INTRODUCTION

Cardiovascular diseases, including coronary heart disease, cerebrovascular disease, peripheral arterial disease, rheumatic and congenital heart diseases, and venous thromboembolism, are a leading cause of death globally (Stewart, Manmathan, Wilkinson, 2017). One important risk factor for cardiovascular diseases is dyslipidemia, defined as high levels of low-density lipoprotein cholesterol (LDL) and triglycerides (TG) and low levels of high-density lipoprotein cholesterol (HDL) (Sarzynski et al., 2015). The underlying causes of dyslipidemias include genetic and lifestyle factors. Familial hypercholesterolemia is a genetic condition characterized by a mutation in the LDL-receptor, leading to the accumulation of LDL in the blood (Lozano et al., 2016). Hyperlipidemia is a disorder characterized by high levels of LDL and/or very low-density lipoprotein cholesterol (VLDL) (Nelson, 2013). Hypertriglyceridemia is characterized by high levels of TG (>150 mg/dL) or ≥1.7 mmol/L (Perez-Martinez et al., 2016). Many lipid disorders are associated with lifestyle factors, such as lack of exercise, consuming high-saturated fat diet, metabolic disorders, and drug therapy (e.g., immunosuppressants) (Patel, Brocks, 2010; Zhang et al., 2016). However, suitable lifestyle changes, along with drug therapy, can lead to a 30%–40% reduction in coronary heart disease mortality (Gurr, Harwood, Frayn, 2008; Clark et al., 2012).

Dyslipidemia is an abnormal lipid profile associated with many common diseases, including coronary heart disease and atherosclerosis. Cholesteryl ester transfer protein (CETP) is a hydrophobic plasma glycoprotein that is responsible for the transfer of cholesteryl ester from high-density lipoprotein athero-protective particles to pro-atherogenic very low-density lipoprotein and low-density lipoprotein particles. The requirement for new CETP inhibitors, which block this process has driven our current work. Here, the synthesis as well as the ligand-based and structure-based design of seven oxoacetamido-benzamides 9a–g with CETP inhibitory activity is described. An in vitro study demonstrated that most of these compounds have appreciable CETP inhibitory activity. Compound 9g showed the highest inhibitory activity against CETP with an IC₅₀ of 0.96 μM. Glide docking data for compounds 9a–g and torcetrapib provide evidence that they are accommodated in the CETP active site where hydrophobic interactions drive ligand/CETP complex formation. Furthermore, compounds 9a–g match the features of known CETP active inhibitors, providing a rationale for their high docking scores against the CETP binding domain. Therefore, these oxoacetamido-benzamides show potential for use as novel CETP inhibitors.

Keywords: CETP Inhibitors. Cholesteryl ester transfer protein. Dyslipidemia. Glide docking. Oxoacetamido-benzamides. Pharmacophoric features.
of 2.59 Å) comprises a 60 Å-long hydrophobic tunnel occupied by two cholesteryl ester (CE) molecules. Two phospholipid molecules also occupy CETP, and while their polar heads are exposed to plasma, their acyl chains are buried in the hydrophobic tunnel. In addition, CETP has two β-barrel domains at the N and C termini, each with a twisted sheet and a long α-helix, a central β-sheet between the two β-barrels, and a C-terminal α-helix (Mezdour et al., 1994). CETP is involved in reverse cholesterol transport and is responsible for increasing VLDL-triglyceride levels, and subsequently LDL levels, through the transfer of CE from HDL particles to VLDL. An increase in the influx of free fatty acids into the liver causes an increase in the level of VLDL-triglyceride secretion and a decrease in HDL-cholesterol levels (Regieli et al., 2008; Suhy et al., 2014; Yassine et al., 2014; Chirasani, Revanasiddappa, Senapati, 2016). Four CETP inhibitors have reached the clinical trial stage, including torcetrapib, dalcetrapib, evacetrapib, and anacetrapib. While the other three CETP inhibitors demonstrated adverse effects, mainly cardiovascular, anacetrapib showed lower side effects and an enhancement of the lipid profile (Mullard, 2017).

Previously, our group designed and synthesized a range of different CETP inhibitors, including benzylidene-amino methanones (Abu Khalaf et al., 2010), benzylamino methanones (Abu Sheikha et al., 2010), N-(4-benzyloxyphenyl)-4-methyl-benzenesulfonamides (Abu Khalaf et al., 2012), N-(4-benzylamino-phenyl)-toluene-4-sulfonic acid esters (Abu Khalaf et al., 2012), chlorobenzyl benzamides (Abu Khalaf et al., 2017a), fluorinated benzamides (Abu Khalaf et al., 2017b), and substituted benzyl benzamides (Abu Khalaf et al., 2017c). In an attempt to optimize our previously synthesized CETP inhibitors, compound A (% inhibition = 50% at 10 µM, Figure 1) was chosen as a lead (Abu Khalaf et al., 2017c). New oxoacetamido-benzamide analogs 9a–g were designed and synthesized by varying the aromatic ring meta substitution (H, Cl, OCH3, CH3) for the F-atom, in addition to varying the aromatic ring para substitution with either trifluoromethoxy or trifluoromethyl groups. These substitutions were followed by an in vitro biological evaluation of their activity as CETP inhibitors.

**MATERIAL AND METHODS**

**Synthesis**

All chemicals, reagents, and solvents were of analytical grade. Chemicals and solvents were purchased from the following companies (Alfa Aesar, Acros Organics, Sigma-Aldrich, Fluka, SD fine ChemLimite, Tedia, and Fisher Scientific). Melting points were measured using a Gallenkamp melting point apparatus. Infrared (IR) spectra were recorded using a Shimadzu IR Affinity1 FTIR spectrophotometer. All samples were prepared with potassium bromide and pressed into a disc. 1H- and 13C-Nuclear Magnetic resonance (NMR) spectra were measured using a Bruker, Avance DPX-500 spectrometer, and 400 spectrometer, at The University of Jordan and the Hashemite University, respectively. Chemical shifts are given in δ (ppm) using TMS as an internal reference; the samples were dissolved in deuterated chloroform (CDCl3) or dimethylsulfoxide (DMSO). An AFLX800TBI Microplate Fluorimeter (BioTek Instruments, Winooski, VT, USA) was used for the in vitro bioassay. Thin-layer chromatography (TLC) was performed on 20 × 20 cm aluminum cards with a layer thickness of 0.2 mm, pre-coated with fluorescent silica gel GF254 DC-alufolien-kieselgel (Fluka Analytical, Germany), and visualized using UV light (at 254 and/or 360 nm).
General procedure for the synthesis of the methyl benzoates intermediates 5a and 5b

Preparation of 3-aminobenzoic acid methyl ester (3) and the next methyl 3-(4-(trifluoromethoxy)benzylamino) benzoate intermediate (5a) were carried out as previously described (Abu Khalaf et al., 2017a; Abu Khalaf et al., 2017b; Abu Khalaf et al., 2017c). Purification was achieved by column chromatography using cyclohexane:ethyl acetate (8.5:1.5) as the eluent. Synthesis of 5b was commenced by dissolving 2.0 g (13.2 mmol) of ester 3 in 20 mL of dichloromethane (DCM). Then, 1-(bromomethyl)-4-(trifluoromethyl) benzene (4b, 6.14 mL, 39.6 mmol), and (TEA 9.3 mL, 66.2 mmol) were added. The mixture was stirred at 20-25°C for 7 days, evaporated, and the intermediate methyl 3-(4-(trifluoromethyl)benzylamino) benzoate (5b) was purified by column chromatography using cyclohexane:ethyl acetate (9:1) as the eluent. The intermediate 5b was obtained as a yellow powder (3.19 g, % yield = 78%); C_{16}H_{14}F_{3}NO_{2}; mp. 126–127°C; R_f = 0.4 (cyclohexane:ethyl acetate, 9:1); ^1H-NMR (500 MHz, CDCl_3): δ 2.34, 3.24, 3.28, 4.28 (m, 9H, Ar-H), 6.14 (d, J = 7.1 Hz, 1H, Ar-H), 7.12 (d, J = 7.5 Hz, 2H, Ar-H), 7.18 (d, J = 5.0 Hz, 2H, Ar-H); 13C-NMR (125 MHz, CDCl_3): δ 112.0, 117.1, 117.2, 123.7, 125.6, 125.9, 128.2, 129.1, 130.8, 145.4, 149.0, 161.7 ppm; IR (KBr): 3394, 3039, 2916, 1643, 1581, 1535, 1481, 1427, 1265, 1226, 1157 cm$^{-1}$.

General procedure for the synthesis of the targeted compounds 9a–c

The preparation of the acyl intermediate 7a from 5a was carried out as previously described (Abu Khalaf et al., 2017a; Abu Khalaf et al., 2017b; Abu Khalaf et al., 2017c).

3-(N-(4-(Trifluoromethoxy)benzyl)-2-(benzylamino)-2-oxoacetamido)-N-benzylbenzamide (9a)

Benzylation (8a, 0.155 mL, 1.37 mmol), 5 mL of triethylamine, and 10 mL of dichloromethane were added to 7a (0.64 mmol), then the reaction mixture was stirred at 20-25°C for 5 days. The crude product was purified by column chromatography using chloroform:ethyl acetate (8.5:1.5) as the eluent. An off-white viscous liquid was obtained as 9a (0.180 g, % yield = 43%); C_{31}H_{26}F_{3}N_{3}O_{4}; R_f = 0.29 (chloroform:ethyl acetate, 8.5:1.5); ^1H-NMR (400 MHz, CDCl_3): δ 2.86, 2.87, 4.28 (m, 9H, Ar-H), 6.14 (d, J = 4.5 Hz, 2H, NHCCH), 4.62 (d, J = 3.9 Hz, 2H, NHCCH), 4.93 (s, 2H, NCH$_2$), 6.45 (s, 1H, Ar-H), 7.06 (d, J = 7.1 Hz, 1H, Ar-H), 7.12 (d, J = 7.5 Hz, 2H, Ar-H), 7.18 (d, J = 5.0 Hz, 2H, Ar-H); 13C-NMR (100 MHz, CDCl_3): δ 46.3, 52.4, 113.2, 117.1, 117.2, 123.7, 125.6, 125.9, 128.2, 129.1, 130.8, 145.4, 149.0, 161.7 ppm; IR (KBr): 3434, 3394, 3039, 2962, 1712, 1612, 1527, 1257, 1157 cm$^{-1}$.

N-(3-Methylbenzyl)-3-(2-(3-methylbenzylamino)-N-(4-(trifluoromethyl)benzyl)-2-oxoacetamido)benzamide (9b)

3-Methyl benzylamine (8c, 0.15 mL, 1.2 mmol), 5 mL of triethylamine, and 10 mL of dichloromethane were added to 7a (0.64 mmol), then the reaction mixture was stirred at 20-25°C for 5 days. The crude product was purified by column chromatography using chloroform:acetone (9:5.0:0.5) as the eluent. A pale yellow viscous liquid was obtained as 9b (0.117 g, % yield = 30%); C_{33}H_{30}F_{3}N_{3}O_{4}; R_f = 0.5 (chloroform:acetone, 9:1); ^1H-NMR (400 MHz, CDCl_3): δ 2.34 (s, 3H, CH$_3$), 2.38 (s, 3H, CH$_3$), 4.28 (d, J = 4.3 Hz, 2H, NHCCH), 4.56 (t, J = 4.2 Hz, 2H, NHCCH), 4.94 (s, 2H, NCH$_2$), 6.37 (s, 1H, Ar-H), 6.94–7.29 (m, 13H, Ar-H), 7.36 (t, J = 7.5 Hz, 1H, Ar-H), 7.45 (s, 1H, NH), 7.59 (s, 1H, NH), 7.69 (d, J = 7.5 Hz, 1H, Ar-H) ppm; ^13C-NMR (100 MHz, CDCl_3): δ 21.3 (1C, CH$_3$), 29.7 (1C, CH$_3$), 43.5 (1C, CH$_3$), 44.3 (1C, NHCCH), 54.2 (1C, NHCCH), 112.0 (2C, Ar-C), 124.9 (1C, Ar-C), 125.1 (1C, Ar-C), 125.7 (1C, Ar-C), 126.1 (1C, Ar-C), 127.8 (2C, Ar-C), 128.0 (2C, Ar-C), 128.7 (2C, Ar-C), 128.8 (2C, Ar-C), 129.3 (1C, Ar-C), 130.1 (1C, Ar-C), 130.4 (2C, Ar-C), 134.4 (1C, Ar-C), 135.7 (1C, Ar-C), 136.9 (1C, Ar-C), 137.9 (1C, Ar-C), 142.2 (1C, Ar-C), 144.8 (1C, Ar-C), 159.8 (1C, CO), 162.0 (1C, CO), 166.1 (1C, CO) ppm; IR (KBr): 3371, 3248, 3086, 2916, 1643, 1581, 1535, 1481, 1427, 1265, 1226, 1157 cm$^{-1}$.
N-(3-Methoxybenzyl)-3-(2-(3-methoxybenzylamino)-N-(4-(trifluoromethoxy)benzyl)-2-oxoacetamido)benzamide (9c)

3-Methoxy benzylamine (8d, 0.15 mL, 1.16 mmol), 5 mL of triethylamine, and 10 mL of dichloromethane were added to 7a (0.64 mmol); then, the reaction mixture was stirred at 20-25°C for 5 days. The crude product was purified by column chromatography using chloroform:acetone (9.5:0.5) as the eluent.

A pale yellow viscous liquid was obtained as 9c (0.175 g, % yield = 46%); C_{23}H_{20}F_3N_3O_6; Rf = 0.3 (chloroform:acetone, 93:7); 1^H-NMR (400 MHz, CDCl_3): δ 3.78 (s, 3H, OCH_3), 3.82 (s, 3H, OCH_3), 4.28 (s, 2H, HNCH_2), 4.59 (s, 2H, HNCH_2), 4.93 (s, 2H, NCH_3), 6.47 (s, 1H, Ar-H), 6.72 (s, 1H, Ar-H), 6.76 (d, J = 7.0 Hz, 1H, Ar-H), 6.81 (d, J = 7.8 Hz, 1H, Ar-H), 6.85-6.95 (m, 4H, Ar-H), 7.05 (d, J = 7.2 Hz, 1H, Ar-H), 7.12 (d, J = 7.4 Hz, 2H, Ar-H), 7.16-7.31 (m, 3H, Ar-H), 7.34 (t, J = 6.6 Hz, 1H, Ar-H), 7.47 (s, 1H, NH), 7.59 (s, 1H, NH), 7.68 (d, J = 7.3 Hz, 2H, Ar-H) ppm; 1^3C-NMR (100 MHz, CDCl_3): δ 43.4 (1C, HNCH_2), 44.2 (1C, HNCH_3), 54.1 (1C, NCH_3), 55.3 (2C, OCH_3), 113.1 (1C, Ar-C), 113.2 (1C, Ar-C), 113.5 (1C, Ar-C), 113.7 (1C, Ar-C), 119.1 (1C, OCF_3), 120.0 (2C, Ar-C), 120.2 (1C, Ar-C), 121.0 (1C, Ar-C), 121.7 (1C, Ar-C), 125.7 (1C, Ar-C), 126.1 (1C, Ar-C), 129.3 (1C, Ar-C), 129.8 (2C, Ar-C), 129.9 (1C, Ar-C), 130.1 (1C, Ar-C), 130.4 (2C, Ar-C), 134.4 (1C, Ar-C), 135.8 (1C, Ar-C), 138.5 (1C, Ar-C), 139.4 (1C, Ar-C), 142.2 (1C, Ar-C), 148.9 (1C, Ar-C), 159.9 (1C, CO), 162.0 (1C, CO), 166.2 (1C, CO) ppm; IR (KBr): 3317, 3070, 2930, 1651, 1589, 1442, 1404, 1319, 1265, 1157 cm^{-1}.

General procedure for the synthesis of the targeted compounds 9d–g

Methyl 3-(4-(trifluoromethyl)benzylamino) benzoate (5b, 0.25 g) was hydrolyzed to benzoic acid 6b, as reported previously (Abu Khalaf et al., 2017a; Abu Khalaf et al., 2017b; Abu Khalaf et al., 2017c). Subsequently, 6b (0.2 g, 0.64 mmol) was dissolved in 10 mL of dichloromethane and then oxalyl chloride (2, 0.11 mL, 1.2 mmol, (COCl)_2) was added. The reaction was left under stirring for 5 days at 50–60°C. The reaction mixture was then evaporated to obtain the acyl intermediate 7b.

3-(N-(4-(Trifluoromethyl)benzyl)-2-(benzylamino)-2-oxoacetamido)-N benzylbenzamide (9d)

Next, benzylamine (8a, 0.12 mL, 1.14 mmol), 5 mL of triethylamine, and 10 mL of dichloromethane were added to 7b, and then the reaction mixture was stirred at 20-25°C for 5 days. The crude product was purified by column chromatography using cyclohexanecarbonyl acetate (6:4) as the eluent.

A white sticky powder was obtained as 9d (0.1 g, % yield = 31%); C_{31}H_{26}F_3N_3O_3; mp. 79–80°C; Rf= 0.29 (chloroform:ethyl acetate, 8.5:1.5); 1^H-NMR (500 MHz, CDCl_3): δ 2.96 (s, 3H, OCH_3), 4.09 (d, J = 5.65 Hz, 3H, Ar-H), 5.04 (s, 2H, NCH_2), 5.38 (d, J = 6.5 Hz, 1H, Ar-H), 7.12 (d, J = 6.9 Hz, 3H, Ar-H), 7.20 (m, 2H, Ar-H), 7.25 (t, J = 5.65 Hz, 4H, Ar-H), 7.43 (t, 3H, Ar-H), 7.60 (m, 2H, Ar-H), 7.78 (d, J = 7.6 Hz, 1H, Ar-H), 7.83 (s, 1H, Ar-H), 9.00 (t, J = 5.85 Hz, 1H, NH), 9.18 (t, J = 10.9 Hz, 1H, NH) ppm; 1^3C-NMR (125 MHz, DMSO-d6): δ 41.9 (1C, HNCH_2), 43.1 (1C, HNCH_3), 51.4 (IC, NCH_3), 123.7 (1C, CF_3), 125.5 (1C, Ar-C), 126.9 (1C, Ar-C), 127.0 (1C, Ar-C), 127.5 (2C, Ar-C), 129.0 (1C, Ar-C), 128.3 (1C, Ar-C), 128.4 (2C, Ar-C), 128.5 (1C, Ar-C), 128.8 (1C, Ar-C), 128.9 (1C, Ar-C), 135.8 (1C, Ar-C), 138.5 (1C, Ar-C), 139.4 (1C, Ar-C), 139.8 (1C, Ar-C), 139.9 (1C, Ar-C), 141.0 (1C, Ar-C), 141.8 (1C, Ar-C), 163.4 (1C, Ar-C), 164.1 (1C, Ar-C), 165.4 (1C, CO), 165.5 (1C, CO), 167.4 (1C, CO) ppm; IR (KBr): 3332, 3263, 2962, 1651, 1543, 1411, 1327 cm^{-1}.

N-(3-Chlorobenzyl)-3-(2-(3-chlorobenzylamino)-N-(4-(trifluoromethyl)benzyl)-2-oxoacetamido)benzamide (9g)

Next, 3-chlorobenzylamine (8b, 0.25 mL, 2.05 mmol), 5 mL of triethylamine, and 10 mL of dichloromethane were added to 7b, then the reaction...
mixture was stirred at 20-25°C for 5 days. The crude product was purified by column chromatography using chloroform:ethyl acetate (7.5:2.5) as the eluent.

A white sticky powder was obtained as 9e (0.1 g, % yield = 22%); C_{31}H_{24}Cl_{2}F_{3}N_{3}O_{3}; mp. 89–90°C; RF = 0.46 (chloroform:ethyl acetate, 7.5:2.5); H-NMR (400 MH$_2$, CDCl$_3$): δ 4.30 (d, J = 4.9 Hz, 2H, HNC$_2$; 1H, Ar-H), 7.05–7.20 (m, 5H, Ar-H), 5.00 (s, 2H, NHC$_2$), 6.50 (s, 1H, Ar-H), 7.08 (d, J = 8.4 Hz, 2H, Ar-H), 7.17 (s, 1H, Ar-H), 7.20–7.45 (m, 9H, Ar-H), 7.63 (s, 1H, NAr-H), 7.68 (d, J = 7.3 Hz, 1H, Ar-H) ppm; 13C-NMR (100 MH$_2$, CDCl$_3$): δ 42.8 (1C, CH$_2$), 43.6 (1C, CH$_3$), 54.4 (1C, CH$_2$), 122.6 (1C, CF$_2$), 125.3 (1C, Ar-C), 126.0 (2C, Ar-C), 125.6 (IC, Ar-C), 125.7 (1C, Ar-C), 125.8 (1C, Ar-C), 126.0 (IC, Ar-C), 126.1 (IC, Ar-C), 127.8 (1C, Ar-C), 127.9 (1C, Ar-C), 128.0 (2C, Ar-C), 129.1 (2C, Ar-C), 129.5 (1C, Ar-C), 130.1 (2C, Ar-C), 133.4 (1C, Ar-C), 134.6 (1C, Ar-C), 135.5 (1C, Ar-C), 138.9 (1C, Ar-C), 139.5 (1C, Ar-C), 140.0 (1C, Ar-C), 142.2 (1C, Ar-C), 159.8 (1C, CO), 162.0 (1C, CO), 166.1 (1C, CO) ppm; IR (KBr): 3394, 3263, 3070, 2962, 1651, 1589, 1543, 1411, 1327 cm$^{-1}$. N-(3-Methoxybenzyl)-3-(2-(3-methoxybenzylamino)-N-(4-(trifluoromethyl)benzyl)-2-oxoacetamido)benzamide (9g)

Next, 3-methoxybenzylamine (8d, 0.1 mL, 0.77 mmol), 5 mL of triethylamine, and 10 mL of dichloromethane were added to 7b, then the reaction mixture was stirred at 20-25°C for 5 days. The crude product was purified by column chromatography using chloroform:acetone (97:3) as the eluent.

An off-white sticky powder was obtained as 9g (0.05 g, % yield = 17%); C_{33}H_{36}F_{3}N_{3}O_{5}; mp. 109–111°C; RF = 0.4 (cyclohexane:ethyl acetate, 9:1); H-NMR (400 MH$_2$, DMSO-d$_6$); δ 3.70 (s, 3H, OC$_3$), 3.72 (s, 3H, OCH$_3$), 4.10 (d, J = 5.5 Hz, 2H, HNC$_2$), 4.46 (d, J = 5.8 Hz, 2H, HNC$_2$), 5.09 (s, 2H, NHC$_2$), 6.42 (d, J = 7.2 Hz, 1H, Ar-H), 6.67 (s, 1H, Ar-H), 6.74 (d, J = 9.7 Hz, 1H, Ar-H), 6.81 (d, J = 2.3 Hz, 1H, Ar-H), 6.84–6.90 (m, 1H, Ar-H), 7.08 (t, J = 7.8 Hz, 1H, Ar-H), 7.22 (t, J = 8.0 Hz, 1H, Ar-H), 7.32–7.36 (m, 2H, Ar-H), 7.48 (d, J = 8.1 Hz, 1H, Ar-H), 7.67–7.74 (m, 4H, Ar-H), 7.80 (d, J = 2.1 Hz, 1H, Ar-H), 7.87 (s, 1H, Ar-H), 9.03 (t, J = 5.6 Hz, 1H, NH), 9.24 (t, J = 5.5 Hz, 1H, NH) ppm; 13C-NMR (100 MH$_2$, DMSO-d$_6$): δ 42.0 (1C, HN$_3$), 43.1 (1C, HN$_3$), 51.3 (1C, NCH$_3$), 55.4 (2C, OCH$_3$), 112.6 (1C, Ar-C), 112.7 (1C, Ar-C), 113.4 (1C, Ar-C), 113.5 (1C, Ar-C), 119.6 (1C, Ar-C), 119.9 (1C, Ar-C), 125.8 (1C, CF$_2$), 126.4 (1C, Ar-C), 126.8 (1C, Ar-C), 129.0 (2C, Ar-C), 129.1 (2C, Ar-C), 129.5 (1C, Ar-C), 129.8 (1C, Ar-C), 130.4 (1C, Ar-C), 132.1 (2C, Ar-C), 132.2 (1C, Ar-C), 135.8 (1C, Ar-C), 140.1 (1C, Ar-C), 140.9 (1C, Ar-C), 141.5 (1C, Ar-C), 159.6 (1C, Ar-C), 159.8 (1C, Ar-C), 163.3 (1C, CO), 165.6 (1C, CO), 167.5 (1C, CO) ppm; IR (KBr): 3302, 3062, 2962, 2916, 1651, 1589, 1543, 1411, 1327 cm$^{-1}$; HR-MS (ESI, negative mode) m/z [M$^-1$]+ 604.21043 (C_{33}H_{36}F_{3}N_{3}O$_5$ requires 604.21376).
### Computational methods

#### Preparation of protein structures

The coordinates of CETP (PDB ID: 4EWS, resolution of 2.59 Å) (Liu et al., 2012) were obtained from the RCSB Protein Data Bank. The CETP structure was prepared and energetically minimized using the protein preparation wizard (Protein Preparation Wizard, 2016) in the Schrödinger software to optimize H-bond interactions.

#### Preparation of ligand structures

The synthesized compounds (ligands) were modeled based on the structure of the co-crystallized ligand (0RP) in 4EWS (Liu et al., 2012). Ligands were built using the MAESTRO build panel and energetically minimized in MacroModel script (Protein Preparation Wizard, 2016) using the OPLS2005 force field.

#### Glide docking

The grid file for CETP was extracted using the Glide Grid Generation protocol (Protein Preparation Wizard, 2016) with the embedded ligand as the centroid. The van der Waals scaling factor for the nonpolar atoms was calibrated to 0.8 to promote flexibility for the protein side chains. No water molecules were considered. All other parameters were scaled to default. The binding energies were used to determine the docking scores (kcal/mol). A highly negative docking score indicates a better binding interaction.

#### In vitro CETP inhibition bioassay

An aliquot of rabbit serum (1 µL) was mixed with the testing sample (2 µL). Next, donor molecule (5 µL) and acceptor molecule (5 µL) in the assay buffer were added, mixed well, and the volume was adjusted to 200 µL using the assay buffer.

The mixture was incubated at 37°C for 1 h. The fluorescence intensity (excitation λ: 480 nm; emission λ: 511 nm) was measured using a FLX800TBI Microplate Fluorimeter (BioTek Instruments, Winooski, VT, USA).

The synthesized molecules were first dissolved in DMSO to yield 10 mM stock solutions. The solutions were then diluted to the required concentration using DMSO. The concentration of all synthesized compounds was adjusted to 10 µM; CETP activity was not affected by DMSO at the final concentration used in diluted solutions. The percentage of residual CETP activity was identified in the presence and absence of the tested molecules. Torcetrapib was used as a positive inhibitor to estimate CETP inhibition (0.08 µM concentration). Negative control samples without rabbit serum were used for the contrast background. The experimental protocol and all measurements were carried out in duplicate.

The percentage inhibition of CETP by the synthesized compounds was calculated using the following equation (Abu Khalaf et al., 2017a):

\[
\% \text{Inhibition} = \left[1 - \frac{[(\text{Inhibitor reading-Blank reading})]}{[(\text{Positive control-Negative control})]} \right] \times 100
\]

The mid-range experimental dose groups responded in a linear fashion with respect to dose, and IC\textsubscript{50} values were determined from this linear portion of the curve. The equation of this dose-response line was correctly determined by plotting the percentage inhibition of CETP against the log concentration of the tested compound, allowing the IC\textsubscript{50} values to be calculated accurately. Primary screening of the inhibitory activity of the synthesized compounds at 10 µM concentration was performed; 10 µM was chosen according to our previous studies on CETP inhibitors. Because several inhibitors demonstrated a % inhibition of approximately 90%, these compounds were also assayed at three additional lower concentrations (5.0 µM, 1.0 µM, and 0.5 µM), to obtain CETP % inhibition values above and below the IC\textsubscript{50} value. A line of best-fit was then drawn.

The correlation coefficient (R\textsuperscript{2}) of the corresponding dose-response line was calculated (see Table I).

### RESULTS AND DISCUSSION

#### Synthesis

A series of oxoacetamido-benzamides 9\textsubscript{a–g} were synthesized as shown in Scheme 1.
The synthesis was commenced with the activation of the carboxylic acid moiety of 3-aminobenzoic acid (1) using oxalyl chloride (2) in the presence of methanol to produce acyl chloride. Subsequently, nucleophilic attack of the OH group of methanol on the carbonyl carbon of the acyl chloride produced the methyl ester protecting group 3.

Next, the amine nitrogen of 3-amino benzoic acid methyl ester (3) attacked the partially positive methylene group of benzyl bromide 4a or 4b in the presence of DCM as a solvent to produce the substituted 3-benzylamino benzoic acid methyl ester intermediates 5a or 5b. Triethylamine was used as an acid scavenger (HBr). It was found that 5a (46% yield) was produced in a lower yield than 5b (78% yield).

Deprotection of the carboxylic acid groups of 3-aminobenzoic acid methyl ester intermediates 5a
and 5b was carried out by alkaline hydrolysis using 1M NaOH under reflux, followed by neutralization with concentrated HCl.

Then, reactivation of the carboxylic acid moiety of 3-benzylamino benzoic acid intermediates 6a or 6b was performed using oxalyl chloride (2) to produce the acyl chloride derivatives in the presence of DCM and the tetrahedral structure left as HCl, CO₂, and CO gases. Additionally, the lone pair of electrons of the nitrogen atom of intermediates 6a and 6b attacked the partially positive carbonyl carbon moiety of oxalyl chloride (2), where the chloride ion was left as a good leaving group.

Subsequently, amide formation was attained by the nucleophilic attack of the amine moiety of one of the used benzylamines 8a–d on the partially positive carbonyl carbon of the previously produced acyl chlorides to obtain the targeted benzamide derivatives 9a–g.

**In vitro CETP inhibition bioassay**

The results of the in vitro CETP inhibition assay, presented in Table I, demonstrate that most of the targeted compounds have an appreciable activity against CETP at a concentration of 10 µM. Three of them (9c, 9e, and 9g) were found to have a % inhibition of approximately 90% at 10 µM concentration. Therefore, the inhibitory activities of 9c, 9e, and 9g were evaluated at lower concentrations (5.0 µM, 1.0 µM, and 0.5 µM), and their IC₅₀ values were determined (Table I).

**Table I - In vitro bioactivities of the synthesized oxoacetamido-benzamides 9a–g**

<table>
<thead>
<tr>
<th>Synthesized compound</th>
<th>% Inhibition (at 10.0 µM)</th>
<th>% Inhibition (at 5.0 µM)</th>
<th>% Inhibition (at 1.0 µM)</th>
<th>% Inhibition (at 0.5 µM)</th>
<th>IC₅₀ (µM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>9a</td>
<td>71.7± 0.4</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>9b</td>
<td>84.4± 0.7</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>9c</td>
<td>92.7± 0.6</td>
<td>69.8±0.7</td>
<td>35.3± 0.2</td>
<td>18.4±0.4</td>
<td>1.89 (R² = 0.99)**</td>
</tr>
<tr>
<td>9d</td>
<td>62.7± 0.5</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>9e</td>
<td>92.3± 0.8</td>
<td>68.3±0.5</td>
<td>26.7± 0.5</td>
<td>16.2±0.4</td>
<td>2.16 (R² = 0.99)**</td>
</tr>
<tr>
<td>9f</td>
<td>20.0± 0.5</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>9g</td>
<td>90.4± 0.7</td>
<td>75.2±0.6</td>
<td>55.9± 0.4</td>
<td>33.7±0.6</td>
<td>0.96 (R² = 0.99)**</td>
</tr>
<tr>
<td>Torcetrapib (0RP)</td>
<td>88.2±±0.8</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>0.04</td>
</tr>
</tbody>
</table>

ND: not determined. *: at concentration of 0.08 µM.
**: This value represents the correlation coefficient of the corresponding dose-response line at four concentrations.

As can be seen in Table I, most of the synthesized compounds demonstrated comparable bioactivities (within the same range). As a general observation, benzamides with p-OCF₃ groups (9a–c) demonstrated slightly higher CETP inhibition at 10 µM concentration than those with the p-CF₃ moiety (9d–g), especially when they were substituted with the m-CH₃ group (9b and 9f). Furthermore, in comparison to the previously synthesized p-substituted analogs (Abu Khalaf et al., 2017c), the m-CH₃ group in 9b demonstrated a higher % inhibition (84.4%) than its p-CH₃ substituted analog (62.1%), and compound 9e with the m-OCH₃ moiety demonstrated higher % inhibition (92.7%) than its p-OCH₃ substituted analog (65.8%).

**Docking study**

To identify the structural basis for CETP inhibition by the co-crystallized ligand (0RP: torcetrapib) and the targeted compounds 9a–g, the glide docking approach was used (Friesner et al., 2004; Friesner et al., 2006) against CETP (PDB ID: 4EWS) (Liu et al., 2012). The Glide docking data for compounds 9a–g and 0RP...
demonstrated that each of these compounds could be accommodated in the active site of 4EWS. Furthermore, as shown in Figure 2, the docked 9a model can be superimposed on the coordinates of 0RP (torcetrapib).

The Glide docking data suggested that hydrophobic interactions drive ligand/4EWS complex formation (Table II; Figure 3 and 4; Supplementary Figures 1S and 2S). Additionally, the backbones of 9e and 9f formed an H-bond with S230 (Figures 3S).

**TABLE II** - The Glide docking scores (kcal/mol) of 9a–g and 0RP

<table>
<thead>
<tr>
<th>Compound</th>
<th>Glide docking scores (kcal/mol)</th>
<th>H-Bond</th>
</tr>
</thead>
<tbody>
<tr>
<td>9a</td>
<td>-10.62</td>
<td>NA</td>
</tr>
<tr>
<td>9b</td>
<td>-11.80</td>
<td>NA</td>
</tr>
<tr>
<td>9c</td>
<td>-11.37</td>
<td>NA</td>
</tr>
<tr>
<td>9d</td>
<td>-11.63</td>
<td>NA</td>
</tr>
<tr>
<td>9e</td>
<td>-11.41</td>
<td>S230</td>
</tr>
<tr>
<td>9f</td>
<td>-12.06</td>
<td>S230</td>
</tr>
<tr>
<td>9g</td>
<td>-12.58</td>
<td>NA</td>
</tr>
<tr>
<td>Torcetrapib (0RP)</td>
<td>-10.57</td>
<td>NA</td>
</tr>
</tbody>
</table>

NA: not available.
The high binding scores obtained for compounds 9a–g against 4EWS indicate that this scaffold has potential inhibitory activity against CETP. Furthermore, the small difference (2 kcal/mol) observed between the binding affinity of the co-crystallized ligand (0RP: torcetrapib) and the binding affinities of 9a–g provides further evidence of the significance of this scaffold for CETP inhibition.

To assess the performance of the Glide program, the structure of the docked 0RP model was compared with the experimental 0RP coordinates from the 4EWS crystal structure (Liu et al., 2012). Figure 5 demonstrates the superimposition of the Glide-produced 0RP model with the experimental structure from 4EWS. The RMSD for the heavy atoms of 0RP in these structures was 1.534 Å. These results indicate that Glide docking is capable of generating the experimental conformation from the 4EWS crystal structure, and thus evaluating the location of ligand binding.

The in vitro biological data demonstrated that compound 9c tailored with X= p-OCF$_3$ and Y= m-OCH$_3$ moieties exhibited promising CETP inhibition. According to the modeling results, the H-bond acceptor and/or hydrophobic pocket interacted with the m-OCH$_3$ and p-OCF$_3$ motifs in 9c. Moreover, the high inhibitory activity of compound 9e substituted with X= p-CF$_3$ and Y= m-Cl groups demonstrated the significance of hydrophobic interactions on 4EWS/ligand complex formation and CETP inhibition. Additionally, compound 9g substituted with X= p-CF$_3$ and Y= m-OCH$_3$ showed comparable inhibitory activity to that of 9e. This finding provided further evidence for the dominance of hydrophobic interactions in the 4EWS binding domain. A comparison of the activities of compounds 9a–e indicated that the m-H-bond acceptor moiety is essential for the activity of analogs bearing p-OCF$_3$.

In contrast, the absence of m-Cl, as exemplified in compound 9d, weakened the inhibitory activity, and the replacement of m-Cl with m-CH$_3$ as in compound 9f decreased the activity further. Together, the observed inhibitory activities of compounds 9d–g provide evidence that the m-electron-withdrawing moiety might induce CETP inhibitory activity. Nevertheless, m-Cl and m-CH$_3$ are hydrophobic and isosteres of each other; the m-electron-withdrawing effect was significant for the inhibitory activity of derivatives tailored to p-CF$_3$.

**Pharmacophore mapping**

To investigate the core structures of compounds 9a–g and their motifs, these structures were scanned against the CETP active inhibitor pharmacophore model (Abu Khalaf et al., 2017a). Compounds 9a–g matched the features of CETP active inhibitors (Figure 6), providing a rationale for their high docking scores against the CETP binding domain. Additionally, the accommodation of compounds 9a–g in the CETP binding domain explained their inhibitory activity.
CONCLUSIONS

The present study identified oxoacetamido-benzamide as a new scaffold targeting CETP activity. The targeted benzamides were found to express similar bioactivities, with compound 9g showing an IC$_{50}$ of 0.96 µM. The results of the study suggest that the presence of a p-trifluoromethoxy group may enhance CETP inhibitory activity. Future optimization of the structure of these inhibitors is required to enhance their physicochemical properties and to clarify the structure-activity relationship.

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CONFLICT OF INTEREST

The authors declare no conflicts of interest.

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SUPPLEMENTARY MATERIAL

**FIGURE 1S** - The ligand/4EWS complex of (A) 9b and (B) 9g. The hydrophobic lining is green colored. Picture made by MAESTRO (Protein Preparation Wizard, 2016)

**FIGURE 2S** - The ligand/4EWS complex of (A) 9c and (B) 0RP. The hydrophobic lining is green colored. Picture made by MAESTRO (Protein Preparation Wizard, 2016)
FIGURE 3S - Glide docked poses of (A) 9e (B) 9f in 4EWS binding site. H-Bond is represented in blue dotted line. Some key binding residues are disclosed and H atoms are invisible for clarification. Picture captured by PYMOL.

FIGURE 4S - Glide docked poses of (A) 9c (B) 9d in 4EWS binding site. Some key binding residues are disclosed and H atoms are invisible for clarification. Picture captured by PYMOL.

FIGURE 5S - Glide docked poses of 9g in 4EWS binding site. Some key binding residues are disclosed and H atoms are invisible for clarification. Picture captured by PYMOL.