858     GTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACGTTT  916
               |||||||||||||||| || |||||||||||||||||||||| |||||||||||||||||
Sbjct  841     GTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAG-ATTTGCCAAGGACGTTT  898

Query  917     TCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTAA  976
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  899     TCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTAA  958

Query  977     CCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGACGCACTCGGCACCTT  1036
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  959     CCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGACGCACTCGGCACCTT  1018

Query  1037    ACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAG  1096
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1019    ACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAG  1078

Query  1097    GAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGG  1156
               |||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||||
Sbjct  1079    GAATTGACGGAAGGGCACCACCAGGAGTKGAGMCTGCGGCTTAATTTGACTCAACACGGG  1138

Query  1157    GAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTT  1216
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1139    GAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTT  1198

Query  1217    GTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCGAT  1276
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1199    GTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCGAT  1258

Query  1277    AACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACTTC  1336
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1259    AACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACTTC  1318

Query  1337    TTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC  1396
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1319    TTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGC  1378

Query  1397    CCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAACGAGTATTAACCTTG  1456
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1379    CCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAACGAGTATTAACCTTG  1438

Query  1457    GCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAATT  1516
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1439    GCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAATT  1498

Query  1517    ATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACGTC  1576
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1499    ATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACGTC  1558

Query  1577    CCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCTCC  1636
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1559    CCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCTCC  1618

Query  1637    GGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTGGT  1696
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1619    GGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTGGT  1678

Query  1697    CATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1728
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              ||||||||||||||||||||||||||||||||
Sbjct  1679   CATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1710


>dbj|AB054268.1| Debaryomyces udenii gene for 18S rRNA, partial sequence,
strain:JCM
7885
Length=1751

 Score = 3133 bits (1696),  Expect = 0.0
 Identities = 1723/1736 (99%), Gaps = 8/1736 (0%)
 Strand=Plus/Plus

Query  3      GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123    ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141    ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183    CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201    CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  258

Query  242    CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  259    CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  318

Query  302    GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  319    GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  378

Query  362    TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  379    TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  438

Query  422    TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  439    TGACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  497

Query  482    AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  498    AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  557

Query  542    GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  558    GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGTT  617

Query  602    TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  618    TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  677

Query  662    AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  678    AACCTCTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  737

Query  722    TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  738    TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  797
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Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  798   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  857

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             |||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||
Sbjct  858   TATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCA  916

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  917   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  976

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  977   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1036

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1037  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1096

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGT-GGAGCCTGCGGCTTA  1139
             |||||||||||||||||||||||||||||||||||||||||||| ||| |||||||||||
Sbjct  1097  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGGA-CCTGCGGCTTA  1155

Query  1140  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1156  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1215

Query  1200  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1216  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1275

Query  1260  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1319
             ||||||||||||   |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1276  GTCTGCTTAATTNNNATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1335

Query  1320  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1336  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1395

Query  1380  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1396  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1455

Query  1440  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1456  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1515

Query  1500  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1516  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1575

Query  1560  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1576  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1635

Query  1620  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1636  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1695

Query  1680  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1696  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1751
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>emb|X83819.1| Debaryomyces castellii 18S rRNA gene (NCYC 604)
Length=1804

 Score = 3133 bits (1696),  Expect = 0.0
 Identities = 1736/1761 (98%), Gaps = 5/1761 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  46    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  105

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  106   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  165

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  166   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  225

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||||
Sbjct  226   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGNNTTGTGCTGGC  285

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  286   GATGGTTCATTCAAATTTCTGCCCTATCAACTTNCGATGGTAGGATAGTGGCCTACCATG  345

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  346   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  405

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  406   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  465

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  466   GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  524

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  525   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  584

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             |||||||||||||||||||||   ||||||||||||||||||   |||||||||||||||
Sbjct  585   CTCCAATAGCGTATATTAAAGNNNTTGCAGTTAAAAAGCTCGNNNTTGAACCTTGGGCTT  644

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||||||||| |||  ||||||||||||||||||||||||||||||||||
Sbjct  645   GGTTGGCCGGTCCGCCTTTTCGGCNTGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  704

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  705   ACCTCTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  764

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  765   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  824

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  825   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  884
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Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  885   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  943

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  944   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  1003

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1004  CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1063

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  1064  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCNGGGGGGAGTATGGTCGCAA  1123

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1124  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1183

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1184  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1243

Query  1202  CTCTTTCTTGATTTTGTGGGT-GGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  1244  CTCTTTCTTGATTTTGTGGGTCGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1303

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Sbjct  1304  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTAGG  1363

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGG-CAA  1379
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  1364  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCCAA  1423

Query  1380  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1424  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1483

Query  1440  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1499
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1484  AGCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1543

Query  1500  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1544  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1603

Query  1560  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1604  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1663

Query  1620  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1664  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1723

Query  1680  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGA  1739
             |||| ||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  1724  AGCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTNCGTAGGTGA  1783

Query  1740  ACCTGCGGAAGGATCATTACA  1760
             |||| ||||||||||||||||
Sbjct  1784  ACCTNCGGAAGGATCATTACA  1804
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>dbj|AB054266.1| Debaryomyces yamadae gene for 18S rRNA, partial sequence,
strain:JCM
6191
Length=1752

 Score = 3131 bits (1695),  Expect = 0.0
 Identities = 1721/1734 (99%), Gaps = 3/1734 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   CTCTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  440

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  500

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  560

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  620

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  621   GGTTGGCCGGTCCGCCTTTTCGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  680

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  681   ACCTCTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  740

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  800

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
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                   ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  801    CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  860

Query  843    ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
              ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  861    ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  919

Query  902    TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  920    TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  979

Query  962    CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  980    CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1039

Query  1022   CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1040   CGGACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1099

Query  1082   GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
              ||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Sbjct  1100   GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTAAT  1158

Query  1142   TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1159   TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1218

Query  1202   CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1219   CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1278

Query  1262   CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
              ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||  ||
Sbjct  1279   CTGCTTAATTNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTAGGC  1338

Query  1322   TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1339   TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1398

Query  1382   ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1399   ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1458

Query  1442   CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1459   CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1518

Query  1502   TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1519   TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1578

Query  1562   TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1579   TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1638

Query  1622   CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1639   CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1698

Query  1682   CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1699   CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1752
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>gb|AY520192.1| Candida sp. BG02-7-14-001I-1-1 18S ribosomal RNA gene, partial
sequence
Length=1748

 Score = 3131 bits (1695),  Expect = 0.0
 Identities = 1728/1743 (99%), Gaps = 6/1743 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  130   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  188

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  248

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  308

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  309   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  368

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  369   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  428

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  429   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  488

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  489   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  548

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  549   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  608

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  609   GGTTGGCCGGTCCGC-TTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  667

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  668   ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  727

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  787

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  847
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Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  848   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  906

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  966

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1026

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1086

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             |||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Sbjct  1087  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGTTGCTTAAT  1146

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1206

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1266

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1326

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1386

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1387  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1446

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||| | ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1447  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1505

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1506  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1565

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1566  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1625

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1626  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1685

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1686  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1745

Query  1741  CCT  1743
             |||
Sbjct  1746  CCT  1748
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>dbj|AB054274.1| Debaryomyces vanrijiae gene for 18S rRNA, partial sequence,
strain:JCM
3657
Length=1752

 Score = 3127 bits (1693),  Expect = 0.0
 Identities = 1721/1734 (99%), Gaps = 3/1734 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  440

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  500

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  560

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  620

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||||||||| |||| ||||||||||||||||||||||||||||||||||
Sbjct  621   GGTTGGCCGGTCCGCCTTTTCGGCGTGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  680

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||| ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  681   ACCTCTCGTCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  740

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  800

Query  783   CTATTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  801   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  860

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  861   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  919

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  920   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  979

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  980   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1039

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1040  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1099

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Sbjct  1100  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTAAT  1158

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1159  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1218

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1219  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1278

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Sbjct  1279  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTAGGC  1338

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1339  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1398

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1399  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1458

Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1459  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1518

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1519  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1578

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1579  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1638

Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1639  CTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1698

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             || |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1699  CTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1752
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>dbj|AB105434.1| Pichia guilliermondii gene for 18S rRNA, partial sequence,
strain:IAM
14500
Length=1734

 Score = 3127 bits (1693),  Expect = 0.0
 Identities = 1717/1728 (99%), Gaps = 5/1728 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  189

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  247

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  307

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  308   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  367

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  368   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  427

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  428   TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  487

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  488   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  547

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  548   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  607

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  608   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  667

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  668   AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  727

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  787

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  847
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Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             ||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Sbjct  848   TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  906

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  966

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1026

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1086

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1146

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1206

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1266

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  TCTGCTTAATTGCNATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1326

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1386

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1387  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1446

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1447  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1506

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1507  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1566

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1567  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1626

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1627  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1686

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1728
             ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1687  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1734


>gb|AY520212.1| Candida sp. BG02-6-15-010A-3 18S ribosomal RNA gene, partial
sequence
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Length=1739

 Score = 3125 bits (1692),  Expect = 0.0
 Identities = 1721/1734 (99%), Gaps = 6/1734 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  130   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  188

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  248

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  308

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  309   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  368

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  369   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  428

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  429   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  488

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  489   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  548

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  549   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  608

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  609   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  667

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  668   ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  727

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  787

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  847

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
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Sbjct  848   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  906

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  966

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1026

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1086

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1146

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1206

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1266

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1326

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1386

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1387  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1446

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||| | ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1447  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1505

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1506  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1565

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1566  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1625

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1626  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1685

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1734
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1686  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1739


>dbj|AB013542.1| Candida sophiae-reginae 18S rRNA gene, strain JCM 8925, partial
sequence
Length=1781

 Score = 3123 bits (1691),  Expect = 0.0
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 Identities = 1739/1760 (98%), Gaps = 12/1760 (0%)
 Strand=Plus/Plus

Query  3    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30   GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123  ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
            |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150  ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183  CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
            || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209  CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  266

Query  242  CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267  CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  326

Query  302  GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327  GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  386

Query  362  TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387  TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  446

Query  422  TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  447  TGACAATAAATAACGATACAGGGCCCTTACGGGTCTTGTAATTGGAATGAGTACAATGTA  506

Query  482  AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507  AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  566

Query  542  GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  567  GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  626

Query  602  TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
            ||||||||||||||| |||| |||||||||||||||||||||||||||||||||||||||
Sbjct  627  TGGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  685

Query  662  AACCTT-TCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGT  720
            |||||| | |||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  686  AACCTTGT-GCCCTTGTGGTGCTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGT  744

Query  721  GTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGG  780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  745  GTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGG  804

Query  781  TTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCA  840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  805  TTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCA  864

Query  841  GTATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGC  899
            ||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||
Sbjct  865  GTATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGC  923

Query  900  ATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGA  959
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  924   ATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGA  983

Query  960   TACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCttttttt  1019
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  984   TACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTT  1043

Query  1020  GACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGC  1079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1044  GACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGC  1103

Query  1080  AAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTA  1139
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1104  AAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTA  1163

Query  1140  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1164  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1223

Query  1200  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1224  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1283

Query  1260  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1284  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1343

Query  1320  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1344  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1403

Query  1380  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1404  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1463

Query  1440  AACGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGG  1498
             | ||||| | ||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  1464  AGCGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGG  1522

Query  1499  GGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCA  1558
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1523  GGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCA  1582

Query  1559  GCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAA  1618
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1583  GCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAA  1642

Query  1619  TGGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAA  1678
             |||||||||||||| |||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  1643  TGGCTTAGTGAGGCTTCCGGATTGGTTTAGAGAAGGGGGCAACTCCATCTTGGAACCGAA  1702

Query  1679  AAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTG  1738
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1703  AAGCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TG  1761

Query  1739  AACCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||||
Sbjct  1762  AACCTGCGGAAGGATCATTA  1781


>dbj|AB013535.1| Candida multigemmis 18S rRNA gene, strain JCM 9559, partial
sequence
Length=1783
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 Score = 3120 bits (1689),  Expect = 0.0
 Identities = 1738/1760 (98%), Gaps = 10/1760 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  266

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  326

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  386

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  446

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  447   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  506

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  566

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  567   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  626

Query  602   TGGTTGGCCGGTCCGCCTTTT-TGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGC  660
             |||||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||
Sbjct  627   TGGTTGGCCGGTCCGCTTTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGC  686

Query  661   TAACCTTTC-GCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAG  719
             ||| || ||  || || |||||  | ||||||||||||||||||||||||||||||||||
Sbjct  687   TAA-CTATCTTCCTTTTTGGTGGGTAGCGAACCAGGACTTTTACTTTGAAAAAATTAGAG  745

Query  720   TGTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATG  779
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  746   TGTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATG  805

Query  780   GTTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATC  839
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  806   GTTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATC  865

Query  840   AGTATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAG  898
             |||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||
Sbjct  866   AGTATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAG  924
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Query  899   CATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAG  958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  925   CATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAG  984

Query  959   ATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttt  1018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  985   ATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTT  1044

Query  1019  tGACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCG  1078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1045  TGACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCG  1104

Query  1079  CAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT  1138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1105  CAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT  1164

Query  1139  AATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGA  1198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1165  AATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGA  1224

Query  1199  GAGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATT  1258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1225  GAGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATT  1284

Query  1259  TGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTT  1318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1285  TGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTT  1344

Query  1319  TGCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCA  1378
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1345  GGCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCA  1404

Query  1379  ATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGC  1438
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1405  ATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGC  1464

Query  1439  CAACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGG  1498
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1465  CAGCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGG  1524

Query  1499  GGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCA  1558
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1525  GGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCA  1584

Query  1559  GCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAA  1618
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1585  GCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAA  1644

Query  1619  TGGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAA  1678
             |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1645  TGGCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAA  1704

Query  1679  AAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTG  1738
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  1705  AAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TG  1763

Query  1739  AACCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||||
Sbjct  1764  AACCTGCGGAAGGATCATTA  1783


>dbj|AB013519.1| Candida glucosophila 18S rRNA gene, strain JCM 9440, partial
sequence
Length=1783
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 Score = 3120 bits (1689),  Expect = 0.0
 Identities = 1736/1758 (98%), Gaps = 6/1758 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACTGCTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  209

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  210   CTCTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  269

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  270   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  329

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  330   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  389

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  390   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  449

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  450   GACAATAAATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  508

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  509   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  568

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  569   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  628

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||| ||||||||| ||||||||||||||||||| |||||||||||||||| |||||||
Sbjct  629   GGTTGCCCGGTCCGCTTTTTTGGCGAGTACTGGACGCAACCGAGCCTTTCCTCCTGGCTA  688

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  689   ACCTTTCGCCCTTGTGGTGATTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  748

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||| || |||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  749   TCAAAGCAGGCGTTAGCTCGAATATGTTAGCATGGAATAATAGAATAGGACGTTATGGTT  808

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  809   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  868

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  869   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  927
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Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  928   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  987

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  988   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGATGTTCTTTTTTTGA  1047

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1048  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1107

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1108  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1167

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1168  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1227

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1228  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1287

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1288  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1347

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1348  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1407

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1408  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1467

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||| | || |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1468  CGAGTTTGTA-CCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1526

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1527  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1586

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1587  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1646

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||||| |||||||||||||||| |||||||||||||||||| |||||||||
Sbjct  1647  GCTTAGTGAGGCCTTCGGATTGGTTTAAAGAGGGGGGCAACTCCATCTTGAAACCGAAAA  1706

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  1707  GTTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TGAA  1765

Query  1741  CCTGCGGAAGGATCATTA  1758
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Sbjct  1766  CCTGCGGAAGGATCATTA  1783


>dbj|AB054267.1| Debaryomyces vanrijiae var. yarrowii gene for 18S rRNA, partial
sequence, strain:JCM 6190
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Length=1753

 Score = 3118 bits (1688),  Expect = 0.0
 Identities = 1719/1735 (99%), Gaps = 4/1735 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  440

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  500

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  560

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  620

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||||||||| |||| ||||||||||||||||||||||||||||||||||
Sbjct  621   GGTTGGCCGGTCCGCCTTTTCGGCGTGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  680

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  681   ACCTCTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  740

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  800

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  801   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  860

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
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Sbjct  861   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  919

Query  902   TT-GCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  920   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  979

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  980   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1039

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1040  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1099

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             |||||||||||||||||||||||||||||||||||||||||||||| | |||||||||||
Sbjct  1100  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTAA  1158

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1159  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1218

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1219  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1278

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             |||||||||||   |||||||||||||||||||||||||||||||||||||||||||  |
Sbjct  1279  TCTGCTTAATTNNNATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTAGG  1338

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1339  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1398

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1399  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1458

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1459  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1518

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1519  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1578

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1579  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1638

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1639  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1698

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1699  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1753


>gb|AY242152.1| Candida athensensis strain BG99-8-11-1-C1 18S ribosomal RNA gene,
partial sequence
Length=1730

 Score = 3118 bits (1688),  Expect = 0.0
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 Identities = 1713/1724 (99%), Gaps = 5/1724 (0%)
 Strand=Plus/Plus

Query  3    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
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Sbjct  10   GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123  ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130  ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  189

Query  183  CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
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Sbjct  190  CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  247

Query  242  CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248  CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  307

Query  302  GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  308  GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  367

Query  362  TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  368  TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  427

Query  422  TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  428  TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  487

Query  482  AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  488  AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  547

Query  542  GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
            |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  548  GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  607

Query  602  TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  608  TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  667

Query  662  AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  668  AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  727

Query  722  TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728  TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  787

Query  782  TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788  TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  847

Query  842  TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
            ||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Sbjct  848  TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  906

Query  901  TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  966

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1026

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
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Sbjct  1027  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1086

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1146

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1206

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1266

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1326

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1386

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1387  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1446

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1447  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1506

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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Sbjct  1507  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1566

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1567  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1626

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
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Sbjct  1627  GCTTAGTGAGGCCTCCGGATTGGTTTAGAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1686

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAA  1724
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Sbjct  1687  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAA  1730


>dbj|AB013579.1| Candida quercitrusa 18S rRNA gene, strain JCM 9832, partial
sequence
Length=1782

 Score = 3118 bits (1688),  Expect = 0.0
 Identities = 1736/1758 (98%), Gaps = 7/1758 (0%)
 Strand=Plus/Plus
```

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Query  3    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30   GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90   AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123  ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
            |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150  ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183  CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
            || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209  CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  266

Query  242  CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267  CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  326

Query  302  GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327  GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  386

Query  362  TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387  TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  446

Query  422  TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
            |||||||||||| ||||||||||||||||||||||||||| |||||||||||||||| ||
Sbjct  447  TGACAATAAATACCGATACAGGGCCCTTTCGGGTCTTGTATTTGGAATGAGTACAATCTA  506

Query  482  AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507  AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  566

Query  542  GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
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Sbjct  567  GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  626

Query  602  TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
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Sbjct  627  TGGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  685

Query  662  AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
            |||||||| || || |||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  686  AACCTTTCACCTTTTTGGTGTCTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  745

Query  722  TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  746  TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  805

Query  782  TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  806  TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  865

Query  842  TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
            |||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||
Sbjct  866  TATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCA  924

Query  901  TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  925  TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  984
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Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  985   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1044

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
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Sbjct  1045  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1104

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
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Sbjct  1105  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1164

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
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Sbjct  1165  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATGAGGATTGACAGATTGAGA  1224

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1225  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1284

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1285  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1344

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
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Sbjct  1345  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1404

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
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Sbjct  1405  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1464

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
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Sbjct  1465  GCGAGTTTTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1524

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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Sbjct  1525  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1584

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
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Sbjct  1585  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1644

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
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Sbjct  1645  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1704

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
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Sbjct  1705  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1764

Query  1741  CCTGCGGAAGGATCATTA  1758
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Sbjct  1765  CCTGCGGAAGGATCATTA  1782


>dbj|AB013541.1| Candida natalensis 18S rRNA gene, strain JCM 1445, partial
sequence
Length=1781

 Score = 3118 bits (1688),  Expect = 0.0
 Identities = 1736/1758 (98%), Gaps = 8/1758 (0%)
 Strand=Plus/Plus
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Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  266

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  326

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  386

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  446

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  447   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATCTA  506

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  566

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  567   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGTT  626

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||| |||| |||||||||||||||||||||||||||||||||||||||
Sbjct  627   TGGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  685

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             |||||||| || || |||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  686   AACCTTTCACCTTTTTGGTGTCTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  745

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  746   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  805

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  806   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  865

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             |||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||
Sbjct  866   TATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCA  924

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  925   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  984
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Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  985   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1044

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1045  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1104

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1105  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1164

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  1165  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATGAGGATTGACAGATTGAGA  1224

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1225  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1284

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1285  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1344

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1345  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1404

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1405  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1464

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              ||||| |||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1465  GCGAGTTTTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1524

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1525  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1584

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1585  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1644

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1645  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1704

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  1705  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TGAA  1763

Query  1741  CCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||
Sbjct  1764  CCTGCGGAAGGATCATTA  1781


>gb|DQ534404.1| Debaryomyces hansenii strain JHSa 18S ribosomal RNA gene, partial
sequence
Length=1741

 Score = 3114 bits (1686),  Expect = 0.0
 Identities = 1711/1722 (99%), Gaps = 6/1722 (0%)
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 Strand=Plus/Plus

Query  3      GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  76

Query  63     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  77     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  136

Query  123    ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  137    ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  196

Query  183    CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  197    CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  254

Query  242    CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  255    CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  314

Query  302    GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  315    GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  374

Query  362    TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  375    TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  434

Query  422    TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  435    TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  494

Query  482    AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  495    AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  554

Query  542    GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  555    GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  614

Query  602    TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  615    TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  674

Query  662    AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  675    AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  734

Query  722    TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  735    TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  794

Query  782    TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  795    TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  854

Query  842    TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
              ||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Sbjct  855    TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  913

Query  901    TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  914   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  973

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  974   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1033

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1034  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1093

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1094  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1153

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1154  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1213

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1214  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1273

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1274  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1333

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1334  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1393

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1394  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1453

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1454  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1513

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1514  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1573

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1574  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1633

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1634  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1693

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAAC  1722
             |||||||||||||||||||||||||||||||||||||| |||
Sbjct  1694  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCG-AAC  1734


>gb|AY520250.1| Candida sp. BG02-5-27-4-5-1 18S ribosomal RNA gene, partial
sequence
Length=1739

 Score = 3114 bits (1686),  Expect = 0.0
 Identities = 1719/1734 (99%), Gaps = 6/1734 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
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Sbjct  10        GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63        AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70        AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123       ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
                 |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  130       ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  188

Query  183       CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189       CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  248

Query  243       GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249       GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  308

Query  303       GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  309       GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  368

Query  363       ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  369       ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  428

Query  423       GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  429       GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  488

Query  483       ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  489       ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  548

Query  543       CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  549       CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  608

Query  603       GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
                 |||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  609       GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  667

Query  663       ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
                 |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  668       ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  727

Query  723       TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728       TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  787

Query  783       CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788       CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  847

Query  843       ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
                 |||| |||||||||||||||||||||||| ||| | ||||||||||||||||||||||||
Sbjct  848       ATTCCGTTGTCAGAGGTGAAATTCTTGGATTTA-CGGAAGACTAACTACTGCGAAAGCAT  906

Query  902       TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907       TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  966

Query  962       CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1026

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1086

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1146

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1206

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1266

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1326

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1386

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1387  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1446

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||| | ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1447  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1505

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1506  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1565

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1566  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1625

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1626  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1685

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1734
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1686  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1739


>dbj|AB054263.1| Debaryomyces occidentalis var. persoonii gene for 18S rRNA, 
partial
sequence, strain:JCM 8127
Length=1753

 Score = 3112 bits (1685),  Expect = 0.0
 Identities = 1718/1735 (99%), Gaps = 4/1735 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80
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Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   CTCTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  440

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  500

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  560

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  620

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||||||||| |||| ||||||||||||||||||||||||||||||||||
Sbjct  621   GGTTGGCCGGTCCGCCTTTTCGGCGTGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  680

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  681   ACCATTCACCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  740

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             |||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TCAAAGCAGGCCTT-GCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  799

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  800   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  859

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  860   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  918

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  919   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  978

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  979   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1038
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Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  1039  CGCACTCGGCACCTTACGGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1098

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1099  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1158

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1159  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1218

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTT-CTTAGTTGGTGGAGTGATTTG  1260
             |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Sbjct  1219  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTTCTTAGTTGGTGGAGTGATTTG  1278

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||   ||||||||||||||||||||||||||||||||||||||||||||  |
Sbjct  1279  TCTGCTTAATNNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTAGG  1338

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1339  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1398

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1399  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1458

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1459  GCGAGTATTAGCCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1518

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1519  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1578

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1579  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1638

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1639  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1698

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAGGTTTCCGTAG  1735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1699  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAGGTTTCCGTAG  1753


>dbj|AB054276.1| Debaryomyces castellii gene for 18S rRNA, partial sequence,
strain:JCM
6177
Length=1751

 Score = 3109 bits (1683),  Expect = 0.0
 Identities = 1717/1734 (99%), Gaps = 4/1734 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  440

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  441   GACAATAAATAACGATACAGGGCC-TTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  499

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  559

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  619

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||||||||| |||| ||||||||||||||||||||||||||||||||||
Sbjct  620   GGTTGGCCGGTCCGCCTTTTCGGCGTGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  679

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||| ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  680   ACCTCTCGTCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  739

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  799

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  800   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  859

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  860   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  918

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  919   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  978

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  979   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1038

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1039  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1098

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Sbjct  1099  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTAAT  1157

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1158  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1217

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1218  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1277

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||  |||||||||||||||||||||||||||||||||||||||||| |  ||
Sbjct  1278  CTGCTTAATTNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCATAAGC  1337

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1338  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1397

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCTACACTGACGGAGCCAA  1441
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1398  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCTACACTGACGGAGCCAG  1457

Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1458  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1517

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1518  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1577

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1578  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1637

Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
             ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1638  CTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1697

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             || |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1698  CTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1751


>gb|AY520269.1| Candida sp. BG02-5-27-4-2-1 18S ribosomal RNA gene, partial
sequence
Length=1739

 Score = 3109 bits (1683),  Expect = 0.0
 Identities = 1718/1734 (99%), Gaps = 6/1734 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAGCCGTGGTAATTCTAGAGCTA  129
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Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  130   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  188

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  248

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  308

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  309   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  368

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  369   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  428

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  429   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  488

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
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Sbjct  489   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  548

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
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Sbjct  549   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  608

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
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Sbjct  609   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  667

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
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Sbjct  668   ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  727

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  787

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
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Sbjct  788   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  847

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
             |||| |||||||||||||||||||||||| ||| | ||||||||||||||||||||||||
Sbjct  848   ATTCCGTTGTCAGAGGTGAAATTCTTGGATTTA-CGGAAGACTAACTACTGCGAAAGCAT  906

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  966

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
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Sbjct  967   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1026

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
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Sbjct  1027  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1086
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Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
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Sbjct  1087  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1146

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1206

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1266

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1326

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1386

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
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Sbjct  1387  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1446

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
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Sbjct  1447  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1505

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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Sbjct  1506  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1565

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1566  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1625

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1626  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1685

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1734
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1686  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1739


>gb|AY520264.1| Candida sp. BG02-7-18-022A-1-1 18S ribosomal RNA gene, partial
sequence
Length=1739

 Score = 3109 bits (1683),  Expect = 0.0
 Identities = 1719/1735 (99%), Gaps = 8/1735 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAGCCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  130   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  188
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Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
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Sbjct  189   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  248

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  308

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
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Sbjct  309   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  368

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  369   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  428

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  429   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  488

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
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Sbjct  489   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  548

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
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Sbjct  549   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  608

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             ||||||||||||||| ||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  609   GGTTGGCCGGTCCGC-TTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  667

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  668   ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  727

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  787

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
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Sbjct  788   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  847

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  848   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  906

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  966

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
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Sbjct  967   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1026

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
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Sbjct  1027  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1086

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
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Sbjct  1087  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1146
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Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
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Sbjct  1147  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1206

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
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Sbjct  1207  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1266

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTG-CTAGCTTTTG  1320
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Sbjct  1267  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGC-GACTAGCTTTTG  1325

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
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Sbjct  1326  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1385

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
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Sbjct  1386  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1445

Query  1441  ACGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1499
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Sbjct  1446  GCGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGG  1504

Query  1500  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1559
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Sbjct  1505  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1564

Query  1560  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1619
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Sbjct  1565  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1624

Query  1620  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1679
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Sbjct  1625  GGCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1684

Query  1680  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1734
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Sbjct  1685  AGCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1739


>gb|EF532297.1| Pichia guilliermondii strain gao1zhong2 18S ribosomal RNA gene,
partial sequence
Length=1714

 Score = 3107 bits (1682),  Expect = 0.0
 Identities = 1705/1715 (99%), Gaps = 5/1715 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
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Sbjct  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
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Sbjct  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
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Sbjct  183   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  240

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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  300

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  360

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  420

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
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Sbjct  421   TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  480

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
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Sbjct  481   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  540

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
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Sbjct  541   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  600

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
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Sbjct  601   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  660

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
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Sbjct  661   AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  720

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
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Sbjct  721   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  780

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
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Sbjct  781   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  840

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
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Sbjct  841   TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  899

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  900   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  959

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  960   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1019

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1020  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1079

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
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Sbjct  1080  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1139

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
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Sbjct  1140  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1199

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
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Sbjct  1200  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1259

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1260  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1319

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1320  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1379

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1380  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1439

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1440  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1499

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1500  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1559

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1560  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1619

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1620  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1679

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAG  1715
             |||||||||||||||||||||||||||||||||||
Sbjct  1680  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAG  1714


>gb|EF061756.1| Debaryomyces hansenii strain G7a1 18S ribosomal RNA gene, partial
sequence
Length=1682

 Score = 3107 bits (1682),  Expect = 0.0
 Identities = 1682/1682 (100%), Gaps = 0/1682 (0%)
 Strand=Plus/Plus

Query  25    CAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATAGTA  84
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     CAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATAGTA  60

Query  85    CCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAATCCCGACT  144
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAATCCCGACT  120

Query  145   GTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCTTTTCGGAGCTCTTTGATGAT  204
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCTTTTCGGAGCTCTTTGATGAT  180

Query  205   TCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAAATTTCTGC  264
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAAATTTCTGC  240

Query  265   CCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAACGGGGAAT  324
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   CCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAACGGGGAAT  300

Query  325   AAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCA  384
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCA  360

Query  385   GGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACGATACAGGG  444
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACGATACAGGG  420

Query  445   CCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGGAACAATTG  504
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   CCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGGAACAATTG  480

Query  505   GAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGT  564
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGT  540

Query  565   TGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGTTGGCCGGTCCGCCTTTTTG  624
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   TGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGTTGGCCGGTCCGCCTTTTTG  600

Query  625   GCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCTTTCGCCCTTGTGGTGTTT  684
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   GCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCTTTCGCCCTTGTGGTGTTT  660

Query  685   GGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTTTGCTCGAA  744
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   GGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTTTGCTCGAA  720

Query  745   TATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTTTCTAGGAC  804
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   TATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTTTCTAGGAC  780

Query  805   CATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGAGGTGAAAT  864
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   CATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGAGGTGAAAT  840

Query  865   TCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACGTTTTCATTAAT  924
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841   TCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACGTTTTCATTAAT  900

Query  925   CAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTAACCATAAAC  984
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  901   CAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTAACCATAAAC  960

Query  985   TATGCCGACTAGGGATCGGGTGTTGTTCtttttttGACGCACTCGGCACCTTACGAGAAA  1044
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  961   TATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGACGCACTCGGCACCTTACGAGAAA  1020

Query  1045  TCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATTGAC  1104
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1021  TCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATTGAC  1080

Query  1105  GGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTCA  1164
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1081  GGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAACTCA  1140

Query  1165  CCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTTGTGGGTGG  1224
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1141  CCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTTGTGGGTGG  1200

Query  1225  TGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCGATAACGAACG  1284
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1201  TGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCGATAACGAACG  1260

Query  1285  AGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACTTCTTAGAGGG  1344
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1261  AGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACTTCTTAGAGGG  1320

Query  1345  ACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCCTTAGAC  1404
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1321  ACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCCTTAGAC  1380

Query  1405  GTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAACGAGTATTAACCTTGGCCGAGAG  1464
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1381  GTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAACGAGTATTAACCTTGGCCGAGAG  1440

Query  1465  GTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAATTATTGCTCT  1524
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1441  GTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAATTATTGCTCT  1500

Query  1525  TCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACGTCCCTGCCCT  1584
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1501  TCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACGTCCCTGCCCT  1560

Query  1585  TTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCTCCGGATTGGT  1644
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1561  TTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCTCCGGATTGGT  1620

Query  1645  TTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTGGTCATTTAGA  1704
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1621  TTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTGGTCATTTAGA  1680

Query  1705  GG  1706
             ||
Sbjct  1681  GG  1682


>gb|DQ534403.1| Pichia guilliermondii strain JHSd 18S ribosomal RNA gene, partial
sequence
Length=1738

 Score = 3105 bits (1681),  Expect = 0.0
 Identities = 1711/1724 (99%), Gaps = 7/1724 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17    GCC-TGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  75

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  76    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  135

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  136   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  195

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  196   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  253

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  254   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  313
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Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  314   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  373

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  374   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  433

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  434   TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  493

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  494   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  553

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  554   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  613

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  614   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  673

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  674   AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  733

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  734   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  793

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  794   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  853

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             ||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Sbjct  854   TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  912

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  913   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  972

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  973   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1032

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1033  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1092

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1093  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1152

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1153  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1212

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1213  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1272
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Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1273  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1332

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1333  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1392

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1393  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1452

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1453  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1512

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1513  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1572

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1573  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1632

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1633  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1692

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAA  1724
             |||||||||||||||||||| ||||||||||||||||||| |||
Sbjct  1693  GCTGGTCAAACTTGGTCATT-AGAGGAAGTAAAAGTCGTAGCAA  1735


>dbj|AB054282.1| Pichia guilliermondii gene for 18S rRNA, partial sequence,
strain:JCM
10735
Length=1752

 Score = 3105 bits (1681),  Expect = 0.0
 Identities = 1718/1736 (98%), Gaps = 7/1736 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGG-ATAACCGTGGTAATTCTAGAGCT  121
             |||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGTATAACCGTGGTAATTCTAGAGCT  140

Query  122   AATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAAT  181
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   AATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAAT  200

Query  182   GCT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTG  240
             ||| |||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   GCTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTG  258

Query  241   GCGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCA  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  259   GCGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCA  318

Query  301   TGGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGG  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  319   TGGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGG  378

Query  361   CTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  379   CTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTA  438

Query  421   GTGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGT  480
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  439   GTGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGT  498

Query  481   AAATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  499   AAATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCC  558

Query  541   AGCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGC  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  559   AGCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGC  618

Query  601   TTGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGC  660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  619   TTGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGC  678

Query  661   TAACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGT  720
             ||||| |||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  679   TAACCATTCGTCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGT  738

Query  721   GTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGG  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  739   GTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGG  798

Query  781   TTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCA  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  799   TTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCA  858

Query  841   GTATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGC  899
             |||||||||||||||||||||||||||| || ||| ||||||||||||||||||||||||
Sbjct  859   GTATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGC  917

Query  900   ATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGA  959
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  918   ATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGA  977

Query  960   TACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCttttttt  1019
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  978   TACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTT  1037

Query  1020  GACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGC  1079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1038  GACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGC  1097

Query  1080  AAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTA  1139
             ||||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||
Sbjct  1098  AAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTA  1156

Query  1140  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1157  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1216

Query  1200  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1259
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  1217  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTCCTTAGTTGGTGGAGTGATTT  1276

Query  1260  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1319
             |||||||||||   ||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1277  GTCTGCTTAATNNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1336

Query  1320  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1337  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1396

Query  1380  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1397  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1456

Query  1440  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1499
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1457  AGCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1516

Query  1500  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1517  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1576

Query  1560  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1577  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1636

Query  1620  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1637  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1696

Query  1680  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1697  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1752


>dbj|AB000950.1| Taphrina farlowii gene for 18S rRNA, complete sequence
Length=1776

 Score = 3105 bits (1681),  Expect = 0.0
 Identities = 1737/1761 (98%), Gaps = 15/1761 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  22    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  81

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  82    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  141

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  142   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  201

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  202   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTAGAATCGCATGGCCTTGTGCTGG  259

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  260   CGATGGTTCATTCAAATTTTTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  319

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  379

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  380   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  439

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             |||||||| |||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  440   TGACAATACATAACGATACAGGG-CCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  498

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  499   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  558

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  559   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  618

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  619   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  678

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  679   AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  738

Query  722   TTCAAAGCAGGCCTTTGCTCGAATA-TATTAGCATGGAATAATAGAATAGGACGTTATGG  780
             ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  739   TTCAAAGCAGGCCTTTGCTCGAATACTATTAGCATGGAATAATAGAATAGGACGTTATGG  798

Query  781   TTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATA-GGGACGGTCGGGGGCATC  839
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  799   TTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGGACGGTCGGGGGCATC  858

Query  840   AGTATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAG  898
             ||||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||
Sbjct  859   AGTATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAG  917

Query  899   CATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAG  958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  918   CATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAG  977

Query  959   ATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttt  1018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  978   ATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTT  1037

Query  1019  tGACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCG  1078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1038  TGACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCG  1097

Query  1079  CAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT  1138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1098  CAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT  1157

Query  1139  AATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGA  1198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1158  AATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGA  1217

Query  1199  GAGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATT  1258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1218  GAGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATT  1277

Query  1259  TGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTT  1318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1278  TGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTT  1337

Query  1319  TGCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCA  1378
             |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
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Sbjct  1338   TGCTGGTATAGTCACTTCCTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCA  1397

Query  1379   ATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGC  1438
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1398   ATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGT  1457

Query  1439   -CAACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTG  1497
               || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1458   TCAGCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTG  1517

Query  1498   GGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCC-TAGTAAGCGCAAGTCAT  1556
              |||||||||||||||| ||||||||||||||||||||||||| | |||||||||||||||
Sbjct  1518   GGGATAGAGCATTGTA-TTATTGCTCTTCAACGAGGAATTCCCT-GTAAGCGCAAGTCAT  1575

Query  1557   CAGCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTG  1616
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1576   CAGCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTG  1635

Query  1617   AATGGCTTAGTGAGGCCTCCGGATTGGTTTAAA-GAA-GGGGGCAACTCCATCTTGGAAC  1674
              ||||||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||
Sbjct  1636   AATGGCTTAGTGAGGCCTCCGGATTGGTTTAAACGAACGGGGGCAACTCCATCTTGGAAC  1695

Query  1675   CGAAAAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1696   CGAAAAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1755

Query  1735   -GGTGAACCTGCGGAAGGATC  1754
               ||||||||||||||||||||
Sbjct  1756   CGGTGAACCTGCGGAAGGATC  1776


>gb|EU784644.1| Pichia guilliermondii strain CXF-1 18S ribosomal RNA gene, partial
sequence
Length=1739

 Score = 3103 bits (1680),  Expect = 0.0
 Identities = 1703/1713 (99%), Gaps = 5/1713 (0%)
 Strand=Plus/Plus

Query  3      GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123    ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  150    ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  209

Query  183    CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  210    CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  267

Query  242    CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  268    CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  327

Query  302    GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  328    GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  387

Query  362    TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  388      TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  447

Query  422      TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
                |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  448      TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  507

Query  482      AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  508      AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  567

Query  542      GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
                |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  568      GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  627

Query  602      TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  628      TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  687

Query  662      AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
                |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  688      AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  747

Query  722      TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  748      TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  807

Query  782      TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  808      TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  867

Query  842      TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
                ||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Sbjct  868      TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  926

Query  901      TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  927      TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  986

Query  961      ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  987      ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1046

Query  1021     ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1047     ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1106

Query  1081     AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1107     AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1166

Query  1141     TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1167     TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1226

Query  1201     GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1227     GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1286

Query  1261     TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1287     TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1346

Query  1321     CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1347  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1406

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1407  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1466

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1467  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1526

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1527  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1586

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1587  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1646

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1647  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1706

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAA  1713
             |||||||||||||||||||||||||||||||||
Sbjct  1707  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAA  1739


>dbj|AB013573.1| Candida fragi 18S rRNA gene, strain JCM 1791, partial sequence
Length=1781

 Score = 3101 bits (1679),  Expect = 0.0
 Identities = 1733/1758 (98%), Gaps = 8/1758 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  89

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  149

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  150   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  208

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  266

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  326

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  386

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  446

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
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                ||||||||||||||| ||||||| |||||||||||||||||| |||||||||||||| ||
Sbjct  447   TGACAATAAATAACGTTACAGGGGCCTTTCGGGTCTTGTAATCGGAATGAGTACAATCTA  506

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  566

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  567   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  626

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||| |||| |||||||||||||||||||||||||||||||||||||||
Sbjct  627   TGGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  685

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             |||||||| || || |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  686   AACCTTTCTCCTTTTTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  745

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  746   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  805

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  806   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  865

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             |||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||||
Sbjct  866   TATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCA  924

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  925   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  984

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  985   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1044

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1045  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1104

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1105  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1164

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  1165  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATGAGGATTGACAGATTGAGA  1224

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1225  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1284

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  1285  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCATTTG  1344

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1345  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1404

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1405  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1464

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              ||||| |||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1465  GCGAGTTTTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1524

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  1525  ATAGAGCATTGTAATTTTTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1584

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1585  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1644

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1645  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1704

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAGGTGAA  1740
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Sbjct  1705  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG-TGAA  1763

Query  1741  CCTGCGGAAGGATCATTA  1758
             ||||||||||||||||||
Sbjct  1764  CCTGCGGAAGGATCATTA  1781


>emb|FN690501.1| Uncultured fungus partial 18S rRNA gene, clone 3b-D8
Length=1686

 Score = 3097 bits (1677),  Expect = 0.0
 Identities = 1683/1686 (99%), Gaps = 1/1686 (0%)
 Strand=Plus/Plus

Query  7     TGCATGTCTAAGTATAAGCAATTTATACAGT-GAAACTGCGAATGGCTCATTAAATCAGT  65
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1     TGCATGTCTAAGTATAAGCAATTTATACAGTGGAAACTGCGAATGGCTCATTAAATCAGT  60

Query  66    TATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATA  125
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATA  120

Query  126   CATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCTT  185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   CATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCTT  180

Query  186   TTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGAT  245
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGAT  240

Query  246   GGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTT  305
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTT  300

Query  306   TCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACC  365
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACC  360

Query  366   ACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGAC  425
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   ACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGAC  420

Query  426   AATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATA  485
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATA  480

Query  486   CCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTC  545
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTC  540

Query  546   CAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGT  605
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGT  600

Query  606   TGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACC  665
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   TGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACC  660

Query  666   TTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCA  725
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   TTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCA  720

Query  726   AAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTA  785
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   AAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTA  780

Query  786   TTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATT  845
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   TTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATT  840

Query  846   CAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATTTGC  905
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841   CAGTTGTCAGAGGTGAAATTCTTGGATTACCTGAAGACTAACTACTGCGAAAGCATTTGC  900

Query  906   CAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGT  965
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  901   CAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGT  960

Query  966   CGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGACGCA  1025
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  961   CGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGACGCA  1020

Query  1026  CTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCT  1085
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1021  CTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCT  1080

Query  1086  GAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGA  1145
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1081  GAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGA  1140

Query  1146  CTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCT  1205
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1141  CTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCT  1200

Query  1206  TTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGC  1265
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1201  TTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGC  1260

Query  1266  TTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGT  1325
             |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1261  TTAATTGCAATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGT  1320

Query  1326  ATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAG  1385
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1321  ATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAG  1380

Query  1386  GTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAACGAG  1445
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1381  GTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAACGAG  1440

Query  1446  TATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGA  1505
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1441  TATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGA  1500

Query  1506  GCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCG  1565
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1501  GCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCG  1560

Query  1566  TTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTA  1625
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1561  TTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTA  1620

Query  1626  GTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGG  1685
             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  1621  GTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTNGGAACCGAAAAGCTGG  1680

Query  1686  TCAAAC  1691
             ||||||
Sbjct  1681  TCAAAC  1686


>dbj|AB054275.1| Debaryomyces polymorphus gene for 18S rRNA, partial sequence,
strain:JCM 3647
Length=1751

 Score = 3097 bits (1677),  Expect = 0.0
 Identities = 1715/1734 (98%), Gaps = 4/1734 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             |||||||||||||||||||||||||||||||||||||||||||| | |||||||||||||
Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCAATACGGGGAGGTAGT  440

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  441   GACAATAAATAACGATACAGGGCC-TTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  499
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Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  559

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  619

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
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Sbjct  620   GGTTGGCCGGTCCGCCTTTTCGGCGTGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  679

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
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Sbjct  680   ACCTCTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  739

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  799

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
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Sbjct  800   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  859

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  860   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  918

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  919   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  978

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  979   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1038

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
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Sbjct  1039  CGGACTCGGCACCTTACGGGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1098

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
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Sbjct  1099  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTAAT  1157

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1158  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1217

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1218  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1277

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||  ||||||||||||||||||||||||||||||||||||||||||||  ||
Sbjct  1278  CTGCTTAATTNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTAGGC  1337

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
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Sbjct  1338  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1397

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
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Sbjct  1398  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1457
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Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
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Sbjct  1458  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1517

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
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Sbjct  1518  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1577

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
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Sbjct  1578  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1637

Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
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Sbjct  1638  CTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1697

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
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Sbjct  1698  CTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1751


>dbj|AB054273.1| Debaryomyces pseudopolymorphus gene for 18S rRNA, partial
sequence,
strain:JCM 3652
Length=1751

 Score = 3097 bits (1677),  Expect = 0.0
 Identities = 1715/1734 (98%), Gaps = 4/1734 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
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Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAA-GGATGTATTTATTAGATAAAAAATCAATG  199

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
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Sbjct  200   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  259

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
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Sbjct  260   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  319

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  379

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
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Sbjct  380   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  439

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
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Sbjct  440   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  499

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
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Sbjct  500   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  559

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
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Sbjct  560   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  619

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
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Sbjct  620   GGTTGGCCGGTCCGCCTTTTCGGCGTGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  679

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
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Sbjct  680   ACCTCTCGTCCTAGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  739

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
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Sbjct  740   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  799

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
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Sbjct  800   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  859

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  860   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  918

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
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Sbjct  919   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  978

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
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Sbjct  979   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1038

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             || ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  1039  CGGACTCGGCACCTTACGGGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1098

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
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Sbjct  1099  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTAAT  1157

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
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Sbjct  1158  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1217

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
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Sbjct  1218  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1277

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
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Sbjct  1278  CTGCTTAATNNCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTAGGC  1337

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
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Sbjct  1338  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1397

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
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Sbjct  1398  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1457

Query  1442  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1501
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Sbjct  1458  CGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGA  1517

Query  1502  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1561
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Sbjct  1518  TAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCT  1577

Query  1562  TGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGG  1621
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Query  1622  CTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1681
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Sbjct  1638  CTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAG  1697

Query  1682  CTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
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Sbjct  1698  CTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1751


>dbj|AB054265.1| Debaryomyces polymorphus var. africanus gene for 18S rRNA, partial
sequence, strain:JCM 7443
Length=1752

 Score = 3097 bits (1677),  Expect = 0.0
 Identities = 1716/1735 (98%), Gaps = 5/1735 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
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Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
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Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
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Sbjct  201   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
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Sbjct  261   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
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Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
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Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCAATACGGGGAGGTAGT  440

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
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Sbjct  441   GACAATAAATAACGATACAGGGCC-TTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  499

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  559

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
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Sbjct  560   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  619

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
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Sbjct  620   GGTTGGCCGGTCCGCCTTTTCGGCGTGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  679

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
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Sbjct  680   ACCTCTCGTCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  739

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
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Sbjct  740   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  799

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
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Sbjct  800   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  859

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
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Sbjct  860   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  918

Query  902   TT-GCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  919   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  978

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  979   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1038

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
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Sbjct  1039  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1098

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
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Sbjct  1099  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTAA  1157

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1158  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1217

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
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Sbjct  1218  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1277

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             |||||||||||  ||||||||||||||||||||||||||||||||||||||||||||  |
Sbjct  1278  TCTGCTTAATTNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTAGG  1337

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1338  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1397

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1398  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1457

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1458  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1517

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1518  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1577

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1578  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1637

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1638  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1697

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             ||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1698  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1752


>gb|AY520271.1| Candida sp. BG02-5-27-1-2-C 18S ribosomal RNA gene, partial
sequence
Length=1718

 Score = 3097 bits (1677),  Expect = 0.0
 Identities = 1702/1713 (99%), Gaps = 7/1713 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  189

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  247

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  307

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  308   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  367

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  368   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  427

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  428   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  487

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  488   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  547

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  548   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGTT  607
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Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  608   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  667

Query  662   AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
             ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  668   AACCTTTCGCCCTTGTGGTGTCTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  727

Query  722   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728   TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  787

Query  782   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  847

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCA  900
             |||||||||||||||||||||||||||||||| || ||||||||||||||||||||||||
Sbjct  848   TATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCA  906

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTTGTCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  966

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1026

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1086

Query  1081  AGGCTGAAACTTAAAGGAATT-GACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTA  1139
             |||||||||||||||||| || ||||||||||||||||||||||||||||||||||||||
Sbjct  1087  AGGCTGAAACTTAAAGGA-TTAGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTA  1145

Query  1140  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1146  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1205

Query  1200  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1206  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1265

Query  1260  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1319
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1266  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1325

Query  1320  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1379
             |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1326  GCTGGTATAGNCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1385

Query  1380  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1386  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1445

Query  1440  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1499
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1446  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1505

Query  1500  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1506  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1565
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Query  1560  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1566  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1625

Query  1620  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1679
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1626  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1685

Query  1680  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAA  1712
             |||||||||||||||||||||||||||||||||
Sbjct  1686  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAA  1718


>dbj|AB054262.1| Debaryomyces occidentalis gene for 18S rRNA, partial sequence,
strain:JCM 8123
Length=1754

 Score = 3096 bits (1676),  Expect = 0.0
 Identities = 1716/1736 (98%), Gaps = 5/1736 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  140

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  141   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  200

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  201   CTCTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  260

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  261   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  320

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  321   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  380

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  381   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  440

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  441   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  500

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  501   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  560

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  561   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  620

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||||||||| |||| ||||||||||||||||||||||||||||||||||
Sbjct  621   GGTTGGCCGGTCCGCCTTTTCGGCGTGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  680
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Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  681   ACCATTCACCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  740

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  741   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  800

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  801   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  860

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCAT  901
             ||||||||||||||||||||||||||||||| || |||||||||||||||||||||||||
Sbjct  861   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCAT  919

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  920   TTGCCAAGGACGTTTTCATTAATCAAGAACGGAAGTTAGGGGATCGAAGATGATCAGATA  979

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  980   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1039

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1040  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1099

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-AGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||
Sbjct  1100  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGGA-CCTGCGGCTTAA  1158

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1159  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1218

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTT-CTTAGTTGGTGGAGTGATTT  1259
             ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Sbjct  1219  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTTCTTAGTTGGTGGAGTGATTT  1278

Query  1260  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1319
             |||||||||||   ||||||||||||||||||||||||||||||||||||||||||||  
Sbjct  1279  GTCTGCTTAATNNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTAG  1338

Query  1320  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1339  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1398

Query  1380  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1399  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1458

Query  1440  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1499
             | ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1459  AGCGAGTATTAGCCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1518

Query  1500  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1519  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1578

Query  1560  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1619
             |||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  1579  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGGTACTACCGATTGAAT  1638
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Query  1620  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1679
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  1639  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCTTCTTGGAACCGAAA  1698

Query  1680  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1699  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1754


>gb|GU570441.1| Candida sp. NN-2010a 18S ribosomal RNA gene, partial sequence
Length=1710

 Score = 3092 bits (1674),  Expect = 0.0
 Identities = 1701/1713 (99%), Gaps = 5/1713 (0%)
 Strand=Plus/Plus

Query  18    GTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTT  77
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTT  60

Query  78    GATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAAT  137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAAT  120

Query  138   CCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCT-TTTCGGAGCTCT  196
             ||||||||||||||||||||||||||||||||||||||||||||||| |||  |||||||
Sbjct  121   CCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCTCTTT--GAGCTCT  178

Query  197   TTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAA  256
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  179   TTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAA  238

Query  257   ATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAA  316
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239   ATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAA  298

Query  317   CGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGA  376
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299   CGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGA  358

Query  377   AGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACG  436
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  359   AGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATACATAACG  418

Query  437   ATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGG  496
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  419   ATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGG  478

Query  497   AACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTAT  556
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479   AACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTAT  538

Query  557   ATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGTTGGCCGGTCCG  616
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  539   ATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCTTGGTTGGCCGGTCCG  598

Query  617   CCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCTTTCGCCCTTG  676
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  599   CCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCATTCGCCCTTG  658

Query  677   TGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTT  736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  659   TGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTT  718
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Query  737   TGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTT  796
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719   TGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTT  778

Query  797   TCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGA  856
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  779   TCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGA  838

Query  857   GGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACGTT  915
             |||||||||||| || ||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  839   GGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACGTT  897

Query  916   TTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTA  975
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  898   TTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTA  957

Query  976   ACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGACGCACTCGGCACCT  1035
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  958   ACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGACGCACTCGGCACCT  1017

Query  1036  TACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAA  1095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1018  TACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAA  1077

Query  1096  GGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGG  1155
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1078  GGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGG  1137

Query  1156  GGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTT  1215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1138  GGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTT  1197

Query  1216  TGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCGA  1275
             ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1198  TGTGGGTGGCGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCGA  1257

Query  1276  TAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACTT  1335
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1258  TAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACTT  1317

Query  1336  CTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATG  1395
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1318  CTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATG  1377

Query  1396  CCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAACGAGTATTAACCTT  1455
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  1378  CCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAGCGAGTATTAACCTT  1437

Query  1456  GGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAAT  1515
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1438  GGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAAT  1497

Query  1516  TATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACGT  1575
             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  1498  TATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCACCTTGCGTTGATTACGT  1557

Query  1576  CCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCTC  1635
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1558  CCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCTC  1617

Query  1636  CGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTGG  1695
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1618  CGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTGG  1677
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Query  1696  TCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1728
             |||||||||||||||||||||||||||||||||
Sbjct  1678  TCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1710


>emb|AJ508276.1| Pichia caribbica partial 18S rRNA gene, strain CBS 5265T
Length=1710

 Score = 3092 bits (1674),  Expect = 0.0
 Identities = 1701/1713 (99%), Gaps = 5/1713 (0%)
 Strand=Plus/Plus

Query  18    GTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTT  77
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTT  60

Query  78    GATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAAT  137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAAT  120

Query  138   CCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCT-TTTCGGAGCTCT  196
             ||||||||||||||||||||||||||||||||||||||||||||||| |||  |||||||
Sbjct  121   CCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCTCTTT--GAGCTCT  178

Query  197   TTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAA  256
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  179   TTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAA  238

Query  257   ATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAA  316
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239   ATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAA  298

Query  317   CGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGA  376
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299   CGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGA  358

Query  377   AGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACG  436
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  359   AGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATACATAACG  418

Query  437   ATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGG  496
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  419   ATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGG  478

Query  497   AACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTAT  556
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479   AACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTAT  538

Query  557   ATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGTTGGCCGGTCCG  616
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  539   ATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCTTGGTTGGCCGGTCCG  598

Query  617   CCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCTTTCGCCCTTG  676
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  599   CCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCATTCGCCCTTG  658

Query  677   TGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTT  736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  659   TGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTT  718

Query  737   TGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTT  796
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719   TGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTT  778
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Query  797   TCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGA  856
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  779   TCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGA  838

Query  857   GGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACGTT  915
             |||||||||||| || ||| ||||||||| ||||||||||||||||||||||||||||||
Sbjct  839   GGTGAAATTCTTAGATTTA-CTGAAGACTTACTACTGCGAAAGCATTTGCCAAGGACGTT  897

Query  916   TTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTA  975
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  898   TTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTA  957

Query  976   ACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGACGCACTCGGCACCT  1035
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  958   ACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGACGCACTCGGCACCT  1017

Query  1036  TACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAA  1095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1018  TACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAA  1077

Query  1096  GGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGG  1155
             ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  1078  GGAATTGACGGAAGGGCACCACCAGGAGTGGAGACTGCGGCTTAATTTGACTCAACACGG  1137

Query  1156  GGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTT  1215
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1138  GGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTT  1197

Query  1216  TGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCGA  1275
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1198  TGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCGA  1257

Query  1276  TAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACTT  1335
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1258  TAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACTT  1317

Query  1336  CTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATG  1395
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1318  CTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATG  1377

Query  1396  CCCTTAGACGTTCTGGGCCGCACGCGCTACACTGACGGAGCCAACGAGTATTAACCTT  1455
             ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  1378  CCCTTAGACGTTCTGGGCCGCACGCGCTACACTGACGGAGCCAGCGAGTATTAACCTT  1437

Query  1456  GGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAAT  1515
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1438  GGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAAT  1497

Query  1516  TATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACGT  1575
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1498  TATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACGT  1557

Query  1576  CCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCTC  1635
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1558  CCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCTC  1617

Query  1636  CGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTGG  1695
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1618  CGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTGG  1677

Query  1696  TCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1728
             |||||||||||||||||||||||||||||||||
Sbjct  1678  TCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1710
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>gb|AY227715.1| Candida xestobii strain ATCC 24001 18S ribosomal RNA gene, partial
sequence
Length=1715

 Score = 3090 bits (1673),  Expect = 0.0
 Identities = 1698/1709 (99%), Gaps = 5/1709 (0%)
 Strand=Plus/Plus

Query  3      GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70     AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123    ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  130    ATACATGCTACAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  189

Query  183    CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190    CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  247

Query  242    CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248    CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  307

Query  302    GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  308    GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  367

Query  362    TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  368    TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  427

Query  422    TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  428    TGACAATACATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  487

Query  482    AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  488    AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  547

Query  542    GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  548    GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  607

Query  602    TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  608    TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  667

Query  662    AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  668    AACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  727

Query  722    TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728    TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  787

Query  782    TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  788   TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  847

Query  842   TATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCA  900
             ||||||||||||||||||||||||||| || ||| |||||||||||||||||||||||||
Sbjct  848   TATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCA  906

Query  901   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  966

Query  961   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTG  1026

Query  1021  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1086

Query  1081  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1146

Query  1141  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1206

Query  1201  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1266

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1326

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1386

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1387  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1446

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1447  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1506

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1507  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1566

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1567  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1626

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1627  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1686

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAG  1709
             |||||||||||||||||||||||||||||
Sbjct  1687  GCTGGTCAAACTTGGTCATTTAGAGGAAG  1715


>gb|AY242159.1| Candida sp. BG01-7-21-003B-1-1 18S ribosomal RNA gene, partial
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sequence
Length=1720

 Score = 3090 bits (1673),  Expect = 0.0
 Identities = 1702/1715 (99%), Gaps = 6/1715 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  130   ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  188

Query  183   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189   CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  248

Query  243   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249   GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  308

Query  303   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  309   GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  368

Query  363   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  369   ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  428

Query  423   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  429   GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  488

Query  483   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  489   ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  548

Query  543   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  549   CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  608

Query  603   GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
             |||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  609   GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  667

Query  663   ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
             |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  668   ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  727

Query  723   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728   TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  787

Query  783   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788   CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  847

Query  843   ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
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             ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  848   ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  906

Query  902   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907   TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  966

Query  962   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGA  1021
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967   CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1026

Query  1022  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027  CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1086

Query  1082  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1146

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1206

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1266

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1326

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1386

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1387  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1446

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||| | ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1447  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1505

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1506  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1565

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1566  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1625

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1626  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1685

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAG  1715
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Sbjct  1686  GCTAGTCAAACTTGGTCATTTAGAGGAAGTAAAAG  1720


>dbj|AB054258.1| Debaryomyces etchellsii gene for 18S rRNA, partial sequence, 
strain:JCM 3656
Length=1752
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 Score = 3086 bits (1671),  Expect = 0.0
 Identities = 1715/1736 (98%), Gaps = 7/1736 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGG-ATAACCGTGGTAATTCTAGAGCT  121
             |||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTAC-TGGTATAACCGTGGTAATTCTAGAGCT  139

Query  122   AATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAAT  181
             |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  140   AATACATGCTGAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAAC  199

Query  182   GCTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  200   GCTCTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  259

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  319

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  379

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  439

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  499

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  559

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  619

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||| ||||| |||| |||||||||||||||||||||||||||||||||
Sbjct  620   TGGTTGGCCGGTCCGTCTTTTCGGCGTGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  679

Query  662   AACCT-TTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGT  720
             ||||| || |||||||||||| | ||||||||||||||||||||||||||||||||||||
Sbjct  680   AACCTATT-GCCCTTGTGGTGGTAGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGT  738

Query  721   GTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGG  780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  739   GTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGG  798

Query  781   TTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCA  840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  799   TTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCA  858

Query  841   GTATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGC  899
             ||||||||||||||||||||||||||||||||| || |||||||||||||||||||||||
Sbjct  859   GTATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGC  917
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Query  900   ATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGA  959
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  918   ATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGA  977

Query  960   TACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCttttttt  1019
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  978   TACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTT  1037

Query  1020  GACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGC  1079
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1038  GACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGC  1097

Query  1080  AAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTA  1139
             ||||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||
Sbjct  1098  AAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGG-GACTGCGGCTTA  1156

Query  1140  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1199
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1157  ATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAG  1216

Query  1200  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1259
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1217  AGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTT  1276

Query  1260  GTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1319
             ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1277  GTCTGCTTAATTNNGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTT  1336

Query  1320  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1379
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1337  GCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAA  1396

Query  1380  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1439
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1397  TAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCC  1456

Query  1440  AACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1499
             | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1457  AGCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGG  1516

Query  1500  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1559
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1517  GATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAG  1576

Query  1560  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1619
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1577  CTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAAT  1636

Query  1620  GGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1679
             ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1637  GGCTTAGTGAGGCCTTCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAA  1696

Query  1680  AGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1697  AGTTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1752


>gb|AY227020.1| Pichia guilliermondii strain CCO 8 18S ribosomal RNA gene, partial
sequence
Length=1701

 Score = 3086 bits (1671),  Expect = 0.0
 Identities = 1694/1704 (99%), Gaps = 5/1704 (0%)
 Strand=Plus/Plus
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Query  24   GCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATAGT  83
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATAGT  60

Query  84   ACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAATCCCGAC  143
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   ACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAATCCCGAC  120

Query  144  TGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCT-TTTCGGAGCTCTTTGATG  202
            ||||||||||||||||||||||||||||||||||||||||| |||  |||||||||||||
Sbjct  121  TGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCTCTTT--GAGCTCTTTGATG  178

Query  203  ATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAAATTTCT  262
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  179  ATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAAATTTCT  238

Query  263  GCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAACGGGGA  322
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239  GCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAACGGGGA  298

Query  323  ATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAG  382
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299  ATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAG  358

Query  383  CAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACGATACAG  442
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  359  CAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATACATAACGATACAG  418

Query  443  GGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGGAACAAT  502
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  419  GGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGGAACAAT  478

Query  503  TGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAA  562
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479  TGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAA  538

Query  563  GTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGTTGGCCGGTCCGCCTTTT  622
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  539  GTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCTTGGTTGGCCGGTCCGCCTTTT  598

Query  623  TGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCTTTCGCCCTTGTGGTGT  682
            ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  599  TGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCATTCGCCCTTGTGGTGT  658

Query  683  TTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTTTGCTCG  742
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  659  TTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTTTGCTCG  718

Query  743  AATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTTTCTAGG  802
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719  AATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTTTCTAGG  778

Query  803  ACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGAGGTGAA  862
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  779  ACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGAGGTGAA  838

Query  863  ATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACGTTTTCATT  921
            |||||| || ||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  839  ATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACGTTTTCATT  897

Query  922  AATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTAACCATA  981
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  898  AATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTAACCATA  957
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Query  982   AACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGACGCACTCGGCACCTTACGAG  1041
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  958   AACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGACGCACTCGGCACCTTACGAG  1017

Query  1042  AAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATT  1101
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1018  AAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATT  1077

Query  1102  GACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAAC  1161
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1078  GACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAAAC  1137

Query  1162  TCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTTGTGGG  1221
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1138  TCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATTTTGTGGG  1197

Query  1222  TGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCGATAACGA  1281
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1198  TGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCGATAACGA  1257

Query  1282  ACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACTTCTTAGA  1341
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1258  ACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACTTCTTAGA  1317

Query  1342  GGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCCTTA  1401
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1318  GGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCCTTA  1377

Query  1402  GACGTTCTGGGCCGCACGCGCTACACTGACGGAGCCAACGAGTATTAACCTTGGCCGA  1461
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  1378  GACGTTCTGGGCCGCACGCGCTACACTGACGGAGCCAGCGAGTATTAACCTTGGCCGA  1437

Query  1462  GAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAATTATTGC  1521
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1438  GAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAATTATTGC  1497

Query  1522  TCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACGTCCCTGC  1581
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1498  TCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACGTCCCTGC  1557

Query  1582  CCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCTCCGGATT  1641
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1558  CCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCTCCGGATT  1617

Query  1642  GGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTGGTCATTT  1701
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1618  GGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTGGTCATTT  1677

Query  1702  AGAGGAAGTAAAAGTCGTAACAAG  1725
             ||||||||||||||||||||||||
Sbjct  1678  AGAGGAAGTAAAAGTCGTAACAAG  1701


>gb|AY520226.1| Candida sp. BG02-5-23-003D-5 18S ribosomal RNA gene, partial
sequence
Length=1740

 Score = 3086 bits (1671),  Expect = 0.0
 Identities = 1716/1736 (98%), Gaps = 9/1736 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  130   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAACG  189

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  190   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  247

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  248   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  307

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  308   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  367

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  368   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  427

Query  422   TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
             ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  428   TGACAATAAATAACGATACAGGGCCCTTTAGGGTCTTGTAATTGGAATGAGTACAATGTA  487

Query  482   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  488   AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  547

Query  542   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  548   GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCT  607

Query  602   TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
             ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  608   TGGTTGGCCGGTCCGCC-TTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  666

Query  662   AACC-TTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGT  720
             ||||   | |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  667   AACCAAGT-GCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGT  725

Query  721   GTTCAAAGCAGGCCTTT-GCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATG  779
             |||||||||| || ||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  726   GTTCAAAGCAAGCGTTTCGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATG  785

Query  780   GTTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATC  839
             |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct  786   GTTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAACAGGGACGGTCGGGGGCATC  845

Query  840   AGTATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAG  898
             |||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||
Sbjct  846   AGTATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAG  904

Query  899   CATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAG  958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  905   CATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAG  964

Query  959   ATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttt  1018
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  965   GTACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTT  1024

Query  1019  tGACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCG  1078
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1025  TGACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCG  1084

Query  1079  CAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT  1138
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1085  CAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT  1144

Query  1139  AATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGA  1198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1145  AATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGA  1204

Query  1199  GAGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATT  1258
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1205  GAGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATT  1264

Query  1259  TGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTT  1318
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1265  TGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTT  1324

Query  1319  TGCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCA  1378
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1325  GGCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCA  1384

Query  1379  ATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGC  1438
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1385  ATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGC  1444

Query  1439  CAACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGG  1498
             || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1445  CAGCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGG  1504

Query  1499  GGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCA  1558
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1505  GGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCA  1564

Query  1559  GCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAA  1618
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1565  GCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAA  1624

Query  1619  TGGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAA  1678
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1625  TGGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAA  1684

Query  1679  AAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1734
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1685  AAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTA  1740


>emb|AJ508269.1| Pichia caribbica partial 18S rRNA gene, strain CBS 2022T
Length=1710

 Score = 3086 bits (1671),  Expect = 0.0
 Identities = 1701/1714 (99%), Gaps = 7/1714 (0%)
 Strand=Plus/Plus

Query  18    GTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTT  77
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTT  60

Query  78    GATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAAT  137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  61    GATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAAT  120

Query  138   CCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCT-TTTCGGAGCTCT  196
             ||||||||||||||||||||||||||||||||||||||||||||||| |||  |||||||
Sbjct  121   CCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCTCTTT--GAGCTCT  178

Query  197   TTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAA  256
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  179   TTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAA  238

Query  257   ATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAA  316
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239   ATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAA  298

Query  317   CGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGA  376
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299   CGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGA  358

Query  377   AGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACG  436
             ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  359   AGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATACATAACG  418

Query  437   ATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGG  496
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  419   ATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGG  478

Query  497   AACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTAT  556
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479   AACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTAT  538

Query  557   ATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGTTGGCCGGTCCG  616
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  539   ATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCTTGGTTGGCCGGTCCG  598

Query  617   CCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCTTTCGCCCTTG  676
             ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  599   CCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCATTCGCCCTTG  658

Query  677   TGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTT  736
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  659   TGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTT  718

Query  737   TGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTT  796
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719   TGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTT  778

Query  797   TCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGA  856
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  779   TCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGA  838

Query  857   GGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACGTT  915
             |||||||||||| || ||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  839   GGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACGTT  897

Query  916   TTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTA  975
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  898   TTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTA  957

Query  976   ACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGACGCACTCGGCACCT  1035
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  958   ACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGACGCACTCGGCACCT  1017

Query  1036  TACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAA  1095
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1018  TACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAA  1077

Query  1096  GGAATTGACGGAAGGGCACCACCAGGAG-TGGAGCCTGCGGCTTAATTTGACTCAACACG  1154
             |||||||||||||||||||||||||||| ||| | |||||||||||||||||||||||||
Sbjct  1078  GGAATTGACGGAAGGGCACCACCAGGAGTTGG-GACTGCGGCTTAATTTGACTCAACACG  1136

Query  1155  GGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATT  1214
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1137  GGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATT  1196

Query  1215  TTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCG  1274
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1197  TTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCG  1256

Query  1275  ATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACT  1334
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1257  ATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACT  1316

Query  1335  TCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGAT  1394
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1317  TCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGAT  1376

Query  1395  GCCCTTAGACGTTCTGGCCGCACGCGCGCTACACTGACGGAGCCAACGAGTATTAACCT  1454
             ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Sbjct  1377  GCCCTTAGACGTTCTGGCCGCACGCGCGCTACACTGACGGAGCCAGCGAGTATTAACCT  1436

Query  1455  TGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAA  1514
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1437  TGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAA  1496

Query  1515  TTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG  1574
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1497  TTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG  1556

Query  1575  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCT  1634
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1557  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCT  1616

Query  1635  CCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTG  1694
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1617  CCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTG  1676

Query  1695  GTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1728
             ||||||||||||||||||||||||||||||||||
Sbjct  1677  GTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1710


>gb|AY242197.1| Candida sp. BG01-7-21-009A-1-1 18S ribosomal RNA gene, partial
sequence
Length=1716

 Score = 3083 bits (1669),  Expect = 0.0
 Identities = 1698/1711 (99%), Gaps = 6/1711 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  10    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  69

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  70    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  129

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
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                 |||||||||||||||||||||| | |||||||||||||||||||||||||||||||||||
Sbjct  130       ATACATGCTAAAAATCCCGACT-TCTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  188

Query  183       CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  242
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189       CTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGC  248

Query  243       GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  302
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249       GATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATG  308

Query  303       GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  362
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  309       GTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCT  368

Query  363       ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  422
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  369       ACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGT  428

Query  423       GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  482
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  429       GACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAA  488

Query  483       ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  542
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  489       ATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAG  548

Query  543       CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  602
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  549       CTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTT  608

Query  603       GGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  662
                 |||||||||||||| |||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  609       GGTTGGCCGGTCCG-CTTTATGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTA  667

Query  663       ACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  722
                 |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  668       ACCTTTCGCCCTTGTGGTGTTTGGAGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGT  727

Query  723       TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  782
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  728       TCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTT  787

Query  783       CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  842
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  788       CTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGT  847

Query  843       ATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCAT  901
                 ||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Sbjct  848       ATTCAGTTGTCAGAGGTGAAATTCTTGGATTTA-CTGAAGACTAACTACTGCGAAAGCAT  906

Query  902       TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  961
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  907       TTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATA  966

Query  962       CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCttttttGA  1021
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  967       CCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGA  1026

Query  1022      CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1081
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1027      CGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAA  1086

Query  1082      GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1141
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1087  GGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAAT  1146

Query  1142  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1201
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1147  TTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAG  1206

Query  1202  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1207  CTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGT  1266

Query  1262  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1321
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1267  CTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGC  1326

Query  1322  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1381
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1327  TGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATA  1386

Query  1382  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAA  1441
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  1387  ACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAG  1446

Query  1442  CGAGTAT-TAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
             ||||| | ||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  1447  CGAGT-TCTAACCTTGGCCGAGAGGTCTGGGTAATCTTGTGAAACTCCGTCGTGCTGGGG  1505

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1506  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1565

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1566  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1625

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
             |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1626  GCTTAGTGAGGCTTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1685

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTA  1711
             ||| |||||||||||||||||||||||||||
Sbjct  1686  GCTAGTCAAACTTGGTCATTTAGAGGAAGTA  1716


>emb|AJ508270.1| Candida carpophila partial 18S rRNA gene, strain CBS 5256T
Length=1710

 Score = 3083 bits (1669),  Expect = 0.0
 Identities = 1700/1714 (99%), Gaps = 7/1714 (0%)
 Strand=Plus/Plus

Query  18    GTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTT  77
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTT  60

Query  78    GATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAAT  137
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAAT  120

Query  138   CCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCT-TTTCGGAGCTCT  196
             ||||||||||||||||||||||||||||||||||||||||||||||| |||  |||||||
Sbjct  121   CCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATGCTCTTT--GAGCTCT  178

Query  197   TTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAA  256
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Sbjct  179    TTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGGCGATGGTTCATTCAA  238

Query  257    ATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAA  316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  239    ATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCATGGTTTCAACGGGTAA  298

Query  317    CGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGA  376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  299    CGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGA  358

Query  377    AGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATAAATAACG  436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  359    AGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAGTGACAATACATAACG  418

Query  437    ATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGG  496
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  419    ATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTAAATACCTTAACGAGG  478

Query  497    AACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTAT  556
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  479    AACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTAT  538

Query  557    ATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCTTGGTTGGCCGGTCCG  616
              ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct  539    ATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACTTTGGGCTTGGTTGGCCGGTCCG  598

Query  617    CCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCTTTCGCCCTTG  676
              ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Sbjct  599    CCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCTAACCATTCGCCCTTG  658

Query  677    TGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTT  736
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  659    TGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTT  718

Query  737    TGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTT  796
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719    TGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGTTCTATTTTGTTGGTT  778

Query  797    TCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGA  856
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  779    TCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAGTATTCAGTTGTCAGA  838

Query  857    GGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACGTT  915
              |||||||||||| || ||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  839    GGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGAAAGCATTTGCCAAGGACGTT  897

Query  916    TTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTA  975
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  898    TTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGATACCGTCGTAGTCTTA  957

Query  976    ACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttGACGCACTCGGCACCT  1035
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  958    ACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTTTTTTGACGCACTCGGCACCT  1017

Query  1036   TACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAA  1095
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  1018   TACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCAAGGCTGAAACTWAAA  1077

Query  1096   GGAATTGACGGAAGGGCACCACCAGGAG-TGGAGCCTGCGGCTTAATTTGACTCAACACG  1154
              |||||||||||||||||||||||||||| ||| | |||||||||||||||||||||||||
Sbjct  1078   GGAATTGACGGAAGGGCACCACCAGGAGTTGG-GACTGCGGCTTAATTTGACTCAACACG  1136

Query  1155   GGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATT  1214
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1137  GGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGAGCTCTTTCTTGATT  1196

Query  1215  TTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCG  1274
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1197  TTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTGTCTGCTTAATTGCG  1256

Query  1275  ATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACT  1334
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1257  ATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTGCTGGTATAGTCACT  1316

Query  1335  TCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGAT  1394
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1317  TCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAATAACAGGTCTGTGAT  1376

Query  1395  GCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAACGAGTATTAACCT  1454
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  1377  GCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCAGCGAGTATTAACCT  1436

Query  1455  TGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAA  1514
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1437  TGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGGATAGAGCATTGTAA  1496

Query  1515  TTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG  1574
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1497  TTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGCTTGCGTTGATTACG  1556

Query  1575  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCT  1634
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1557  TCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATGGCTTAGTGAGGCCT  1616

Query  1635  CCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTG  1694
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1617  CCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAAGCTGGTCAAACTTG  1676

Query  1695  GTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1728
             ||||||||||||||||||||||||||||||||||
Sbjct  1677  GTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTT  1710


>emb|AM261069.1| Debaryomyces sp. MTCC 7061 18S rRNA gene, strain MTCC 7061
Length=1753

 Score = 3079 bits (1667),  Expect = 0.0
 Identities = 1713/1735 (98%), Gaps = 4/1735 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  21    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  80

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGG-ATAACCGTGGTAATTCTAGAGCT  121
             |||||||||||||||||||||||||||||||| ||| |||||||||||||||||||||||
Sbjct  81    AGTTATCGTTTATTTGATAGTACCTTTACTAC-TGGTATAACCGTGGTAATTCTAGAGCT  139

Query  122   AATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAAT  181
             |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  140   AATACATGCTGAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAAC  199

Query  182   GCTTTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  200   GCTCTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  259

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
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Sbjct  260       CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  319

Query  302       GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320       GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  379

Query  362       TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380       TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  439

Query  422       TGACAATAAATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  481
                 |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  440       TGACAATATATAACGATACAGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGTA  499

Query  482       AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  541
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  500       AATACCTTAACGAGGAACAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCA  559

Query  542       GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  601
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  560       GCTCCAATAGCGTATATTAAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGAACCTTGGGCT  619

Query  602       TGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  661
                 ||||||||||||||| ||||| |||| |||||||||||||||||||||||||||||||||
Sbjct  620       TGGTTGGCCGGTCCGTCTTTTCGGCGTGTACTGGACCCAACCGAGCCTTTCCTTCTGGCT  679

Query  662       AACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  721
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Sbjct  680       AACCTATCGCCCTTGTGGTGGTAGGCGAACCAGGACTTTTACTTTGAAAAAATTAGAGTG  739

Query  722       TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  781
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  740       TTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTTATGGT  799

Query  782       TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  841
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Sbjct  800       TCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGCATCAG  859

Query  842       TATTCAGTTGTCAGAGGTGAAATTCTTGGATT-ACCTGAAGACTAACTACTGCGAAAGCA  900
                 |||||||||||||||||||||||||||||||| || ||||||||||||||||||||||||
Sbjct  860       TATTCAGTTGTCAGAGGTGAAATTCTTGGATTTAC-TGAAGACTAACTACTGCGAAAGCA  918

Query  901       TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  960
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  919       TTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGATCAGAT  978

Query  961       ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCtttttttG  1020
                 |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  979       ACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGGTGTTCTTTTTTTG  1038

Query  1021      ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1080
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Sbjct  1039      ACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGGTCGCA  1098

Query  1081      AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1140
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Sbjct  1099      AGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAA  1158

Query  1141      TTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1200
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Sbjct  1159      TTCGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGATTGAGA  1218

Query  1201      GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1260
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Sbjct  1219  GCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTGATTTG  1278

Query  1261  TCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1320
             ||| |||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1279  TCTACTTAATTGTGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGCTTTTG  1338

Query  1321  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1380
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Sbjct  1339  CTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAGGCAAT  1398

Query  1381  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1440
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Sbjct  1399  AACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGGAGCCA  1458

Query  1441  ACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1500
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Sbjct  1459  GCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGCTGGGG  1518

Query  1501  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1560
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Sbjct  1519  ATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCATCAGC  1578

Query  1561  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1620
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Sbjct  1579  TTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATTGAATG  1638

Query  1621  GCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACCGAAAA  1680
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Sbjct  1639  GCTTAGTGAGGCCTTCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACTGAAAA  1698

Query  1681  GCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1735
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Sbjct  1699  GTTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCGTAACAAGGTTTCCGTAG  1753


>gb|DQ499512.1| Candida sp. ny4e 18S ribosomal RNA gene, partial sequence
Length=1735

 Score = 3077 bits (1666),  Expect = 0.0
 Identities = 1706/1723 (99%), Gaps = 11/1723 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  12    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  71

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  72    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  131

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
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Sbjct  132   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  191

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
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Sbjct  192   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  249

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
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Sbjct  250   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  309

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
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Sbjct  310      GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  369

Query  362      TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
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Sbjct  370      TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  429

Query  422      TGACAATAAATAACGATACA-GGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGT  480
                |||||||| ||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  430      TGACAATACATAACGATACAGGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGT  489

Query  481      AAATACCTT-AACGAGGAACAATT-GGAGGGCAAGTCTGGTGCCAGCAG-CCGCGGTAAT  537
                ||||||||| |||||||||||||| |||||||||||||||||||||||| ||||||||| 
Sbjct  490      AAATACCTTAAACGAGGAACAATTGGGAGGGCAAGTCTGGTGCCAGCAGCCCGCGGTAAA  549

Query  538      TCCAGCTCCAATAGCGTATATTAAAGTTGTT-GCAGTTAAAAAGCTCGTAGTTGAACCTT  596
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Sbjct  550      TCCAGCTCCAATAGCGTATATTAAAGTTGTTGGCAGTTAAAAAGCTCGTAGTTGAACTTT  609

Query  597      GGCTTGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTC  656
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  610      GGGCTTGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTC  669

Query  657      TGGCTAACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTA  716
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Sbjct  670      TGGCTAACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTA  729

Query  717      GAGTGTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTT  776
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Sbjct  730      GAGTGTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTT  789

Query  777      ATGGTTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGC  836
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Sbjct  790      ATGGTTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGC  849

Query  837      ATCAGTATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGA  895
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Sbjct  850      ATCAGTATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGA  908

Query  896      AAGCATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGAT  955
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Sbjct  909      AAGCATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGAT  968

Query  956      CAGATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCttt  1015
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Sbjct  969      CAGATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTT  1028

Query  1016     ttttGACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGG  1075
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Sbjct  1029     TTTTGACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGG  1088

Query  1076     TCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGG  1135
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Sbjct  1089     TCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGG  1148

Query  1136     CTTAATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGAT  1195
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Sbjct  1149     CTTAATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGAT  1208

Query  1196     TGAGAGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTG  1255
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1209     TGAGAGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTG  1268

Query  1256     ATTTGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGC  1315
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Sbjct  1269  ATTTGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGC  1328

Query  1316  TTTTGCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAG  1375
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Sbjct  1329  TTTTGCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAG  1388

Query  1376  GCAATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGG  1435
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Sbjct  1389  GCAATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGG  1448

Query  1436  AGCCAACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGC  1495
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Query  1496  TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCA  1555
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Sbjct  1509  TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCA  1568

Query  1556  TCAGCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATT  1615
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Sbjct  1569  TCAGCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATT  1628

Query  1616  GAATGGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACC  1675
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Sbjct  1629  GAATGGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACC  1688

Query  1676  GAAAAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCG  1718
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>gb|DQ438179.1| Candida sp. N12C 18S ribosomal RNA gene, partial sequence
Length=1735

 Score = 3077 bits (1666),  Expect = 0.0
 Identities = 1706/1723 (99%), Gaps = 11/1723 (0%)
 Strand=Plus/Plus

Query  3     GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  62
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  12    GCCATGCATGTCTAAGTATAAGCAATTTATACAGTGAAACTGCGAATGGCTCATTAAATC  71

Query  63    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  72    AGTTATCGTTTATTTGATAGTACCTTTACTACTTGGATAACCGTGGTAATTCTAGAGCTA  131

Query  123   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  182
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  132   ATACATGCTAAAAATCCCGACTGTTTGGAAGGGATGTATTTATTAGATAAAAAATCAATG  191

Query  183   CT-TTTCGGAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  241
             || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  192   CTCTTT--GAGCTCTTTGATGATTCATAATAACTTTTCGAATCGCATGGCCTTGTGCTGG  249

Query  242   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  301
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Sbjct  250   CGATGGTTCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACCAT  309

Query  302   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  361
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Sbjct  310   GGTTTCAACGGGTAACGGGGAATAAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGC  369

Query  362   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  421
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Sbjct  370   TACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCCGACACGGGGAGGTAG  429

Query  422   TGACAATAAATAACGATACA-GGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGT  480
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Sbjct  430   TGACAATACATAACGATACAGGGGCCCTTTCGGGTCTTGTAATTGGAATGAGTACAATGT  489

Query  481   AAATACCTT-AACGAGGAACAATT-GGAGGGCAAGTCTGGTGCCAGCAG-CCGCGGTAAT  537
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Sbjct  490   AAATACCTTAAACGAGGAACAATTGGGAGGGCAAGTCTGGTGCCAGCAGCCCGCGGTAAA  549

Query  538   TCCAGCTCCAATAGCGTATATTAAAGTTGTT-GCAGTTAAAAAGCTCGTAGTTGAACCTT  596
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Sbjct  550   TCCAGCTCCAATAGCGTATATTAAAGTTGTTGGCAGTTAAAAAGCTCGTAGTTGAACTTT  609

Query  597   GGGCTTGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTC  656
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Sbjct  610   GGGCTTGGTTGGCCGGTCCGCCTTTTTGGCGAGTACTGGACCCAACCGAGCCTTTCCTTC  669

Query  657   TGGCTAACCTTTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTA  716
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Sbjct  670   TGGCTAACCATTCGCCCTTGTGGTGTTTGGCGAACCAGGACTTTTACTTTGAAAAAATTA  729

Query  717   GAGTGTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTT  776
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Sbjct  730   GAGTGTTCAAAGCAGGCCTTTGCTCGAATATATTAGCATGGAATAATAGAATAGGACGTT  789

Query  777   ATGGTTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGC  836
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Sbjct  790   ATGGTTCTATTTTGTTGGTTTCTAGGACCATCGTAATGATTAATAGGGACGGTCGGGGGC  849

Query  837   ATCAGTATTCAGTTGTCAGAGGTGAAATTCTTGGA-TTACCTGAAGACTAACTACTGCGA  895
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Sbjct  850   ATCAGTATTCAGTTGTCAGAGGTGAAATTCTTAGATTTA-CTGAAGACTAACTACTGCGA  908

Query  896   AAGCATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGAT  955
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Sbjct  909   AAGCATTTGCCAAGGACGTTTTCATTAATCAAGAACGAAAGTTAGGGGATCGAAGATGAT  968

Query  956   CAGATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCttt  1015
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Sbjct  969   CAGATACCGTCGTAGTCTTAACCATAAACTATGCCGACTAGGGATCGGGTGTTGTTCTTT  1028

Query  1016  ttttGACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGG  1075
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Sbjct  1029  TTTTGACGCACTCGGCACCTTACGAGAAATCAAAGTCTTTGGGTTCTGGGGGGAGTATGG  1088

Query  1076  TCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGG  1135
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Sbjct  1089  TCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGG  1148

Query  1136  CTTAATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGAT  1195
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Sbjct  1149  CTTAATTTGACTCAACACGGGGAAACTCACCAGGTCCAGACACAATAAGGATTGACAGAT  1208

Query  1196  TGAGAGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTG  1255
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Sbjct  1209  TGAGAGCTCTTTCTTGATTTTGTGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGTG  1268

Query  1256  ATTTGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGC  1315
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1269  ATTTGTCTGCTTAATTGCGATAACGAACGAGACCTTAACCTACTAAATAGTGCTGCTAGC  1328

Query  1316  TTTTGCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAG  1375
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Sbjct  1329  TTTTGCTGGTATAGTCACTTCTTAGAGGGACTATCGATTTCAAGTCGATGGAAGTTTGAG  1388

Query  1376  GCAATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGG  1435
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Sbjct  1389  GCAATAACAGGTCTGTGATGCCCTTAGACGTTCTGGGCCGCACGCGCGCTACACTGACGG  1448

Query  1436  AGCCAACGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGC  1495
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Sbjct  1449  AGCCAGCGAGTATTAACCTTGGCCGAGAGGTCTGGGAAATCTTGTGAAACTCCGTCGTGC  1508

Query  1496  TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCA  1555
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Sbjct  1509  TGGGGATAGAGCATTGTAATTATTGCTCTTCAACGAGGAATTCCTAGTAAGCGCAAGTCA  1568

Query  1556  TCAGCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATT  1615
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Sbjct  1569  TCAGCTTGCGTTGATTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTACTACCGATT  1628

Query  1616  GAATGGCTTAGTGAGGCCTCCGGATTGGTTTAAAGAAGGGGGCAACTCCATCTTGGAACC  1675
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Query  1676  GAAAAGCTGGTCAAACTTGGTCATTTAGAGGAAGTAAAAGTCG  1718
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Sbjct  1689  GAAAAGCTGGTCAAACTTGGTCATT-AGAGGAAGTAAAAGTCG  1730



  Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
    Posted date:  Jun 26, 2010  5:44 PM
  Number of letters in database: 1,817,769,445
  Number of sequences in database:  12,090,198

Lambda     K      H
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Gapped
Lambda     K      H
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Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 12090198
Number of Hits to DB: 8629390
Number of extensions: 69897
Number of successful extensions: 69897
Number of sequences better than 10: 36836
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 57168
Number of HSP's successfully gapped: 57081
Length of query: 2961
Length of database: 31882540517
Length adjustment: 34
Effective length of query: 2927
Effective length of database: 31471473785
Effective search space: 92117003768695
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A: 0
X1: 15 (28.8 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 15 (28.8 bits)
S2: 23 (43.6 bits)
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BLASTN 2.2.23+
Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and
Webb Miller (2000), "A greedy algorithm for aligning DNA
sequences", J Comput Biol 2000; 7(1-2):203-14.


RID: 2DDABPEZ014


Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
           12,090,198 sequences; 31,882,540,517 total letters
Query= gi|65306735|gb|AY939792.1| Pichia guilliermondii strain ATCC 6260 18S
ribosomal RNA gene, partial sequence; internal transcribed spacer 1,
5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607


                                                                   Score     E
Sequences producing significant alignments:                       (Bits)  Value

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gb|EU568963.1|  Pichia guilliermondii isolate CNRMA 200600335 ...  1122    0.0
gb|EU568961.1|  Pichia guilliermondii isolate CNRMA 200600561 ...  1122    0.0
gb|EU568959.1|  Pichia guilliermondii isolate CNRMA 200600938 ...  1122    0.0
gb|EU568957.1|  Pichia guilliermondii isolate CNRMA 200601010 ...  1122    0.0
gb|EU568955.1|  Pichia guilliermondii isolate CNRMA 200601023 ...  1122    0.0
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gb|EU568947.1|  Pichia guilliermondii isolate CNRMA 200500030 ...  1122    0.0
gb|EU568945.1|  Pichia guilliermondii isolate CNRMA 200500086 ...  1122    0.0
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gb|EU568933.1|  Pichia guilliermondii isolate CNRMA 200501305 ...  1122    0.0
gb|EU568931.1|  Pichia guilliermondii isolate CNRMA 200501314 ...  1122    0.0
gb|EU568929.1|  Pichia guilliermondii isolate CNRMA 200501320 ...  1122    0.0
gb|EU568911.1|  Pichia guilliermondii 18S ribosomal RNA gene, ...  1122    0.0
dbj|AB369917.1|  Pichia guilliermondii genes for small subunit...  1122    0.0
gb|EU177579.1|  Pichia guilliermondii strain EQ 18S ribosomal ...  1122    0.0
gb|EF191048.1|  Pichia guilliermondii strain HJM 18S ribosomal...  1122    0.0
gb|DQ663478.1|  Pichia guilliermondii isolate JHSd 18S ribosom...  1122    0.0
gb|DQ680842.1|  Pichia guilliermondii strain G7A1 18S ribosoma...  1122    0.0
gb|AY939795.1|  Pichia guilliermondii isolate UR 9406-03 18S r...  1122    0.0
gb|AY939792.1|  Pichia guilliermondii strain ATCC 6260 18S rib...  1122    0.0
gb|GU385845.1|  Pichia guilliermondii strain SMB 18S ribosomal...  1120    0.0
gb|GQ334393.1|  Pichia guilliermondii isolate SD 337 18S ribos...  1116    0.0
gb|FJ969194.1|  Pichia guilliermondii strain UAF-214 18S ribos...  1116    0.0
gb|EU568993.1|  Pichia guilliermondii isolate CNRMA 200500950 ...  1116    0.0
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gb|EU568989.1|  Pichia guilliermondii isolate CNRMA 200501343 ...  1116    0.0
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gb|EU568985.1|  Pichia guilliermondii isolate CNRMA 200601042 ...  1116    0.0
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gb|DQ663479.1|  Pichia guilliermondii isolate hn-2 18S ribosom...  1116    0.0
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gb|GQ497898.1|  Pichia guilliermondii strain PX-PAT 18S riboso...  1110    0.0
gb|GQ149493.1|  Pichia guilliermondii strain UAF-130 18S ribos...  1110    0.0
gb|FJ662408.1|  Pichia guilliermondii isolate ZA043 18S riboso...  1110    0.0
gb|EU568969.1|  Pichia guilliermondii isolate CNRMA 200501202 ...  1110    0.0
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gb|DQ663476.1|  Pichia guilliermondii isolate L2-8 18S ribosom...  1109    0.0
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gb|EF375704.1|  Pichia guilliermondii strain N12c 18S ribosoma...  1107    0.0
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emb|FM199963.1|  Pichia caribbica 18S rRNA gene (partial), ITS...  1092    0.0
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ALIGNMENTS
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gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
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 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

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ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
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 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

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gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

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Query  601  CGGAGGA  607
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Sbjct  601  CGGAGGA  607


>gb|EU568961.1| Pichia guilliermondii isolate CNRMA 200600561 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568959.1| Pichia guilliermondii isolate CNRMA 200600938 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601   CGGAGGA  607
             |||||||
Sbjct  601   CGGAGGA  607


>gb|EU568957.1| Pichia guilliermondii isolate CNRMA 200601010 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
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Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568955.1| Pichia guilliermondii isolate CNRMA 200601023 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568953.1| Pichia guilliermondii isolate CNRMA 200700041 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
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sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568951.1| Pichia guilliermondii isolate CNRMA 200700261 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568949.1| Pichia guilliermondii isolate CNRMA 200700329 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
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Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568947.1| Pichia guilliermondii isolate CNRMA 200500030 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
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Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568945.1| Pichia guilliermondii isolate CNRMA 200500086 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601   CGGAGGA  607
             |||||||
Sbjct  601   CGGAGGA  607


>gb|EU568943.1| Pichia guilliermondii isolate CNRMA 200500816 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568941.1| Pichia guilliermondii isolate CNRMA 200500861 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568939.1| Pichia guilliermondii isolate CNRMA 200501141 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
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ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568937.1| Pichia guilliermondii isolate CNRMA 200501142 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568935.1| Pichia guilliermondii isolate CNRMA 200501144 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601   CGGAGGA  607
             |||||||
Sbjct  601   CGGAGGA  607


>gb|EU568933.1| Pichia guilliermondii isolate CNRMA 200501305 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
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Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568931.1| Pichia guilliermondii isolate CNRMA 200501314 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
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Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568929.1| Pichia guilliermondii isolate CNRMA 200501320 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568911.1| Pichia guilliermondii 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene, and
internal transcribed spacer 2, complete sequence; and 28S
ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>dbj|AB369917.1| Pichia guilliermondii genes for small subunit rRNA, ITS1, 5.8S
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rRNA, ITS2 and large subunit rRNA, partial and complete sequence,
strain: IFM 5492
Length=631

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  25   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  84

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  85   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  144

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  145  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  204

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  205  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  264

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  265  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  324

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  325  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  384

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  385  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  444

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  445  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  504

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  505  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  564

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  565  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  624

Query  601  CGGAGGA  607
            |||||||
Sbjct  625  CGGAGGA  631


>gb|EU177579.1| Pichia guilliermondii strain EQ 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EF191048.1| Pichia guilliermondii strain HJM 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=631

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  25   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  84

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  85   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  144

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  145  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  204

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  205  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  264

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  265  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  324

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  325  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  384

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  385  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  444

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  445  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  504

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  505  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  564

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  565  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  624

Query  601  CGGAGGA  607
            |||||||
Sbjct  625  CGGAGGA  631


>gb|DQ663478.1| Pichia guilliermondii isolate JHSd 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=617

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  70

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  71   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  130

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  131  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  190

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  191  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  250

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  310
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Query  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  370

Query  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  371   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  430

Query  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  431   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  490

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  491   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  550

Query  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  551   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  610

Query  601   CGGAGGA  607
             |||||||
Sbjct  611   CGGAGGA  617


>gb|DQ680842.1| Pichia guilliermondii strain G7A1 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=636

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  29    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  88

Query  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  89    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  148

Query  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  149   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  208

Query  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  268

Query  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  269   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  328

Query  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  329   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  388

Query  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  389   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  448
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Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  449  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  508

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  509  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  568

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  569  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  628

Query  601  CGGAGGA  607
            |||||||
Sbjct  629  CGGAGGA  635


>gb|AY939795.1| Pichia guilliermondii isolate UR 9406-03 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|AY939792.1| Pichia guilliermondii strain ATCC 6260 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1122 bits (607),  Expect = 0.0
 Identities = 607/607 (100%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|GU385845.1| Pichia guilliermondii strain SMB 18S ribosomal RNA gene, partial
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sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=610

 Score = 1120 bits (606),  Expect = 0.0
 Identities = 606/606 (100%), Gaps = 0/606 (0%)
 Strand=Plus/Plus

Query  2    CCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCG  61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCG  60

Query  62   GCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAG  121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAG  120

Query  122  AGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAA  181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAA  180

Query  182  TTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGA  241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGA  240

Query  242  ACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTG  301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTG  300

Query  302  AACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTC  361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTC  360

Query  362  TCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAA  421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAA  420

Query  422  AGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCC  481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCC  480

Query  482  AACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACC  541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACC  540

Query  542  AAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGC  601
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGC  600

Query  602  GGAGGA  607
            ||||||
Sbjct  601  GGAGGA  606


>gb|GQ334393.1| Pichia guilliermondii isolate SD 337 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=609

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus
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Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  62

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  63   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  122

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  182

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct  183  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGGAG  242

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  243  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  302

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  303  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  362

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  363  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  422

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  423  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  482

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  483  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  542

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  543  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  602

Query  601  CGGAGGA  607
            |||||||
Sbjct  603  CGGAGGA  609


>gb|FJ969194.1| Pichia guilliermondii strain UAF-214 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568993.1| Pichia guilliermondii isolate CNRMA 200500950 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568991.1| Pichia guilliermondii isolate CNRMA 200501319 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
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Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568989.1| Pichia guilliermondii isolate CNRMA 200501343 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
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Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568987.1| Pichia guilliermondii isolate CNRMA 200600803 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607
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>gb|EU568985.1| Pichia guilliermondii isolate CNRMA 200601042 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568983.1| Pichia guilliermondii isolate CNRMA 200500719 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus
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Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
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Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
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Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
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Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
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Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
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Sbjct  601  CGGAGGA  607


>gb|EU568981.1| Pichia guilliermondii isolate CNRMA 200601191 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
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Query  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421   AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601   CGGAGGA  607
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Sbjct  601   CGGAGGA  607


>gb|EU568979.1| Pichia guilliermondii isolate CNRMA 200700040 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568977.1| Pichia guilliermondii isolate CNRMA 200500809 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
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Sbjct  601  CGGAGGA  607


>gb|EU568975.1| Pichia guilliermondii isolate CNRMA 200500821 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
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Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568973.1| Pichia guilliermondii isolate CNRMA 200500863 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607
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>gb|EU568971.1| Pichia guilliermondii isolate CNRMA 200500864 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 606/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|DQ663480.1| Pichia guilliermondii isolate hn-3 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=610

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 607/608 (99%), Gaps = 1/608 (0%)
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 Strand=Plus/Plus

Query  1    TCC-GTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCG  59
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3    TCCTGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCG  62

Query  60   CGGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCT  119
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  63   CGGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCT  122

Query  120  AGAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCA  179
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123  AGAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCA  182

Query  180  AATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAA  239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  183  AATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAA  242

Query  240  GAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTT  299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  243  GAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTT  302

Query  300  TGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTC  359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  303  TGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTC  362

Query  360  TCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGA  419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  363  TCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGA  422

Query  420  AAAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTAT  479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  423  AAAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTAT  482

Query  480  CCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAA  539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  483  CCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAA  542

Query  540  CCAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  599
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  543  CCAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  602

Query  600  GCGGAGGA  607
            ||||||||
Sbjct  603  GCGGAGGA  610


>gb|DQ663479.1| Pichia guilliermondii isolate hn-2 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=611

 Score = 1116 bits (604),  Expect = 0.0
 Identities = 607/608 (99%), Gaps = 1/608 (0%)
 Strand=Plus/Plus

Query  1    TCC-GTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCG  59
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3    TCCTGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCG  62

Query  60   CGGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCT  119
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  63   CGGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCT  122
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Query  120  AGAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCA  179
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123  AGAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCA  182

Query  180  AATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAA  239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  183  AATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAA  242

Query  240  GAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTT  299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  243  GAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTT  302

Query  300  TGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTC  359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  303  TGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTC  362

Query  360  TCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGA  419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  363  TCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGA  422

Query  420  AAAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTAT  479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  423  AAAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTAT  482

Query  480  CCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAA  539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  483  CCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAA  542

Query  540  CCAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  599
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  543  CCAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  602

Query  600  GCGGAGGA  607
            ||||||||
Sbjct  603  GCGGAGGA  610


>gb|GQ913349.1| Pichia guilliermondii strain W1171 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1110 bits (601),  Expect = 0.0
 Identities = 605/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
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Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAG  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|GQ497898.1| Pichia guilliermondii strain PX-PAT 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1110 bits (601),  Expect = 0.0
 Identities = 605/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCCTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAACTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|GQ149493.1| Pichia guilliermondii strain UAF-130 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1110 bits (601),  Expect = 0.0
 Identities = 605/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGAGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|FJ662408.1| Pichia guilliermondii isolate ZA043 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=616

 Score = 1110 bits (601),  Expect = 0.0
 Identities = 606/608 (99%), Gaps = 1/608 (0%)
 Strand=Plus/Plus

Query  1    TCCGTA-GGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCG  59
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4    TCCGTAGGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCG  63

Query  60   CGGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCT  119
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  64   CGGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCT  123

Query  120  AGAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCA  179
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  124  AGAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCA  183

Query  180  AATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAA  239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  184  AATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAA  243

Query  240  GAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTT  299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  244  GAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTT  303

Query  300  TGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTC  359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  304  TGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTC  363

Query  360  TCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGA  419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  364  TCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGA  423

Query  420  AAAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTAT  479
            ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  424  AAAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTAT  483

Query  480  CCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAA  539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  484  CCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAA  543

Query  540  CCAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  599
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  544  CCAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  603

Query  600  GCGGAGGA  607
            ||||||||
Sbjct  604  GCGGAGGA  611
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>gb|EU568969.1| Pichia guilliermondii isolate CNRMA 200501202 18S ribosomal RNA
gene, partial sequence; internal transcribed spacer 1, 5.8S
ribosomal RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1110 bits (601),  Expect = 0.0
 Identities = 605/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  CTTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|AF209874.1|AF209874 Debaryomyces hansenii var. fabryi CBS8417 internal
transcribed
spacer 1, 5.8S ribosomal RNA gene, and internal transcribed
spacer 2, complete sequence
Length=607

 Score = 1110 bits (601),  Expect = 0.0
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 Identities = 605/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            |||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTTTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|FJ515205.1| Pichia guilliermondii strain UN44 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=602

 Score = 1109 bits (600),  Expect = 0.0
 Identities = 600/600 (100%), Gaps = 0/600 (0%)
 Strand=Plus/Plus

Query  8    GTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCGGCGAAA  67
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCGGCGAAA  60

Query  68   AACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGAGATAG  127
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  61   AACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGAGATAG  120

Query  128  GTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAATTTTGA  187
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAATTTTGA  180

Query  188  ATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAG  247
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAG  240

Query  248  CGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCA  307
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCA  300

Query  308  CATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAAC  367
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAAC  360

Query  368  CCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATT  427
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATT  420

Query  428  GGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCAACTCG  487
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCAACTCG  480

Query  488  TTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACCAAACAA  547
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  TTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACCAAACAA  540

Query  548  GTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  607
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  600


>gb|DQ663476.1| Pichia guilliermondii isolate L2-8 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=616

 Score = 1109 bits (600),  Expect = 0.0
 Identities = 605/607 (99%), Gaps = 1/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            |||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Sbjct  2    TCCGTAGGTGAACCTGCGGAAGGATCATAACAGTATTCTTTTGCCAGCGCTTAACTGCGC  61

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  62   GGCG-AAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
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Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EF643576.1| Pichia guilliermondii strain S0201 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=639

 Score = 1107 bits (599),  Expect = 0.0
 Identities = 599/599 (100%), Gaps = 0/599 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  28   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  87

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  88   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  147

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  148  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  207

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  208  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  267

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  268  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  327

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  328  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  387

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  388  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  447
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Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  448  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  507

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  508  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  567

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  599
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  568  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  626


>gb|EF222224.1| Pichia guilliermondii strain WC43-1 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=636

 Score = 1107 bits (599),  Expect = 0.0
 Identities = 606/609 (99%), Gaps = 2/609 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  27   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  86

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  87   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  146

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  147  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  206

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  207  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  266

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  326

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  386

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  446

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  447  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  506

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  566

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  567  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  626

Query  601  -CGGA-GGA  607
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             |||| |||
Sbjct  627  GCGGAAGGA  635


>gb|EF375704.1| Pichia guilliermondii strain N12c 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 26S ribosomal RNA gene, partial sequence
Length=628

 Score = 1107 bits (599),  Expect = 0.0
 Identities = 599/599 (100%), Gaps = 0/599 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  76

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  77   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  136

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  137  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  196

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  197  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  256

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  257  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  316

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  317  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  376

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  377  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  436

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  437  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  496

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  497  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  556

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  599
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  557  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  615


>gb|AY700139.1| Fungal endophyte sp. CEY 20 18S small subunit ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S large subunit ribosomal RNA gene, partial
sequence
Length=608

 Score = 1107 bits (599),  Expect = 0.0
 Identities = 599/599 (100%), Gaps = 0/599 (0%)
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 Strand=Plus/Plus

Query  2    CCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCG  61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCG  60

Query  62   GCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAG  121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAG  120

Query  122  AGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAA  181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  AGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAA  180

Query  182  TTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGA  241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGA  240

Query  242  ACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTG  301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  ACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTG  300

Query  302  AACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTC  361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  AACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTC  360

Query  362  TCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAA  421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAA  420

Query  422  AGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCC  481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCC  480

Query  482  AACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACC  541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  AACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACC  540

Query  542  AAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  599


>gb|GQ149494.1| Pichia guilliermondii strain UAF-62 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=608

 Score = 1105 bits (598),  Expect = 0.0
 Identities = 605/608 (99%), Gaps = 1/608 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
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Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGATTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAAC-TTAAGCATATCAATAA  599
            ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACCTTAAGCATATCAATAA  600

Query  600  GCGGAGGA  607
            ||||||||
Sbjct  601  GCGGAGGA  608


>gb|EF532299.1| Pichia guilliermondii strain JHSa 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 26S ribosomal RNA gene, partial sequence
Length=641

 Score = 1105 bits (598),  Expect = 0.0
 Identities = 604/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  30   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  89

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  90   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  149

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  150  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  209

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  210  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  269

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  270  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  329
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Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  330  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  389

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  390  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  449

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  450  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  509

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  510  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  569

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| || 
Sbjct  570  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAAAAAA  629

Query  601  CGGAGGA  607
            ||| |||
Sbjct  630  CGGGGGA  636


>gb|EF197814.1| Pichia guilliermondii strain HK53 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=635

 Score = 1105 bits (598),  Expect = 0.0
 Identities = 605/608 (99%), Gaps = 2/608 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  28   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  87

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  88   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  147

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  148  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  207

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  208  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  267

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  268  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  327

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  328  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  387

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  388  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  447

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
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            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  448  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  507

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  508  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  567

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  568  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA-AAG  626

Query  601  C-GGAGGA  607
            | ||||||
Sbjct  627  CCGGAGGA  634


>gb|DQ683005.1| Pichia guilliermondii strain L11-2 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=635

 Score = 1105 bits (598),  Expect = 0.0
 Identities = 606/609 (99%), Gaps = 3/609 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  27   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  86

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  87   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  146

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  147  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  206

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  207  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  266

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  326

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  386

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  446

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  447  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  506

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  566

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
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Sbjct  567  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCA-TAAG  625

Query  601  -C-GGAGGA  607
             | ||||||
Sbjct  626  GCCGGAGGA  634


>emb|AM176627.1| Pichia guilliermondii 18S rRNA gene, 5.8S rRNA gene, 26S rRNA
gene, ITS1 and ITS2, clone (54)32
Length=604

 Score = 1105 bits (598),  Expect = 0.0
 Identities = 602/604 (99%), Gaps = 0/604 (0%)
 Strand=Plus/Plus

Query  4    GTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCGGC  63
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCGGC  60

Query  64   GAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGAG  123
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGAG  120

Query  124  ATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAATT  183
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAATT  180

Query  184  TTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAAC  243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAAC  240

Query  244  GCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAA  303
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  GCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAA  300

Query  304  CGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTC  363
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTC  360

Query  364  AAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAG  423
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  AAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAG  420

Query  424  TATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCAA  483
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCAA  480

Query  484  CTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACCAA  543
            ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  481  CTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACGACAACCAA  540

Query  544  ACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGG  603
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  ACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGG  600

Query  604  AGGA  607
            ||||
Sbjct  601  AGGA  604


>gb|AY700141.1| Fungal endophyte sp. CEY 22 18S small subunit ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S large subunit ribosomal RNA gene, partial
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sequence
Length=607

 Score = 1105 bits (598),  Expect = 0.0
 Identities = 598/598 (100%), Gaps = 0/598 (0%)
 Strand=Plus/Plus

Query  3    CGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCGG  62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    CGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCGG  60

Query  63   CGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGA  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGA  120

Query  123  GATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAAT  182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAAT  180

Query  183  TTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAA  242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAA  240

Query  243  CGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGA  302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGA  300

Query  303  ACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCT  362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCT  360

Query  363  CAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAA  422
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAA  420

Query  423  GTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCA  482
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCA  480

Query  483  ACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACCA  542
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACCA  540

Query  543  AACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  598


>gb|GQ280287.1| Pichia guilliermondii isolate ZA016 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=614

 Score = 1103 bits (597),  Expect = 0.0
 Identities = 607/611 (99%), Gaps = 4/611 (0%)
 Strand=Plus/Plus

Query  1    TCCGTA-GGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCG  59
            |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  3    TCCGTAGGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCG  62

Query  60   CGGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTG-C-TTTGGTTTGGC  117
            |||||||||||||||||||||||||||||||||||||||||||||| | |||||||||||
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Sbjct  63    CGGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCCTTTTGGTTTGGC  122

Query  118   CTAGAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGT  177
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  123   CTAGAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGT  182

Query  178   CAAATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATG  237
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  183   CAAATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATG  242

Query  238   AAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATC  297
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  243   AAGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATC  302

Query  298   TTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTC  357
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  303   TTTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTC  362

Query  358   TCTCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTT  417
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  363   TCTCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTT  422

Query  418   GAAAAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTT  477
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  423   GAAAAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTT  482

Query  478   ATCCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAAC  537
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  483   ATCCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAAC  542

Query  538   AACCAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAAT  597
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  543   AACCAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAAT  602

Query  598   AAGC-GGAGGA  607
             |||| ||||||
Sbjct  603   AAGCCGGAGGA  613


>gb|EF222226.1| Pichia guilliermondii strain HK55a 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=616

 Score = 1101 bits (596),  Expect = 0.0
 Identities = 598/599 (99%), Gaps = 0/599 (0%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  18    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  77

Query  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  78    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  137

Query  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  138   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  197

Query  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  198   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  257
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Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  258  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  317

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  318  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  377

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  378  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  437

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  438  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  497

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  498  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  557

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  599
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  558  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  616


>gb|EF190233.1| Pichia guilliermondii strain 3-2 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=642

 Score = 1101 bits (596),  Expect = 0.0
 Identities = 596/596 (100%), Gaps = 0/596 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  31   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  90

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  91   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  150

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  151  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  210

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  211  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  270

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  271  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  330

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  331  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  390

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  391  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  450
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Query  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  451   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  510

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  511   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  570

Query  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA  596
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  571   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA  626


>gb|EF192233.1| Pichia guilliermondii strain gaozhong 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=624

 Score = 1101 bits (596),  Expect = 0.0
 Identities = 596/596 (100%), Gaps = 0/596 (0%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  27    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  86

Query  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  87    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  146

Query  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  147   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  206

Query  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  207   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  266

Query  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  326

Query  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  386

Query  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  446

Query  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  447   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  506

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  566

Query  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA  596
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  567   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA  622
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>gb|EF193071.1| Pichia guilliermondii voucher MCCC2E00277 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=627

 Score = 1101 bits (596),  Expect = 0.0
 Identities = 596/596 (100%), Gaps = 0/596 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  31   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  90

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  91   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  150

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  151  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  210

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  211  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  270

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  271  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  330

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  331  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  390

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  391  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  450

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  451  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  510

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  511  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  570

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA  596
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  571  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA  626


>gb|DQ668353.1| Pichia guilliermondii isolate L4-1 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=622

 Score = 1101 bits (596),  Expect = 0.0
 Identities = 596/596 (100%), Gaps = 0/596 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  85
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Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  86   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  145

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  146  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  205

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  206  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  265

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  266  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  325

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  326  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  385

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  386  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  445

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  446  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  505

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  506  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  565

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA  596
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  566  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA  621


>gb|FJ515181.1| Pichia guilliermondii strain SN4 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=605

 Score = 1099 bits (595),  Expect = 0.0
 Identities = 602/605 (99%), Gaps = 2/605 (0%)
 Strand=Plus/Plus

Query  4    GTA-GGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCGG  62
            ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTAGGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCGG  60

Query  63   CGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGA  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGA  120

Query  123  GATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAAT  182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAAT  180

Query  183  TTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAA  242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAA  240
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Query  243  CGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGA  302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGA  300

Query  303  ACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCT  362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  ACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCT  360

Query  363  CAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAA  422
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAA  420

Query  423  GTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCA  482
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  421  GTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCA  480

Query  483  ACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACCA  542
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  ACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACCA  540

Query  543  AACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCG  602
            |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  AACAAGTT-GACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCG  599

Query  603  GAGGA  607
            |||||
Sbjct  600  GAGGA  604


>gb|EF643595.1| Pichia guilliermondii strain LN-9 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=648

 Score = 1099 bits (595),  Expect = 0.0
 Identities = 597/598 (99%), Gaps = 0/598 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  35   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  94

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  95   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  154

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  155  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  214

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  215  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  274

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  275  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  334

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  335  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  394

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  395  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  454

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  455  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  514

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  515  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  574

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATA  598
            ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  575  CAAACAAGTTTGACCTCAAATCAGGCAGGAATACCCGCTGAACTTAAGCATATCAATA  632


>gb|EF197809.1| Pichia guilliermondii strain HK51b 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=624

 Score = 1098 bits (594),  Expect = 0.0
 Identities = 599/601 (99%), Gaps = 1/601 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  15   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  74

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  75   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  134

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  135  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  194

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  195  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  254

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  255  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  314

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  315  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  374

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  375  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  434

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  435  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  494

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  495  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  554

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
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Sbjct  555   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA-AAG  613

Query  601   C  601
             |
Sbjct  614   C  614


>gb|DQ663477.1| Pichia guilliermondii isolate hn-4 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1098 bits (594),  Expect = 0.0
 Identities = 597/598 (99%), Gaps = 1/598 (0%)
 Strand=Plus/Plus

Query  10    GAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCGGCGAAAAA  69
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCGGCGAAAAA  60

Query  70    CCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGAGATAGGT  129
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGAGATAGGT  120

Query  130   TGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAATTTTGAAT  189
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAATTTTGAAT  180

Query  190   TAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCG  249
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCG  240

Query  250   AAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACA  309
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACA  300

Query  310   TTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCC  369
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCC  360

Query  370   CCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATTGG  429
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATTGG  420

Query  430   CATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCAACTCGTT  489
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   CATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCAACTCGTT  480

Query  490   GAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACCAAACAAGT  549
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACCAAACAAGT  540

Query  550   TTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  607
             |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Sbjct  541   TTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCA-TAAGCGGAGGA  597


>gb|DQ534408.1| Debaryomyces hansenii strain JHSa 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=611
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 Score = 1098 bits (594),  Expect = 0.0
 Identities = 597/598 (99%), Gaps = 1/598 (0%)
 Strand=Plus/Plus

Query  10   GAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCGGCGAAAAA  69
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14   GAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCGGCGAAAAA  73

Query  70   CCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGAGATAGGT  129
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  74   CCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAGAGATAGGT  133

Query  130  TGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAATTTTGAAT  189
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134  TGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAATTTTGAAT  193

Query  190  TAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCG  249
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  194  TAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGAACGCAGCG  253

Query  250  AAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACA  309
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  254  AAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTGAACGCACA  313

Query  310  TTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCC  369
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  314  TTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTCTCAAACCC  373

Query  370  CCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATTGG  429
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  374  CCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAAAGTATTGG  433

Query  430  CATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCAACTCGTT  489
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  434  CATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCCAACTCGTT  493

Query  490  GAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACCAAACAAGT  549
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  494  GAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACCAAACAAGT  553

Query  550  TTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAGCGGAGGA  607
            ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  554  TTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATA-GCGGAGGA  610


>gb|EF197816.1| Pichia guilliermondii strain NA-3 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=624

 Score = 1096 bits (593),  Expect = 0.0
 Identities = 595/596 (99%), Gaps = 0/596 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  27   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  86

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  87   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  146

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  147  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  206

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  207  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  266

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  267  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  326

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  327  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  386

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  387  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  446

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  447  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  506

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  507  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  566

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA  596
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  567  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA  622


>emb|FN428931.1| Pichia caribbica ITS1, 5.8S rRNA gene, ITS2 and 26S rRNA gene
(partial), strain IMUFRJ 51970
Length=1167

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  63

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  64   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  123

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  124  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  183

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  184  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  243

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  244  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  303

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  304  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  363
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Query  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  364   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  423

Query  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  424   AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  483

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  484   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  543

Query  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  544   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  603

Query  601   CGGAGGA  607
             |||||||
Sbjct  604   CGGAGGA  610


>gb|GU248264.1| Pichia caribbica strain XTWJX 18S ribosomal RNA gene, partial
sequence; internal transcribed spacer 1, 5.8S ribosomal RNA
gene, and internal transcribed spacer 2, complete sequence;
and 26S ribosomal RNA gene, partial sequence
Length=631

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  25    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  84

Query  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  85    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  144

Query  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
             |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  145   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  204

Query  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  205   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  264

Query  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  265   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  324

Query  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  325   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  384

Query  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  385   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  444

Query  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  445   AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  504

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  505    CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  564

Query  541    CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  565    CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  624

Query  601    CGGAGGA  607
              |||||||
Sbjct  625    CGGAGGA  631


>gb|FJ183437.1| Pichia guilliermondii strain VAL-05-030 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=592

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 592/592 (100%), Gaps = 0/592 (0%)
 Strand=Plus/Plus

Query  1      TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1      TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61     GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61     GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121    GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121    GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181    ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181    ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241    AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241    AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301    GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301    GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361    CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361    CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421    AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421    AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481    CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481    CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541    CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATA  592
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541    CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATA  592


>gb|FJ183435.1| Pichia guilliermondii strain VAL-05-015 18S ribosomal RNA gene,
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partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=592

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 592/592 (100%), Gaps = 0/592 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATA  592
            ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATA  592


>gb|EU569029.1| Pichia caribbica isolate CNRMA 200500812 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
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Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569027.1| Pichia caribbica isolate CNRMA 200500862 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
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             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
             ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
             |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421   AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601   CGGAGGA  607
             |||||||
Sbjct  601   CGGAGGA  607


>gb|EU569025.1| Pichia caribbica isolate CNRMA 200501000 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
             |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569023.1| Pichia caribbica isolate CNRMA 200501146 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
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Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569021.1| Pichia caribbica isolate CNRMA 200501145 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
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Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569019.1| Pichia caribbica isolate CNRMA 200501201 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569017.1| Pichia caribbica isolate CNRMA 200500949 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
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Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569015.1| Pichia caribbica isolate CNRMA 200501317 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
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Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569013.1| Pichia caribbica isolate CNRMA 200600033 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180
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Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569011.1| Pichia caribbica isolate CNRMA 200501316 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
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            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569009.1| Pichia caribbica isolate CNRMA 200600196 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
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Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569007.1| Pichia caribbica isolate CNRMA 200600368 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
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Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569005.1| Pichia caribbica isolate CNRMA 200601082 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569003.1| Pichia caribbica isolate CNRMA 200700035 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
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sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU569001.1| Pichia caribbica isolate CNRMA 200700593 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EU568913.1| Pichia caribbica 18S ribosomal RNA gene, partial sequence; internal
transcribed spacer 1, 5.8S ribosomal RNA gene, and internal
transcribed spacer 2, complete sequence; and 28S ribosomal
RNA gene, partial sequence
Length=607

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 602/607 (99%), Gaps = 0/607 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180
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Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGGA  607
            |||||||
Sbjct  601  CGGAGGA  607


>gb|EF190227.1| Pichia guilliermondii strain gao1zhong2 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete
sequence; and 28S ribosomal RNA gene, partial sequence
Length=624

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 595/596 (99%), Gaps = 1/596 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  29   TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  88

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  89   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  148

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  149  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  208

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  209  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  268

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  269  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  328
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Query  301   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  329   GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  388

Query  361   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  389   CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  448

Query  421   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  449   AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  508

Query  481   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  509   CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  568

Query  541   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAA  596
             |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  569   CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATA-CAA  623


>emb|AM158922.1| Candida xestobii partial 18S rRNA gene, ITS1, 5.8S rRNA gene,
ITS2 and partial 26S rRNA gene, strain CBS 5975
Length=895

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 603/608 (99%), Gaps = 2/608 (0%)
 Strand=Plus/Plus

Query  1     TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  26    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  85

Query  61    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  86    GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  145

Query  121   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTA-CAGTTAGTCA  179
             |||||||||||||||||||||||||||||||||||||||||||||||||  || ||||| 
Sbjct  146   GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTAG-TAGTCG  204

Query  180   AATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAA  239
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  205   AATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAA  264

Query  240   GAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTT  299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  265   GAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTT  324

Query  300   TGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTC  359
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  325   TGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTC  384

Query  360   TCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGA  419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  385   TCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGA  444

Query  420   AAAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTAT  479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  445   AAAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTAT  504

Query  480   CCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAA  539
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  505   CCAACTCGTTGAACGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAA  564
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Query  540  CCAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  599
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  565  CCAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  624

Query  600  GCGGAGGA  607
            ||||||||
Sbjct  625  GCGGAGGA  632


>gb|DQ249193.1| Pichia guilliermondii strain WM 02.91 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=657

 Score = 1094 bits (592),  Expect = 0.0
 Identities = 597/599 (99%), Gaps = 1/599 (0%)
 Strand=Plus/Plus

Query  2    CCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCG  61
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  51   CCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGCG  110

Query  62   GCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAG  121
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  111  GCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTAG  170

Query  122  AGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAA  181
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  171  AGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAAA  230

Query  182  TTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGA  241
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  231  TTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAGA  290

Query  242  ACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTG  301
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  291  ACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTTG  350

Query  302  AACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTC  361
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  351  AACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCTC  410

Query  362  TCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAA  421
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  411  TCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAAA  470

Query  422  AGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCC  481
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  471  AGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATCC  530

Query  482  AACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACC  541
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  531  AACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAACC  590

Query  542  AAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAA-GCATATCAATAA  599
            |||||||||||||||||||||||||||||||||||||||||| ||| ||||||||||||
Sbjct  591  AAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACATAAAGCATATCAATAA  649


>emb|FM199963.1| Pichia caribbica 18S rRNA gene (partial), ITS1, 5.8S rRNA gene,
ITS2 and 26S rRNA gene (partial), strain H5MandK13
Length=606
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 Score = 1092 bits (591),  Expect = 0.0
 Identities = 601/606 (99%), Gaps = 0/606 (0%)
 Strand=Plus/Plus

Query  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TCCGTAGGTGAACCTGCGGAAGGATCATTACAGTATTCTTTTGCCAGCGCTTAACTGCGC  60

Query  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   GGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCCTA  120

Query  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTCAA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||  | |||||||
Sbjct  121  GAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTATTGATAGTCAA  180

Query  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGAAG  240

Query  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCTTT  300

Query  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCTCT  360

Query  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTGAA  420
            ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  361  CTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGAACTAGGCGTTTGCTTGAA  420

Query  421  AAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480
            |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  421  AAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTATC  480

Query  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  CAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACAAC  540

Query  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  CAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAAG  600

Query  601  CGGAGG  606
            ||||||
Sbjct  601  CGGAGG  606


>gb|EU520225.1| Mycena pura isolate NW473 18S ribosomal RNA gene, partial sequence;
internal transcribed spacer 1, 5.8S ribosomal RNA gene,
and internal transcribed spacer 2, complete sequence; and
28S ribosomal RNA gene, partial sequence
Length=612

 Score = 1083 bits (586),  Expect = 0.0
 Identities = 601/609 (98%), Gaps = 3/609 (0%)
 Strand=Plus/Plus

Query  1    TCCGTA-GGTGAACCTGCGGAAGGATCATTAC-AGTATTCTTTTGCCAGCGCTTAACTGC  58
            |||||| |||| |||||||||||||||||| |  | ||||||||||||||||||||||||
Sbjct  3    TCCGTAGGGTG-ACCTGCGGAAGGATCATTRCRCGKATTCTTTTGCCAGCGCTTAACTGC  61
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Query  59   GCGGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCC  118
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  62   GCGGCGAAAAACCTTACACACAGTGTCTTTTTGATACAGAACTCTTGCTTTGGTTTGGCC  121

Query  119  TAGAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTC  178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  122  TAGAGATAGGTTGGGCCAGAGGTTTAACAAAACACAATTTAATTATTTTTACAGTTAGTC  181

Query  179  AAATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGA  238
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  182  AAATTTTGAATTAATCTTCAAAACTTTCAACAACGGATCTCTTGGTTCTCGCATCGATGA  241

Query  239  AGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCT  298
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  242  AGAACGCAGCGAAATGCGATAAGTAATATGAATTGCAGATTTTCGTGAATCATCGAATCT  301

Query  299  TTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCT  358
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  302  TTGAACGCACATTGCGCCCTCTGGTATTCCAGAGGGCATGCCTGTTTGAGCGTCATTTCT  361

Query  359  CTCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTG  418
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  362  CTCTCAAACCCCCGGGTTTGGTATTGAGTGATACTCTTAGTCGGACTAGGCGTTTGCTTG  421

Query  419  AAAAGTATTGGCATGGGTAGTACTAGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTA  478
            |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Sbjct  422  AAAAGTATTGGCATGGGTAGTACTGGATAGTGCTGTCGACCTCTCAATGTATTAGGTTTA  481

Query  479  TCCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACA  538
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  482  TCCAACTCGTTGAATGGTGTGGCGGGATATTTCTGGTATTGTTGGCCCGGCCTTACAACA  541

Query  539  ACCAAACAAGTTTGACCTCAAATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATA  598
            |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  542  ACCAAACAAGTTTGACCTCAAATCAGGTAGSAATACCCGCTGAACTTAAGCATATCAATA  601

Query  599  AGCGGAGGA  607
            |||||||||
Sbjct  602  AGCGGAGGA  610



  Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS,
GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
    Posted date:  Jun 26, 2010  5:44 PM
  Number of letters in database: 1,817,769,445
  Number of sequences in database:  12,090,198

Lambda     K      H
    1.33    0.621     1.12
Gapped
Lambda     K      H
    1.28    0.460    0.850
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 0, Extension: 0
Number of Sequences: 12090198
Number of Hits to DB: 1854205
Number of extensions: 12817
Number of successful extensions: 12817
Number of sequences better than 10: 9418
Number of HSP's better than 10 without gapping: 0
Number of HSP's gapped: 12671
Number of HSP's successfully gapped: 12667
Length of query: 607
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Length of database: 31882540517
Length adjustment: 32
Effective length of query: 575
Effective length of database: 31495654181
Effective search space: 18110001154075
Effective search space used: 18110001154075
A: 0
X1: 14 (26.9 bits)
X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 14 (27.0 bits)
S2: 22 (41.7 bits)
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