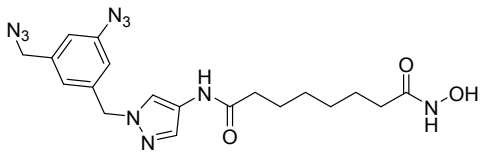
SUPPORTING INFORMATION

Design and development of histone deacetylase (HDAC) chemical probes for cell-based profiling

Victoria E. Albrow,[a] Rachel L. Grimley,[a] James Clulow,[b] Colin R. Rose,[c] Jianmin Sun,[c] Joseph S. Warmus,[c] Edward W. Tate,[b] Lyn H. Jones,[d] and R. Ian Storer.[e]

[a] Biology, Pfizer Ltd, The Portway Building, Granta Park, Great Abington, Cambridge, CB21 6GS, UK.
[b] Department of Chemistry and Institute of Chemical Biology, Imperial College London, London, SW7 2AZ, UK.
[c] Worldwide Research and Development, Pfizer Neusentis Chemistry, Eastern Point Road, Groton, Connecticut 06340, USA.
[d] Worldwide Medicinal Chemistry, Pfizer Rare Disease Chemistry, 610 Main Street, Cambridge, MA 02139, USA.
[e] Worldwide Medicinal Chemistry, Pfizer Ltd, The Portway Building, Granta Park, Great Abington, Cambridge, CB21 6GS, UK.

Table of contents



	Lit. HDAC1	Current HDAC1	Lit. HDAC4	Current HDAC4
SAHA	0.022[1] 0.014[2]	0.051	0.122[1] >50[2]	>30
SAHA diazide[1]	0.099[1]	0.138	0.379[1]	13.048
SAHABPyne[3, 4]		0.236		>50

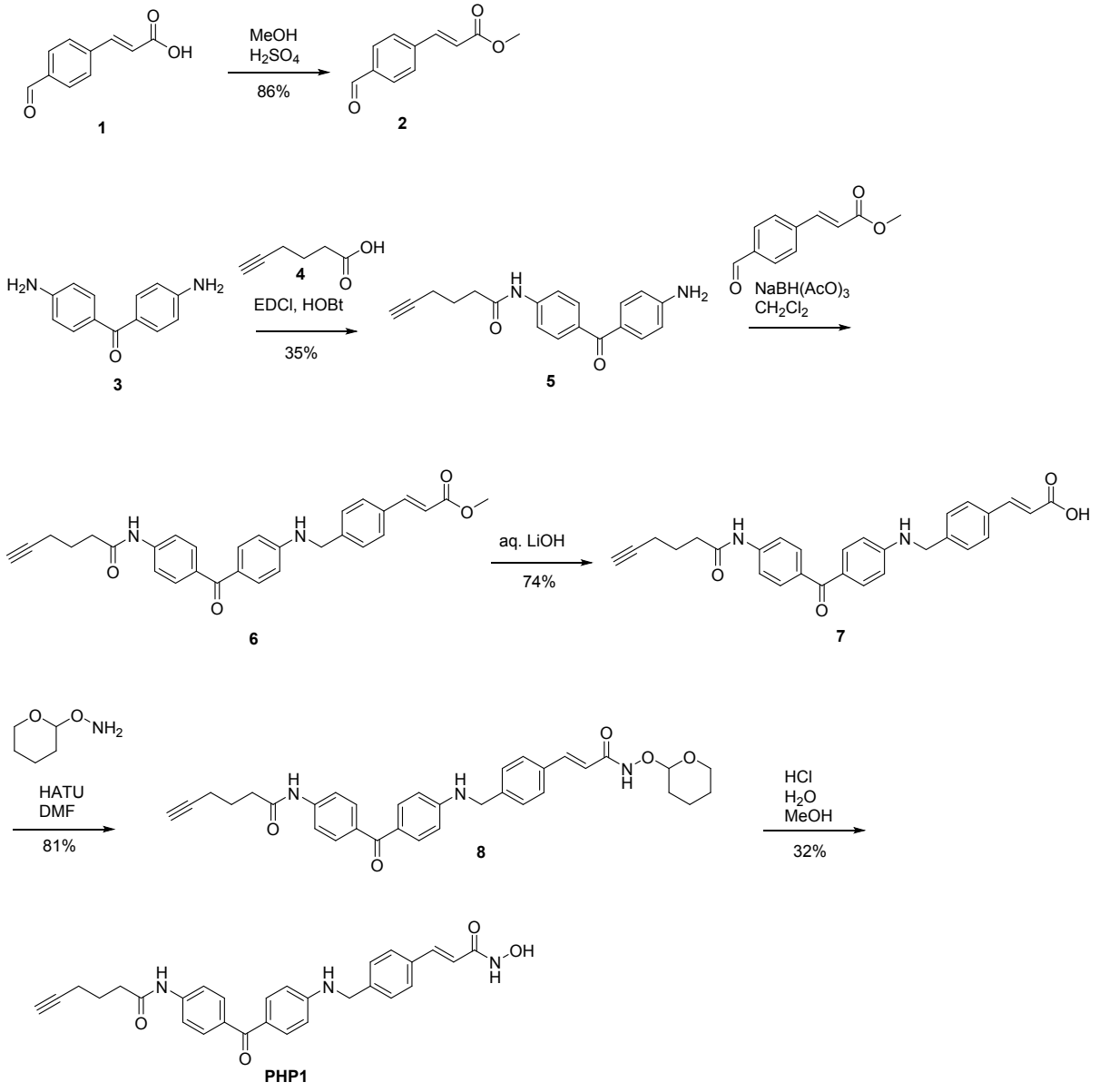
SI Figure S1: Structure and enzyme activity data for literature SAHA diazide probe. Structure of reported SAHA-based diazide probe[1] and table of IC_{50} values generated in this study for inhibitory activity against recombinant HDAC1 and 4 in a fluorgenic plate based assay. The mean IC_{50} values from duplicate runs of the compounds in μM are summarized.

Supporting Experimental Procedures

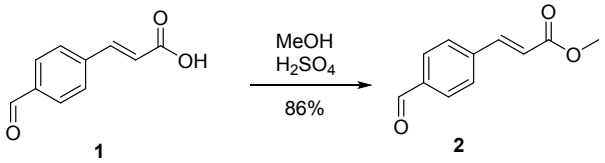
Synthesis of Chemical Probes

Unless otherwise noted, all chemical compounds were obtained from commercial suppliers and used without purification. SAHA and SAHABPyne were purchased from Cayman chemicals. TMP269 was purchased from Xcessbio. Pandacostat[5] and intermediates **37**[6] and **43**[7] were prepared according to literature methods.

Synthesis of (*E*)-*N*-(4-(4-((4-(3-(hydroxyamino)-3-oxoprop-1-en-1-yl)benzyl)amino)benzoyl)phenyl)hex-5-ynamide (PHP1)



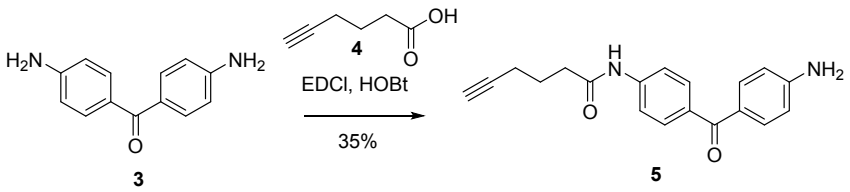
Synthesis of methyl (*E*)-3-(4-formylphenyl)acrylate (2)



1 2

To a solution of (*E*)-3-(4-formylphenyl)acrylic acid (**1**) (1.0 g, 5.68 mmol) in MeOH (30 mL) at 0 °C was added conc. H_2SO_4 (3 mL). The resulting mixture was stirred at 80 °C for half an hour. The solvent was removed by evaporation and the obtained compound was stirred with water (100 mL) for 15minutes. The precipitated white solid was filtered, washed with water (300 mL) and dried to give pure methyl (*E*)-3-(4-formylphenyl)acrylate (**2**) (1.9 g, 86%). ^{1}H NMR (400 MHz, $CDCl_3$) δ ppm 3.81 (3H, s), 6.52 (2H, d), 7.67 (3H, m), 7.87 (2H, m), 10.0 (1H, s).

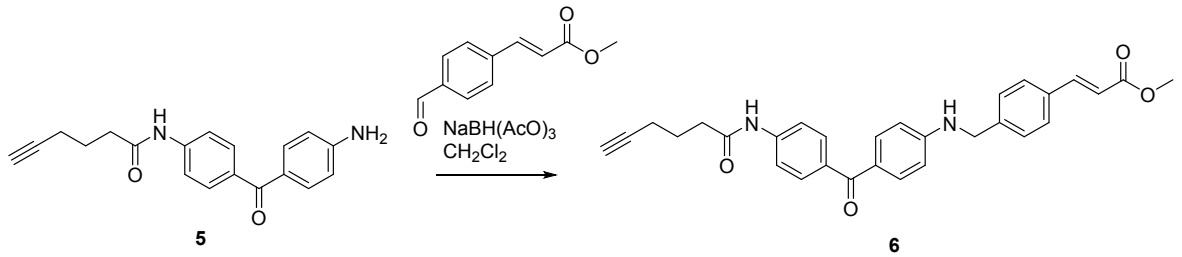
Synthesis of *N*-(4-(4-aminobenzoyl)phenyl)hex-5-ynamide (5)



3 5

To a 50 mL flask fitted with a stir bar under N_2 was added hex-5-ynoic acid (**4**) (104 µL, 0.94 mmol), 1-hydroxybenzotriazole (HOBt) (144 mg, 0.94 mmol), and DMF (2.4 mL). To the solution was added 1-(3-dimethylaminopropyl)-3-ethylcarbodiimide hydrochloride (EDCI) (181 mg, 0.94 mmol). The mixture was stirred for 5 minutes and bis(4-aminophenyl)methanone (**3)** (100 mg, 0.47 mmol) was added. After stirring the mixture overnight, EtOAc (30 mL) was added. The organic layer was washed with saturated $NaHCO_3$ (2 × 25 mL) and 10% aqueous citric acid (2 × 25 mL), dried with Na_2SO_4, filtered, and concentrated. Purification over silica gel (3% MeOH in $CHCl_3$) yielded compound **5** (75 mg, 52%) as a brown-yellow solid. ^{1}H NMR (400 MHz, $CDCl_3$) δ ppm 1.76 (quintet, *J* = 7.3, 2H), 2.20 (td, *J* = 7.0, 2.6, 2H), 2.45 (t, *J* = 7.4, 2H), 2.80 (t, *J* = 2.6, 1H), 6.05 (s, 2H), 6.57 (d, *J* = 8.7, 2H), 7.48 (d, *J* = 8.6, 2H), 7.58(d, *J* = 8.6, 2H), 7.69 (d, *J* = 8.6, 2H), 10.19 (s, 1H).

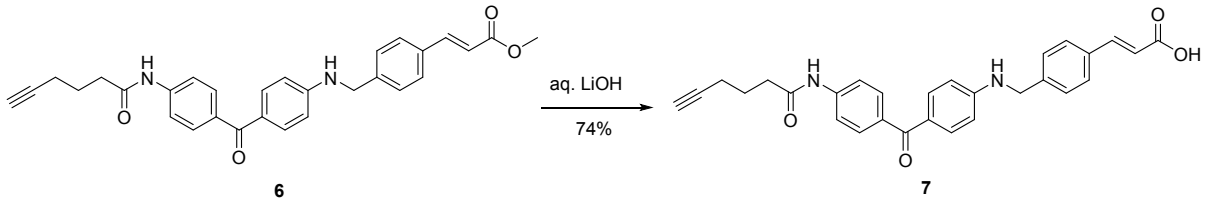
Synthesis of methyl (*E*)-3-(4-(((4-(4-(hex-5-ynamido)benzoyl)phenyl)amino)methyl)phenyl)acrylate (6)



5 6

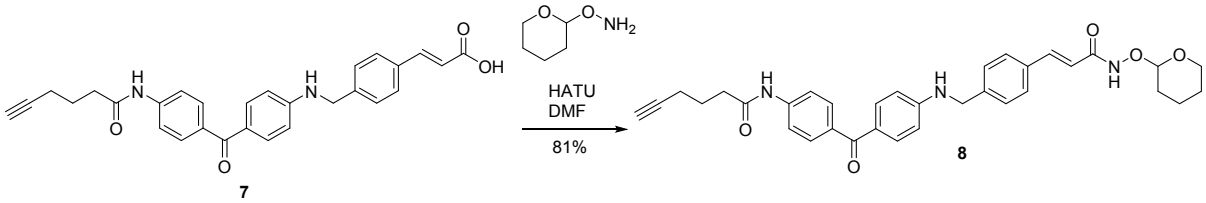
A mixture of **5** (307 mg, 1.0 mmol), 2 (209 mg, 1.1 mmol), and AcOH (280 µL, 5 mmol) in CH_2Cl_2 (5 mL) was stirred at room temperature for 10 minutes. The mixture was treated with $NaBH(OAc)_3$ (850 mg, 2.0 mmol) at 0 °C, and the resulting mixture was stirred at room temperature for 20 minutes. The reaction was quenched with saturated aqueous $NaHCO_3$ (50 mL), and the mixture was extracted with AcOEt (80 mL). The organic layers were washed with saturated aqueous $NaHCO_3$ (50 mL) and brine (50 mL), dried (Na_2SO_4), filtered, and concentrated to afford the desired product **6** that was used for the next step without further purification.

Synthesis of (*E*)-3-(4-(((4-(4-(hex-5-ynamido)benzoyl)phenyl)amino)methyl)phenyl)acrylic acid



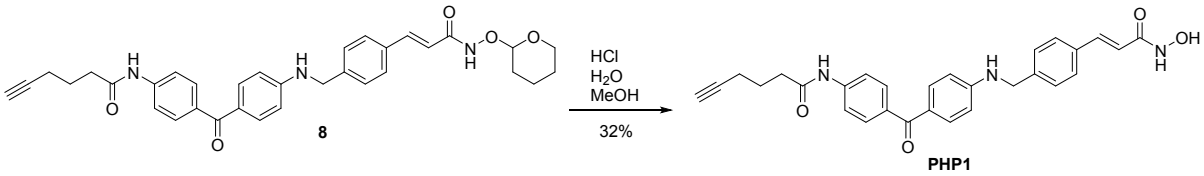
To a solution of **6** (100 mg, 0.208 mmol) in THF/H_2O (20/20, 40 mL) was added LiOH.H_2O (106 mg, 2.5 mmol). The solution was then stirred at room temperature for 2 hours. After completion, the solvent was then concentrated in vacuo to give the crude compound **7** (71 mg, 74%), which was used directly for next step.

Synthesis of (*E*)-*N*-(4-(4-((4-(3-oxo-3-(((tetrahydro-2H-pyran-2-yl)oxy)amino)prop-1-en-1-yl)benzyl)amino)benzoyl)phenyl)hex-5-ynamide



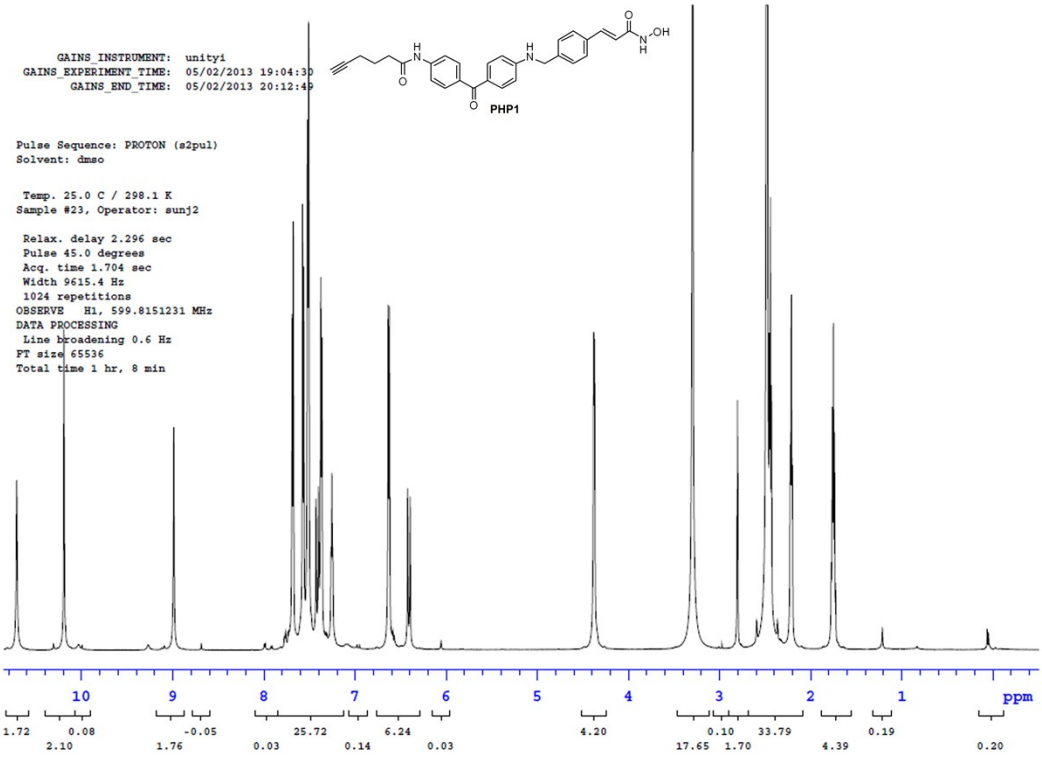
To a solution of **7** (96.9 mg, 0.21 mmol), O-(tetrahydro-2H-pyran-2-yl)hydroxylamine (24 mg, 0.208 mmol), TEA (84 mg, 0.832 mmol) in THF (20/20, 40 mL) was added HATU (87 mg, 0.23 mmol). The solution was then stirred at room temperature for 2 hours. After completion, brine was added, extracted twice with ethyl acetate, dried with Na_2SO_4, concentrated in vacuo to give the crude **8** (95 mg, 81%), which was used directly for next step.

Synthesis of (*E*)-*N*-(4-(4-((4-(3-(hydroxyamino)-3-oxoprop-1-en-1-yl)benzyl)amino)benzoyl)phenyl)hex-5-ynamide (PHP1)

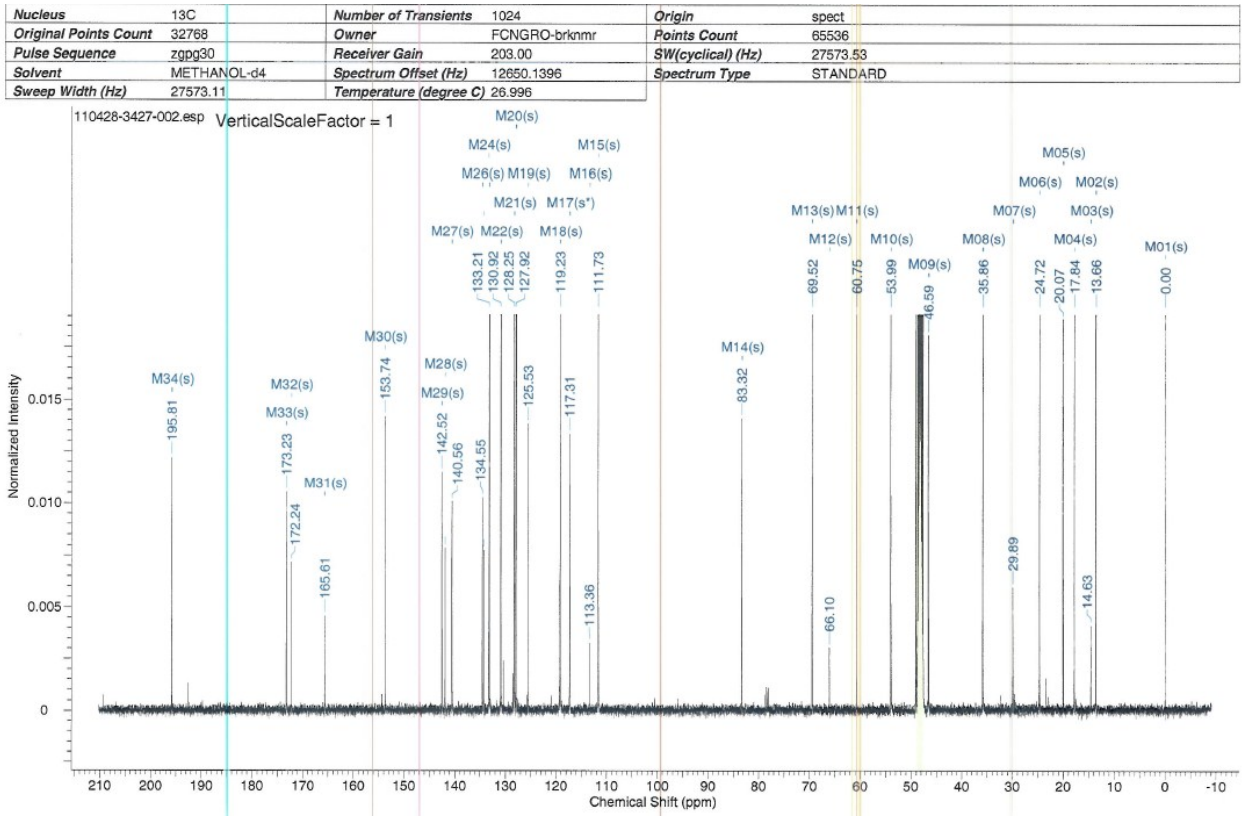


A solution of compound **8** (200 mg, 0.35 mmol) in 1N HCl (50 mL) was stirred at room temperature for 2 hours. After completion, the solution was extracted three times with ethyl acetate, dried with Na_2SO_4, concentrated in vacuo to give crude desired compound, which was purified by Prepare HPLC to afford pure **PHP1** (54 mg, 32%). ^{1}H NMR (600 MHz, DMSO-d6) δ ppm 1.77 (quin, *J* = 7.19 Hz, 3H), 2.23 (td, *J* = 7.04, 2.35 Hz, 2H), 2.46 (t, *J* = 7.34 Hz, 3H), 2.82 (t, *J* = 2.64 Hz, 1H), 4.40 (d, *J* = 5.87 Hz, 2H), 6.43 (d, *J* = 15.85 Hz, 1H), 6.65 (d, *J* = 8.80 Hz, 2H), 7.27 (t, *J* = 5.87 Hz, 1H), 7.39 (d, *J* = 7.63 Hz, 2H), 7.43 (d, *J* = 15.85 Hz, 1H), 7.53 (d, *J* = 7.04 Hz, 4H), 7.59 (d, *J* = 8.80 Hz, 2H), 7.70 (d, *J* = 8.22 Hz, 2H), 9.01 (s, 1H), 10.21 (s, 1H), 10.73 (br. s., 1H); ^{13}C NMR (126 MHz, methanol-d4) δ ppm 195.8, 173.2, 172.2, 165.6, 153.7, 142.5, 141.9, 140.6, 134.5, 134.3, 133.3, 133.2, 130.9, 128.3, 127.9, 125.5, 119.2, 117.3, 111.7, 83.3, 69.5, 60.8, 54.0, 46.6, 35.9, 29.9, 24.7, 20.1, 17.8, 14.6, 13.7; Melting point: 171-173 °C; HPLC (12 min) R_t 7.84 min UV 254 nm >90% purity; LRMS *m/z* 482.5 $[M+H]^+$;HRMS calculated for $[M+H^+, C_{29}H_{28}N_3O_4^+]$ requires *m/z* 482.2080. Found 482.2074.

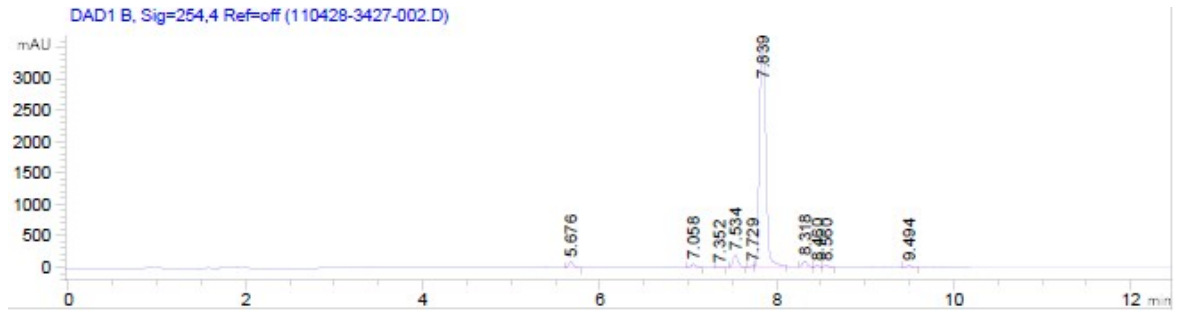
^{1}H NMR (**PHP1**):



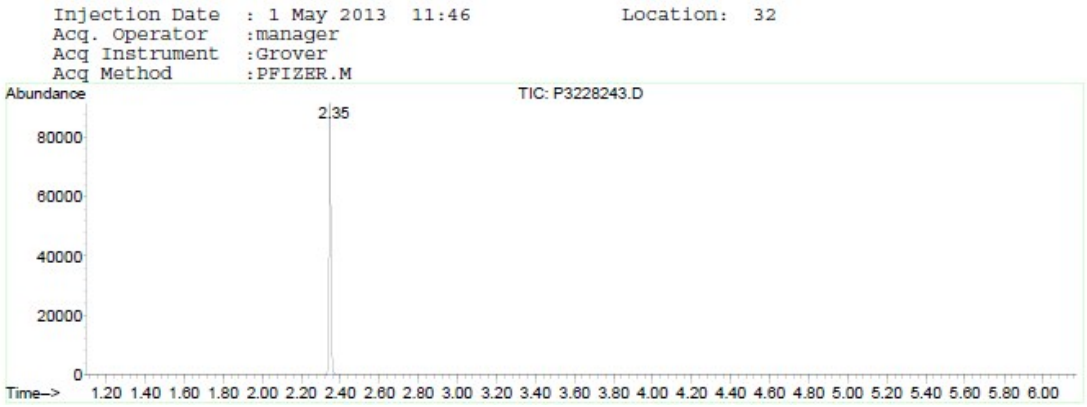
^{13}C NMR (**PHP1**):



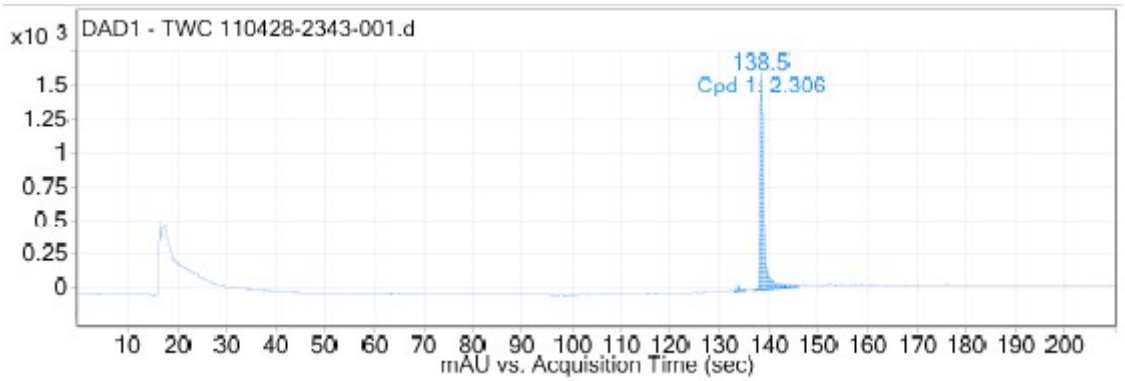
HPLC UV 254nm (**PHP1**): (>90% purity)



GC trace (**PHP1**): (>95% purity)

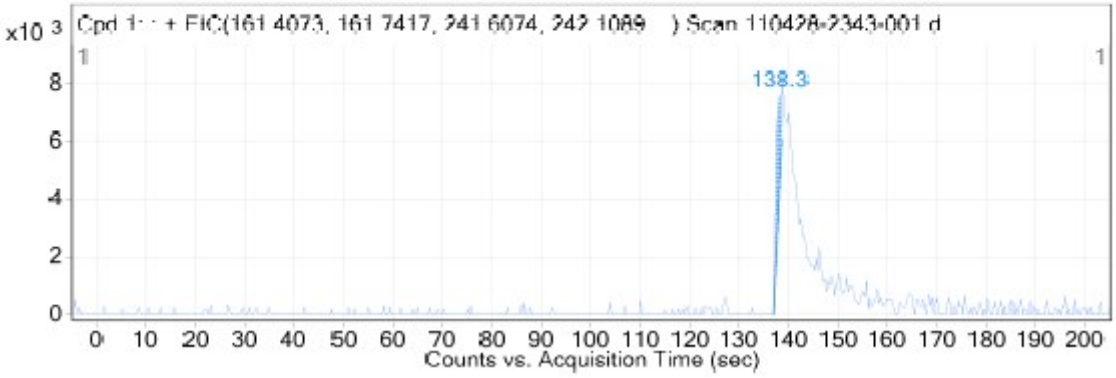


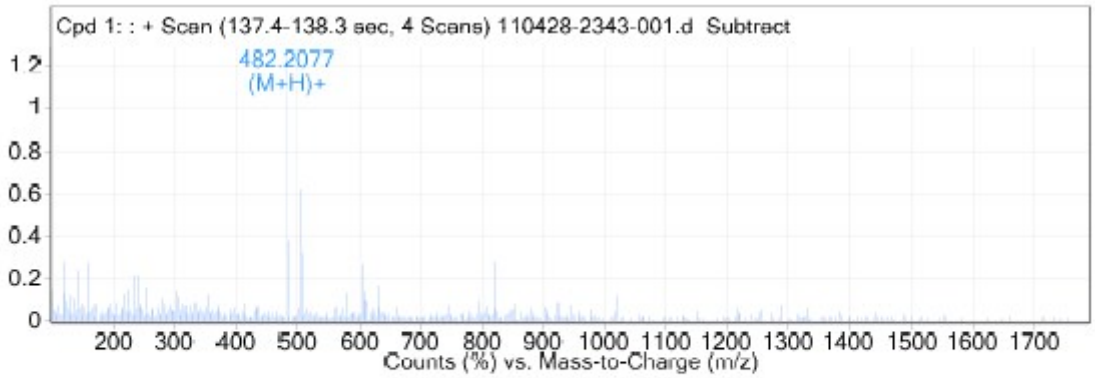
HR-LCMS (**PHP1**): (>95% purity)



Compound Table

Compound Label	Formula	Tgt Mass	Diff (ppm)	Purity Value	Purity Result
Cpd 1:	C29H27N3O4	NaN	NaN	95.3	Pass



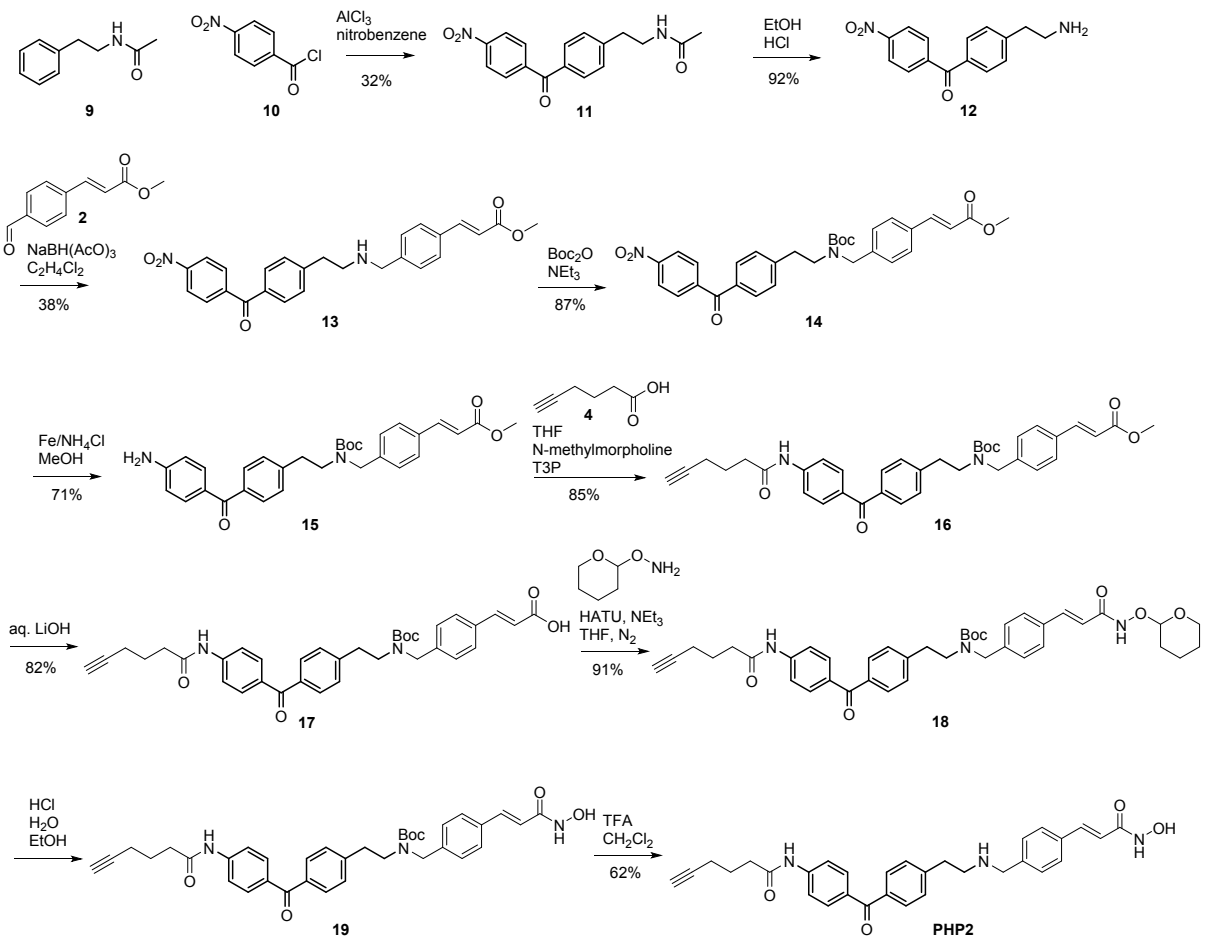


MS Spectrum Peak List

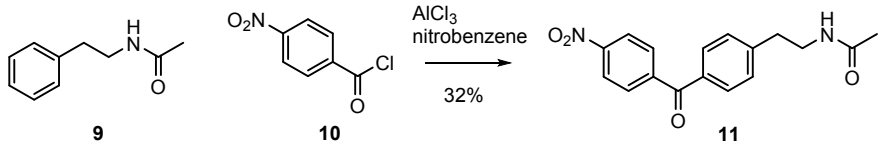
m/z	*Calc m/z*	Diff(ppm)	z	Abund	Formula	Ion
482.2077	482.2074	-0.48	1	4527.4	C29H28N3O4	(M+H)+
483.208	483.2106	5.31	1	1333.2	C29H28N3O4	(M+H)+
484.2153	484.2135	-3.71	1	210.6	C29H28N3O4	(M+H)+

--- End Of Report ---

Synthesis of 2,2,2-trifluoro-1-(5-(3-((4-(4-(prop-2-yn-1-yloxy)benzoyl)phenoxy)methyl)-1,2,4-oxadiazol-5-yl)thiophen-2-yl)ethanone (PHP2)

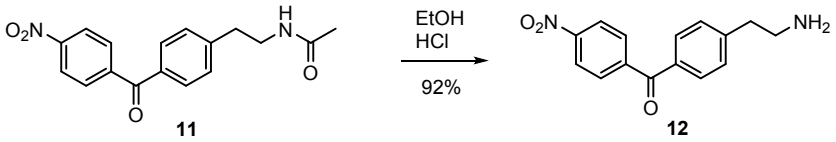


Synthesis of *N*-(4-(4-nitrobenzoyl)phenethyl)acetamide (11)



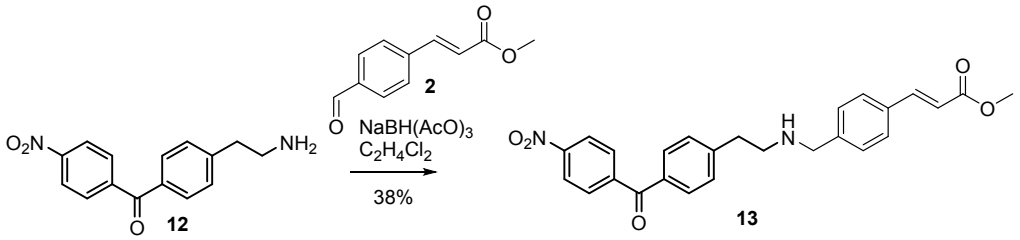
A suspension of *N*-phenethyl-acetamide **9** (10 g, 61.27 mmol), 4-nitro-benzoyl chloride **10** and $AlCl_3$ (16.3 g, 122.54 mmol) in nitrobenzene (31.4 mL, 306.35 mmol) was heated at 90 °C for 18 hours. The nitrobenzene was evaporated under vacuo. The residue was quenched with cold water under cold conditions. The resultant solid was washed with diethyl ether and dried under vacuo to afford **11** as a brown solid (6 g, 32%).

Synthesis of (4-(2-aminoethyl)phenyl)(4-nitrophenyl)methanone (12)



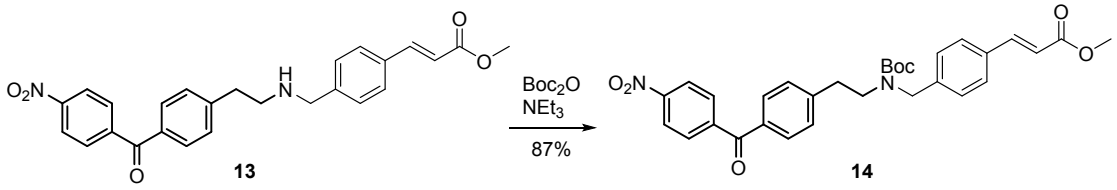
A solution of **11** (2 g, 6.4 mmol) in ethanol:HCl (6 mL, 1:2) was heated under reflux for 24 hours in sealed tube. The reaction mixture was concentrated under reduced pressure and solid obtained was washed with ethyl acetate and dried under vacuo to obtain **12** as brown solid (1.6 g, 92%).

Synthesis of methyl (*E*)-3-(4-(((4-(4-nitrobenzoyl)phenethyl)amino)methyl)phenyl)acrylate (13)



To a stirred solution of **12** (500 mg, 1.63 mmol) in dry dichloroethane (5 mL) was added triethylamine (0.68 mL, 4.90 mmol) and stirred for 30 minutes. Molecular sieves (3A°) (200 mg), methyl (*E*)-3-(4-formylphenyl)acrylate (**2**) (310 mg, 1.633 mmol) and acetic acid (0.39 mL, 6.53 mmol) was added to the reaction mixture and allowed to stir for 18 hours at room temperature. $NaBH(OAc)_3$ (415 mg, 1.96 mmol) was added and stirred for 45 minutes. The reaction mixture was quenched with saturated sodium bicarbonate solution (5 mL), extracted with DCM (3 × 30 mL), the combined organic extract was washed with water (10 mL), brine (10 mL) and dried over anhydrous Na_2SO_4, concentrated under reduced pressure to afford crude residue which was purified by column chromatography to give **13** (275 mg, 38%).

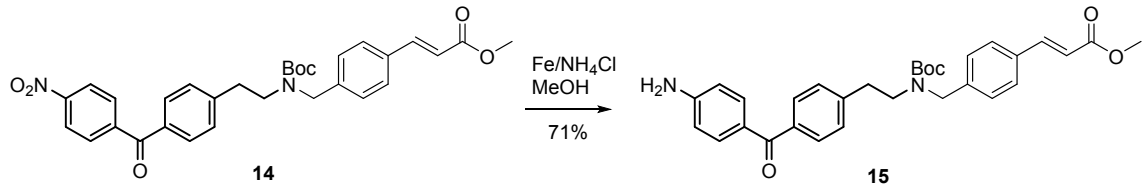
Synthesis of methyl (*E*)-3-(4-(((tert-butoxycarbonyl)(4-(4-nitrobenzoyl)phenethyl)amino)methyl)phenyl)acrylate (14)



To a stirred solution of **13** (300 mg, 0.68 mmol) in dry dichloromethane (6 mL) was added boc-anhydride (0.17 mL, 0.74 mmol) and triethylamine (0.28 mL, 2.03 mmol) in cold conditions and stirred for 18 hours at ambient temperature. The reaction mixture was diluted with dichloromethane (50 mL), washed with water (10 mL), brine (10 mL) and dried over anhydrous Na_2SO_4,

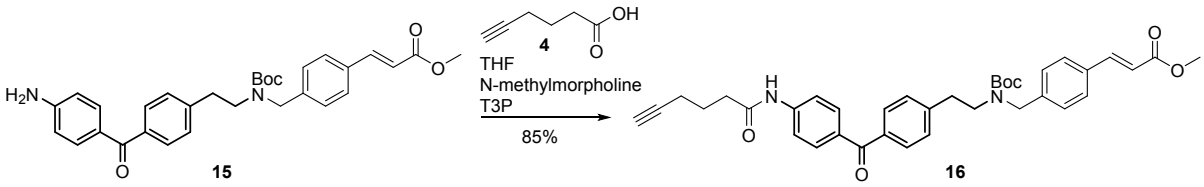
concentrated under reduced pressure to afford crude residue which was purified by column chromatography to give **14** as yellowish oil (320 mg, 87%).

Synthesis of methyl (*E*)-3-(4-(((4-(4-aminobenzoyl)phenethyl)(tert-butoxycarbonyl)amino)methyl)phenyl)acrylate (15)



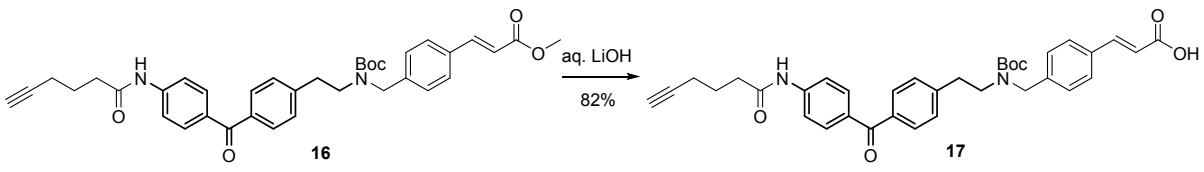
To a stirred solution of **14** (325 mg, 0.60 mmol) in methanol (7 mL) was added Iron powder (113.4 mg, 2.03 mmol) and ammonium chloride (159.6 mg, 2.99 mmol) in water (0.6 mL). The reaction mixture was refluxed at 100 °C for 16 hours. The reaction mixture was cooled to room temperature and filtered through celite. The filtrate was concentrated under reduced pressure to afford crude, which was purified by column chromatography to obtain **15** as a yellowish solid (220 mg, 71%).

Synthesis of methyl (*E*)-3-(4-(((tert-butoxycarbonyl)(4-(4-(hex-5-ynamido)benzoyl)phenethyl)amino)methyl)phenyl)acrylate (16)



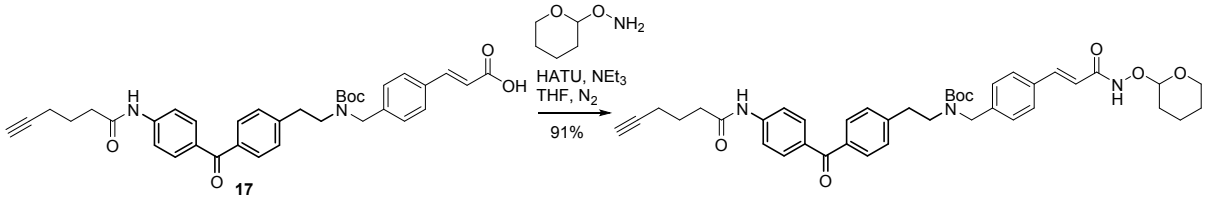
A solution of **15** (375 mg, 0.73 mmol) and hex-5-ynoic acid (**4**) (81.7 mg, 0.73 mmol) in dry THF (8 mL) was cooled to 0 °C. N-methylmorpholine (0.4 mL, 3.65 mmol) followed by T3P (0.76 mL, 2.55 mmol) was added and the resulting reaction mixture was refluxed for 14 hours. THF was evaporated and the residue was dissolved in ethyl acetate (50 mL). The organic fraction was washed with water (10 mL), 1N HCl (5 mL) 5% $NaHCO_3$ solution (5 mL) and brine (10 mL). The organic part was dried over anhydrous Na_2SO_4, concentrated under reduced pressure to afford crude residue, which was purified by column chromatography to give **16** (380 mg, 85%).

Synthesis of (*E*)-3-(4-(((tert-butoxycarbonyl)(4-(4-(hex-5-ynamido)benzoyl)phenethyl)amino)methyl)phenyl)acrylic acid (17)



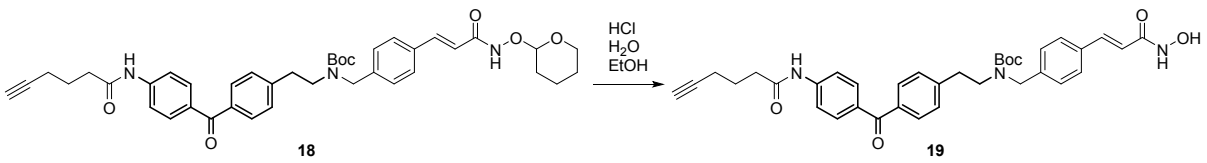
To a solution of **16** (750 mg, 1.23 mmol) in THF: water (15 mL, 1:1) was added LiOH (32.5 mg, 1.36 mmol) and the reaction mixture was heated at 60 °C for 2.5 hours. The reaction mixture was cooled to room temperature and concentrated to solid residue. The residue was dissolved in water (10 mL). The aqueous part was washed with ethyl acetate (2 × 20 mL) to remove organic impurities. The aqueous part was acidified (pH~4) with 0.5N HCl and extracted with ethyl acetate (3 × 50 mL). The combined organic extract was washed with water (30 mL), brine (30 mL) and dried over anhydrous Na_2SO_4, concentrated under reduced pressure to afford **17** as a brown solid (600 mg, 82%).

Synthesis of *tert*-butyl (*E*)-(4-(4-(hex-5-ynamido)benzoyl)phenethyl)(4-(3-oxo-3-(((tetrahydro-2H-pyran-2-yl)oxy)amino)prop-1-en-1-yl)benzyl)carbamate (18)



To a solution of **17** (400 mg, 0.67 mmol) and O-(tetrahydro-2H-pyran-2-yl)hydroxylamine (164 mg, 1.35 mmol) in THF (6.8 mL) under N_2 was added TEA (377 µl, 2.69 mmol) and HATU (310 mg, 0.77 mmol). The reaction was stirred at ambient temperature overnight. The mixture was diluted with ethyl acetate (30 mL), washed with brine and dried over anhydrous Na_2SO_4 then concentrated under reduced pressure. The crude reaction product was purified using silica column chromatography 0-5% MeOH in dichloromethane to give the desired product (427 mg, 91%).

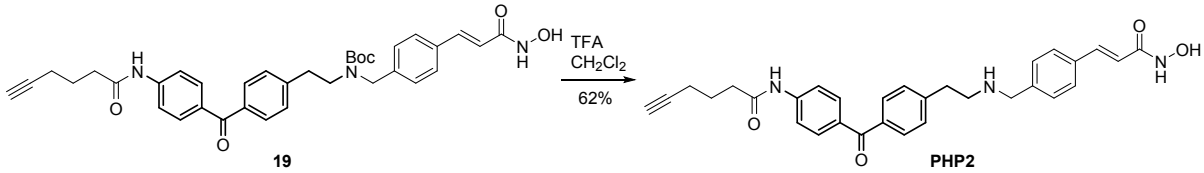
Synthesis of *tert*-butyl (*E*)-(4-(4-(hex-5-ynamido)benzoyl)phenethyl)(4-(3-(hydroxyamino)-3-oxoprop-1-en-1-yl)benzyl)carbamate (19)



To a solution of **18** (427 mg, 0.62 mmol) in EtOH (2 mL) was added 1M HCl (2 mL). The reaction was stirred at ambient temperature for 2 hours then extracted with ethyl acetate (3 × 20 mL) and the solvent evaporated. LCMS showed the reaction was only about 55% complete. 1M HCl (13 mL) was

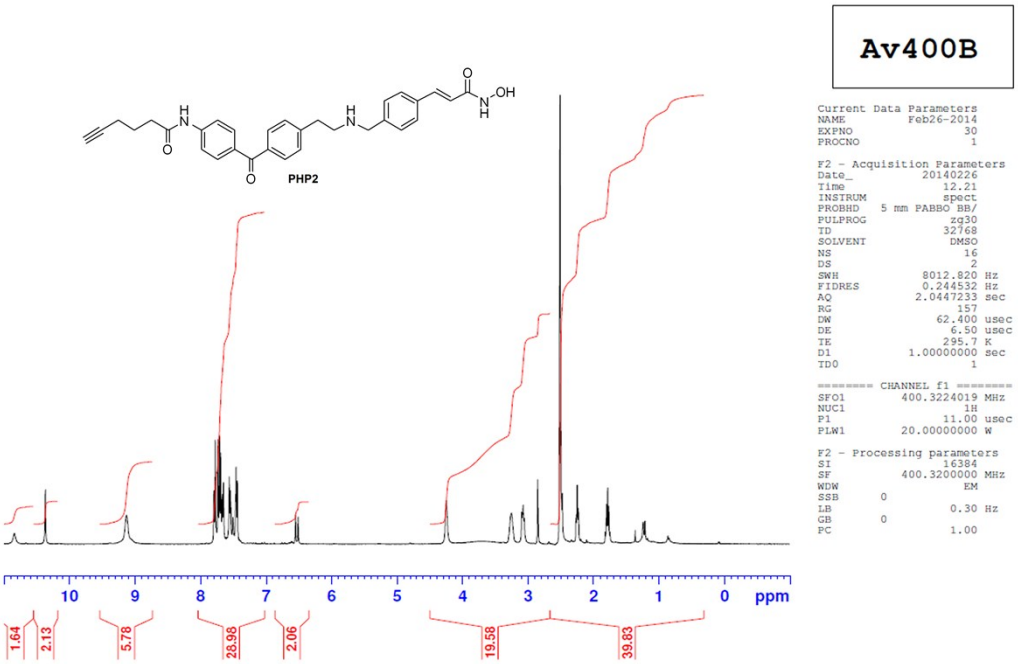
added and the recation stirred for a further 4 hours until all starting material was consumed. The reaction was evaporated to dryness and used without further purification.

Synthesis of (*E*)-*N*-(4-(4-(2-((4-(3-(hydroxyamino)-3-oxoprop-1-en-1-yl)benzyl)amino)ethyl)benzoyl)phenyl)hex-5-ynamide (PHP2)

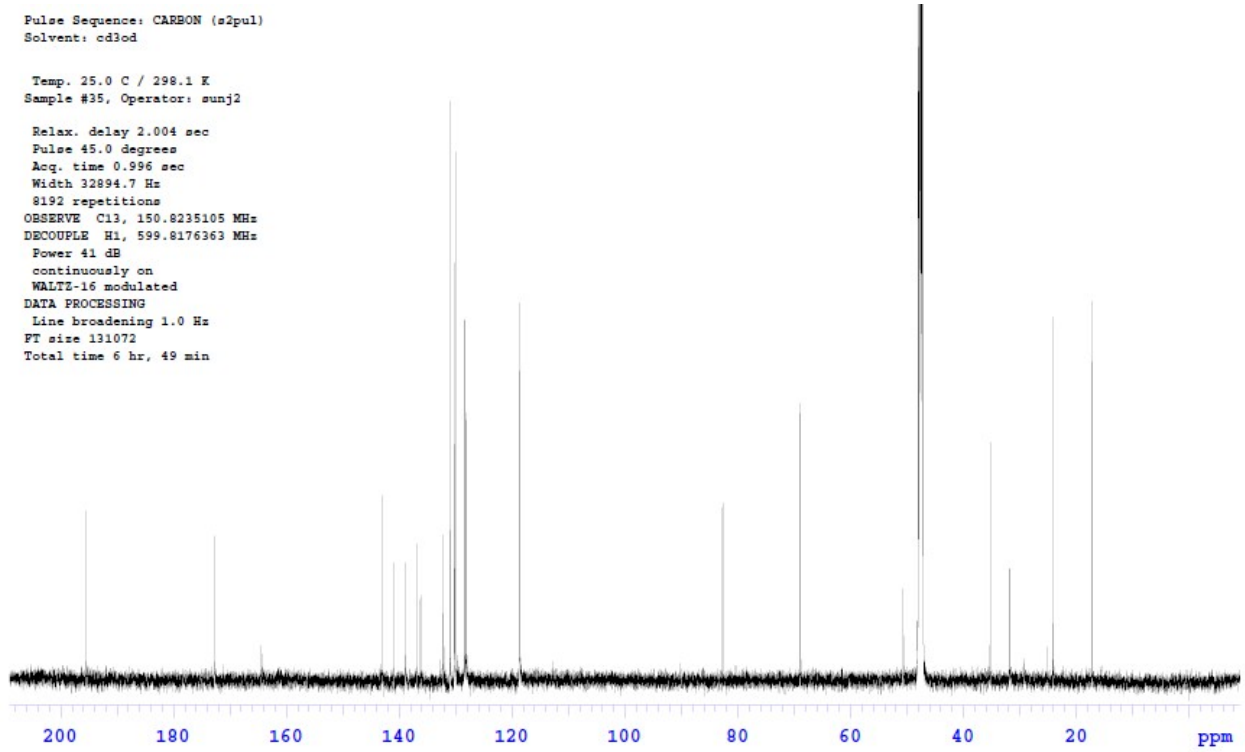


A solution of **19** (375 mg, 0.62 mmol) in dichloromethane (3 mL) was cooled to 0 °C before addition of TFA (940 µL, 12.3 mmol). The reaction was allowed to warm to ambient temperature and stirred for 3 hours. The solvent was removed by co-evaporation with ethyl acetate and heptane. The product was triturated with 1:5 ethyl acetate/heptanes then filtered and dried top give **PHP2** as a pink solid (238 mg, 62%). ^{1}H NMR (400 MHz, DMSO-d6) δ ppm 1.23 (br. s., 1 H) 1.78 (t, *J*=7.32 Hz, 2 H) 2.24 (td, *J*=7.01, 2.56 Hz, 2 H) 2.83 (t, J=2.56 Hz, 1 H) 3.01 - 3.12 (m, 2 H) 3.25 (br. s., 2 H) 4.24 (br. s., 2 H) 6.52 (d, *J*=15.86 Hz, 1 H) 7.40 - 7.58 (m, 5 H) 7.61 - 7.84 (m, 7 H) 9.08 (br. s., 2 H) 10.34 (s, 1 H) 10.76-10.87 (m, 1 H); ^{13}C NMR (126 MHz, methanol-d4) δ ppm 197.1, 174.3, 166.0, 144.7, 142.6, 140.5, 138.4, 137.8, 133.9, 133.7, 132.5, 131.8, 131.6, 131.2, 130.0, 129.7, 120.2, 84.2, 70.5, 52.2, 36.8, 33.3, 26.8, 25.6, 18.8; Melting point: 153-155 °C; HPLC (12 min) R_t 7.06 min UV 254nm >90% purity; LRMS *m/z* 510.6 $[M+H]^+$; HRMS calculated for $[M+H^+, C_{31}H_{32}N_3O_4^+]$ requires *m/z* 510.2393. Found 510.2407.

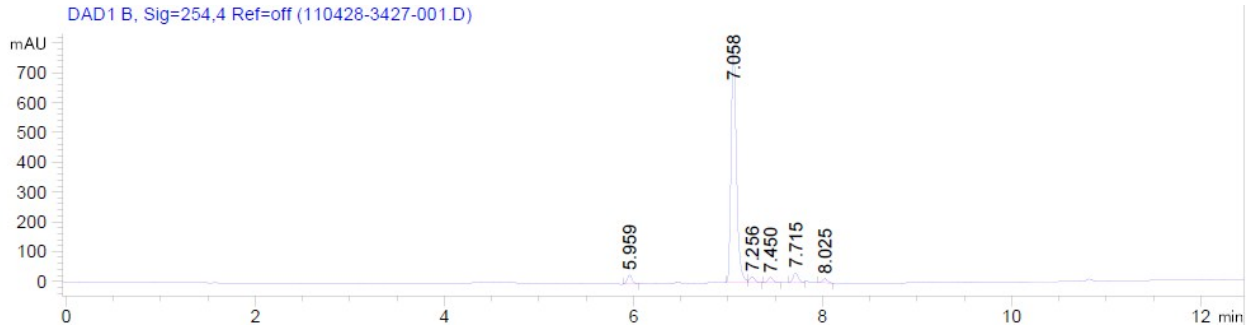
^{1}H NMR (**PHP2**):



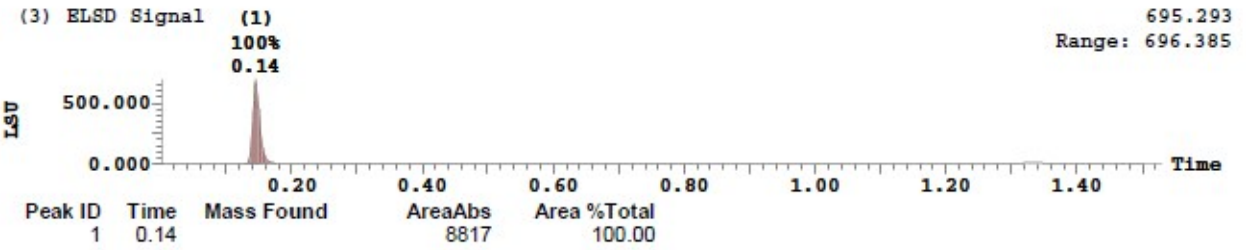
^{13}C NMR (**PHP2**):



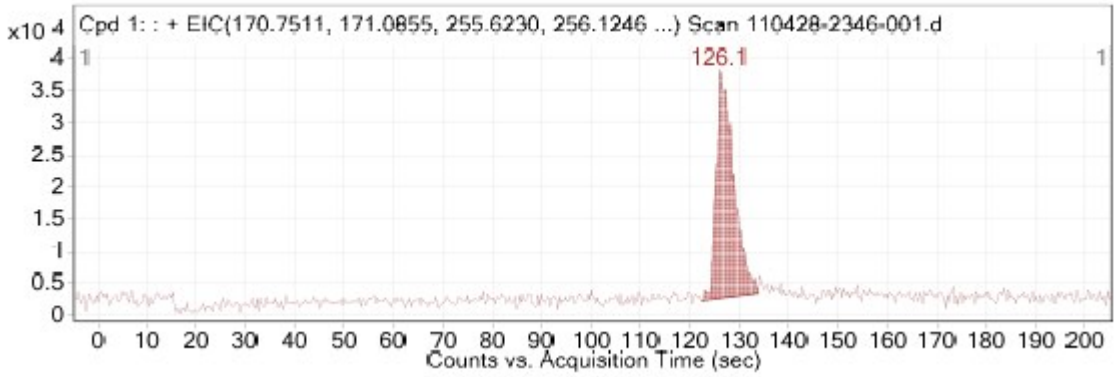
HPLC UV 254nm (**PHP2**): (>90% purity)

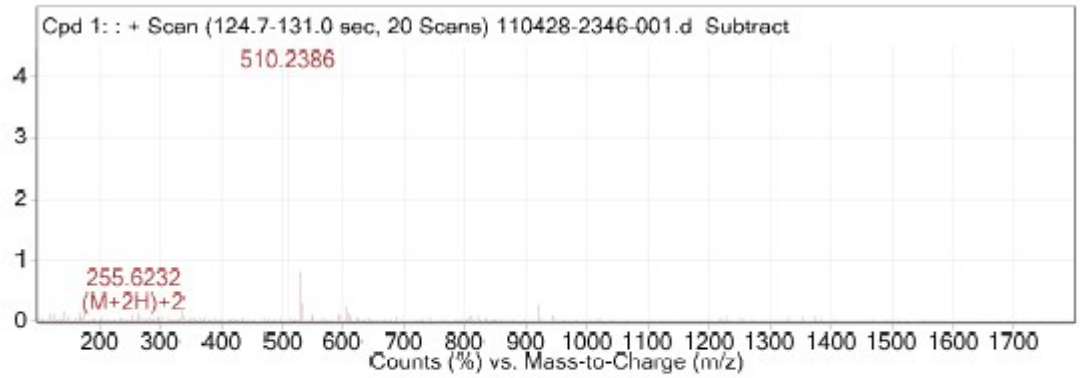


HPLC ELSD (**PHP2**): (>95% purity)



HR-LCMS (**PHP2**): (>95% purity)

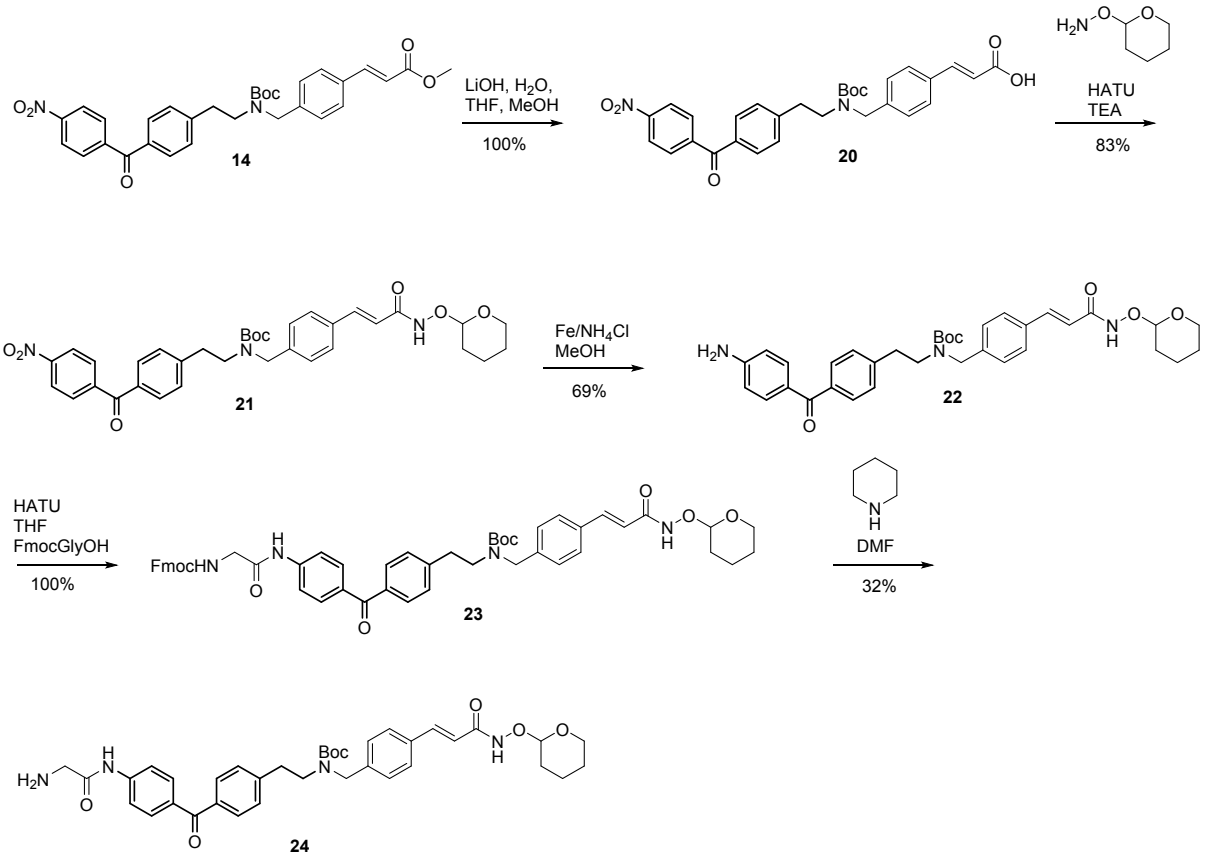




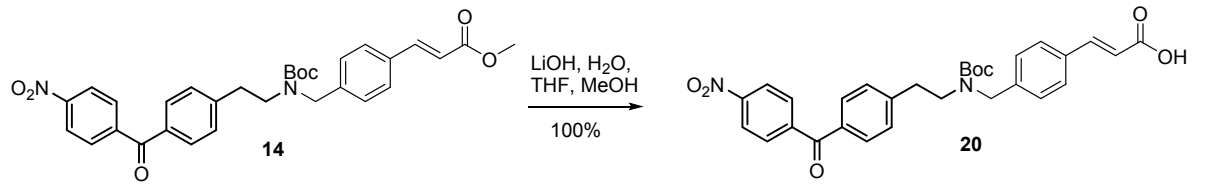
MS Spectrum Peak List

m/z	*Calc m/z*	Diff(ppm)	z	Abund	Formula	Ion
255.6232	255.623	-0.73	2	332	C31H33N3O4	(M+2H)+2
256.1241	256.1246	2.13	2	174.2	C31H33N3O4	(M+2H)+2
510.2386	510.2387	0.27		15758.3	C31H32N3O4	(M+H)+
510.2386			1	15758.3		
511.242	511.2419	-0.1	1	5322.7	C31H32N3O4	(M+H)+
512.245	512.2449	-0.31	1	1226	C31H32N3O4	(M+H)+
513.2456	513.2476	3.96	1	172.4	C31H32N3O4	(M+H)+

Synthesis of *tert*-butyl (*E*)-(4-(4-(2-aminoacetamido)benzoyl)phenethyl)(4-(3-oxo-3-(((tetrahydro-2H-pyran-2-yl)oxy)amino)prop-1-en-1-yl)benzyl)carbamate (24) intermediate for biotin probes

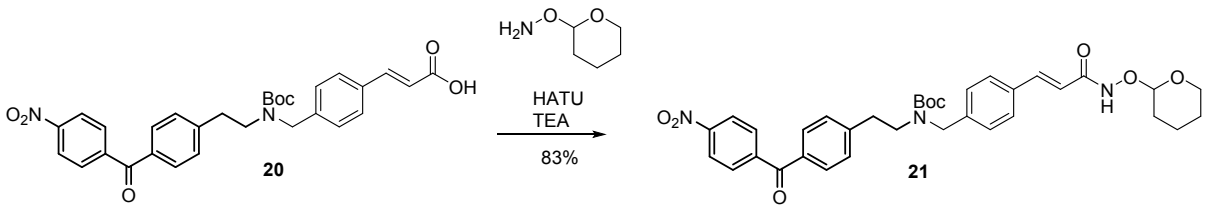


Synthesis of (*E*)-3-(4-(((tert-butoxycarbonyl)(4-(4-nitrobenzoyl)phenethyl)amino)methyl)phenyl)acrylic acid (20)



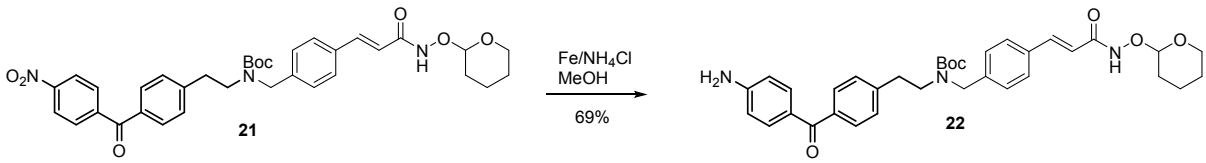
To a stirred solution of **14** (200 mg, 0.37 mmol) in a mixture of THF, MeOH and H_2O was added $LiOH.H_2O$ (2:1:1, 4 mL) and stirred at ambient temperature until all starting material was completely consumed. Most of the solvent was removed in vacuo and the remainder acidified with 10% critic acid to pH<4, then partitioned between H_2O and DCM. The collected organic layer was dried, concentrated to afford compound **20** as yellow oil (196 mg, 100%), which was pure enough for the next step.

Synthesis of *tert*-butyl (*E*)-(4-(4-nitrobenzoyl)phenethyl)(4-(3-oxo-3-(((tetrahydro-2*H*-pyran-2-yl)oxy)amino)prop-1-en-1-yl)benzyl)carbamate (21)



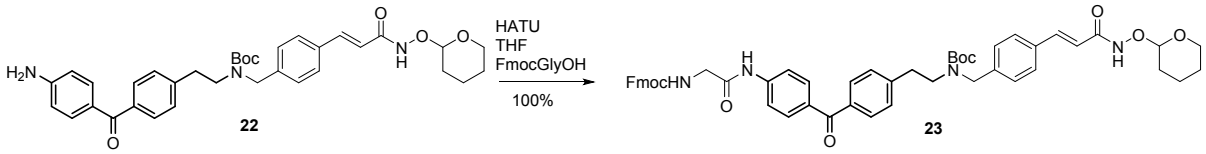
To a stirred solution of compound **20** (2.1 g, 3.96 mmol) in THF (50 mL) was added HATU (1.5 g, 3.96 mmol) and stirred at room temperature for 15 minutes. A solution of O-(tetrahydro-2H-pyran-2-yl)hydroxylamine (456 mg, 3.96 mmol) and TEA (800 mg, 7.9 mmol) in THF (2 mL) was added and stirred till starting material was consumed (ca. 2 hours). Most of the solvent was removed in vacuo and the remainder partitioned between H_2O and DCM. The collected organic layer was dried, concentrated to afford the crude product, which was further purified by column chromatography on silica gel (10-20%, ethyl acetate in PE) to give pure desired compound **21** as oil (2.0 g, 83%). If necessary, the product was further purified by Prep.HPLC(Column: DIKMA Diamonsil(2) C18 200*20mm*5um Mobile phase: from 68% MeCN in water (Base-Ammonia(pH 10)) to 88% MeCN in water (Base-Ammonia(pH 10)); Wavelength: 220 nm) to give a white solid.

Synthesis of *tert*-butyl (*E*)-(4-(4-aminobenzoyl)phenethyl)(4-(3-oxo-3-(((tetrahydro-2*H*-pyran-2-yl)oxy)amino)prop-1-en-1-yl)benzyl)carbamate (22)



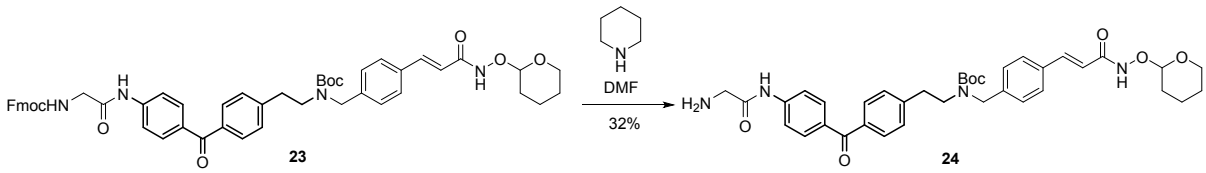
To a stirred solution of **21** (607 mg, 0.97 mmol) in methanol (12 mL) was added Iron powder (189 mg, 3.37 mmol) and ammonium chloride (254 mg, 4.8 mmol) in water (1 mL). The reaction mixture was refluxed at 100 °C for 2 hours. The reaction mixture was cooled to room temperature and filtered through a pad of celite. The filtrate was concentrated under reduced pressure to remove most of the solvent, and then partitioned between H_2O (50 mL) and DCM (2 × 50 mL). The collected organic layer was dried, concentrated to afford crude product, which was purified by column chromatography (50-60% PE in ethyl acetate) to obtain **22** as a yellowish solid (400 mg, 69%). If necessary, the product was further purified by Prep.HPLC(Column: Phenomenex Gemini C18 250*21.2mm*8um Mobile phase: from 50% MeCN in water (Base-Ammonia(pH 10)) to 70% MeCN in water (Base-Ammonia(pH 10)); Wavelength: 220 nm) to give a white solid.

Synthesis of *tert*-butyl (*E*)-(4-(4-(2-((((9*H*-fluoren-9-yl)methoxy)carbonyl)amino)acetamido)benzoyl)phenethyl)(4-(3-oxo-3-(((tetrahydro-2*H*-pyran-2-yl)oxy)amino)prop-1-en-1-yl)benzyl)carbamate (23)



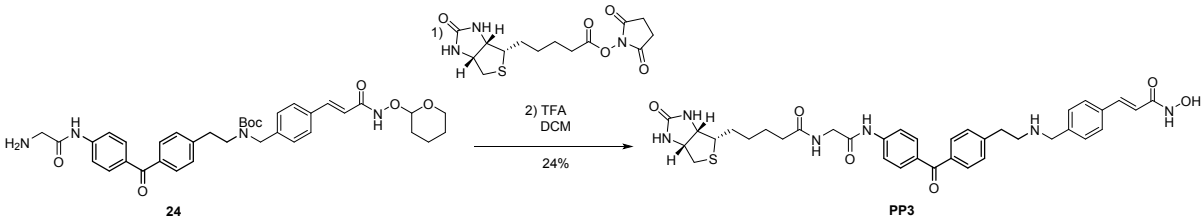
To a stirred solution of FmocGlyOH (2.7 g, 9.18 mmol) in THF (70 mL) was added HATU (3.56 g, 9.3 mmol) and stirred at room temperature for 15 minutes. A solution of compound **22** (1.1 g, 1.83 mmol) and TEA (929 mg, 9.18 mmol) in THF (5 mL) was added and stirred till starting material was consumed (ca. 18 hours). Most of the solvent was removed in vacuo and partitioned between H_2O and DCM. The collected organic layer was dried, concentrated to afford the crude product, which was further purified by column chromatography on silica gel (40-65%, ethyl acetate in PE) to give crude product **23** as oil (1.97 g, 118%). If necessary, the product was further purified by Prep.HPLC(Column: Phenomenex Gemini C18 250*21.2mm*8um Mobile phase: from 68% MeCN in water (Base-Ammonia(pH 10)) to 88% MeCN in water (Base-Ammonia(pH 10)); Wavelength: 220 nm) to give a white solid.

Synthesis of *tert*-butyl (*E*)-(4-(4-(2-aminoacetamido)benzoyl)phenethyl)(4-(3-oxo-3-(((tetrahydro-2*H*-pyran-2-yl)oxy)amino)prop-1-en-1-yl)benzyl)carbamate (24)



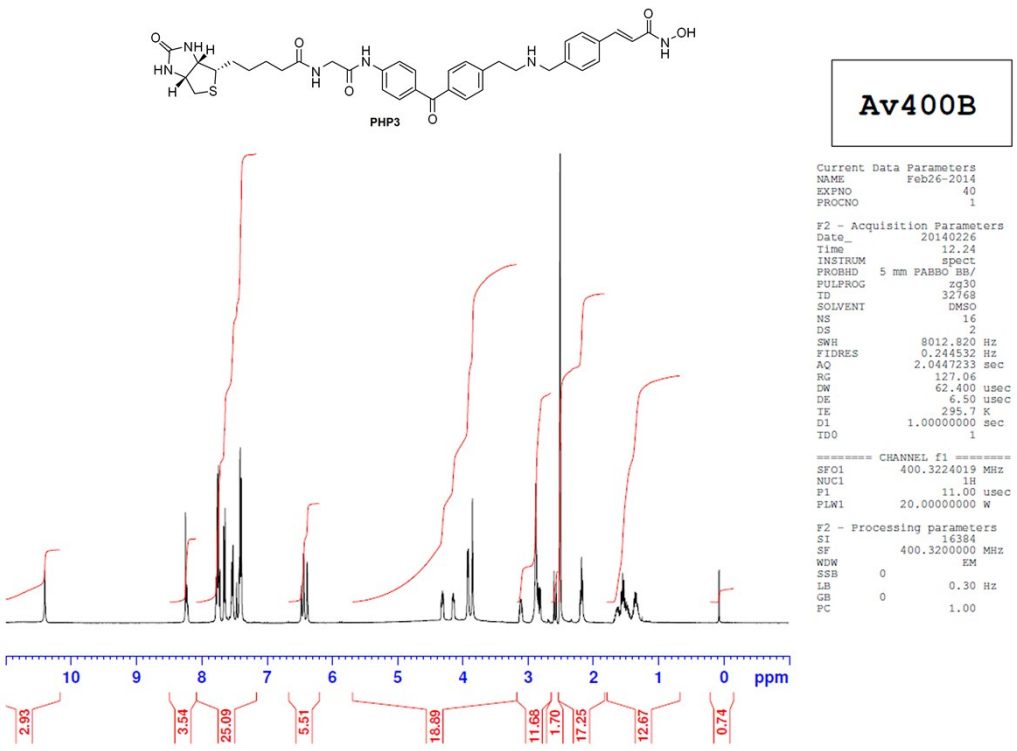
To a stirred solution of **23** (515 mg, 0.58 mmol) in DMF (6 mL) was added piperidine (100 mg, 1.17 mmol) and stirred at room temperature till starting material was consumed (ca. 2 hours). Most of the solvent was removed in vacuo and the remainder partitioned between H_2O and DCM. The collected organic layer was dried, concentrated to afford the crude product, which was purified by Prep.HPLC(Column: Phenomenex Gemini c18 250*21.2mm*8um Mobile phase: from 44% MeCN in water (neu) to 64% MeCN in water (neu); Wavelength: 220 nm) to give **24** (120 mg, 32% yield).

Synthesis of *N*-(2-((4-(4-(2-((4-((*E*)-3-(hydroxyamino)-3-oxoprop-1-en-1-yl)benzyl)amino)ethyl)benzoyl)phenyl)amino)-2-oxoethyl)-5-((3a*S*,4*S*,6a*R*)-2-oxohexahydro-1H-thieno[3,4-d]imidazol-4-yl)pentanamide (PHP3)

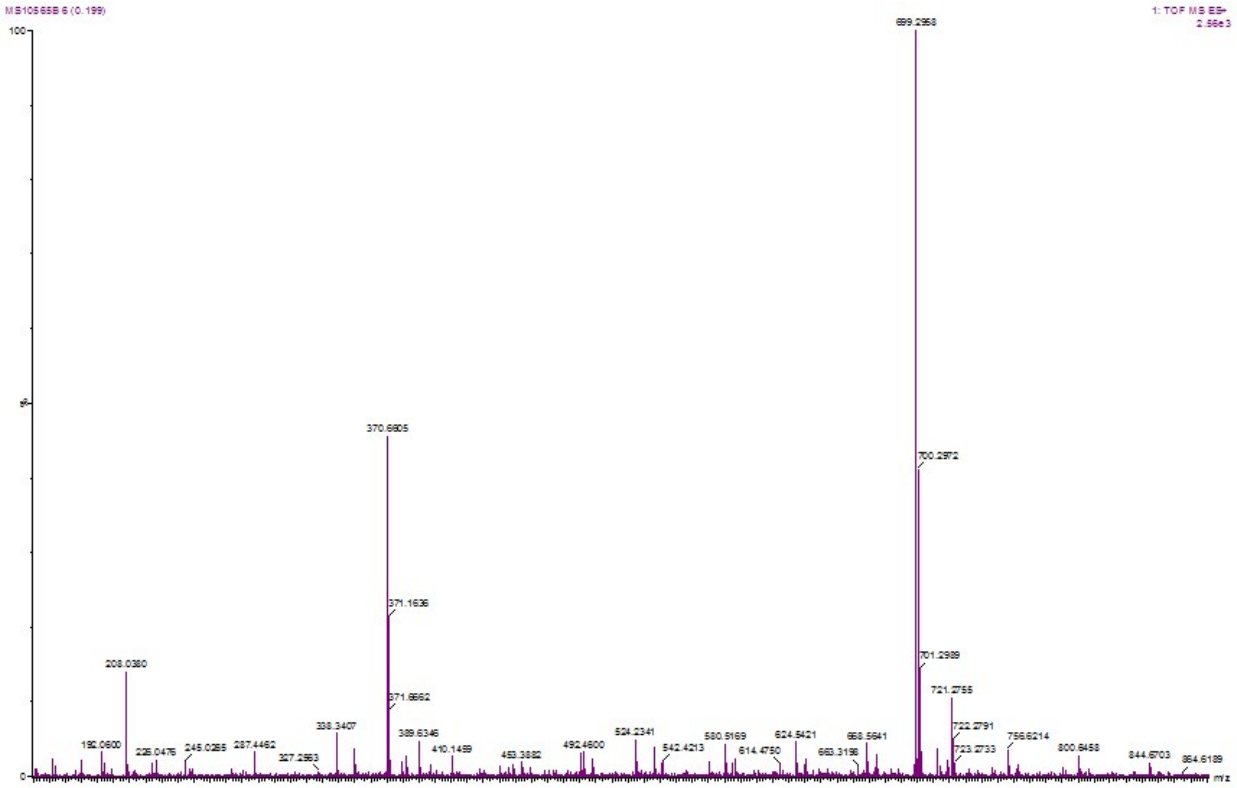


To a solution of **24** (250 mg, 0.38 mmol) in DCM (5 mL) was added NHS-biotin (130 mg, 0.38 mmol) and stirred at ambient temperature until starting material was consumed (ca. 24 hours). TFA (5 mL) and H_2O (1 mL) was added in turn and stirred for another 2 hours. LC-MS showed the reaction was complete. Most of the solvent was removed in vacuo to afford the crude product, which was purified by Prep.HPLC(Column: DIKMA Diamonsil(2) C18 200*20mm*5um Mobile phase: from 10% MeCN in water (0.225%FA) to 30% MeCN in water (0.225%FA); Wavelength: 220 nm) to give **PHP3** (63.2 mg, 24%). ^{1}H NMR (400 MHz, DMSO-d6) δ ppm 1.25-1.70 (m, 6H), 2.11-2.24 (m, 2H), 2.43-2.53 (m, 6H), 2.54-2.62 (m, 1H), 2.78-2.96 (m, 4H), 3.07-3.15(m, 1H), 3.78-3.95 (m, 4H), 4.10-4.18 (m, 1H), 4.26-4.37 (m, 1H), 6.32-6.52 (m, 2H), 7.32-7.83 (m, 12H), 8.18-8.29 (m, 2H), 10.39 (s, 1H); HRMS calculated for [M+H$^+$, $C_{37}H_{43}N_6O_6S^+$] requires *m/z* 699.2965. Found 699.2958.

^{1}H NMR (**PHP3**):



HRMS (**PHP3**):

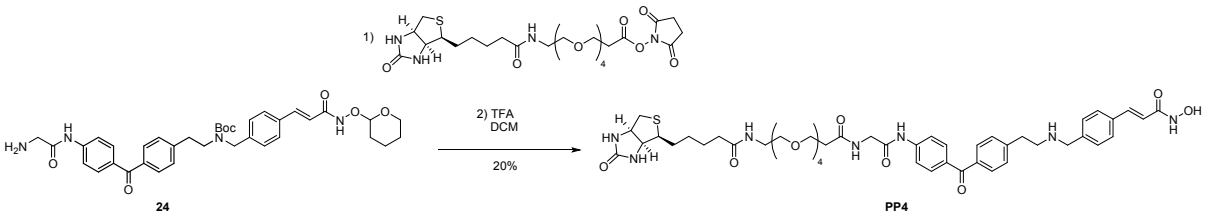


Elements Used:

C: 37-37 H: 0-200 N: 0-10 O: 0-10 Na: 0-1 S: 1-1

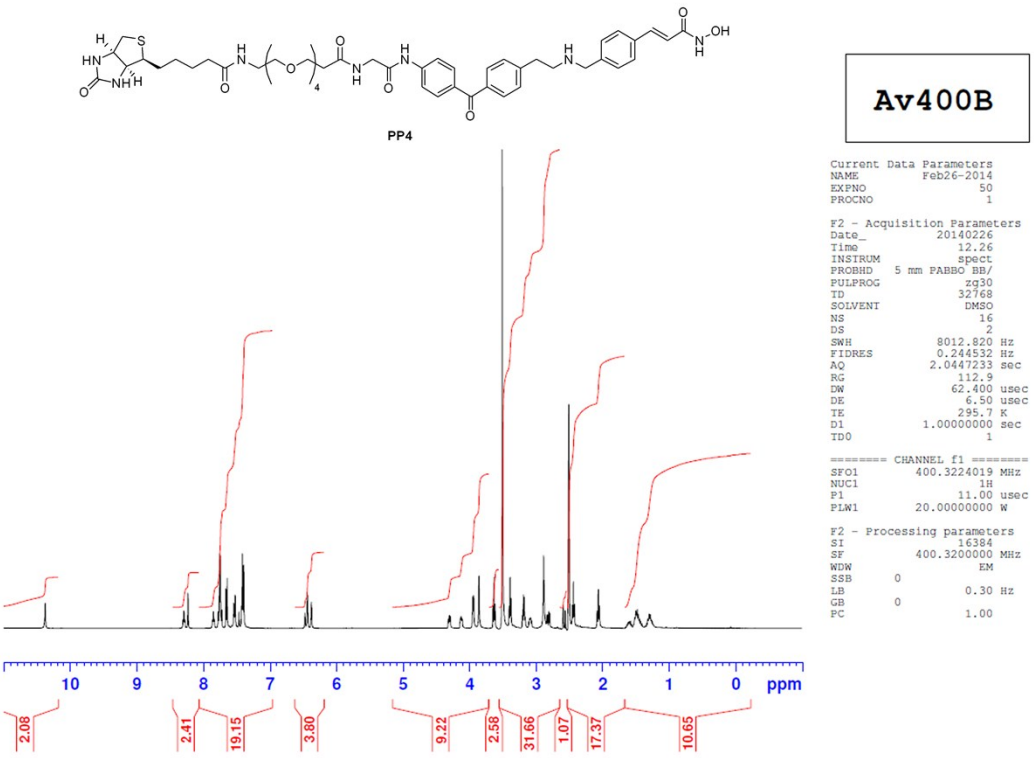
Minimum:				-1.5			
Maximum:		5.0	10.0	50.0			
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Norm)	Formula
699.2958	699.2965	-0.7	-1.0	19.5	78.2	0.0	C37 H43 N6 O6 S

Synthesis of *N*-(2-((4-(4-(2-((4-((*E*)-3-(hydroxyamino)-3-oxoprop-1-en-1-yl)benzyl)amino)ethyl)benzoyl)phenyl)amino)-2-oxoethyl)-1-(5-((3a*S*,4*S*,6a*R*)-2-oxohexahydro-1H-thieno[3,4-d]imidazol-4-yl)pentanamido)-3,6,9,12-tetraoxapentadecan-15-amide (PHP4)

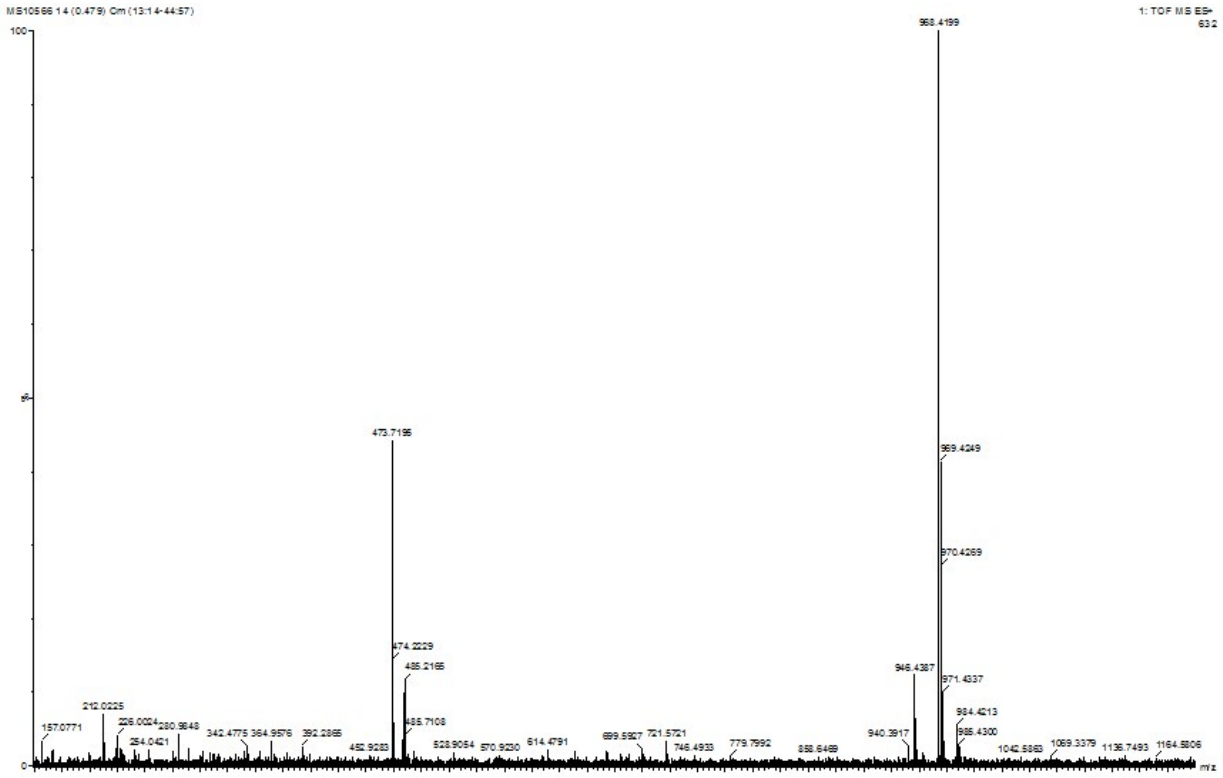


To a stirred solution of **24** (240 mg, 0.36 mmol) in DCM (5 mL) was added NHS-PEG_4-biotin (196 mg, 0.33 mmol) and stirred at room temperature until starting material was consumed (ca. 24 hours). TFA (5 mL) and H_2O (1mL) was added in turn and stirred for another 2 hours. LC-MS show the reaction was complete. Most of the solvent was removed in vacuo to afford the crude product, which was purified by Prep.HPLC(Column: DIKMA Diamonsil(2) C18 200*20mm*5um Mobile phase: from 10% MeCN in water (0.225%FA) to 30% MeCN in water (0.225%FA); Wavelength: 220 nm) to give **PHP4** (69.1 mg, 20%). ^{1}H NMR (400 MHz, DMSO-d6) δ ppm 1.19-1.70 (m, 6H), 2.00-2.11 (m, 2H), 2.39-2.52 (m, 8H), 2.52-2.61 (m, 1H), 2.76-2.96 (m, 4H), 3.03-3.13 (m, 1H), 3.13-3.22 (m, 2H), 3.32-3.42 (m, 2H), 3.43-3.56 (m, 12H), 3.56-3.68 (m, 2H), 3.81-3.89 (m, 2H), 3.90-3.98 (m, 2H), 4.09-4.17 (m, 1H), 4.27-4.34 (m, 1H), 6.34-6.50 (m, 2H), 7.32-7.60 (m, 6H), 7.60-7.69 (m, 2H), 7.69-7.81 (m, 3H), 7.81-7.90 (m, 1H), 8.19-8.35 (m, 2H), 10.39 (s, 1H); HRMS calculated for [M+Na^+, $C_{48}H_{63}N_7O_{11}SNa^+$] requires *m/z* 968.4204. Found 968.4199.

^{1}H NMR (**PHP4**):



HRMS (**PHP4**):

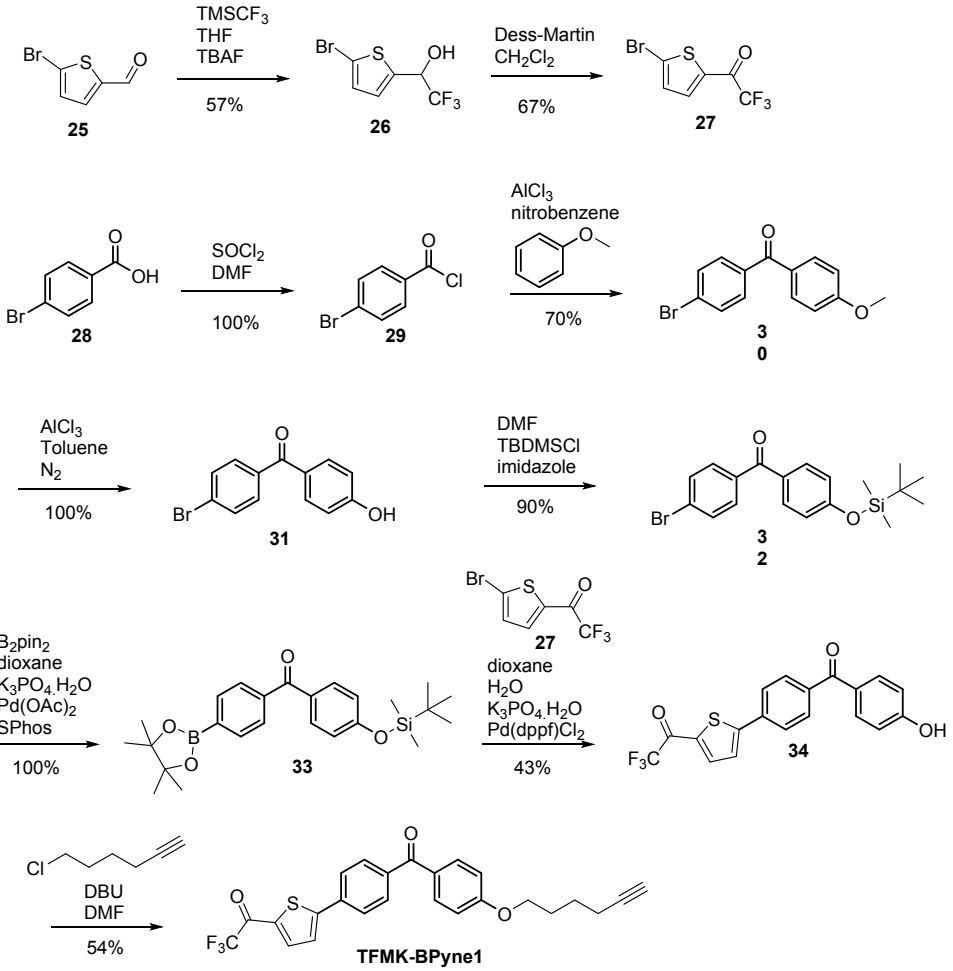


Elements Used:

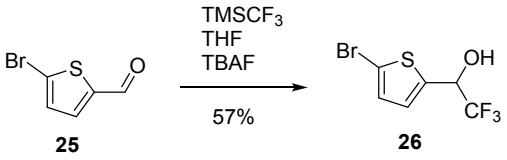
C: 48-48 H: 0-200 N: 0-15 O: 0-15 Na: 0-1 S: 1-1

Minimum:				-1.5			
Maximum:		5.0	10.0	50.0			
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Norm)	Formula
968.4199	968.4204	-0.5	-0.5	20.5	106.6	0.0	C48 H63 N7 O11 Na S
	968.4102	9.7	10.0	29.5	110.4	3.8	C48 H54 N15 O6 S

Synthesis of 2,2,2-trifluoro-1-(5-(4-(4-(hex-5-yn-1-yloxy)benzoyl)phenyl)thiophen-2-yl)ethan-1-one (TFMK-BPyne1)

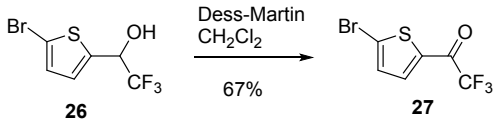


Synthesis of 1-(5-bromothiophen-2-yl)-2,2,2-trifluoroethan-1-ol (26)



To a solution of **25** (4.2 g, 20 mmol) and $TMSCF_3$ (3.4 g, 24 mmol) in THF (20 mL) was added TBAF (1M in THF, 20 mL, 20 mmol) dropwise at 0 ~ 5 °C. The solution was stirred at ambient temperature for 2 days. The reaction mixture was quenched with 6 M of a.q HCl (20 mL) at 0 ~ 5 °C, then extracted with EtOAc (3 × 100 mL). The combined organic layers were dried over $MgSO_4$ and concentrated in vacuo. The residue was purified by silica column chromatography (PE/EtOAc = 100/1 ~ 10/1) to give compound **26** as a yellow oil (3.0 g, 57%).

Synthesis of 1-(5-bromothiophen-2-yl)-2,2,2-trifluoroethan-1-one (27)

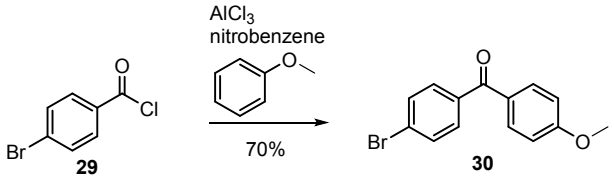


To a cooled solution of **26** (6.0 g, 23 mmol) in DCM (80 mL) was added Dess-Martin (9.7 g, 23 mmol) portion wise, then the solution was stirred at ambient temperature overnight. TLC (PE/EtOAc = 8/1) showed the starting material was consumed completely. To the reaction solution was added a.q Na_2SO_3 (50 mL) and a.q Na_2CO_3 (50 mL), then filtered. The filtrate was extracted with DCM (2 × 100 mL). The combined organic layers were washed with brine (3 × 100 mL), dried over Na_2SO_4, filtered and concentrated in vacuo. The residue was purified through column chromatography (Pe/EtOAc = 1/0 ~ 100/1) to give **27** as a yellow oil (4.0 g, 67%). ^{1}H NMR (400 MHz, $CDCl_3$) δ ppm 7.22 (d, 1H), 7.70 (d, 1H).

Synthesis of 4-bromobenzoyl chloride (29)

To the mixture of **28** (20.1 g, 0.1 mol) in $SOCl_2$ (50 mL) was added DMF (3 drops). The solution heated at reflux for 2 hours. The solution was concentrated in high vacuum to give **29** (22 g, 100%), which was used for the next step directly.

Synthesis of (4-bromophenyl)(4-methoxyphenyl)methanone (30)

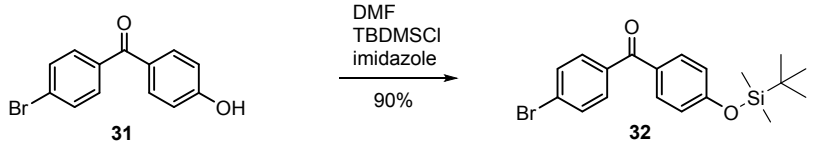


To nitrobenzene (50 mL) was added $AlCl_3$ (14.6 g, 0.11 mol) portionwise at 0 ~ 5 °C, then a solution of **29** (22 g, 0.1 mol) in nitrobenzene (20 mL) was added below 8 °C. The solution was stirred for 10 minutes and anisole (10.3 g, 0.095 mol) was added at < 5 °C. The mixture was stirred at ambient temperature overnight. The reaction solution was poured into ice-water (100 mL) then extracted with DCM (2 × 200 mL). The combined organic layers were washed with brine (2 × 100 mL), dried over Na_2SO_4, filtered and concentrated in vacuo to remove DCM. To the residue was added hexane (500 mL). A white solid was formed. The solid was filtered and dried in vacuo to give **30** (20 g, 70%) as a white solid. ^{1}H NMR (400 MHz, $CDCl_3$) δ ppm 3.90 (s, 3H), 6.96 (d, 2H), 7.63 (m, 4H), 7.79 (d, 2H).

Synthesis of (4-bromophenyl)(4-hydroxyphenyl)methanone (31)

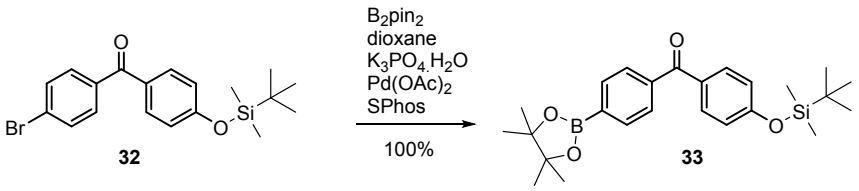
A slurry of **30** (800 mg, 2.75 mmol) in toluene (10 mL) was treated with anhydrous $AlCl_3$ (915 mg, 6.87 mmol) and stirred at reflux under a blanket of nitrogen (slurry immediately became a bright yellow solution upon addition of $AlCl_3$ - slight exotherm). After 2 hours, LCMS indicated reaction was complete. The dark brown mixture was allowed to cool to room temperature and stand overnight. The reaction mixture was poured into 3M HCl (30 mL) and extracted with ethyl acetate (3 × 60 mL). The combined organics were washed with saturated brine (1 × 20 mL), dried ($MgSO_4$) and concentrated under reduced pressure to afford 800 mg of **31** as a reddish-brown solid. Spectral data consistent with desired product in good purity and literature values. Used without further purification. ^{1}H NMR (400 MHz, DMSO-d6) δ ppm 6.88 (d, *J* = 8.80 Hz, 2H), 7.59 (d, *J* = 8.41 Hz, 2H), 7.64 (d, *J* = 8.80 Hz, 2H), 7.70 - 7.75 (m, 2 H), 10.46 (s, 1 H).

Synthesis of (4-bromophenyl)(4-((*tert*-butyldimethylsilyl)oxy)phenyl)methanone (32)



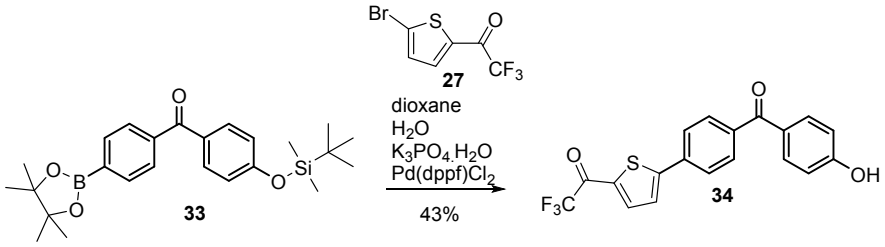
A solution of **31** (2 g crude, 7 mmol theoretical) in DMF (15 mL) was treated with TBDMS-Cl (2.32 g, 15.4 mmol) and imidazole (2.12 g, 30.8 mmol) and the orange solution was stirred at room temperature overnight. LCMS after 22 hours indicated reaction complete: no starting material (0.83 minutes), peak for desired product (1.24 minutes). The orange solution was concentrated under reduced pressure, and the oily residue was diluted with ethyl acetate (250 mL) and washed with water (2 × 50 mL) and saturated brine (1 × 50 mL). The organic layer was dried ($MgSO_4$) and concentrated under reduced pressure to afford 3.15 g of an orange oil. The crude oil was purified using medium-pressure chromatography (40 g silica, 0-11% ethyl acetate/heptane, 11 column volumes). Product fractions (tubes 6-18) were combined and concentrated under reduced pressure to afford **32** (2.47 g, 90%) as an orange oil. More (impure) desired product was found in the other tubes (tubes 2-5), but was not collected. ^{1}H NMR (400 MHz, $CDCl_3$) δ ppm 0.15 (s, 6H), 0.90 (s, 9H), 6.80 (d, *J* = 8.59 Hz, 2H), 7.52 (d, *J* = 2.73 Hz, 4H), 7.63 (d, *J* = 8.59 Hz, 2H).

Synthesis of (4-((*tert*-butyldimethylsilyl)oxy)phenyl)(4-(4,4,5,5-tetramethyl-1,3,2-dioxaborolan-2-yl)phenyl)methanone (33)



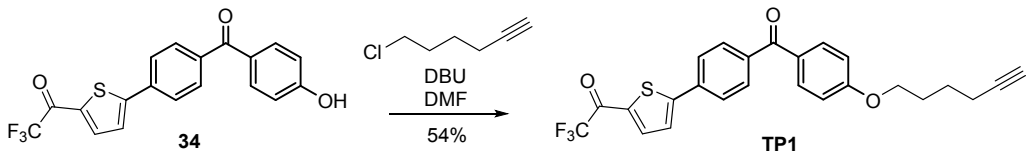
A solution of **32** (1.36 g, 3.48 mmol) and B_2pin_2 (981 mg, 3.82 mmol) in dioxane (40 mL) was treated with K_3PO_4-H_2O (2.53 g, 10.4 mmol), $Pd(OAc)_2$ (40 mg, 0.177 mmol) and SPhos (116 mg, 0.278 mmol) and stirred at 60 °C overnight. LCMS (new peak at 1.30 minutes) after 16 hours indicated reaction was complete (SM peak at 1.24 minutes consumed). The mixture was filtered through celite and concentrated under reduced pressure to afford **33** (1.6 g, 100%) as a brown oil, which was used in the next step directly without further purification. LCMS: ES^+ $(M+H)^+$ 439.3 (100% ELSD) 1.3 minutes (1.5 minutes run-time).

Synthesis of 2,2,2-trifluoro-1-(5-(4-(4-hydroxybenzoyl)phenyl)thiophen-2-yl)ethan-1-one (34)



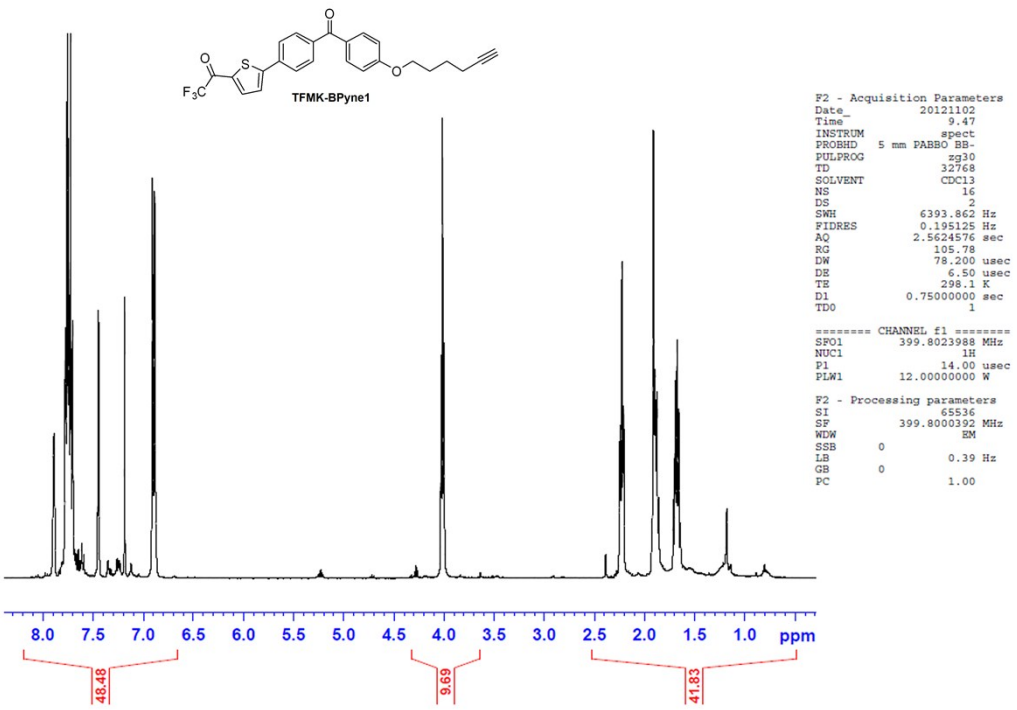
A solution of **33** (assumed 1524 mg, 3.48 mmol) and **27** (900 mg, 3.48 mmol) in pre-sparged dioxane (30 mL) and water (6 mL) was treated with K_3PO_4-H_2O (1.69 g, 6.95 mmol) and $Pd(dppf)Cl_2$ (255 mg, 0.348 mmol) and stirred at 60 °C. LCMS after 3 hours showed starting material (1.3 minutes) was consumed, desired product (0.96 minutes) formed. The mixture was cooled to room temperature and allowed to stand over the next 2 nights. The reaction was filtered through celite. The filtrate was diluted with ethyl acetate (250 mL) and washed with water (1 × 100 mL) and saturated brine (1 × 100 mL). The organic layer was dried ($MgSO_4$) and concentrated under reduced pressure to afford a brown tar that was dissolved in chloroform, loaded onto a 25 g pre-column, and purified using medium-pressure chromatography (120 g silica, 15-30% EtOAc/heptane, 11 column volumes). Product fractions (tubes 46-65) were combined and concentrated to afford an orange solid, which was dissolved in a small amount of hot ethyl acetate and treated with heptane to induce precipitation. The mixture was allowed to cool and then filtered, and the solid was washed with heptane and dried under reduced pressure to afford **34** as an orange solid (376 mg, 29%). Spectral data consistent with desired product (plus a small impurity, 8% by NMR). The filtrate was concentrated under reduced pressure to afford 314 mg of a red-orange solid. The filtrate was dissolved in a small amount of EtOAc/Et_2O at 60 °C. Heptane was added slowly until the mixture became just slightly hazy. The mixture was stirred at 60 °C for 1 hour then allowed to cool slowly to room temperature. The suspension was filtered and washed with heptane then dried under reduced pressure to afford a second crop of **34** as an orange solid (183 mg, 14%). The second filtrate was set aside. Total yield = 43%.

Synthesis of 2,2,2-trifluoro-1-(5-(4-(4-(hex-5-yn-1-yloxy)benzoyl)phenyl)thiophen-2-yl)ethan-1-one (TFMK-BPyne1)

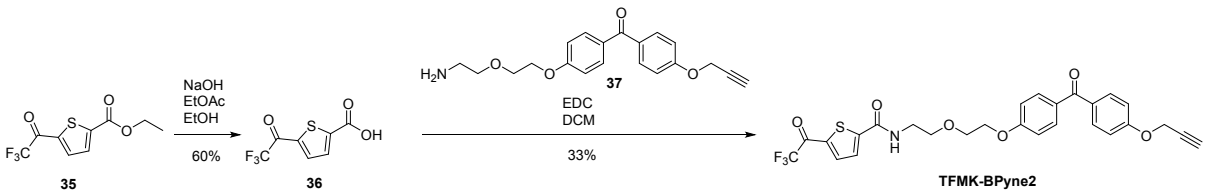


A room temperature solution of **34** (213 mg, 0.567 mmol) in DMF (3 mL) was treated with DBU (100 µL, 0.68 mmol) and 6-chloro-1-hexyne (210 µL, 1.7 mmol). After stirring at room temperature for 1 hour, the mixture was heated to 80 °C overnight. LCMS after 20 hours showed no peak for starting material at 0.96 minutes, large peak for desired product at 1.14 minutes. The mixture was cooled to room temperature, diluted with ethyl acetate, and washed with water (1×) and saturated brine (2×). The organic layer was dried ($MgSO_4$) and concentrated under reduced pressure to afford 230 mg of a yellow-brown solid. The crude was purified using medium-pressure chromatography (12 g silica, 0-25% EtOAc/heptane, 35 column volumes). Product did not emerge as a clean peak. Two fractions were collected, with spectral data indicating both contained primarily desired product: 92 mg of **TFMK-BPyne1** as a bright yellow solid, and a further 47 mg as a "dirty" yellow solid. Total yield = 54%. ^{1}H NMR (400 MHz, $CDCl_3$) δ ppm 1.77 (m, 2H), 1.98 (m, 3H), 2.31 (m, 2H), 4.10 (t, J = 6.24 Hz, 2H), 6.98 (d, J = 8.59 Hz, 2H), 7.54 (d, J = 4.29 Hz, 1H), 7.83 (m, 6H), 7.98 (d, J = 2.34 Hz, 1H); HPLC (1.5 min) R_t 1.15 min ELSD >95% purity; LRMS *m/z* 457.1 $[M+H]^+$.

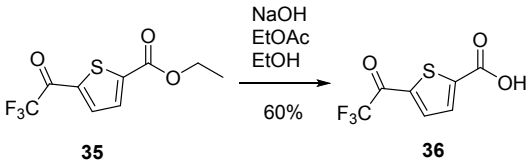
^{1}H NMR (**TFMK-BPyne1**):



Synthesis of N-(2-(2-(4-(4-(prop-2-yn-1-yloxy)benzoyl)phenoxy)ethoxy)ethyl)-5-(2,2,2-trifluoroacetyl)thiophene-2-carboxamide (TFMK-BPyne2)

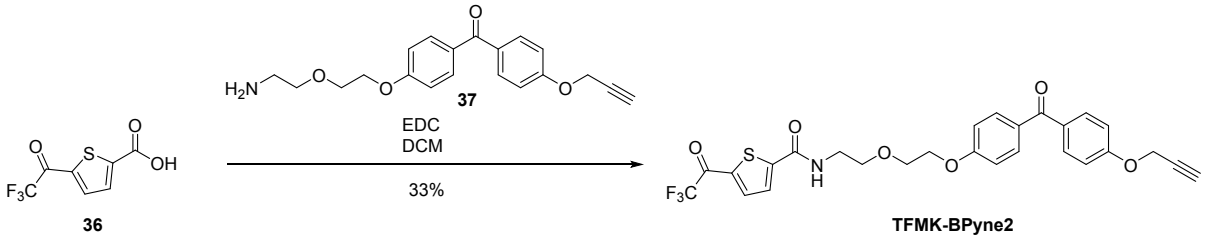


Synthesis of 5-(2,2,2-trifluoroacetyl)thiophene-2-carboxylic acid (36)



Ethyl 5-(2,2,2-trifluoroacetyl)thiophene-2-carboxylate (**35**) (500 mg, 1.98 mmol) was dissolved in ethanol (20 mL). The solution was stirred and sodium hydroxide (2M, 2eq, 2 mL) was added. The reaction was heated to 40 °C for 40 hours. Citric acid (10%) and ethyl acetate were added until the precipitate dissolved. The phases were separated and the aqueaous phase extracted with EtOAc. The combined organic phases were washed with brine (2 × 20 mL) the solution was dried ($MgSO_4$) and evaporated to dryness. Product was purified by silica column chromatography in hexane:EtOAc 4:1 until the remaining starting material had eluted then moved to 100% EtOAC to give product as a yellow solid (265 mg, 60%).

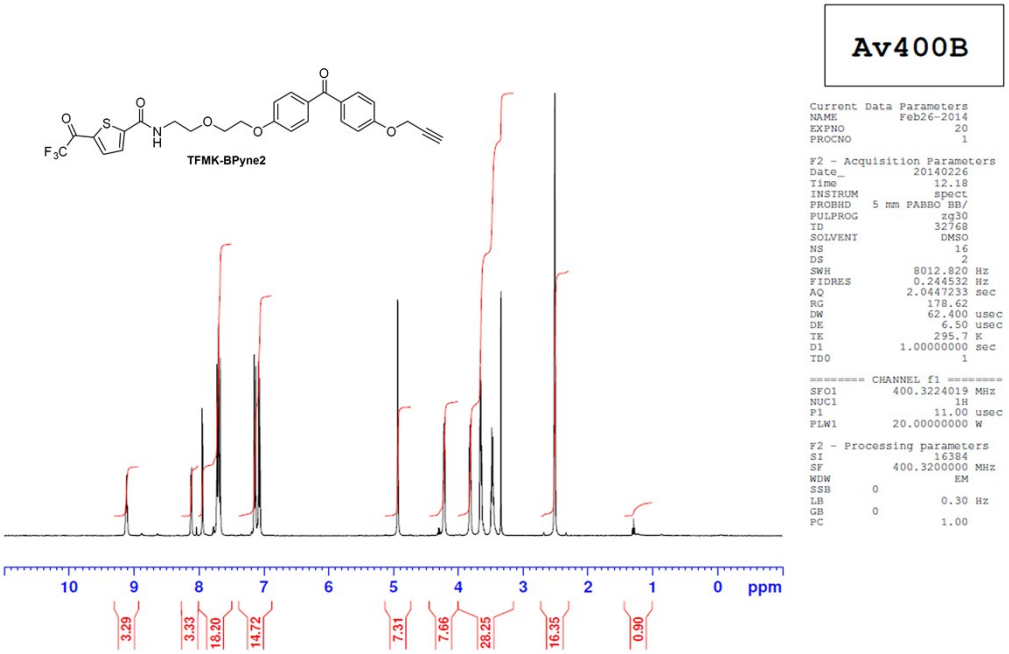
Synthesis of *N*-(2-(2-(4-(4-(prop-2-yn-1-yloxy)benzoyl)phenoxy)ethoxy)ethyl)-5-(2,2,2-trifluoroacetyl)thiophene-2-carboxamide (TFMK-BPyne2)



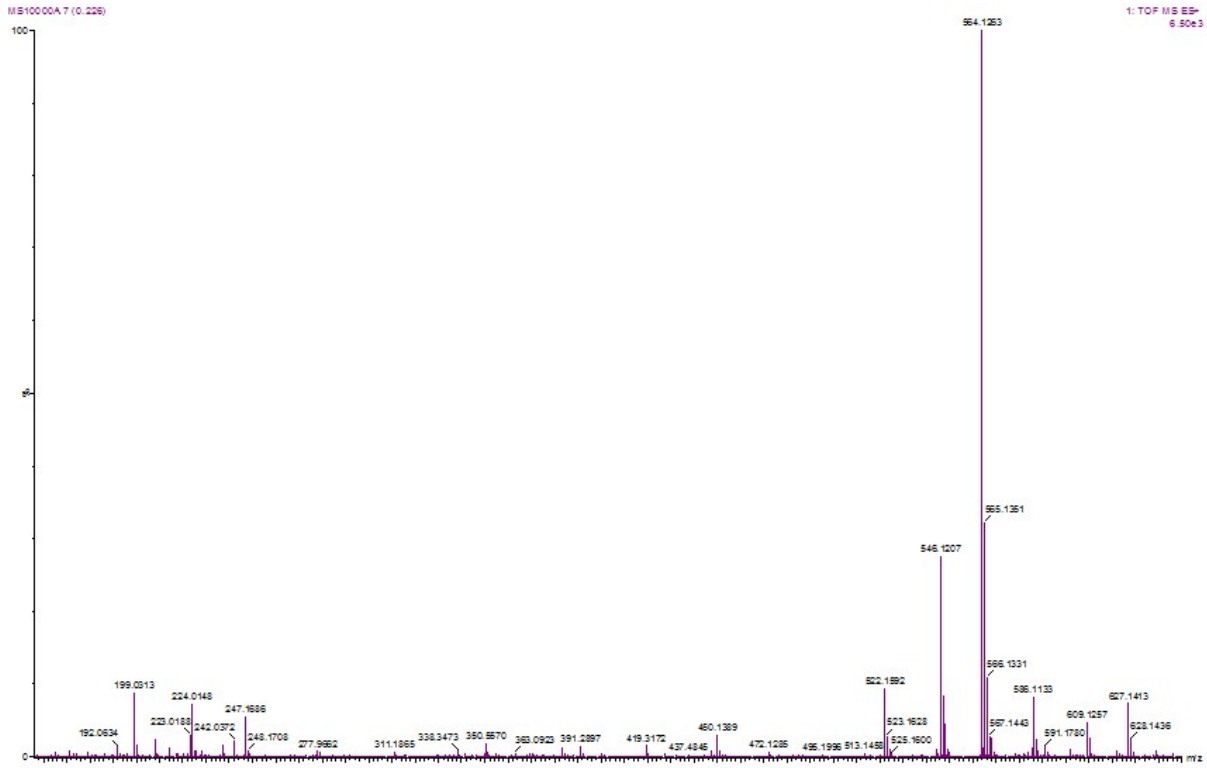
To a stirred solution of carboxylic acid (50 mg, 0.22 mmol) in dichloromethane (5 mL) was added polymer bound EDC (800 mg, >2eq). After 30 minutes a solution of amine **37** (68 mg, 0.2 mmol) in dichloromethane (5 mL) was added and stirred for a further 16 hours. The reaction was filtered then evaporated to dryness to give a pale yellow solid (44 mg). The product was purified by silica column chromatography starting in hexane:EtOAc 1:1 and moving to 2:3 to give the product **TFMK-BPyne2** as an off-white solid (36 mg, 33%). ^{1}H NMR (400 MHz, DMSO-d6) δ ppm 3.39-3.54 (m, 2H), 3.56-3.72 (m, 3H), 3.73-3.89 (m, 2H), 4.18-4.28 (m, 2H), 4.89-5.01 (m, 2H), 7.00-7.20 (m, 4H), 7.61-7.78

(m, 4H), 7.91-8.01 (m, 1H), 8.04-8.15 (m, 1H), 9.04-9.19 (m, 1H); HRMS calculated for [M+H$^+$, $C_{27}H_{23}NO_6SF_3^+$] requires *m/z* 546.1198. Found 546.1207.

^{1}H NMR (**TFMK-BPyne2**):



HRMS (**TFMK-BPyne2**):

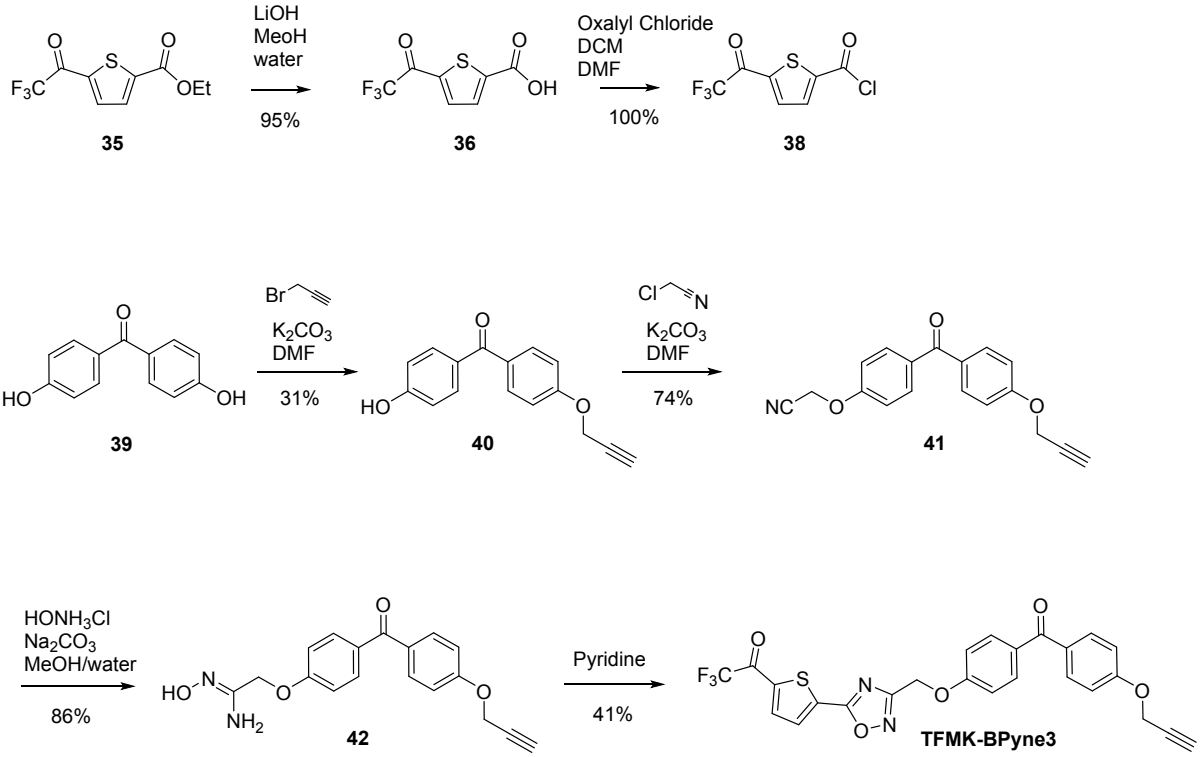


Elements Used:

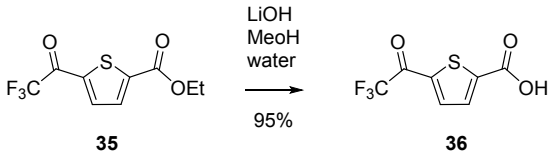
C: 27-27 H: 0-200 N: 0-10 O: 0-10 Na: 0-1 S: 1-1 F: 3-3

Minimum:				-1.5			
Maximum:		5.0	10.0	50.0			
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Norm)	Formula
546.1207	546.1198	0.9	1.6	15.5	99.0	0.0	C27 H23 N O6 S F3

Synthesis of 2,2,2-trifluoro-1-(5-(3-((4-(4-(prop-2-yn-1-yloxy)benzoyl)phenoxy)methyl)-1,2,4-oxadiazol-5-yl)thiophen-2-yl)ethanone (TFMK-BPyne3)

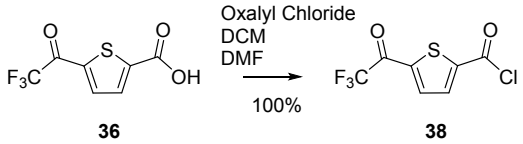


Synthesis of 5-(2,2,2-trifluoroacetyl)thiophene-2-carboxylic acid (36)



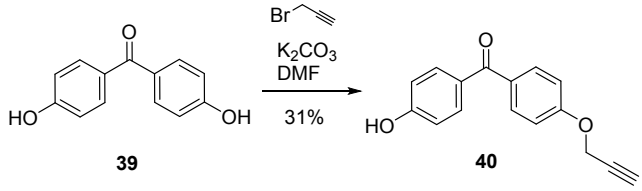
Ethyl 5-(2,2,2-trifluoroacetyl)thiophene-2-carboxylate (**35**) (4.0 g, 15.860 mmol) was dissolved in methanol (40 mL) and water (40 mL). Lithium hydroxide (1.33 g, 31.72 mmol) was added and the mixture was stirred at room temperature for 18 hours. Methanol was removed by rotary evaporation and the aqueous was acidified by the addition of aqueous HCl (2M) and then extracted with ethyl acetate (x4). The combined organics were dried (Na_2SO_4) and solvents removed to give **36** as a solid (3.38 g, 95%); ^{1}H NMR (400 MHz, DMSO-d6) δ ppm 7.83 (s, 1H), 8.10 (s, 1H). LCMS (acidic method) MS ES^-= 222.9.

Synthesis of 5-(2,2,2-trifluoroacetyl)thiophene-2-carbonyl chloride (38)



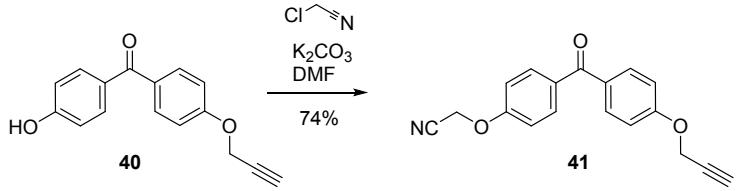
To a stirred solution of **36** (500 mg, 2.23 mmol) and DMF (1 drop) in dichloromethane (10 mL) was added oxalyl chloride (478 µL, 5.58 mmol) dropwise. The resulting mixture was stirred for 16 hours. The mixture was concentrated under reduced pressure to give **38** as a yellow oil, which partially crystallised on standing (563 mg, 104%); ^{1}H NMR (400 MHz, $CDCl_3$) δ ppm 7.94 (d, 1H), 7.99 (d, 1H).

Synthesis of (4-hydroxyphenyl)(4-(prop-2-yn-1-yloxy)phenyl)methanone (40)



Following the method described in WO2011/082488; **39** (4.0 g, 18.67 mmol) was dissolved in dried DMF (35 mL) under Ar and potassium carbonate (3.87 g, 28.01 mmol) was added. The resulting yellow mixture was stirred for 20 minutes and then propargyl bromide (80% solution in toluene, 3.10 mL, 28.01 mmol) was added. The mixture was stirred at room temperature for 18 hours. Water (20 mL) and EtOAc (30 mL) were added and the layers were separated. The aqueous was washed with EtOAc (x2). Organics were washed with water (x3), brine, dried (Na_2SO_4), filtered and solvents removed. The residue was purified by flash chromatography (SiO_2, DCM:EtOAc 95:5) to give **40** as a solid (1.47 g, 31%); ^{1}H NMR (400 MHz, $CDCl_3$) δ ppm 2.56 (t, 1H), 4.77 (d, 2H), 5.38 (s, 1H), 6.88 (d, 2H), 7.03 (d, 2H), 7.74 (d, 2H), 7.78 (d, 2H); UPLC (acidic method) = 100%, 0.71 minutes, 253.01 ($M+H^+$).

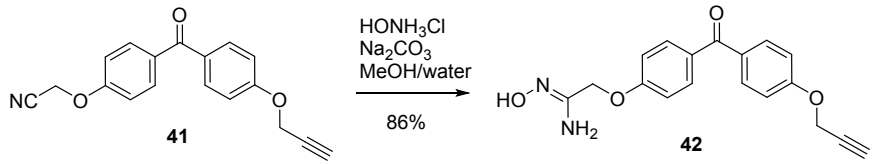
Synthesis of 2-(4-(4-(prop-2-yn-1-yloxy)benzoyl)phenoxy)acetonitrile (41)



To a stirred solution of **40** (1.20 g, 4.76 mmol) in DMF (10 mL) was added potassium carbonate (0.99 g, 7.14 mmol) and the resulting mixture was stirred at room temperature for 20 minutes. Chloroacetonitrile (0.85 mL, 5.11 mmol) was added and the resulting mixture was stirred at room temperature for 16 hours. Water (20 mL) and EtOAc (30 mL) were added and the layers were separated. The aqueous was washed with EtOAc (x3). Organics were washed with water (x4), brine, dried (Na_2SO_4), filtered and solvents removed. Purification by recrystallisation from

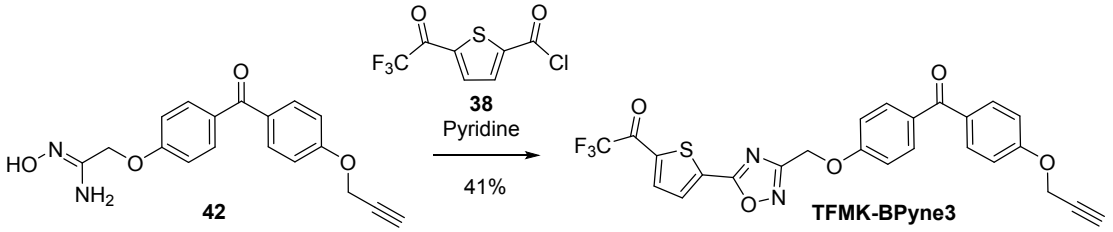
heptanes (heptanes/EtOAc, 7:3) to give **41** as an off-white solid (1.02 g, 74%). ^{1}H NMR (400MHz, $CDCl_3$) δ ppm 4.77 (s, 2H), 4.85 (s, 2H), 7.0-7.10 (m, 4H), 7.80-7.90 (m, 4H).

Synthesis of (*Z*)-N'-hydroxy-2-(4-(4-(prop-2-yn-1-yloxy)benzoyl)phenoxy)acetimidamide (42)



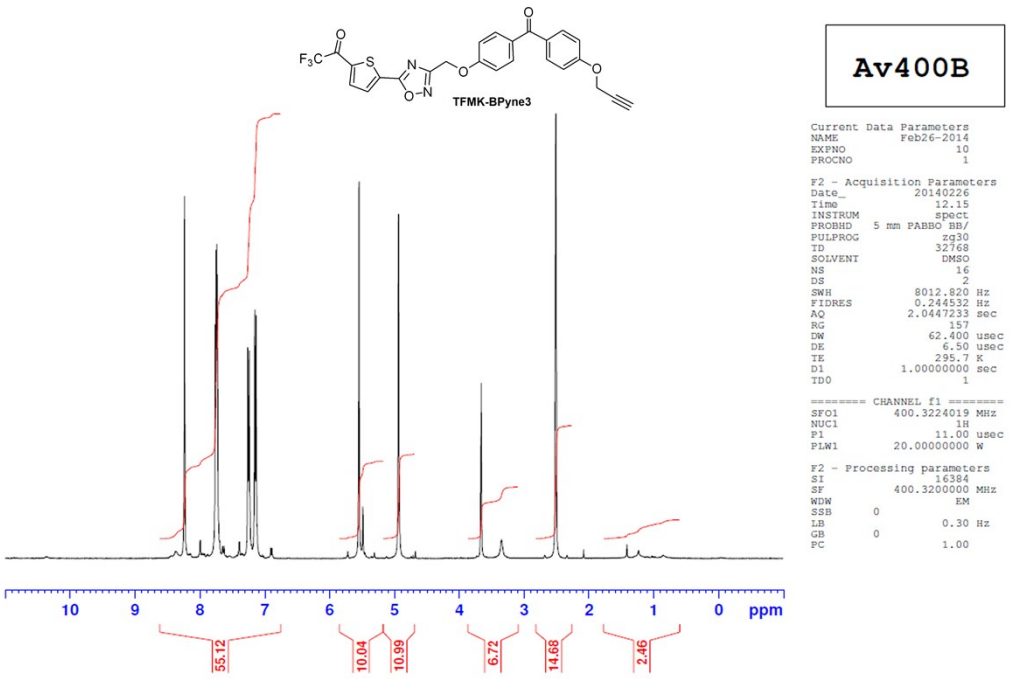
To a stirred suspension of **41** (720 mg, 2.47 mmol) and sodium carbonate (262 mg, 2.47 mmol) in methanol (14 mL) and water (6 mL) was added hydroxylamine hydrochloride (172 mg, 2.47 mmol) at ambient temperature. The mixture was heated to 45 °C and stirred at 45 °C for 1 hour. DMF (20 mL) was added to obtain a solution and the mixture was heated at 45 °C for 16 hours. The resulting mixture was concentrated under reduced pressure. Water (40 mL) and EtOAc (40 mL) were added and the layers were separated. The organic layer was washed with water (3 × 50 mL) and brine (50 mL). The organic layer was dried (Na_2SO_4) and concentrated under reduced pressure to give **42** as a white solid (684 mg, 86% crude yield); ^{1}H NMR (400MHz, $CDCl_3$) δ ppm 2.56 (t, 1H), 4.63 (s, 2H), 4.76 (d, 2H), 4.81-4.91 (m, 1H), 7.03 (d, 4H), 7.77 (d, 2H), 7.79 (d, 2H).

Synthesis of 2,2,2-trifluoro-1-(5-(3-((4-(4-(prop-2-yn-1-yloxy)benzoyl)phenoxy)methyl)-1,2,4-oxadiazol-5-yl)thiophen-2-yl)ethan-1-one (TFMK-BPyne3)

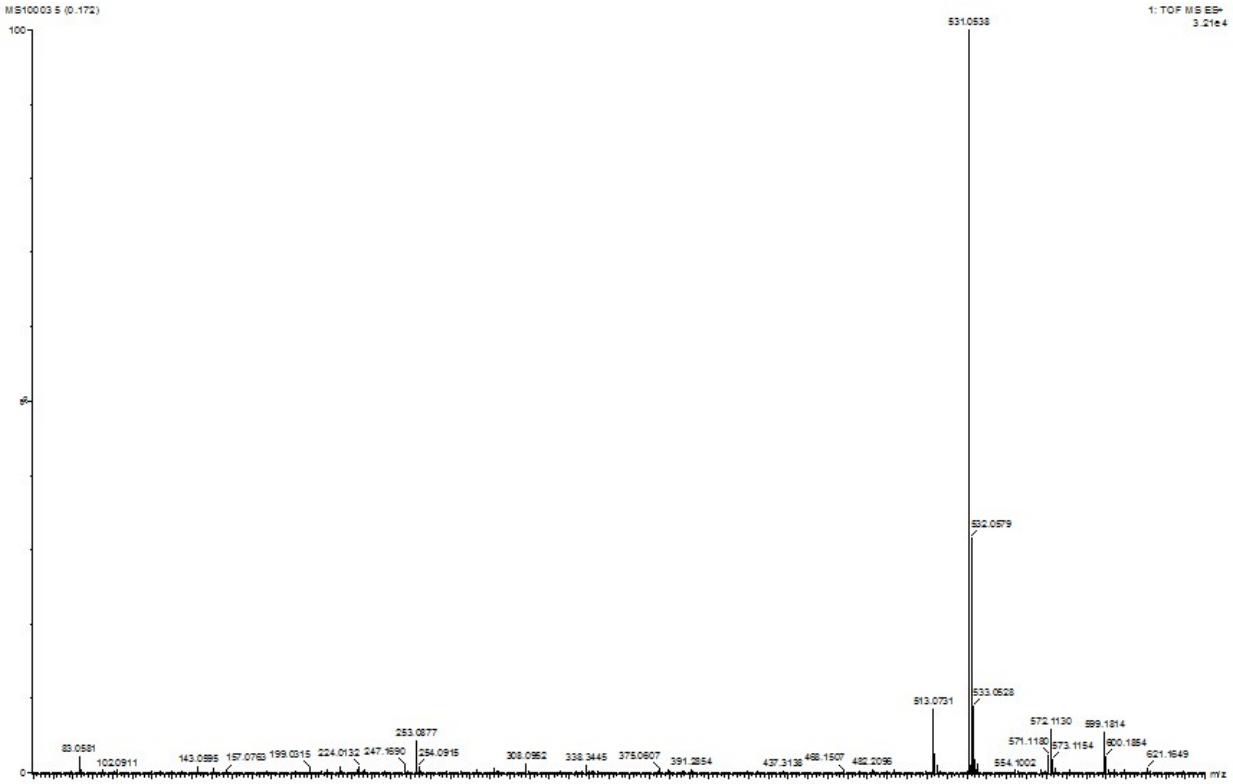


To a stirred solution of **42** (250 mg, 0.86 mmol) in pyridine (2 mL) was added **38** (210 mg, 0.86 mmol). The resulting mixture was heated to 110 °C and stirred at 110 °C for 20 hours. Water (10 mL) was added and the liquids were decanted off. The resulting residue was dissolved in EtOAc (10 mL) and concentrated under reduced pressure. Purification by flash chromatography (SiO_2, EtOAc:heptane 2:3-1:1-3:2) to give **TP3** as a pale yellow solid (180 mg, 41%). ^{1}H NMR (400 MHz, $CDCl_3$) δ ppm 2.56 (t, 1H), 4.77 (d, 2H), 5.34 (s, 2H), 7.40 (d, 2H), 7.71 (d, 2H), 7.90 (d, 2H), 7.81 (d, 2H), 8.00 (s, 1H). HPLC (4 min) R_t 1.66 min ELSD 94% purity; LRMS m/z 531.0 $[M+H_3O]^+$; HRMS calculated for [$M+H^+$, $C_{25}H_{16}N_2O_5SF_3^+$] requires *m/z* 513.0732. Found 513.0731.

^{1}H NMR (**TFMK-BPyne3**):



HRMS (**TFMK-BPyne3**):

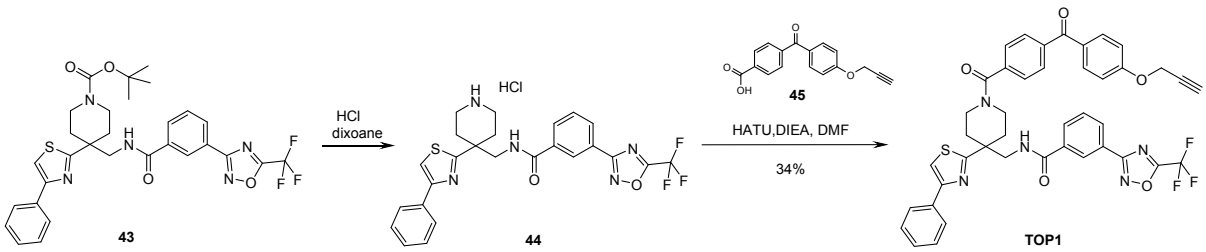


Elements Used:

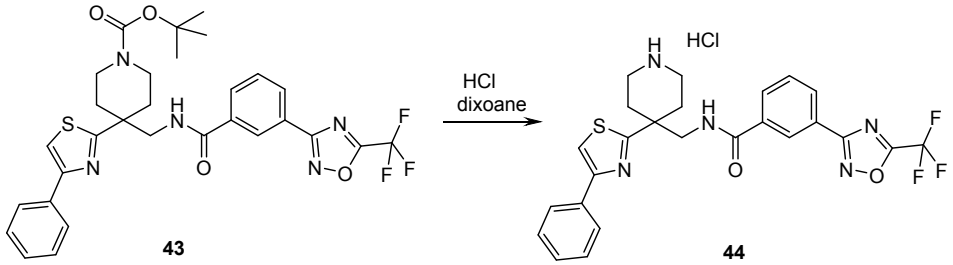
C: 25-25 H: 0-200 N: 0-10 O: 0-10 Na: 0-1 S: 1-1 F: 3-3

Minimum:				-1.5			
Maximum:		5.0	10.0	50.0			
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Norm)	Formula
513.0731	513.0732	-0.1	-0.2	17.5	122.7	0.0	C25 H16 N2 O5 S F3

Synthesis of *N*-((1-(3-(4-(4-(but-3-yn-1-yloxy)benzoyl)phenyl)propanoyl)-4-(4-phenylthiazol-2-yl)piperidin-4-yl)methyl)-3-(5-(trifluoromethyl)-1,2,4-oxadiazol-3-yl)benzamide (TOP1)

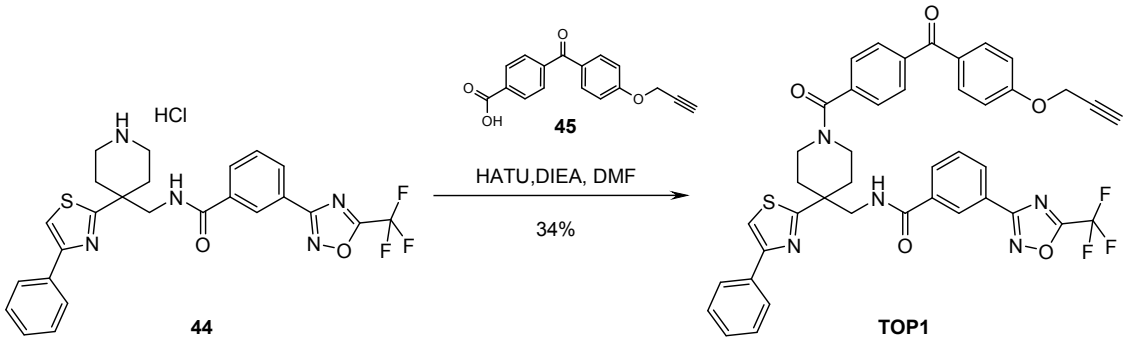


Synthesis of *N*-((4-(4-phenylthiazol-2-yl)piperidin-4-yl)methyl)-3-(5-(trifluoromethyl)-1,2,4-oxadiazol-3-yl)benzamide hydrochloride (44)



To a solution of **43** (80 mg, 0.13 mmol) in DCM (2 mL) was added HCl/Dioxane (1 mL). The mixture was stirred for 1 hour at ambient temperature. TLC showed the reaction was completed. The solution was concentrated to give crude **44** as a white solid which was used for next step directly.

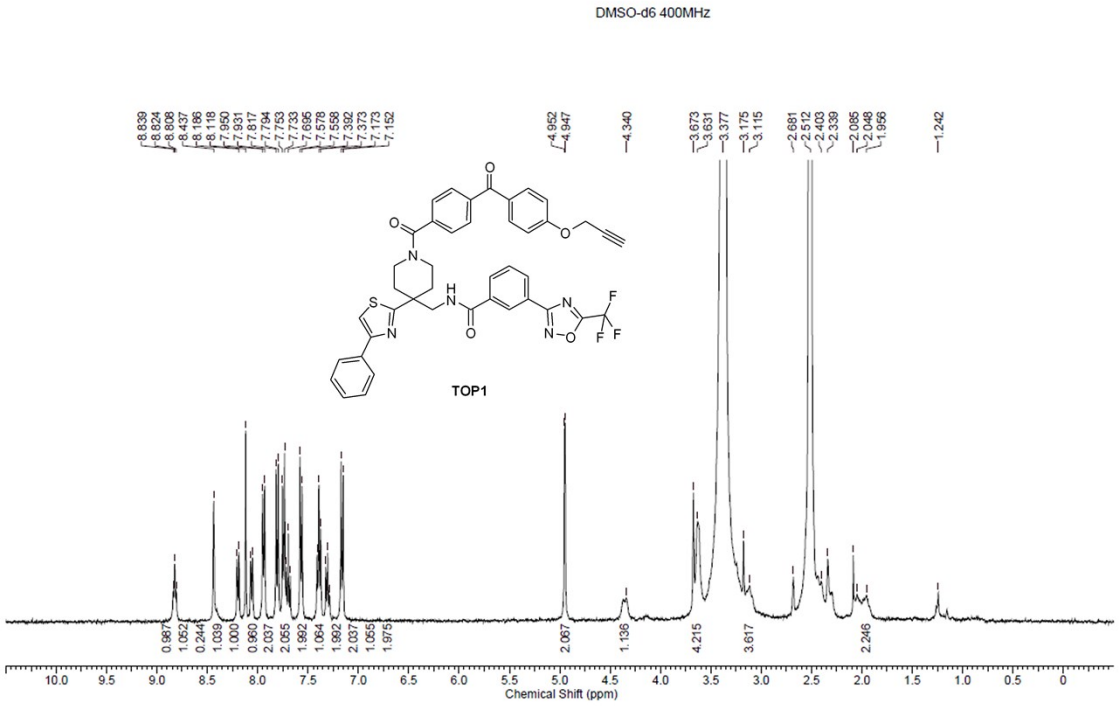
Synthesis of *N*-((4-(4-phenylthiazol-2-yl)-1-(4-(4-(prop-2-yn-1-yloxy)benzoyl)benzoyl)piperidin-4-yl)methyl)-3-(5-(trifluoromethyl)-1,2,4-oxadiazol-3-yl)benzamide (TOP1)



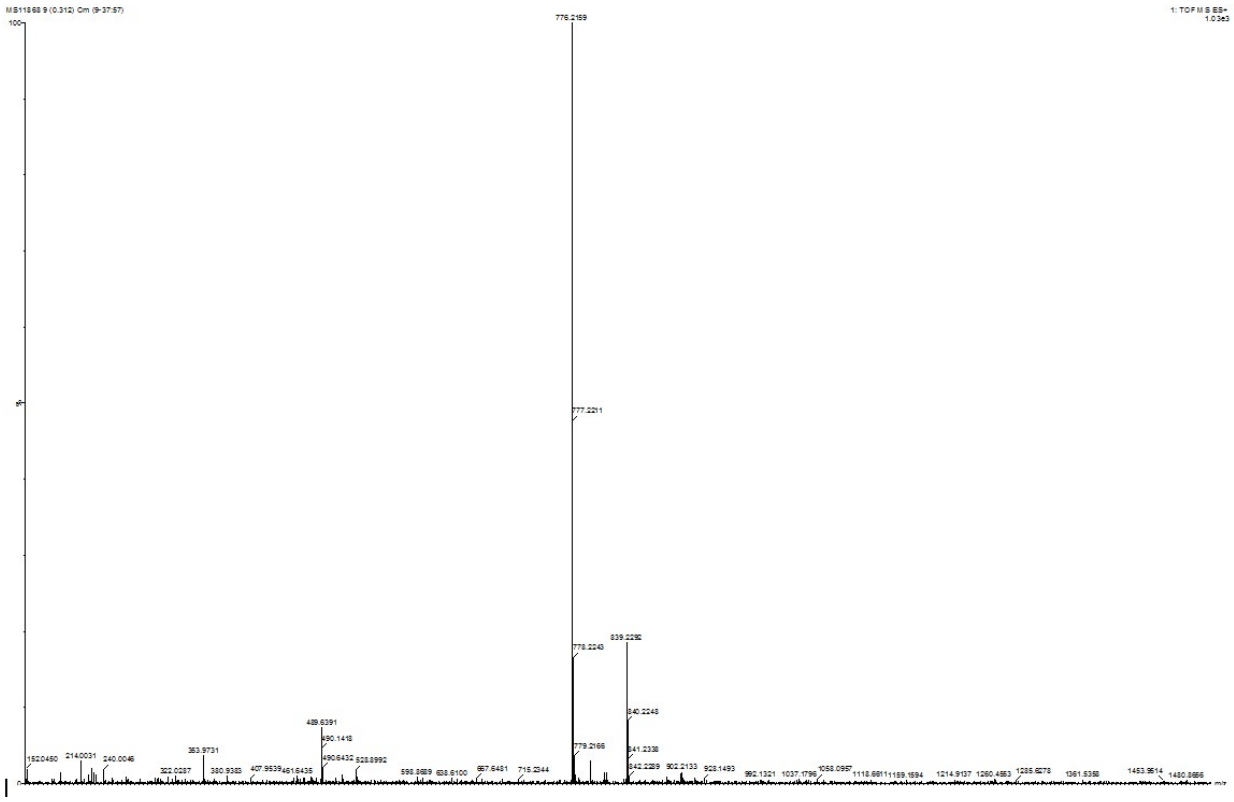
To a stirred solution of compound **44** (67 mg, 0.13 mmol) and **45** (36 mg, 0.13 mmol) in DMF (8 mL) was added HATU (31 mg, 0.14 mmol) and DIEA (17 mg, 0.20 mmol). Stirring was continued at ambient temperature overnight. LCMS showed the reaction was completed. It was evaporated under reduced pressure to give crude residue which was purified by Biotage SP1 (MeOH/DCM=0-10%) to give crude product. The crude product was purified via prep-HPLC to give pure product **TOP1** (34 mg, 34%) as a white solid. ^{1}H NMR (400 MHz, DMSO-d6) δ ppm 1.96-2.08 (m, 2H), 2.33-2.40 (m,

2H), 3.12-3.18 (m, 2H), 3.63-3.67 (m, 4H), 4.34 (br. S, 1H), 4.95 (br. d, *J* = 2.0 Hz, 2H), 7.16 (d, *J* = 8.4 Hz, 2H), 7.31 (m, 1H), 7.37 (t, *J* = 7.6 Hz, 2H), 7.57 (d, *J* = 8.0 Hz, 2H), 7.69-7.75 (m, 3H), 7.81 (d, *J* = 9.2 Hz, 2H), 7.94 (d, *J* = 8.4 Hz, 2H), 8.05 (d, *J* = 9.6 Hz, 1H), 8.12 (s, 1H), 8.18 (d, *J* = 9.6 Hz, 1H), 8.44 (s, 1H), 8.82 (t, *J* = 6.2 Hz, 1H); HRMS calculated for [M+H$^+$, $C_{42}H_{33}F_3N_5O_5S^+$] requires *m/z* 776.2155. Found 776.2159.

^{1}H NMR (**TOP1**):



HRMS (**TOP1**):

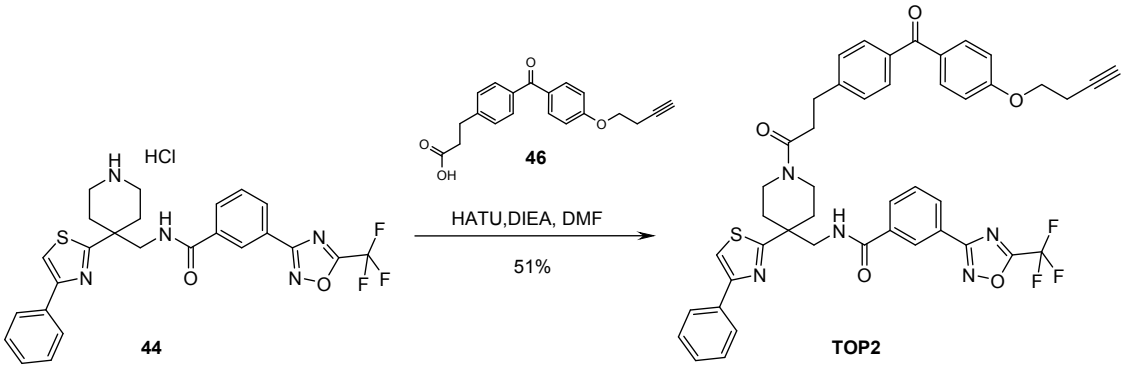


Elements Used:

C: 42-42 H: 0-200 N: 0-10 O: 0-10 Na: 0-1 P: 0-1 S: 1-1 F: 3-3

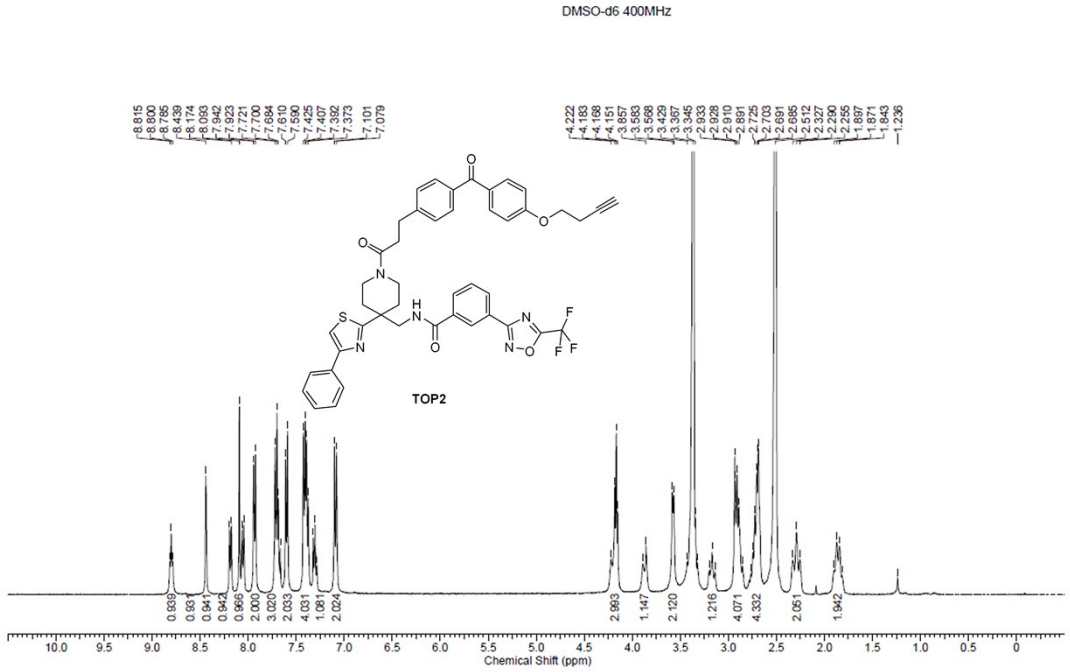
Minimum:				-1.5			
Maximum:		5.0	10.0	50.0			
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Norm)	Formula
776.2159	776.2155	0.4	0.5	27.5	51.8	0.0	C42 H33 N5 O5 S F3

Synthesis of *N*-((1-(3-(4-(4-(but-3-yn-1-yloxy)benzoyl)phenyl)propanoyl)-4-(4-phenylthiazol-2-yl)piperidin-4-yl)methyl)-3-(5-(trifluoromethyl)-1,2,4-oxadiazol-3-yl)benzamide (TOP2)

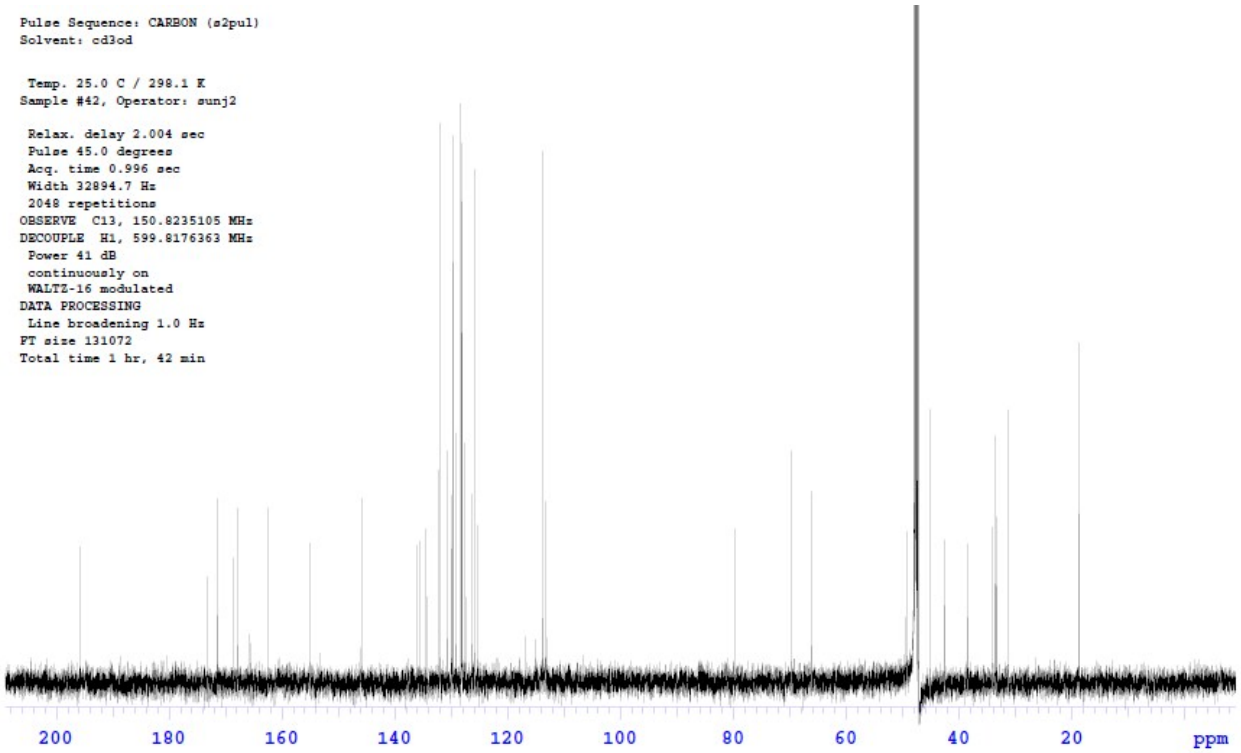


To a stirred solution of **44** (67 mg, 0.13 mmol) and **46** (40 mg, 0.13 mmol) in DMF (8 mL) was added HATU (31 mg, 0.14 mmol) and DIEA (17 mg, 0.20 mmol). Stirring was continued at ambient temperature overnight. LCMS showed the reaction was completed, it was evaporated under reduced pressure to give crude residue which was purified by Biotage SP1 (MeOH/DCM=0-10%) to give crude product. The crude product was purified via prep-HPLC to give pure product **TOP2** (54 mg, 51%) as a white solid. ^{1}H NMR (400 MHz, DMSO-d6) δ ppm 1.86 (dd, *J* = 21.6, 10.4 Hz, 2H), 2.29 (t, *J* = 14.8 Hz, 2H), 2.69-2.73 (m, 4H), 2.89-2.93 (m, 4H), 3.17 (t, *J* = 10.0 Hz, 1H), 3.57 (d, *J* = 6.0 Hz, 2H), 3.85 (t, *J* = 14.8 Hz, 1H), 4.15-4.22 (m, 3H), 7.09 (d, *J* = 8.8 Hz, 2H), 7.26-7.33 (m, 1H), 7.37-7.43 (m, 4H), 7.60 (d, *J* = 8.0 Hz, 2H), 7.68-7.72 (m, 3H), 7.93 (d, *J* = 7.6 Hz, 2H), 7.87-7.96 (d, *J* = 8.4 Hz, 1H), 8.09 (s, 1H), 8.18 (d, *J* = 8.4 Hz, 1H), 8.44 (s, 1H), 8.80 (t, *J* = 6.0 Hz, 1H); ^{13}C NMR (126 MHz, methanol-d4) δ ppm 197.8, 175.3, 173.4, 170.5, 169.8, 164.5, 157.1, 148.0, 138.0, 137.6, 136.4, 134.1, 132.6, 132.0, 132.0, 131.8, 131.2, 130.3, 130.2, 129.5, 128.3, 127.9, 127.3, 115.9, 115.2, 81.8, 71.6, 68.2, 51.3, 50.1, 50.0, 49.9, 49.7, 49.6, 49.4, 49.3, 47.1, 44.5, 40.4, 36.0, 35.5, 35.4, 33.3, 20.7. HPLC (12 min) R_t 9.61 min UV 254nm >95% purity; HRMS calculated for [M+H$^+$, $C_{45}H_{39}F_3N_5O_5S^+$] requires *m/z* 818.2624. Found 818.2623.

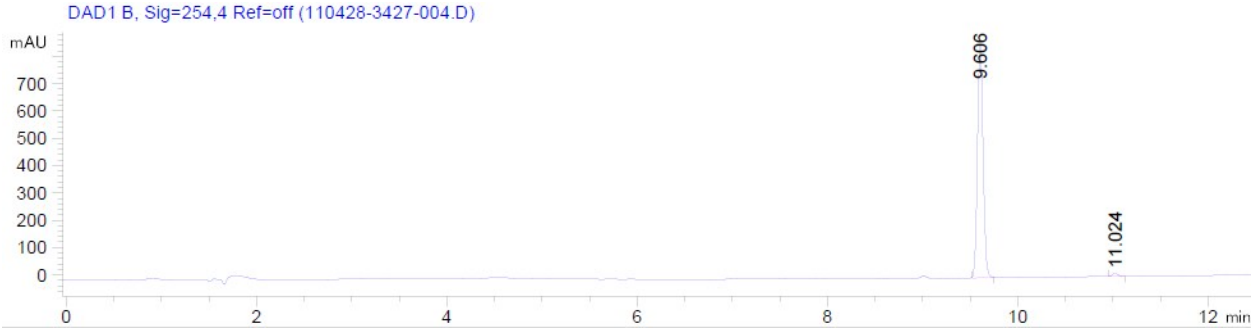
^{1}H NMR (**TOP2**):



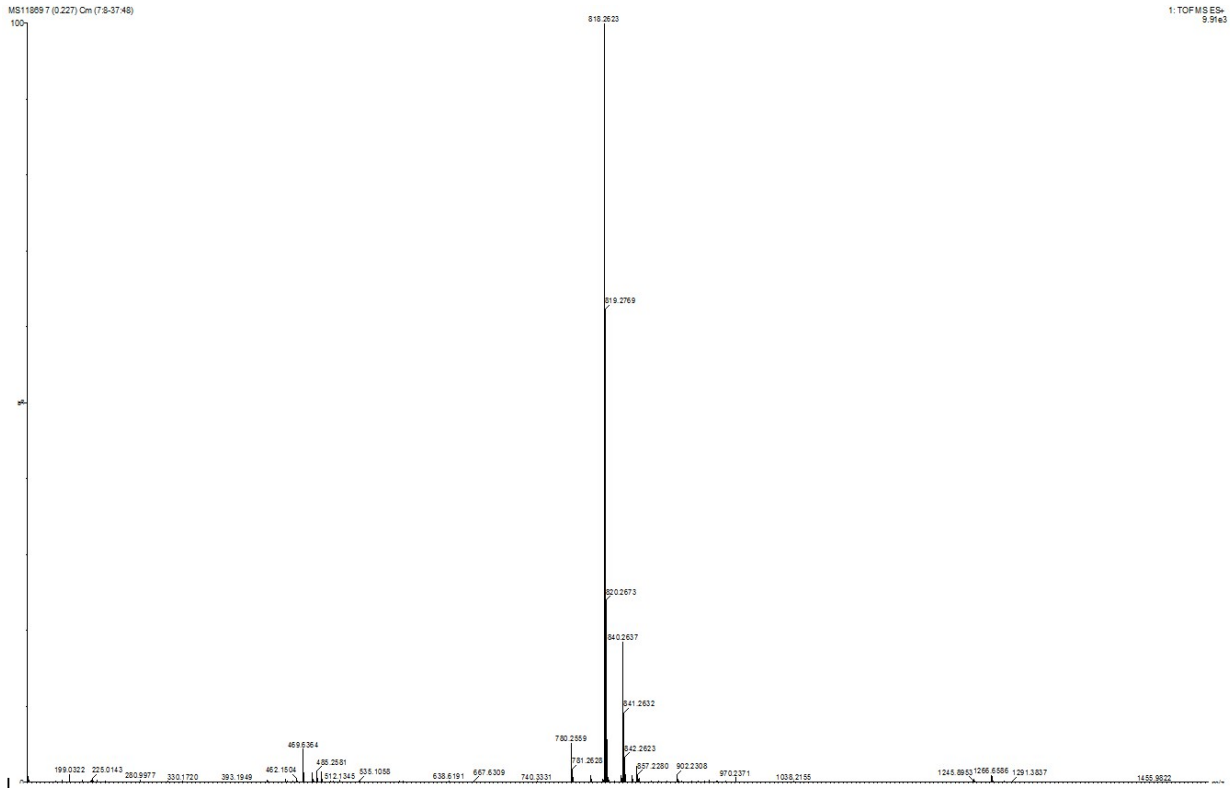
^{13}C NMR (**TOP2**):



HPLC UV 254nm (**TOP2**): (>95% purity)



HRMS (**TOP2**):

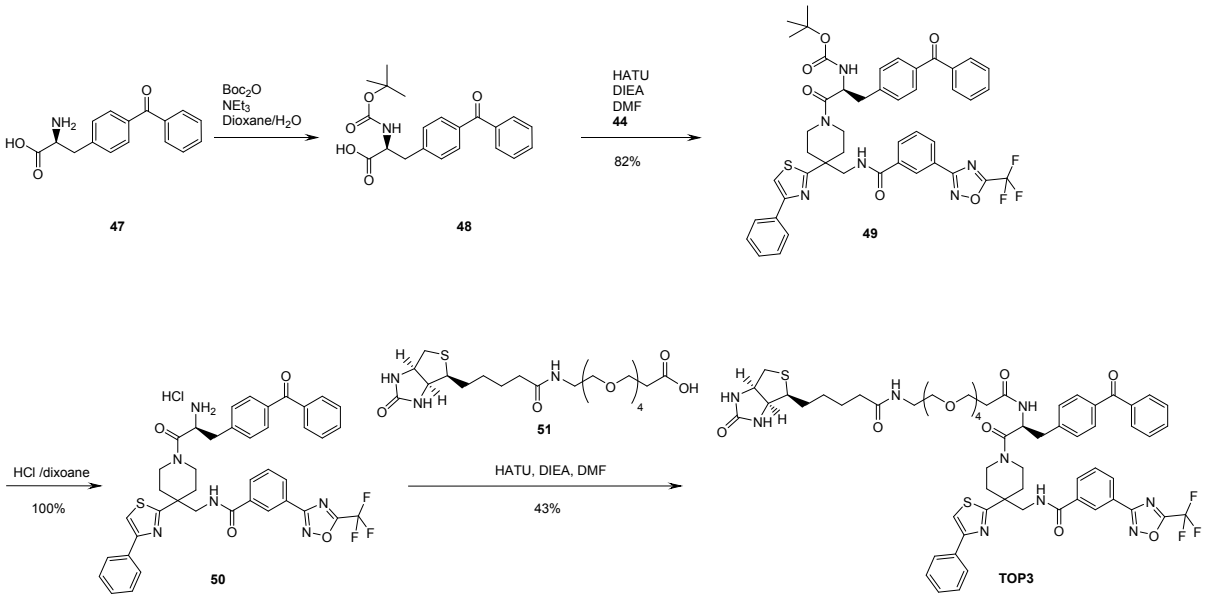


Elements Used:

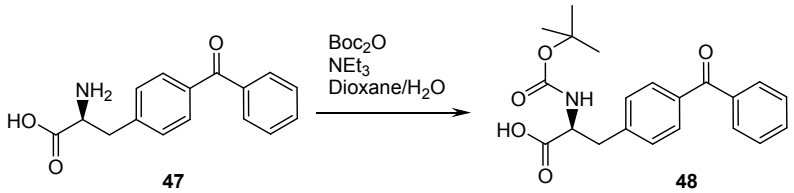
C: 45-45 H: 0-200 N: 0-10 O: 0-10 F: 3-3 Na: 0-1 S: 1-1

Minimum:				-1.5			
Maximum:		5.0	10.0	50.0			
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Norm)	Formula
818.2623	818.2624	-0.1	-0.1	27.5	241.2	0.0	C45 H39 N5 O5 F3 S

Synthesis of *N*-((1-((*S*)-2-(4-benzoylbenzyl)-4,20-dioxo-24-((3a*S*,4*S*,6a*R*)-2-oxohexahydro-1*H*-thieno[3,4-d]imidazol-4-yl)-7,10,13,16-tetraoxa-3,19-diazatetracosanoyl)-4-(4-phenylthiazol-2-yl)piperidin-4-yl)methyl)-3-(5-(trifluoromethyl)-1,2,4-oxadiazol-3-yl)benzamide (TOP3)

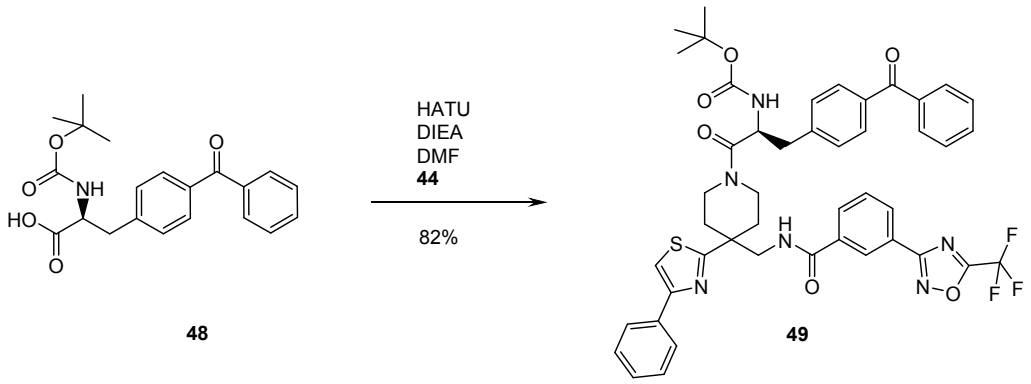


Synthesis of (*S*)-3-(4-benzoylphenyl)-2-((*tert*-butoxycarbonyl)amino)propanoic acid (48)



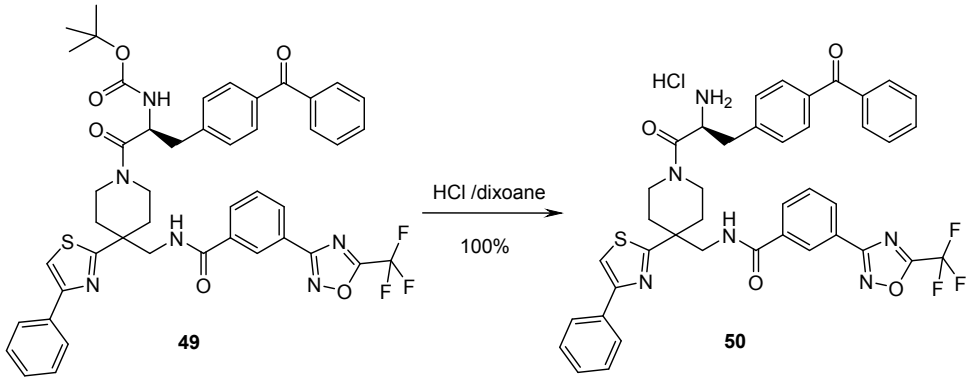
To a stirred solution of **47** (200 mg, 0.74 mmol) in dioxane/H_2O (2 mL/2 mL) was added boc-anhydride (243 mg, 1.12 mmol), followed by Et_3N (224 mg, 2.22 mmol). The mixture was stirred for 4 hours at ambient temperature. TLC (DCM/MeOH=10:1) showed the reaction was completed, 2 mL of water was added to the solution, then the solution was extracted with DCM (3 × 5 mL) , the combined organic layers were dried over Na_2SO_4, It was concentrated to give **48** as a yellow oil.

Synthesis of *tert*-butyl (*S*)-(3-(4-benzoylphenyl)-1-oxo-1-(4-(4-phenylthiazol-2-yl)-4-((3-(5-(trifluoromethyl)-1,2,4-oxadiazol-3-yl)benzamido)methyl)piperidin-1-yl)propan-2-yl)carbamate (49)



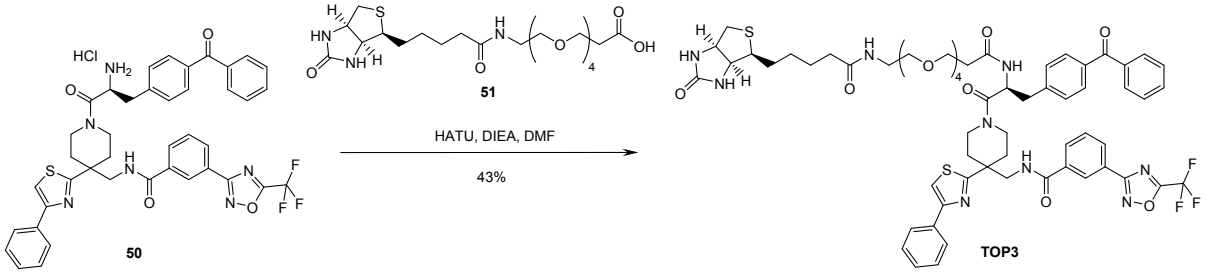
To a stirred solution of **44** (84 mg, 0.16 mmol), **48** (66 mg, 0.16 mmol) and HATU (58 mg, 0.24 mmol) in DMF (4 mL) was added DIEA (63 mg, 0.49 mmol) The reaction was stirred at ambient temperature for 4 hours.LCMS showed the reaction was completed, it was evaporated under reduced pressure to give crude residue which was purified by Biotage SP1 (EA/PE=5-50%) to give crude product **49** (115 mg, 82%) as a yellow oil.

Synthesis of (*S*)-*N*-((1-(2-amino-3-(4-benzoylphenyl)propanoyl)-4-(4-phenylthiazol-2-yl)piperidin-4-yl)methyl)-3-(5-(trifluoromethyl)-1,2,4-oxadiazol-3-yl)benzamide hydrochloride (50)



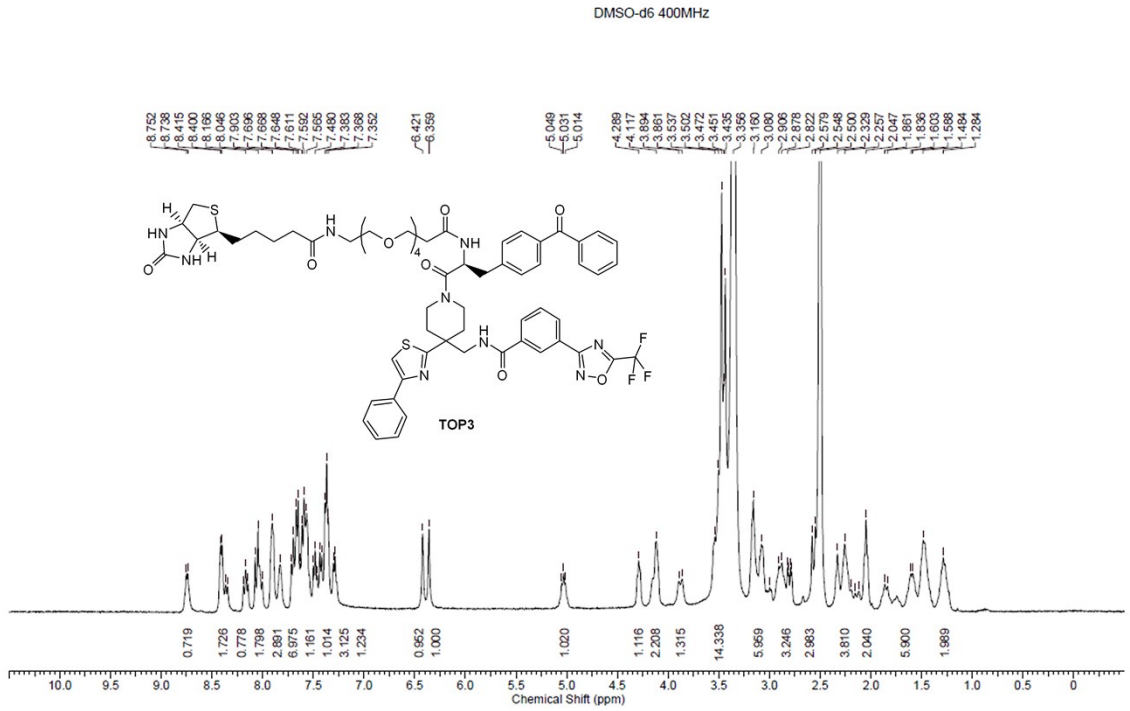
To a solution of **49** (115 mg, 0.13 mmol) in DCM (4 mL) was added HCl/Dioxane (2.5 mL). The mixture was stirred for 1 hour at room temperature, TLC (DCM:MeOH=10:1) showed the reaction was completed, the solution was concentrated to give a crude compound 8 as a white solid which was used for next step directly.

Synthesis of *N*-((1-((*S*)-2-(4-benzoylbenzyl)-4,20-dioxo-24-((3a*S*,4*S*,6a*R*)-2-oxohexahydro-1*H*-thieno[3,4-d]imidazol-4-yl)-7,10,13,16-tetraoxa-3,19-diazatetracosanoyl)-4-(4-phenylthiazol-2-yl)piperidin-4-yl)methyl)-3-(5-(trifluoromethyl)-1,2,4-oxadiazol-3-yl)benzamide (TOP3)

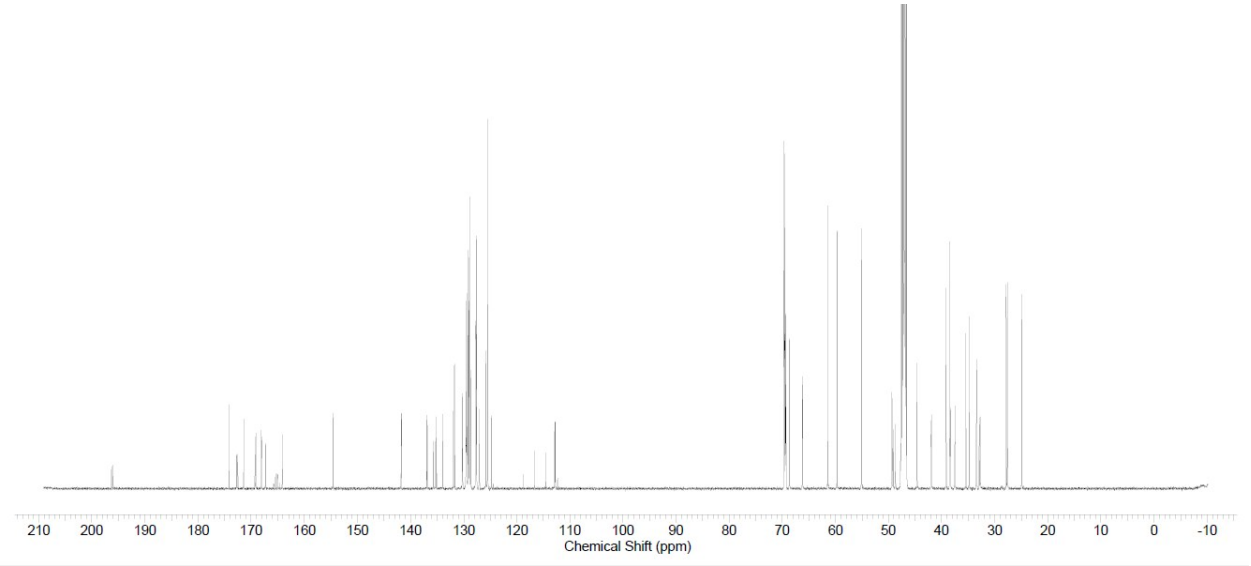


To a stirred solution of **50** (101 mg, 0.13 mmol), **51** (72 mg, 0.15 mmol) and HATU (47 mg, 0.20 mmol) in DMF (5 mL) was added DIEA (52 mg, 0.40 mmol). The reaction was stirred at ambient temperature overnight. LCMS showed the reaction was completed. It was evaporated under reduced pressure to give crude residue which was purified by Biotage SP1 (MeOH/DCM=0-10%) to give crude product. The crude product was purified via prep-HPLC to give pure **TOP3** (70 mg, 43%) as a white solid. ^{1}H NMR (400 MHz, DMSO-d6) δ ppm 1.18-2.41 (m, 14H), 2.42-2.35 (m, 3H), 2.71-3.23 (m, 9H), 3.24-3.63 (m, 14H), 3.88 (d, *J* = 13.2 Hz, 1H), 4.05-4.20 (m, 2H), 4.28-4.29 (m, 1H), 5.03 (br. t, *J* = 7.0 Hz, 1H), 6.36 (s, 1H), 6.42 (s, 1H), 7.18-7.75 (m, 13H), 7.77-7.95 (m, 3H), 7.96-8.12 (m, 2H), 8.16 (t, *J* = 9.0 Hz, 1H), 8.37-8.14 (m, 2H), 8.74 (d, *J* = 5.6 Hz, 1H).); ^{13}C NMR (126 MHz, methanol-d4) δ ppm 196.3, 196.0, 174.2, 172.8, 172.5, 171.4, 169.3, 169.1, 168.1, 168.1, 167.3, 164.2, 154.6, 141.8, 141.7, 136.9, 136.8, 135.7, 135.3, 135.1, 135.1, 134.0, 133.9, 131.9, 131.7, 130.3, 130.2, 129.6, 129.5, 129.5, 129.4, 129.1, 129.1, 128.9, 128.9, 128.7, 128.7, 127.7, 127.7, 127.6, 127.5, 127.1, 127.0, 125.9, 125.5, 124.8, 116.7, 114.5, 112.9, 112.7, 69.7, 69.7, 69.6, 69.6, 69.5, 69.4, 69.4, 69.4, 69.3, 68.7, 68.7, 66.2, 66.2, 61.5, 59.7, 55.1, 46.6, 44.7, 44.6, 42.0, 42.0, 39.2, 38.5, 38.4, 38.4, 37.5, 37.5, 35.4, 34.8, 34.8, 33.4, 32.9, 32.7, 27.9, 27.6, 24.9, 24.9; HPLC (12 min) R_t 11.03 min UV 254 nm >95% purity; HRMS calculated for [M+Na$^+$, $C_{62}H_{70}F_3N_9O_{11}NaS_2^+$] requires *m/z* 1260.4486. Found 1260.4562.

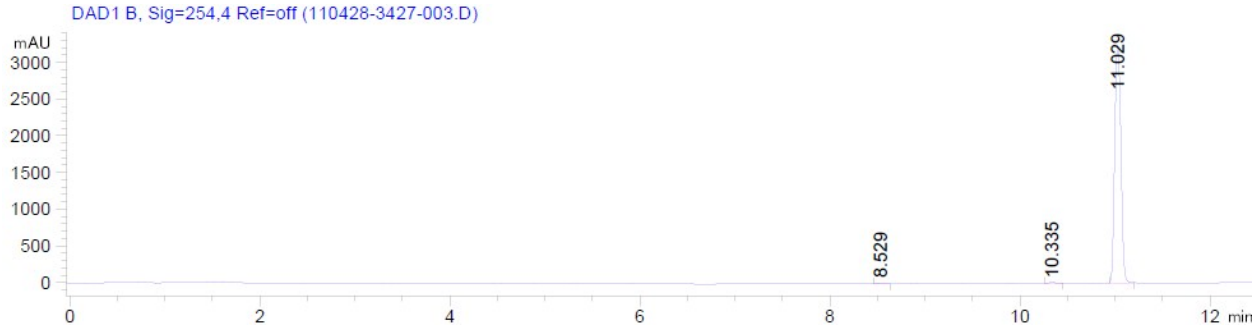
^{1}H NMR (**TOP3**):



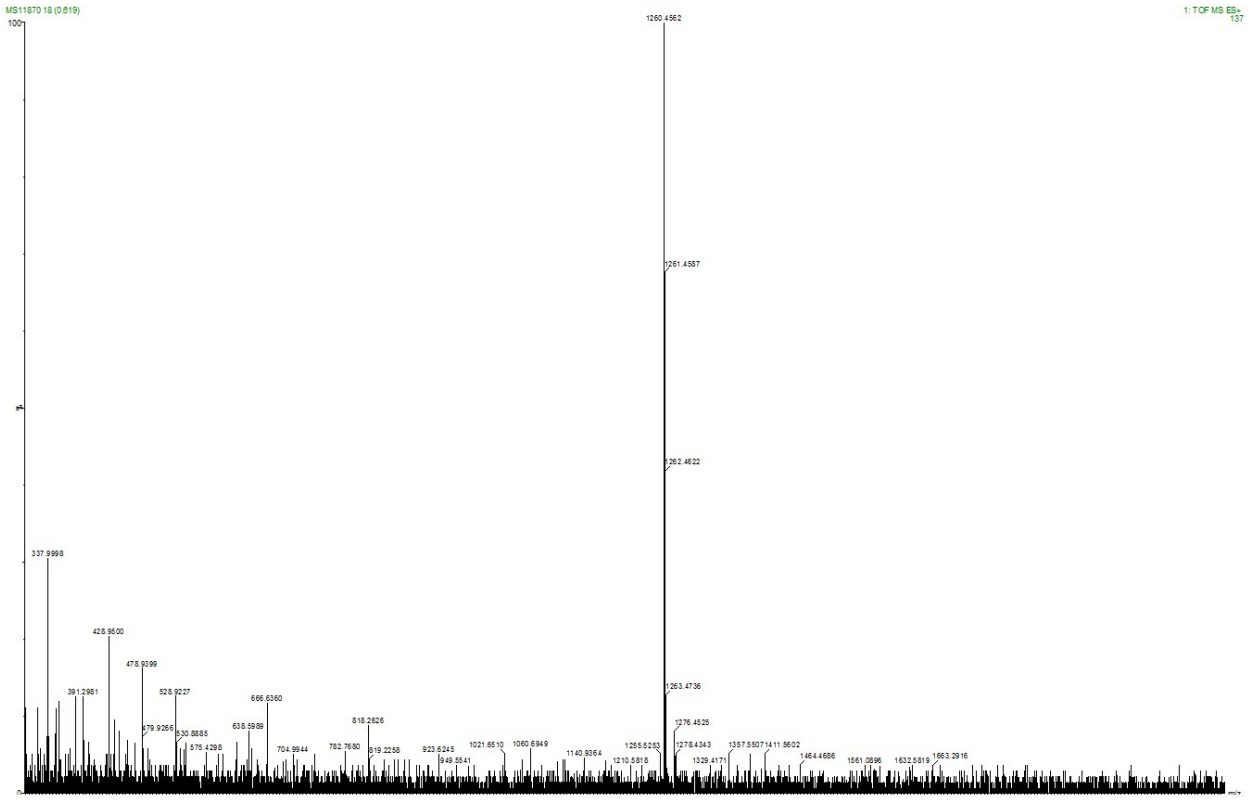
^{13}C NMR (**TOP3**):



HPLC UV 254nm (**TOP3**): (>95% purity):



HRMS (**TOP3**):



Elements Used:

C: 62-62 H: 0-200 N: 0-10 O: 0-15 F: 3-3 Na: 0-1 S: 2-2

Minimum:				-1.5			
Maximum:		5.0	10.0	50.0			
Mass	Calc. Mass	mDa	PPM	DBE	i-FIT	i-FIT (Norm)	Formula
1260.4562	1260.4609	-4.7	-3.7	28.5	23.0	0.4	C62 H73 N7 O14 F3 S2
	1260.4486	7.6	6.0	30.5	23.7	1.1	C62 H70 N9 O11 F3 Na S2

Enzyme Activity Assays

Full HDAC panel screening was carried out at BPS Bioscience

Materials

HDAC Assay Buffer (BPS catalog number 50031)
HDAC Assay Developer (BPS catalog number 50030)
HDAC Substrate 3 (BPS number 50037)
HDAC Class 2a Substrate 1 (BPS number 50040)
SAHA was purchased from Sigma (St. Louis, MO, Catalog Number SML0061)
TSA was purchased from Sigma (St. Louis, MO, Catalog Number T8552)

Assay Conditions

A series of dilutions of the compounds were prepared with 10% DMSO in HDAC assay buffer and 5µl of the dilution was added to a 50µl reaction so that the final concentration of DMSO is 1% in all of reactions. All of the enzymatic reactions were conducted in duplicate at room temperature for 16 hours in a 50µl mixture containing 50mM HEPES, pH7.5, 137mM NaCl, 2.7mM KCl, 0.05% Tween 20, 5µg BSA, Kinetic HDAC developer, an HDAC substrate (see table below), an HDAC enzyme (see table below) and a test compound. For HDAC11 reactions, 0.02% Triton X100 is added. Fluorescence intensity was measured at an excitation of 360 nm and an emission of 460 nm using a Tecan Infinite M1000 microplate reader.

Data Analysis

HDAC activity assays were performed in duplicates at each concentration. The fluorescent intensity data were analyzed using the computer software, Graphpad Prism. In the absence of the compound, the fluorescent intensity (F_t) in each data set was defined as 100% activity. In the absence of HDAC, the fluorescent intensity (F_b) in each data set was defined as 0% activity. The percent activity in the presence of each compound was calculated according to the following equation: %activity = ($F-F_b$)/(F_t-F_b), where F= the fluorescent intensity in the presence of the compound. The values of % activity versus a series of compound concentrations were then plotted using non-linear regression analysis of Sigmoidal dose-response curve generated with the equation $Y=B+(T-B)/1+10^{((LogEC50-X)\times Hill\ Slope)}$, where Y=percent activity, B=minimum percent activity, T=maximum percent activity, X= logarithm of compound and Hill Slope=slope factor or Hill coefficient. The IC50 value was determined by the concentration causing a half-maximal percent activity.

Enzymes and Substrates

Assay	BPS Bioscience Catalog #	Enzyme Used (ng) / Reaction	Substrate
HDAC1	50051	2.5	10µM HDAC Substrate 3
HDAC2	50002	2.5	10µM HDAC Substrate 3
HDAC3/NCOR2	50003	1	10µM HDAC Substrate 3
HDAC4	50004	0.08	2µM HDAC class 2a Substrate 1
HDAC5	50005	3	2µM HDAC class 2a Substrate 1
HDAC6	50006	10	10µM HDAC Substrate 3
HDAC7	50007	0.1	2µM HDAC class 2a Substrate 1
HDAC8	50008	10	2µM HDAC class 2a Substrate 1
HDAC9	50009	4	2µM HDAC class 2a Substrate 1
HDAC10	50010	100	10µM HDAC Substrate 3
HDAC11	50021	60	2µM HDAC class 2a Substrate 1

SI Table 1: Mass spectrometry identified proteins from PHP4 enrichment of HeLa lysates. Sample 1; Steptavidin conjugated sepharose beads (50 µL) were incubated with biotinylated probe **PHP4** (10 µM in 250 µL PBS) for 30 minutes then washed with PBS (3 x 500 µL). HeLa lysates (260 µg total protein) was then incubated with the beads for 1 hour. The beads were washed with PBS (3 x 500 µL) and sent for analysis at the Cambridge Centre for Proteomics. Sample 2; as sample 1 but with pre-treatment of the lysate with probe **PHP2** to compete for binding. Sample 3; as sample 1 but with recombinant truncated HDAC4 (0.5 µg) added to the lysate. Data displayed requires at least 2 peptides identified in any sample. Identified HDACs are highlighted in green.

Identified Proteins (722)	Accession Number	Molecular Weight	sample 1 (spectral counts)	sample 2 (spectral counts)	sample 3 (spectral counts)
Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2	ACACA_HUMAN	266 kDa	177	189	163
Pyruvate carboxylase, mitochondrial OS=Homo sapiens GN=PC PE=1 SV=2	PYC_HUMAN	130 kDa	113	127	112
Tubulin beta-4B chain OS=Homo sapiens GN=TUBB4B PE=1 SV=1	TBB4B_HUMAN	50 kDa	65	65	67
Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2	TBB5_HUMAN	50 kDa	63	69	68
Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	TBA1B_HUMAN	50 kDa	55	53	45
DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	PRKDC_HUMAN	469 kDa	51	56	53
Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	TBA1C_HUMAN	50 kDa	47	45	42
Nuclear receptor corepressor 2 OS=Homo sapiens GN=NCOR2 PE=1 SV=2	NCOR2_HUMAN	275 kDa	46	12	38
Fatty acid synthase OS=Homo sapiens GN=FASN PE=1 SV=3	FAS_HUMAN	273 kDa	45	41	36
Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	TBA4A_HUMAN	50 kDa	45	45	37
Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	MYH9_HUMAN	227 kDa	43	56	37
Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1	EF1A1_HUMAN	50 kDa	39	38	33
60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	CH60_HUMAN	61 kDa	38	39	44
Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2	TBB3_HUMAN	50 kDa	38	43	0
Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1	IQGA1_HUM	189 kDa	31	32	34

SV=1	AN				
Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=MCCC2 PE=1 SV=1	MCCB_HUMAN	61 kDa	31	26	24
Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1	MYOF_HUMAN	235 kDa	30	35	25
Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	ACTB_HUMAN (+1)	42 kDa	29	31	32
Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	FLNA_HUMAN	281 kDa	29	33	24
Nuclear receptor corepressor 1 OS=Homo sapiens GN=NCOR1 PE=1 SV=2	NCOR1_HUMAN	270 kDa	27	4	19
Acetyl-CoA carboxylase 2 OS=Homo sapiens GN=ACACB PE=1 SV=3	ACACB_HUMAN	277 kDa	27	30	27
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial OS=Homo sapiens GN=MCCC1 PE=1 SV=3	MCCA_HUMAN	80 kDa	26	24	19
F-box-like/WD repeat-containing protein TBL1XR1 OS=Homo sapiens GN=TBL1XR1 PE=1 SV=1	TBL1R_HUMAN	56 kDa	26	10	22
Tubulin beta-6 chain OS=Homo sapiens GN=TUBB6 PE=1 SV=1	TBB6_HUMAN	50 kDa	25	30	25
Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	K2C1_HUMAN	66 kDa	23	42	30
Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	TKT_HUMAN	68 kDa	23	28	26
Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	HS90B_HUMAN	83 kDa	23	26	22
Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	ANXA2_HUMAN	39 kDa	22	19	19
Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	XPO2_HUMAN	110 kDa	21	19	20
ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	ATPA_HUMAN	60 kDa	21	21	17
Lysine-specific histone demethylase 1A OS=Homo sapiens GN=KDM1A PE=1 SV=2	KDM1A_HUMAN	93 kDa	21	0	17
4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3	4F2_HUMAN	68 kDa	20	21	21
ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3	ATPB_HUMAN	57 kDa	20	21	14
Propionyl-CoA carboxylase alpha chain, mitochondrial OS=Homo sapiens GN=PCCA PE=1 SV=4	PCCA_HUMAN	80 kDa	19	19	16

Translational activator GCN1 OS=Homo sapiens GN=GCN1L1 PE=1 SV=6	GCN1L_HUMAN	293 kDa	19	21	13
Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	ACTC_HUMAN	42 kDa	19	18	18
Sodium/potassium-transporting ATPase subunit alpha-1 OS=Homo sapiens GN=ATP1A1 PE=1 SV=1	AT1A1_HUMAN	113 kDa	18	17	16
Pyruvate kinase PKM OS=Homo sapiens GN=PKM PE=1 SV=4	KPYM_HUMAN	58 kDa	18	19	19
F-box-like/WD repeat-containing protein TBL1X OS=Homo sapiens GN=TBL1X PE=1 SV=3	TBL1X_HUMAN	62 kDa	18	0	11
Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	K1C9_HUMAN	62 kDa	16	28	22
Propionyl-CoA carboxylase beta chain, mitochondrial OS=Homo sapiens GN=PCCB PE=1 SV=3	PCCB_HUMAN	58 kDa	16	21	15
Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	PRDX1_HUMAN	22 kDa	16	19	14
Histone deacetylase 2 OS=Homo sapiens GN=HDAC2 PE=1 SV=2	HDAC2_HUMAN	55 kDa	16	4	11
Myosin-1 OS=Homo sapiens GN=MYH1 PE=1 SV=3	MYH1_HUMAN	223 kDa	16	1	0
Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	IMB1_HUMAN	97 kDa	15	21	18
Exportin-1 OS=Homo sapiens GN=XPO1 PE=1 SV=1	XPO1_HUMAN	123 kDa	15	16	14
C-1-tetrahydrofolate synthase, cytoplasmic OS=Homo sapiens GN=MTHFD1 PE=1 SV=3	C1TC_HUMAN	102 kDa	15	16	13
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	RPN1_HUMAN	69 kDa	15	12	9
Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	EF2_HUMAN	95 kDa	14	15	15
Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	CALX_HUMAN	68 kDa	14	16	13
Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	SYEP_HUMAN	171 kDa	14	15	18
Carbamoyl-phosphate synthase [ammonia], mitochondrial OS=Homo sapiens GN=CPS1 PE=1 SV=2	CPSM_HUMAN	165 kDa	14	15	11
Brain acid soluble protein 1 OS=Homo sapiens GN=BASP1 PE=1 SV=2	BASP1_HUMAN	23 kDa	14	13	14

D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	SERA_HUMAN	57 kDa	14	11	14
Inosine-5'-monophosphate dehydrogenase 2 OS=Homo sapiens GN=IMPDH2 PE=1 SV=2	IMDH2_HUMAN	56 kDa	14	13	10
Ketosamine-3-kinase OS=Homo sapiens GN=FN3KRP PE=1 SV=2	KT3K_HUMAN	34 kDa	14	6	13
Histone deacetylase 1 OS=Homo sapiens GN=HDAC1 PE=1 SV=1	HDAC1_HUMAN	55 kDa	14	4	12
Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	HSPB1_HUMAN	23 kDa	13	16	16
Importin-5 OS=Homo sapiens GN=IPO5 PE=1 SV=4	IPO5_HUMAN	124 kDa	13	13	17
Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	EFTU_HUMAN	50 kDa	13	13	9
Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	TFR1_HUMAN	85 kDa	13	13	11
Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT2 PE=1 SV=2	K22E_HUMAN	65 kDa	13	19	16
F-box only protein 22 OS=Homo sapiens GN=FBXO22 PE=1 SV=1	FBX22_HUMAN	45 kDa	13	9	12
Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	K2C8_HUMAN	54 kDa	13	14	10
Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	HS90A_HUMAN	85 kDa	13	15	15
Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6	K1C10_HUMAN	59 kDa	12	17	16
Plastin-3 OS=Homo sapiens GN=PLS3 PE=1 SV=4	PLST_HUMAN	71 kDa	12	17	10
NAD(P) transhydrogenase, mitochondrial OS=Homo sapiens GN=NNT PE=1 SV=3	NNTM_HUMAN	114 kDa	12	12	9
Nuclear pore complex protein Nup155 OS=Homo sapiens GN=NUP155 PE=1 SV=1	NU155_HUMAN	155 kDa	12	14	10
40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2	RS3_HUMAN	27 kDa	12	12	13
Basic leucine zipper and W2 domain-containing protein 1 OS=Homo sapiens GN=BZW1 PE=1 SV=1	BZW1_HUMAN	48 kDa	12	8	9
Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	TPM4_HUMAN	29 kDa	12	11	8

Myosin-4 OS=Homo sapiens GN=MYH4 PE=1 SV=2	MYH4_HUMAN	223 kDa	12	0	0
Myosin-2 OS=Homo sapiens GN=MYH2 PE=1 SV=1	MYH2_HUMAN	223 kDa	12	1	0
Metastasis-associated protein MTA2 OS=Homo sapiens GN=MTA2 PE=1 SV=1	MTA2_HUMAN	75 kDa	11	0	13
REST corepressor 1 OS=Homo sapiens GN=RCOR1 PE=1 SV=1	RCOR1_HUMAN	53 kDa	11	0	11
Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B PE=1 SV=5	K2C6B_HUMAN	60 kDa	11	5	7
Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	HSP7C_HUMAN	71 kDa	10	12	11
Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	HNRPK_HUMAN	51 kDa	10	12	12
Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1	IPO7_HUMAN	120 kDa	10	12	10
Elongation factor 1-gamma OS=Homo sapiens GN=EEF1G PE=1 SV=3	EF1G_HUMAN	50 kDa	10	8	6
Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	PCBP1_HUMAN	37 kDa	10	8	9
Trifunctional enzyme subunit alpha, mitochondrial OS=Homo sapiens GN=HADHA PE=1 SV=2	ECHA_HUMAN	83 kDa	10	9	7
Histone deacetylase 3 OS=Homo sapiens GN=HDAC3 PE=1 SV=2	HDAC3_HUMAN	49 kDa	10	3	9
Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4	K1C16_HUMAN	51 kDa	10	6	0
Neuroblast differentiation-associated protein AHNAK OS=Homo sapiens GN=AHNAK PE=1 SV=2	AHNK_HUMAN	629 kDa	9	11	7
Calponin-2 OS=Homo sapiens GN=CNN2 PE=1 SV=4	CNN2_HUMAN	34 kDa	9	10	11
Signal transducer and activator of transcription 3 OS=Homo sapiens GN=STAT3 PE=1 SV=2	STAT3_HUMAN	88 kDa	9	8	11
Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	COF1_HUMAN	19 kDa	9	10	8
T-complex protein 1 subunit theta OS=Homo sapiens GN=CCT8 PE=1 SV=4	TCPQ_HUMAN	60 kDa	9	10	6
3-hydroxyacyl-CoA dehydrogenase type-2 OS=Homo sapiens GN=HSD17B10 PE=1	HCD2_HUMA	27 kDa	9	9	8

SV=3	N				
Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	ITB1_HUMAN	88 kDa	9	8	8
Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV=4	K1C14_HUMAN	52 kDa	9	8	7
Ribonucleoside-diphosphate reductase large subunit OS=Homo sapiens GN=RRM1 PE=1 SV=1	RIR1_HUMAN	90 kDa	9	9	7
Vesicle-fusing ATPase OS=Homo sapiens GN=NSF PE=1 SV=3	NSF_HUMAN	83 kDa	9	7	5
Deoxycytidine kinase OS=Homo sapiens GN=DCK PE=1 SV=1	DCK_HUMAN	31 kDa	9	5	7
Mesoderm induction early response protein 1 OS=Homo sapiens GN=MIER1 PE=1 SV=2	MIER1_HUMAN	58 kDa	9	0	10
Genetic suppressor element 1 OS=Homo sapiens GN=GSE1 PE=1 SV=3	GSE1_HUMAN	136 kDa	9	0	7
Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=2	ANM1_HUMAN	42 kDa	9	3	5
Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	K1C17_HUMAN	48 kDa	9	10	9
ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7	ADT2_HUMAN	33 kDa	9	8	8
Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	DYHC1_HUMAN	532 kDa	8	13	11
Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	TNPO1_HUMAN	102 kDa	8	12	12
ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=1 SV=3	ACLY_HUMAN	121 kDa	8	10	9
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	AT2A2_HUMAN	115 kDa	8	7	10
Glutaminase kidney isoform, mitochondrial OS=Homo sapiens GN=GLS PE=1 SV=1	GLSK_HUMAN	73 kDa	8	8	9
Phospholipase A-2-activating protein OS=Homo sapiens GN=PLAA PE=1 SV=2	PLAP_HUMAN	87 kDa	8	6	6
ATP-dependent RNA helicase DDX39A OS=Homo sapiens GN=DDX39A PE=1 SV=2	DX39A_HUMAN	49 kDa	8	9	7
78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	GRP78_HUMAN	72 kDa	8	11	10
Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1	HNRH1_HUM	49 kDa	8	7	7

PE=1 SV=4	AN				
Synaptic vesicle membrane protein VAT-1 homolog OS=Homo sapiens GN=VAT1 PE=1 SV=2	VAT1_HUMAN	42 kDa	8	7	10
ADP-ribosylation factor 4 OS=Homo sapiens GN=ARF4 PE=1 SV=3	ARF4_HUMAN	21 kDa	8	7	5
Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1	ATX10_HUMAN	53 kDa	8	6	7
Polypeptide N-acetylgalactosaminyltransferase 2 OS=Homo sapiens GN=GALNT2 PE=1 SV=1	GALT2_HUMAN	65 kDa	8	9	7
Perilipin-3 OS=Homo sapiens GN=PLIN3 PE=1 SV=3	PLIN3_HUMAN	47 kDa	8	8	7
40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	RS18_HUMAN	18 kDa	8	8	7
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2 OS=Homo sapiens GN=RPN2 PE=1 SV=3	RPN2_HUMAN	69 kDa	8	6	8
HLA class I histocompatibility antigen, Cw-12 alpha chain OS=Homo sapiens GN=HLA-C PE=2 SV=2	1C12_HUMAN	41 kDa	8	6	7
DNA polymerase delta catalytic subunit OS=Homo sapiens GN=POLD1 PE=1 SV=2	DPOD1_HUMAN	124 kDa	8	4	5
Ras-related protein Rab-7a OS=Homo sapiens GN=RAB7A PE=1 SV=1	RAB7A_HUMAN	23 kDa	8	7	5
Keratin, type II cytoskeletal 7 OS=Homo sapiens GN=KRT7 PE=1 SV=5	K2C7_HUMAN	51 kDa	8	11	7
S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=2	SKP1_HUMAN	19 kDa	8	4	6
Glucosamine-6-phosphate isomerase 1 OS=Homo sapiens GN=GNPDA1 PE=1 SV=1	GNPI1_HUMAN	33 kDa	8	2	7
Myosin-7 OS=Homo sapiens GN=MYH7 PE=1 SV=5	MYH7_HUMAN	223 kDa	8	0	1
Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=1 SV=1	TPM2_HUMAN	33 kDa	8	5	5
Tropomyosin alpha-1 chain OS=Homo sapiens GN=TPM1 PE=1 SV=2	TPM1_HUMAN	33 kDa	8	0	0
Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1	IMA1_HUMAN	58 kDa	7	11	8
ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4	ADT3_HUMAN	33 kDa	7	7	7

Integrin alpha-V OS=Homo sapiens GN=ITGAV PE=1 SV=2	ITAV_HUMAN	116 kDa	7	6	4
Large neutral amino acids transporter small subunit 1 OS=Homo sapiens GN=SLC7A5 PE=1 SV=2	LAT1_HUMAN	55 kDa	7	6	7
T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=4	TCPB_HUMAN	57 kDa	7	5	6
Dihydropyrimidinase-related protein 3 OS=Homo sapiens GN=DPYSL3 PE=1 SV=1	DPYL3_HUMAN	62 kDa	7	6	7
Extended synaptotagmin-1 OS=Homo sapiens GN=ESYT1 PE=1 SV=1	ESYT1_HUMAN	123 kDa	7	7	7
T-complex protein 1 subunit zeta OS=Homo sapiens GN=CCT6A PE=1 SV=3	TCPZ_HUMAN	58 kDa	7	8	6
Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2	AAAT_HUMAN	57 kDa	7	7	6
Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4	MARCS_HUMAN	32 kDa	7	6	7
Src substrate cortactin OS=Homo sapiens GN=CTTN PE=1 SV=2	SRC8_HUMAN	62 kDa	7	7	4
DnaJ homolog subfamily A member 1 OS=Homo sapiens GN=DNAJA1 PE=1 SV=2	DNJA1_HUMAN	45 kDa	7	6	6
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit OS=Homo sapiens GN=DDOST PE=1 SV=4	OST48_HUMAN	51 kDa	7	4	5
RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	RUVB1_HUMAN	50 kDa	7	8	5
Long-chain-fatty-acid--CoA ligase 3 OS=Homo sapiens GN=ACSL3 PE=1 SV=3	ACSL3_HUMAN	80 kDa	7	6	4
Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	CLUS_HUMAN	52 kDa	7	6	6
Hydroxysteroid dehydrogenase-like protein 2 OS=Homo sapiens GN=HSDL2 PE=1 SV=1	HSDL2_HUMAN	45 kDa	7	7	4
Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	QCR2_HUMAN	48 kDa	7	5	6
Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1	UN45A_HUMAN	103 kDa	7	5	5
Histone deacetylase 8 OS=Homo sapiens GN=HDAC8 PE=1 SV=2	HDAC8_HUMAN	42 kDa	7	2	6
Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	HSP71_HUM	70 kDa	7	6	4

	AN				
Histone deacetylase 6 OS=Homo sapiens GN=HDAC6 PE=1 SV=2	HDAC6_HUMAN	131 kDa	7	1	5
Histone-binding protein RBBP4 OS=Homo sapiens GN=RBBP4 PE=1 SV=3	RBBP4_HUMAN	48 kDa	7	1	4
Tetratricopeptide repeat protein 38 OS=Homo sapiens GN=TTC38 PE=1 SV=1	TTC38_HUMAN	53 kDa	7	0	6
HLA class I histocompatibility antigen, A-69 alpha chain OS=Homo sapiens GN=HLA-A PE=1 SV=2	1A69_HUMAN	41 kDa	7	8	6
Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1	RBBP7_HUMAN	48 kDa	7	2	4
Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3	LPPRC_HUMAN	158 kDa	6	11	7
CAD protein OS=Homo sapiens GN=CAD PE=1 SV=3	PYR1_HUMAN	243 kDa	6	7	9
Pachytene checkpoint protein 2 homolog OS=Homo sapiens GN=TRIP13 PE=1 SV=2	PCH2_HUMAN	49 kDa	6	9	7
26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3	PRS6A_HUMAN	49 kDa	6	6	8
Glycerol-3-phosphate dehydrogenase, mitochondrial OS=Homo sapiens GN=GPD2 PE=1 SV=3	GPDM_HUMAN	81 kDa	6	7	6
Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	SERPH_HUMAN	46 kDa	6	8	6
Basigin OS=Homo sapiens GN=BSG PE=1 SV=2	BASI_HUMAN	42 kDa	6	6	6
Fructosamine-3-kinase OS=Homo sapiens GN=FN3K PE=1 SV=1	FN3K_HUMAN	35 kDa	6	4	7
RuvB-like 2 OS=Homo sapiens GN=RUVBL2 PE=1 SV=3	RUVB2_HUMAN	51 kDa	6	7	7
Spermidine synthase OS=Homo sapiens GN=SRM PE=1 SV=1	SPEE_HUMAN	34 kDa	6	7	6
Eukaryotic initiation factor 4A-I OS=Homo sapiens GN=EIF4A1 PE=1 SV=1	IF4A1_HUMAN	46 kDa	6	6	5
Myosin regulatory light chain 12A OS=Homo sapiens GN=MYL12A PE=1 SV=2	ML12A_HUMAN (+1)	20 kDa	6	7	6
Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2	CALU_HUMAN	37 kDa	6	7	6

Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	ENPL_HUMAN	92 kDa	6	11	6
Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	PDCD6_HUMAN	22 kDa	6	5	5
ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	DDX3X_HUMAN	73 kDa	6	6	5
Chromodomain-helicase-DNA-binding protein 4 OS=Homo sapiens GN=CHD4 PE=1 SV=2	CHD4_HUMAN	218 kDa	6	0	4
Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	GRP75_HUMAN	74 kDa	6	3	5
Ras-related protein Rab-1A OS=Homo sapiens GN=RAB1A PE=1 SV=3	RAB1A_HUMAN	23 kDa	6	6	6
Fatty aldehyde dehydrogenase OS=Homo sapiens GN=ALDH3A2 PE=1 SV=1	AL3A2_HUMAN	55 kDa	6	5	4
Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	MYL6_HUMAN	17 kDa	6	5	3
Palladin OS=Homo sapiens GN=PALLD PE=1 SV=3	PALLD_HUMAN	151 kDa	6	4	4
Arginine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=RARS PE=1 SV=2	SYRC_HUMAN	75 kDa	6	5	4
RNA-binding protein 39 OS=Homo sapiens GN=RBM39 PE=1 SV=2	RBM39_HUMAN	59 kDa	6	4	4
Putative N-acetylglucosamine-6-phosphate deacetylase OS=Homo sapiens GN=AMDHD2 PE=1 SV=2	NAGA_HUMAN	44 kDa	6	3	6
Monofunctional C1-tetrahydrofolate synthase, mitochondrial OS=Homo sapiens GN=MTHFD1L PE=1 SV=1	C1TM_HUMAN	106 kDa	6	5	3
Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1	LRC59_HUMAN	35 kDa	6	2	5
GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	RAN_HUMAN	24 kDa	6	4	3
Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3	HNRPF_HUMAN	46 kDa	6	6	6
ADP-ribosylation factor 5 OS=Homo sapiens GN=ARF5 PE=1 SV=2	ARF5_HUMAN	21 kDa	6	6	4
Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	K2C5_HUMAN	62 kDa	6	8	6
Paired amphipathic helix protein Sin3a OS=Homo sapiens GN=SIN3A PE=1 SV=2	SIN3A_HUM	145 kDa	6	0	1

	AN				
ADP-ribosylation factor 1 OS=Homo sapiens GN=ARF1 PE=1 SV=2	ARF1_HUMAN (+1)	21 kDa	6	6	4
Myosin light chain 1/3, skeletal muscle isoform OS=Homo sapiens GN=MYL1 PE=1 SV=3	MYL1_HUMAN	21 kDa	6	0	0
Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2	COPA_HUMAN	138 kDa	5	8	11
Eukaryotic translation initiation factor 4 gamma 1 OS=Homo sapiens GN=EIF4G1 PE=1 SV=4	IF4G1_HUMAN	175 kDa	5	5	8
Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=2	MPCP_HUMAN	40 kDa	5	4	7
Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	G3P_HUMAN	36 kDa	5	7	7
T-complex protein 1 subunit alpha OS=Homo sapiens GN=TCP1 PE=1 SV=1	TCPA_HUMAN	60 kDa	5	10	5
14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	1433T_HUMAN	28 kDa	5	9	7
Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1	PSME3_HUMAN	30 kDa	5	7	6
Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial OS=Homo sapiens GN=SUCLG2 PE=1 SV=2	SUCB2_HUMAN	47 kDa	5	7	4
Alkyldihydroxyacetonephosphate synthase, peroxisomal OS=Homo sapiens GN=AGPS PE=1 SV=1	ADAS_HUMAN	73 kDa	5	5	4
Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=5	EF1D_HUMAN	31 kDa	5	5	6
Protein ERGIC-53 OS=Homo sapiens GN=LMAN1 PE=1 SV=2	LMAN1_HUMAN	58 kDa	5	5	3
Cytosolic phospholipase A2 OS=Homo sapiens GN=PLA2G4A PE=1 SV=2	PA24A_HUMAN	85 kDa	5	6	3
Ras-related protein Rab-14 OS=Homo sapiens GN=RAB14 PE=1 SV=4	RAB14_HUMAN	24 kDa	5	7	5
40S ribosomal protein S2 OS=Homo sapiens GN=RPS2 PE=1 SV=2	RS2_HUMAN	31 kDa	5	2	4
26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=3	PRS7_HUMAN	49 kDa	5	6	6
Ras-related protein Rab-11B OS=Homo sapiens GN=RAB11B PE=1 SV=4	RB11B_HUMAN	24 kDa	5	4	7
40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	RS19_HUMA	16 kDa	5	6	5

	N				
CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3	CD44_HUMAN	82 kDa	5	4	6
DNA mismatch repair protein Msh2 OS=Homo sapiens GN=MSH2 PE=1 SV=1	MSH2_HUMAN	105 kDa	5	5	3
Vesicle-trafficking protein SEC22b OS=Homo sapiens GN=SEC22B PE=1 SV=4	SC22B_HUMAN	25 kDa	5	6	5
Signal recognition particle receptor subunit beta OS=Homo sapiens GN=SRPRB PE=1 SV=3	SRPRB_HUMAN	30 kDa	5	8	2
Pyruvate dehydrogenase E1 component subunit beta, mitochondrial OS=Homo sapiens GN=PDHB PE=1 SV=3	ODPB_HUMAN	39 kDa	5	5	4
Glutathione S-transferase Mu 3 OS=Homo sapiens GN=GSTM3 PE=1 SV=3	GSTM3_HUMAN	27 kDa	5	3	4
40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	RS8_HUMAN	24 kDa	5	4	5
Cytidine deaminase OS=Homo sapiens GN=CDA PE=1 SV=2	CDD_HUMAN	16 kDa	5	3	4
Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1	PCBP2_HUMAN	39 kDa	5	7	6
Beta-1,4-galactosyltransferase 1 OS=Homo sapiens GN=B4GALT1 PE=1 SV=5	B4GT1_HUMAN	44 kDa	5	3	3
Guanine nucleotide-binding protein G(i) subunit alpha-2 OS=Homo sapiens GN=GNAI2 PE=1 SV=3	GNAI2_HUMAN	40 kDa	5	4	3
E3 ubiquitin/ISG15 ligase TRIM25 OS=Homo sapiens GN=TRIM25 PE=1 SV=2	TRI25_HUMAN	71 kDa	5	5	3
CTP synthase 1 OS=Homo sapiens GN=CTPS1 PE=1 SV=2	PYRG1_HUMAN	67 kDa	5	4	3
Ras-related protein Rab-5C OS=Homo sapiens GN=RAB5C PE=1 SV=2	RAB5C_HUMAN	23 kDa	5	4	3
Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	ALDOA_HUMAN	39 kDa	5	3	3
Carnitine O-palmitoyltransferase 1, liver isoform OS=Homo sapiens GN=CPT1A PE=1 SV=2	CPT1A_HUMAN	88 kDa	5	2	2
Glucosamine-6-phosphate isomerase 2 OS=Homo sapiens GN=GNPDA2 PE=1 SV=1	GNPI2_HUMAN	31 kDa	5	2	7
Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1	NDKA_HUMAN	17 kDa	5	6	4
Aldehyde dehydrogenase X, mitochondrial OS=Homo sapiens GN=ALDH1B1 PE=1	AL1B1_HUM	57 kDa	4	7	4

SV=3	AN				
6-phosphofructokinase type C OS=Homo sapiens GN=PFKP PE=1 SV=2	K6PP_HUMAN	86 kDa	4	5	6
T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=4	TCPG_HUMAN	61 kDa	4	7	6
Cyclin-dependent kinase 1 OS=Homo sapiens GN=CDK1 PE=1 SV=3	CDK1_HUMAN	34 kDa	4	5	4
Putative RNA-binding protein Luc7-like 2 OS=Homo sapiens GN=LUC7L2 PE=1 SV=2	LC7L2_HUMAN	47 kDa	4	5	4
Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	FLNB_HUMAN	278 kDa	4	7	5
Trifunctional enzyme subunit beta, mitochondrial OS=Homo sapiens GN=HADHB PE=1 SV=3	ECHB_HUMAN	51 kDa	4	5	5
Glucose-6-phosphate 1-dehydrogenase OS=Homo sapiens GN=G6PD PE=1 SV=4	G6PD_HUMAN	59 kDa	4	4	5
NADH-cytochrome b5 reductase 3 OS=Homo sapiens GN=CYB5R3 PE=1 SV=3	NB5R3_HUMAN	34 kDa	4	6	5
Coatomer subunit beta' OS=Homo sapiens GN=COPB2 PE=1 SV=2	COPB2_HUMAN	102 kDa	4	2	4
ATP synthase subunit O, mitochondrial OS=Homo sapiens GN=ATP5O PE=1 SV=1	ATPO_HUMAN	23 kDa	4	5	6
Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3	THIO_HUMAN	12 kDa	4	5	6
Plasma membrane calcium-transporting ATPase 1 OS=Homo sapiens GN=ATP2B1 PE=1 SV=3	AT2B1_HUMAN	139 kDa	4	4	5
Importin-9 OS=Homo sapiens GN=IPO9 PE=1 SV=3	IPO9_HUMAN	116 kDa	4	7	4
40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4	RS5_HUMAN	23 kDa	4	5	5
Stomatin-like protein 2, mitochondrial OS=Homo sapiens GN=STOML2 PE=1 SV=1	STML2_HUMAN	39 kDa	4	5	5
ATP synthase subunit gamma, mitochondrial OS=Homo sapiens GN=ATP5C1 PE=1 SV=1	ATPG_HUMAN	33 kDa	4	4	4
Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=6	HNRPU_HUMAN	91 kDa	4	2	4
Ras-related protein Rab-2A OS=Homo sapiens GN=RAB2A PE=1 SV=1	RAB2A_HUMAN	24 kDa	4	5	4
Tumor protein D52 OS=Homo sapiens GN=TPD52 PE=1 SV=2	TPD52_HUM	24 kDa	4	5	5

	AN				
ADP-ribosylation factor-like protein 6-interacting protein 4 OS=Homo sapiens GN=ARL6IP4 PE=1 SV=1	AR6P4_HUMAN	38 kDa	4	4	4
Solute carrier family 2, facilitated glucose transporter member 1 OS=Homo sapiens GN=SLC2A1 PE=1 SV=2	GTR1_HUMAN	54 kDa	4	4	4
Podocalyxin OS=Homo sapiens GN=PODXL PE=1 SV=2	PODXL_HUMAN	59 kDa	4	5	4
Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	PPIA_HUMAN	18 kDa	4	4	4
40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=1 SV=2	RS16_HUMAN	16 kDa	4	3	3
Mitochondrial import inner membrane translocase subunit TIM50 OS=Homo sapiens GN=TIMM50 PE=1 SV=2	TIM50_HUMAN	40 kDa	4	3	6
V-type proton ATPase catalytic subunit A OS=Homo sapiens GN=ATP6V1A PE=1 SV=2	VATA_HUMAN	68 kDa	4	4	4
40S ribosomal protein S3a OS=Homo sapiens GN=RPS3A PE=1 SV=2	RS3A_HUMAN	30 kDa	4	3	2
Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3	MAP4_HUMAN	121 kDa	4	7	1
Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	GANAB_HUMAN	107 kDa	4	5	3
Cytochrome c oxidase subunit 4 isoform 1, mitochondrial OS=Homo sapiens GN=COX4I1 PE=1 SV=1	COX41_HUMAN	20 kDa	4	4	3
X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	XRCC5_HUMAN	83 kDa	4	4	3
Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	PDIA1_HUMAN	57 kDa	4	4	3
T-complex protein 1 subunit delta OS=Homo sapiens GN=CCT4 PE=1 SV=4	TCPD_HUMAN	58 kDa	4	3	5
Transforming protein RhoA OS=Homo sapiens GN=RHOA PE=1 SV=1	RHOA_HUMAN	22 kDa	4	4	3
Nuclear cap-binding protein subunit 1 OS=Homo sapiens GN=NCBP1 PE=1 SV=1	NCBP1_HUMAN	92 kDa	4	5	2
Proteasome activator complex subunit 2 OS=Homo sapiens GN=PSME2 PE=1 SV=4	PSME2_HUMAN	27 kDa	4	3	2
Calcium-binding mitochondrial carrier protein Aralar2 OS=Homo sapiens GN=SLC25A13 PE=1 SV=2	CMC2_HUMAN	74 kDa	4	1	2

Coiled-coil domain-containing protein 47 OS=Homo sapiens GN=CCDC47 PE=1 SV=1	CCD47_HUMAN	56 kDa	4	1	1
60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	RL23_HUMAN	15 kDa	4	3	2
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1-related OS=Homo sapiens GN=HMG20B PE=1 SV=1	HM20B_HUMAN	36 kDa	4	0	4
Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2	HPRT_HUMAN	25 kDa	4	3	3
Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	PRDX6_HUMAN	25 kDa	4	3	2
Transmembrane 9 superfamily member 2 OS=Homo sapiens GN=TM9SF2 PE=1 SV=1	TM9S2_HUMAN	76 kDa	4	2	3
14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1	1433E_HUMAN	29 kDa	4	4	6
Coatomer subunit gamma-1 OS=Homo sapiens GN=COPG1 PE=1 SV=1	COPG1_HUMAN	98 kDa	4	4	1
Catechol O-methyltransferase OS=Homo sapiens GN=COMT PE=1 SV=2	COMT_HUMAN	30 kDa	4	4	1
Uridine-cytidine kinase 2 OS=Homo sapiens GN=UCK2 PE=1 SV=1	UCK2_HUMAN	29 kDa	4	3	2
Protein NipSnap homolog 1 OS=Homo sapiens GN=NIPSNAP1 PE=1 SV=1	NIPS1_HUMAN	33 kDa	4	1	2
Epoxide hydrolase 1 OS=Homo sapiens GN=EPHX1 PE=1 SV=1	HYEP_HUMAN	53 kDa	4	1	2
26S protease regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1	PRS4_HUMAN	49 kDa	4	5	0
Ras-related protein Rab-10 OS=Homo sapiens GN=RAB10 PE=1 SV=1	RAB10_HUMAN	23 kDa	4	5	5
Signal peptidase complex subunit 3 OS=Homo sapiens GN=SPCS3 PE=1 SV=1	SPCS3_HUMAN	20 kDa	4	2	2
Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	DPYL2_HUMAN	62 kDa	4	2	2
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2	AIMP2_HUMAN	35 kDa	4	1	2
Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2	RCC2_HUMAN	56 kDa	4	1	1
Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2	SMC2_HUMA	136 kDa	4	2	0

PE=1 SV=2	N				
Peroxiredoxin-4 OS=Homo sapiens GN=PRDX4 PE=1 SV=1	PRDX4_HUMAN	31 kDa	4	4	2
Transcriptional repressor p66-alpha OS=Homo sapiens GN=GATAD2A PE=1 SV=1	P66A_HUMAN	68 kDa	4	0	2
Ras-related protein Rap-1b OS=Homo sapiens GN=RAP1B PE=1 SV=1	RAP1B_HUMAN	21 kDa	4	4	2
REST corepressor 3 OS=Homo sapiens GN=RCOR3 PE=1 SV=2	RCOR3_HUMAN	56 kDa	4	0	5
Isoleucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=IARS PE=1 SV=2	SYIC_HUMAN	145 kDa	3	6	4
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform OS=Homo sapiens GN=PPP2R1A PE=1 SV=4	2AAA_HUMAN	65 kDa	3	6	4
Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2	MAGD2_HUMAN	65 kDa	3	3	5
Poly(U)-binding-splicing factor PUF60 OS=Homo sapiens GN=PUF60 PE=1 SV=1	PUF60_HUMAN	60 kDa	3	5	6
Signal transducer and activator of transcription 1-alpha/beta OS=Homo sapiens GN=STAT1 PE=1 SV=2	STAT1_HUMAN	87 kDa	3	4	4
Peroxisomal multifunctional enzyme type 2 OS=Homo sapiens GN=HSD17B4 PE=1 SV=3	DHB4_HUMAN	80 kDa	3	5	4
Trypsin-1 OS=Homo sapiens GN=PRSS1 PE=1 SV=1	TRY1_HUMAN	27 kDa	3	5	5
40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	RS4X_HUMAN	30 kDa	3	5	4
Serum paraoxonase/arylesterase 2 OS=Homo sapiens GN=PON2 PE=1 SV=3	PON2_HUMAN	39 kDa	3	4	5
T-complex protein 1 subunit eta OS=Homo sapiens GN=CCT7 PE=1 SV=2	TCPH_HUMAN	59 kDa	3	2	5
Sequestosome-1 OS=Homo sapiens GN=SQSTM1 PE=1 SV=1	SQSTM_HUMAN	48 kDa	3	7	3
26S proteasome non-ATPase regulatory subunit 2 OS=Homo sapiens GN=PSMD2 PE=1 SV=3	PSMD2_HUMAN	100 kDa	3	3	3
Sideroflexin-1 OS=Homo sapiens GN=SFXN1 PE=1 SV=4	SFXN1_HUMAN	36 kDa	3	7	2
Basic leucine zipper and W2 domain-containing protein 2 OS=Homo sapiens GN=BZW2 PE=1 SV=1	BZW2_HUMAN	48 kDa	3	4	6

Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	NDKB_HUMAN	17 kDa	3	5	2
Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	ACTN4_HUMAN	105 kDa	3	4	4
ER membrane protein complex subunit 1 OS=Homo sapiens GN=EMC1 PE=1 SV=1	EMC1_HUMAN	112 kDa	3	5	4
Monocarboxylate transporter 4 OS=Homo sapiens GN=SLC16A3 PE=1 SV=1	MOT4_HUMAN	49 kDa	3	4	4
DNA mismatch repair protein Msh6 OS=Homo sapiens GN=MSH6 PE=1 SV=2	MSH6_HUMAN	153 kDa	3	4	3
Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1	S10A4_HUMAN	12 kDa	3	4	4
Tumor protein D54 OS=Homo sapiens GN=TPD52L2 PE=1 SV=2	TPD54_HUMAN	22 kDa	3	4	4
General vesicular transport factor p115 OS=Homo sapiens GN=USO1 PE=1 SV=2	USO1_HUMAN	108 kDa	3	4	3
Squalene synthase OS=Homo sapiens GN=FDFT1 PE=1 SV=1	FDFT_HUMAN	48 kDa	3	4	3
Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=3	TRAP1_HUMAN	80 kDa	3	5	6
Exportin-T OS=Homo sapiens GN=XPOT PE=1 SV=2	XPOT_HUMAN	110 kDa	3	3	5
Catenin alpha-1 OS=Homo sapiens GN=CTNNA1 PE=1 SV=1	CTNA1_HUMAN	100 kDa	3	4	4
Membrane-associated progesterone receptor component 2 OS=Homo sapiens GN=PGRMC2 PE=1 SV=1	PGRC2_HUMAN	24 kDa	3	5	3
Prohibitin-2 OS=Homo sapiens GN=PHB2 PE=1 SV=2	PHB2_HUMAN	33 kDa	3	3	4
40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	RS25_HUMAN	14 kDa	3	3	2
Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	NUCL_HUMAN	77 kDa	3	2	4
Luc7-like protein 3 OS=Homo sapiens GN=LUC7L3 PE=1 SV=2	LC7L3_HUMAN	51 kDa	3	3	2
Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=1 SV=3	ELP1_HUMAN-DECOY	?	3	0	0
B-cell receptor-associated protein 31 OS=Homo sapiens GN=BCAP31 PE=1 SV=3	BAP31_HUM	28 kDa	3	3	3

	AN				
Transmembrane emp24 domain-containing protein 10 OS=Homo sapiens GN=TMED10 PE=1 SV=2	TMEDA_HUMAN	25 kDa	3	4	3
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10 OS=Homo sapiens GN=NDUFB10 PE=1 SV=3	NDUBA_HUMAN	21 kDa	3	3	3
Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2	RTN4_HUMAN	130 kDa	3	4	4
Cytochrome c-type heme lyase OS=Homo sapiens GN=HCCS PE=1 SV=1	CCHL_HUMAN	31 kDa	3	3	3
Extended synaptotagmin-2 OS=Homo sapiens GN=ESYT2 PE=1 SV=1	ESYT2_HUMAN	102 kDa	3	3	3
Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3	ASPH_HUMAN	86 kDa	3	3	2
Surfeit locus protein 4 OS=Homo sapiens GN=SURF4 PE=1 SV=3	SURF4_HUMAN	30 kDa	3	3	3
Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=1 SV=3	SSRA_HUMAN	32 kDa	3	3	5
L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	LDHA_HUMAN	37 kDa	3	4	2
DNA replication licensing factor MCM7 OS=Homo sapiens GN=MCM7 PE=1 SV=4	MCM7_HUMAN	81 kDa	3	3	1
Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	CAND1_HUMAN	136 kDa	3	3	1
Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1	AIFM1_HUMAN	67 kDa	3	3	3
Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1	PTN1_HUMAN	50 kDa	3	3	4
CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2	CD166_HUMAN	65 kDa	3	2	3
ATP synthase F(0) complex subunit B1, mitochondrial OS=Homo sapiens GN=ATP5F1 PE=1 SV=2	AT5F1_HUMAN	29 kDa	3	3	4
Prostaglandin E synthase 2 OS=Homo sapiens GN=PTGES2 PE=1 SV=1	PGES2_HUMAN	42 kDa	3	3	2
Calmodulin OS=Homo sapiens GN=CALM1 PE=1 SV=2	CALM_HUMAN	17 kDa	3	4	2
DnaJ homolog subfamily A member 2 OS=Homo sapiens GN=DNAJA2 PE=1 SV=1	DNJA2_HUMAN	46 kDa	3	2	2

Cytochrome c1, heme protein, mitochondrial OS=Homo sapiens GN=CYC1 PE=1 SV=3	CY1_HUMAN	35 kDa	3	4	2
Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	TAGL2_HUMAN	22 kDa	3	3	3
Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	AIMP1_HUMAN	34 kDa	3	3	2
Ras-related protein Rap-1A OS=Homo sapiens GN=RAP1A PE=1 SV=1	RAP1A_HUMAN	21 kDa	3	2	1
LIM and calponin homology domains-containing protein 1 OS=Homo sapiens GN=LIMCH1 PE=1 SV=4	LIMC1_HUMAN	122 kDa	3	4	1
Catenin delta-1 OS=Homo sapiens GN=CTNND1 PE=1 SV=1	CTND1_HUMAN	108 kDa	3	1	3
Translocon-associated protein subunit delta OS=Homo sapiens GN=SSR4 PE=1 SV=1	SSRD_HUMAN	19 kDa	3	3	3
Dolichol-phosphate mannosyltransferase OS=Homo sapiens GN=DPM1 PE=1 SV=1	DPM1_HUMAN	30 kDa	3	3	2
7-dehydrocholesterol reductase OS=Homo sapiens GN=DHCR7 PE=1 SV=1	DHCR7_HUMAN	54 kDa	3	3	2
TAR DNA-binding protein 43 OS=Homo sapiens GN=TARDBP PE=1 SV=1	TADBP_HUMAN	45 kDa	3	3	2
Mitochondrial 2-oxoglutarate/malate carrier protein OS=Homo sapiens GN=SLC25A11 PE=1 SV=3	M2OM_HUMAN	34 kDa	3	2	3
Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	VDAC1_HUMAN	31 kDa	3	2	4
Protein RER1 OS=Homo sapiens GN=RER1 PE=1 SV=1	RER1_HUMAN	23 kDa	3	3	3
Complement component 1 Q subcomponent-binding protein, mitochondrial OS=Homo sapiens GN=C1QBP PE=1 SV=1	C1QBP_HUMAN	31 kDa	3	3	2
Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1	COPD_HUMAN	57 kDa	3	2	1
Apoptosis regulator BAX OS=Homo sapiens GN=BAX PE=1 SV=1	BAX_HUMAN	21 kDa	3	3	2
Medium-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADM PE=1 SV=1	ACADM_HUMAN	47 kDa	3	3	2
Vesicle-associated membrane protein 7 OS=Homo sapiens GN=VAMP7 PE=1 SV=3	VAMP7_HUMAN	25 kDa	3	3	2
Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	PLAK_HUMA	82 kDa	3	1	3

	N				
Mitotic checkpoint protein BUB3 OS=Homo sapiens GN=BUB3 PE=1 SV=1	BUB3_HUMAN	37 kDa	3	2	1
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-2 OS=Homo sapiens GN=GNB2 PE=1 SV=3	GBB2_HUMAN	37 kDa	3	1	3
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Homo sapiens GN=SDHA PE=1 SV=2	DHSA_HUMAN	73 kDa	3	1	1
14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	1433Z_HUMAN	28 kDa	3	3	5
Vesicle-associated membrane protein 3 OS=Homo sapiens GN=VAMP3 PE=1 SV=3	VAMP3_HUMAN	11 kDa	3	2	3
Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3	TCP4_HUMAN	14 kDa	3	2	3
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 4 OS=Homo sapiens GN=NDUFA4 PE=1 SV=1	NDUA4_HUMAN	9 kDa	3	2	3
LETM1 and EF-hand domain-containing protein 1, mitochondrial OS=Homo sapiens GN=LETM1 PE=1 SV=1	LETM1_HUMAN	83 kDa	3	2	2
40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	RS14_HUMAN	16 kDa	3	3	2
Aspartate--tRNA ligase, cytoplasmic OS=Homo sapiens GN=DARS PE=1 SV=2	SYDC_HUMAN	57 kDa	3	3	2
Protein LSM14 homolog A OS=Homo sapiens GN=LSM14A PE=1 SV=3	LS14A_HUMAN	51 kDa	3	1	2
Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1	HM13_HUMAN	41 kDa	3	3	1
Vesicle-associated membrane protein-associated protein B/C OS=Homo sapiens GN=VAPB PE=1 SV=3	VAPB_HUMAN	27 kDa	3	3	1
Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1	PUR2_HUMAN	108 kDa	3	4	1
Ras-related protein Rab-8A OS=Homo sapiens GN=RAB8A PE=1 SV=1	RAB8A_HUMAN	24 kDa	3	5	3
Nicotinamide N-methyltransferase OS=Homo sapiens GN=NNMT PE=1 SV=1	NNMT_HUMAN	30 kDa	3	2	2
Retinol dehydrogenase 11 OS=Homo sapiens GN=RDH11 PE=1 SV=2	RDH11_HUMAN	35 kDa	3	2	2
Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2	GLU2B_HUMAN	59 kDa	3	3	1

Prohibitin OS=Homo sapiens GN=PHB PE=1 SV=1	PHB_HUMAN	30 kDa	3	1	2
Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	B2MG_HUMAN	14 kDa	3	2	2
Dual specificity mitogen-activated protein kinase kinase 2 OS=Homo sapiens GN=MAP2K2 PE=1 SV=1	MP2K2_HUMAN	44 kDa	3	1	2
Proteasome-associated protein ECM29 homolog OS=Homo sapiens GN=ECM29 PE=1 SV=2	ECM29_HUMAN	204 kDa	3	1	1
Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	IF2G_HUMAN	51 kDa	3	3	0
60S ribosomal protein L31 OS=Homo sapiens GN=RPL31 PE=1 SV=1	RL31_HUMAN	14 kDa	3	3	0
Glutamate--cysteine ligase regulatory subunit OS=Homo sapiens GN=GCLM PE=1 SV=1	GSH0_HUMAN	31 kDa	3	2	1
Methyl-CpG-binding domain protein 3 OS=Homo sapiens GN=MBD3 PE=1 SV=1	MBD3_HUMAN	33 kDa	3	0	3
Transcriptional repressor p66-beta OS=Homo sapiens GN=GATAD2B PE=1 SV=1	P66B_HUMAN	65 kDa	3	0	4
Protein dopey-1 OS=Homo sapiens GN=DOPEY1 PE=2 SV=1	DOP1_HUMAN-DECOY	?	3	0	2
Ras-related protein Rab-32 OS=Homo sapiens GN=RAB32 PE=1 SV=3	RAB32_HUMAN	25 kDa	3	1	1
Secretory carrier-associated membrane protein 3 OS=Homo sapiens GN=SCAMP3 PE=1 SV=3	SCAM3_HUMAN	38 kDa	3	1	1
Keratin, type II cytoskeletal 2 oral OS=Homo sapiens GN=KRT76 PE=1 SV=2	K22O_HUMAN	66 kDa	3	2	2
Very long-chain specific acyl-CoA dehydrogenase, mitochondrial OS=Homo sapiens GN=ACADVL PE=1 SV=1	ACADV_HUMAN	70 kDa	3	0	2
Mesoderm induction early response protein 3 OS=Homo sapiens GN=MIER3 PE=1 SV=2	MIER3_HUMAN	61 kDa	3	0	1
FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2	FAF2_HUMAN	53 kDa	3	0	1
Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2	K2C79_HUMAN	58 kDa	3	5	0
Cyclin-dependent kinase 2 OS=Homo sapiens GN=CDK2 PE=1 SV=2	CDK2_HUMAN	34 kDa	3	3	3
Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1	CATZ_HUMAN	34 kDa	3	0	1

Hemicentin-1 OS=Homo sapiens GN=HMCN1 PE=1 SV=2	HMCN1_HUMAN-DECOY	?	3	0	0
Nucleoporin NUP188 homolog OS=Homo sapiens GN=NUP188 PE=1 SV=1	NU188_HUMAN	196 kDa	3	0	0
Arf-GAP with SH3 domain, ANK repeat and PH domain-containing protein 1 OS=Homo sapiens GN=ASAP1 PE=1 SV=4	ASAP1_HUMAN-DECOY	?	3	0	0
Myosin regulatory light chain 2, skeletal muscle isoform OS=Homo sapiens GN=MYLPF PE=2 SV=1	MLRS_HUMAN	19 kDa	3	0	0
Titin OS=Homo sapiens GN=TTN PE=1 SV=4	TITIN_HUMAN	3816 kDa	2	2	4
Titin OS=Homo sapiens GN=TTN PE=1 SV=4	TITIN_HUMAN-DECOY	?	2	2	2
Methionine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=MARS PE=1 SV=2	SYMC_HUMAN	101 kDa	2	4	3
26S proteasome non-ATPase regulatory subunit 3 OS=Homo sapiens GN=PSMD3 PE=1 SV=2	PSMD3_HUMAN	61 kDa	2	5	5
Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A PE=1 SV=1	2ABA_HUMAN	52 kDa	2	5	2
Signal recognition particle 54 kDa protein OS=Homo sapiens GN=SRP54 PE=1 SV=1	SRP54_HUMAN	56 kDa	2	1	2
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE=1 SV=2	STT3A_HUMAN	81 kDa	2	3	3
T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1	TCPE_HUMAN	60 kDa	2	4	3
Neural cell adhesion molecule L1 OS=Homo sapiens GN=L1CAM PE=1 SV=2	L1CAM_HUMAN	140 kDa	2	5	3
X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	XRCC6_HUMAN	70 kDa	2	5	3
Serine/threonine-protein kinase ATR OS=Homo sapiens GN=ATR PE=1 SV=3	ATR_HUMAN	301 kDa	2	4	0
F-actin-capping protein subunit beta OS=Homo sapiens GN=CAPZB PE=1 SV=4	CAPZB_HUMAN	31 kDa	2	2	3
Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	YBOX1_HUMAN	36 kDa	2	2	2
Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	DESP_HUMAN	332 kDa	2	4	2
Lon protease homolog, mitochondrial OS=Homo sapiens GN=LONP1 PE=1 SV=2	LONM_HUMAN	106 kDa	2	3	3

Rootletin OS=Homo sapiens GN=CROCC PE=1 SV=1	CROCC_HUMAN	229 kDa	2	0	2
Cleft lip and palate transmembrane protein 1 OS=Homo sapiens GN=CLPTM1 PE=1 SV=1	CLPT1_HUMAN	76 kDa	2	4	2
NADPH--cytochrome P450 reductase OS=Homo sapiens GN=POR PE=1 SV=2	NCPR_HUMAN	77 kDa	2	3	2
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3	GFPT1_HUMAN	79 kDa	2	4	3
Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	ENOA_HUMAN	47 kDa	2	4	1
Microsomal glutathione S-transferase 1 OS=Homo sapiens GN=MGST1 PE=1 SV=1	MGST1_HUMAN	18 kDa	2	2	4
Centrosomal protein of 290 kDa OS=Homo sapiens GN=CEP290 PE=1 SV=2	CE290_HUMAN	290 kDa	2	0	2
Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	S10AB_HUMAN	12 kDa	2	3	0
Coiled-coil domain-containing protein 18 OS=Homo sapiens GN=CCDC18 PE=2 SV=1	CCD18_HUMAN	169 kDa	2	0	0
Signal peptidase complex catalytic subunit SEC11A OS=Homo sapiens GN=SEC11A PE=1 SV=1	SC11A_HUMAN	21 kDa	2	3	3
Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial OS=Homo sapiens GN=IDH3A PE=1 SV=1	IDH3A_HUMAN	40 kDa	2	4	3
Eukaryotic peptide chain release factor GTP-binding subunit ERF3A OS=Homo sapiens GN=GSPT1 PE=1 SV=1	ERF3A_HUMAN	56 kDa	2	4	3
Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=2	TMED9_HUMAN	27 kDa	2	3	3
Sulfide:quinone oxidoreductase, mitochondrial OS=Homo sapiens GN=SQRDL PE=1 SV=1	SQRD_HUMAN	50 kDa	2	2	3
Histone H2B type 1-B OS=Homo sapiens GN=HIST1H2BB PE=1 SV=2	H2B1B_HUMAN (+12)	14 kDa	2	3	4
Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3	EF1B_HUMAN	25 kDa	2	3	3
S-adenosylmethionine synthase isoform type-2 OS=Homo sapiens GN=MAT2A PE=1 SV=1	METK2_HUMAN	44 kDa	2	4	2
Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	HNRPM_HUMAN	78 kDa	2	4	1
Bone marrow stromal antigen 2 OS=Homo sapiens GN=BST2 PE=1 SV=1	BST2_HUMA	20 kDa	2	3	3

	N				
Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	QCR1_HUMAN	53 kDa	2	4	2
Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1	RCN1_HUMAN	39 kDa	2	3	2
Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24 PE=1 SV=2	SCMC1_HUMAN	53 kDa	2	2	2
Ran GTPase-activating protein 1 OS=Homo sapiens GN=RANGAP1 PE=1 SV=1	RAGP1_HUMAN	64 kDa	2	3	3
Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens GN=VDAC2 PE=1 SV=2	VDAC2_HUMAN	32 kDa	2	2	4
26S proteasome non-ATPase regulatory subunit 6 OS=Homo sapiens GN=PSMD6 PE=1 SV=1	PSMD6_HUMAN	46 kDa	2	3	3
tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2	NSUN2_HUMAN	86 kDa	2	2	2
Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	MOES_HUMAN	68 kDa	2	2	3
Calcineurin-like phosphoesterase domain-containing protein 1 OS=Homo sapiens GN=CPPED1 PE=1 SV=3	CPPED_HUMAN	36 kDa	2	1	2
40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3	RS27_HUMAN	9 kDa	2	3	2
Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	PCNA_HUMAN	29 kDa	2	4	1
60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	RL22_HUMAN	15 kDa	2	1	2
Nuclear pore complex protein Nup93 OS=Homo sapiens GN=NUP93 PE=1 SV=2	NUP93_HUMAN	93 kDa	2	1	1
Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	LAMP1_HUMAN	45 kDa	2	3	2
26S proteasome non-ATPase regulatory subunit 1 OS=Homo sapiens GN=PSMD1 PE=1 SV=2	PSMD1_HUMAN	106 kDa	2	4	2
Neuron navigator 2 OS=Homo sapiens GN=NAV2 PE=1 SV=3	NAV2_HUMAN	268 kDa	2	1	0
Protein transport protein Sec61 subunit beta OS=Homo sapiens GN=SEC61B PE=1 SV=2	SC61B_HUMAN	10 kDa	2	2	3
Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=1 SV=1	EIF3F_HUMAN	38 kDa	2	2	3

Protein TBRG4 OS=Homo sapiens GN=TBRG4 PE=1 SV=1	TBRG4_HUMAN	71 kDa	2	2	3
Glutathione S-transferase P OS=Homo sapiens GN=GSTP1 PE=1 SV=2	GSTP1_HUMAN	23 kDa	2	2	3
Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	NUDC_HUMAN	38 kDa	2	2	3
Protein disulfide-isomerase A6 OS=Homo sapiens GN=PDIA6 PE=1 SV=1	PDIA6_HUMAN	48 kDa	2	3	2
Serine/threonine-protein phosphatase 6 regulatory subunit 3 OS=Homo sapiens GN=PPP6R3 PE=1 SV=2	PP6R3_HUMAN	98 kDa	2	2	2
26S proteasome non-ATPase regulatory subunit 12 OS=Homo sapiens GN=PSMD12 PE=1 SV=3	PSD12_HUMAN	53 kDa	2	3	2
Nicotinamide phosphoribosyltransferase OS=Homo sapiens GN=NAMPT PE=1 SV=1	NAMPT_HUMAN	56 kDa	2	3	2
Delta(24)-sterol reductase OS=Homo sapiens GN=DHCR24 PE=1 SV=2	DHC24_HUMAN	60 kDa	2	3	2
Receptor expression-enhancing protein 5 OS=Homo sapiens GN=REEP5 PE=1 SV=3	REEP5_HUMAN	21 kDa	2	3	2
Monocarboxylate transporter 1 OS=Homo sapiens GN=SLC16A1 PE=1 SV=3	MOT1_HUMAN	54 kDa	2	2	2
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1	STT3B_HUMAN	94 kDa	2	2	3
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating OS=Homo sapiens GN=NSDHL PE=1 SV=2	NSDHL_HUMAN	42 kDa	2	3	1
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1 OS=Homo sapiens GN=DAD1 PE=1 SV=3	DAD1_HUMAN	12 kDa	2	2	2
7,8-dihydro-8-oxoguanine triphosphatase OS=Homo sapiens GN=NUDT1 PE=1 SV=3	8ODP_HUMAN	23 kDa	2	2	2
26S proteasome non-ATPase regulatory subunit 13 OS=Homo sapiens GN=PSMD13 PE=1 SV=2	PSD13_HUMAN	43 kDa	2	3	1
Tubulin-specific chaperone D OS=Homo sapiens GN=TBCD PE=1 SV=2	TBCD_HUMAN	133 kDa	2	4	0
PRA1 family protein 3 OS=Homo sapiens GN=ARL6IP5 PE=1 SV=1	PRAF3_HUMAN	22 kDa	2	2	2
ATP synthase subunit f, mitochondrial OS=Homo sapiens GN=ATP5J2 PE=1 SV=3	ATPK_HUMAN	11 kDa	2	2	2
Signal peptidase complex subunit 2 OS=Homo sapiens GN=SPCS2 PE=1 SV=3	SPCS2_HUM	25 kDa	2	2	2

	AN				
40S ribosomal protein SA OS=Homo sapiens GN=RPSA PE=1 SV=4	RSSA_HUMAN	33 kDa	2	2	2
Cleft lip and palate transmembrane protein 1-like protein OS=Homo sapiens GN=CLPTM1L PE=1 SV=1	CLP1L_HUMAN	62 kDa	2	2	2
40S ribosomal protein S26 OS=Homo sapiens GN=RPS26 PE=1 SV=3	RS26_HUMAN	13 kDa	2	2	2
Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2	SCRB2_HUMAN	54 kDa	2	2	2
5'-nucleotidase domain-containing protein 2 OS=Homo sapiens GN=NT5DC2 PE=1 SV=1	NT5D2_HUMAN	61 kDa	2	2	2
40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=2	RS15A_HUMAN	15 kDa	2	1	2
Lysophosphatidylcholine acyltransferase 1 OS=Homo sapiens GN=LPCAT1 PE=1 SV=2	PCAT1_HUMAN	59 kDa	2	2	1
60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1	RL24_HUMAN	18 kDa	2	1	1
PI-PLC X domain-containing protein 2 OS=Homo sapiens GN=PLCXD2 PE=2 SV=1	PLCX2_HUMAN	35 kDa	2	2	2
Mannose-P-dolichol utilization defect 1 protein OS=Homo sapiens GN=MPDU1 PE=1 SV=2	MPU1_HUMAN	27 kDa	2	2	2
Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=3	PUR6_HUMAN	47 kDa	2	2	2
F-actin-capping protein subunit alpha-1 OS=Homo sapiens GN=CAPZA1 PE=1 SV=3	CAZA1_HUMAN	33 kDa	2	1	2
Protein pelota homolog OS=Homo sapiens GN=PELO PE=1 SV=2	PELO_HUMAN	43 kDa	2	3	1
Reticulocalbin-2 OS=Homo sapiens GN=RCN2 PE=1 SV=1	RCN2_HUMAN	37 kDa	2	1	1
CD97 antigen OS=Homo sapiens GN=CD97 PE=1 SV=4	CD97_HUMAN	92 kDa	2	3	1
Ras-related protein Rab-6A OS=Homo sapiens GN=RAB6A PE=1 SV=3	RAB6A_HUMAN	24 kDa	2	3	2
Saccharopine dehydrogenase-like oxidoreductase OS=Homo sapiens GN=SCCPDH PE=1 SV=1	SCPDL_HUMAN	47 kDa	2	1	1
ATP synthase-coupling factor 6, mitochondrial OS=Homo sapiens GN=ATP5J PE=1 SV=1	ATP5J_HUMAN	13 kDa	2	2	1

60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	RL7A_HUMAN	30 kDa	2	2	1
Glutamine--tRNA ligase OS=Homo sapiens GN=QARS PE=1 SV=1	SYQ_HUMAN	88 kDa	2	3	0
Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	ITA3_HUMAN	117 kDa	2	0	3
Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1	PDS5A_HUMAN	151 kDa	2	0	2
Collagen alpha-3(VI) chain OS=Homo sapiens GN=COL6A3 PE=1 SV=5	CO6A3_HUMAN-DECOY	?	2	0	0
RNA-binding protein EWS OS=Homo sapiens GN=EWSR1 PE=1 SV=1	EWS_HUMAN	68 kDa	2	2	1
40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	RS6_HUMAN	29 kDa	2	2	1
ER membrane protein complex subunit 2 OS=Homo sapiens GN=EMC2 PE=1 SV=1	EMC2_HUMAN	35 kDa	2	2	1
Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1	SPTC1_HUMAN	53 kDa	2	2	1
Up-regulated during skeletal muscle growth protein 5 OS=Homo sapiens GN=USMG5 PE=1 SV=1	USMG5_HUMAN	6 kDa	2	1	2
40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1	RS10_HUMAN	19 kDa	2	1	1
ADP-ribosylation factor-like protein 1 OS=Homo sapiens GN=ARL1 PE=1 SV=1	ARL1_HUMAN	20 kDa	2	1	2
Ras-related protein Ral-A OS=Homo sapiens GN=RALA PE=1 SV=1	RALA_HUMAN	24 kDa	2	1	2
Vacuole membrane protein 1 OS=Homo sapiens GN=VMP1 PE=1 SV=1	VMP1_HUMAN	46 kDa	2	1	2
Myotrophin OS=Homo sapiens GN=MTPN PE=1 SV=2	MTPN_HUMAN	13 kDa	2	1	1
Transmembrane protein 43 OS=Homo sapiens GN=TMEM43 PE=1 SV=1	TMM43_HUMAN	45 kDa	2	1	2
Thioredoxin-related transmembrane protein 1 OS=Homo sapiens GN=TMX1 PE=1 SV=1	TMX1_HUMAN	32 kDa	2	1	1
Protein S100-A16 OS=Homo sapiens GN=S100A16 PE=1 SV=1	S10AG_HUMAN	12 kDa	2	1	2
40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	RS20_HUMAN	13 kDa	2	1	1
60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=2	RL18_HUMA	22 kDa	2	2	1

	N				
ADP-ribosylation factor-like protein 8B OS=Homo sapiens GN=ARL8B PE=1 SV=1	ARL8B_HUMAN	22 kDa	2	2	1
Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2	H2A1B_HUMAN (+7)	14 kDa	2	2	1
Calponin-3 OS=Homo sapiens GN=CNN3 PE=1 SV=1	CNN3_HUMAN	36 kDa	2	2	4
ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3	ATP5H_HUMAN	18 kDa	2	2	1
Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	K2C80_HUMAN	51 kDa	2	3	2
Protein Shroom3 OS=Homo sapiens GN=SHROOM3 PE=1 SV=2	SHRM3_HUMAN	217 kDa	2	0	1
Mucin-2 OS=Homo sapiens GN=MUC2 PE=1 SV=2	MUC2_HUMAN-DECOY	?	2	1	0
40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	RS12_HUMAN	15 kDa	2	2	0
Mitochondrial import inner membrane translocase subunit TIM44 OS=Homo sapiens GN=TIMM44 PE=1 SV=2	TIM44_HUMAN	51 kDa	2	3	0
Golgin subfamily A member 2 OS=Homo sapiens GN=GOLGA2 PE=1 SV=3	GOGA2_HUMAN	113 kDa	2	1	0
Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52 PE=1 SV=2	RL40_HUMAN (+3)	15 kDa	2	1	1
Delta-1-pyrroline-5-carboxylate synthase OS=Homo sapiens GN=ALDH18A1 PE=1 SV=2	P5CS_HUMAN	87 kDa	2	1	1
Inverted formin-2 OS=Homo sapiens GN=INF2 PE=1 SV=2	INF2_HUMAN	136 kDa	2	1	1
Ras-related protein Rab-18 OS=Homo sapiens GN=RAB18 PE=1 SV=1	RAB18_HUMAN	23 kDa	2	1	1
40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1	RS7_HUMAN	22 kDa	2	1	1
Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4	CBX3_HUMAN	21 kDa	2	1	1
Torsin-1A-interacting protein 1 OS=Homo sapiens GN=TOR1AIP1 PE=1 SV=2	TOIP1_HUMAN	66 kDa	2	1	1
Aldo-keto reductase family 1 member C1 OS=Homo sapiens GN=AKR1C1 PE=1 SV=1	AK1C1_HUMAN	37 kDa	2	1	1
Annexin A1 OS=Homo sapiens GN=ANXA1 PE=1 SV=2	ANXA1_HUM	39 kDa	2	1	1

	AN				
MMS19 nucleotide excision repair protein homolog OS=Homo sapiens GN=MMS19 PE=1 SV=2	MMS19_HUMAN	113 kDa	2	1	1
Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3	DC1I2_HUMAN	71 kDa	2	0	1
60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2	RL27A_HUMAN	17 kDa	2	2	0
Peflin OS=Homo sapiens GN=PEF1 PE=1 SV=1	PEF1_HUMAN	30 kDa	2	2	0
Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2	IPYR_HUMAN	33 kDa	2	2	0
Chromodomain Y-like protein OS=Homo sapiens GN=CDYL PE=1 SV=2	CDYL1_HUMAN	66 kDa	2	0	2
Ubiquitin carboxyl-terminal hydrolase 5 OS=Homo sapiens GN=USP5 PE=1 SV=2	UBP5_HUMAN	96 kDa	2	1	0
ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2	ATPD_HUMAN	17 kDa	2	2	0
Inhibitor of nuclear factor kappa-B kinase-interacting protein OS=Homo sapiens GN=IKBIP PE=1 SV=1	IKIP_HUMAN	39 kDa	2	0	1
Signal recognition particle receptor subunit alpha OS=Homo sapiens GN=SRPR PE=1 SV=2	SRPR_HUMAN	70 kDa	2	0	1
Serine protease 56 OS=Homo sapiens GN=PRSS56 PE=1 SV=1	PRS56_HUMAN-DECOY	?	2	0	0
Bromodomain adjacent to zinc finger domain protein 1A OS=Homo sapiens GN=BAZ1A PE=1 SV=2	BAZ1A_HUMAN	179 kDa	2	0	1
Oxidoreductase HTATIP2 OS=Homo sapiens GN=HTATIP2 PE=1 SV=2	HTAI2_HUMAN	27 kDa	2	0	0
Ectopic P granules protein 5 homolog OS=Homo sapiens GN=EPG5 PE=2 SV=2	EPG5_HUMAN	292 kDa	2	0	0
Leucine-rich repeat flightless-interacting protein 1 OS=Homo sapiens GN=LRRFIP1 PE=1 SV=2	LRRF1_HUMAN	89 kDa	2	1	0
Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1	FA98B_HUMAN	37 kDa	2	1	0
NADH-cytochrome b5 reductase 1 OS=Homo sapiens GN=CYB5R1 PE=1 SV=1	NB5R1_HUMAN	34 kDa	2	1	0
Catenin beta-1 OS=Homo sapiens GN=CTNNB1 PE=1 SV=1	CTNB1_HUMAN	85 kDa	2	1	0

Endophilin-A2 OS=Homo sapiens GN=SH3GL1 PE=1 SV=1	SH3G1_HUMAN	41 kDa	2	0	1
Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=1 SV=2	S61A1_HUMAN	52 kDa	2	1	0
Actin-binding protein anillin OS=Homo sapiens GN=ANLN PE=1 SV=2	ANLN_HUMAN	124 kDa	2	1	0
Sodium-coupled neutral amino acid transporter 5 OS=Homo sapiens GN=SLC38A5 PE=1 SV=1	S38A5_HUMAN	51 kDa	2	0	1
Tripartite motif-containing protein 16 OS=Homo sapiens GN=TRIM16 PE=1 SV=3	TRI16_HUMAN	64 kDa	2	1	0
Equilibrative nucleoside transporter 1 OS=Homo sapiens GN=SLC29A1 PE=1 SV=3	S29A1_HUMAN	50 kDa	2	0	0
Junction-mediating and -regulatory protein OS=Homo sapiens GN=JMY PE=1 SV=2	JMY_HUMAN	111 kDa	2	0	0
Regulating synaptic membrane exocytosis protein 2 OS=Homo sapiens GN=RIMS2 PE=1 SV=2	RIMS2_HUMAN	160 kDa	2	0	0
Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4	SYVC_HUMAN	140 kDa	2	0	0
Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=1 SV=3	SYTC_HUMAN	83 kDa	2	0	0
Ubiquitin carboxyl-terminal hydrolase isozyme L5 OS=Homo sapiens GN=UCHL5 PE=1 SV=3	UCHL5_HUMAN	38 kDa	2	0	0
Mitogen-activated protein kinase kinase kinase 10 OS=Homo sapiens GN=MAP3K10 PE=1 SV=3	M3K10_HUMAN	104 kDa	2	0	0
Coiled-coil domain-containing protein 60 OS=Homo sapiens GN=CCDC60 PE=2 SV=2	CCD60_HUMAN	63 kDa	2	0	0
Nesprin-2 OS=Homo sapiens GN=SYNE2 PE=1 SV=3	SYNE2_HUMAN	796 kDa	1	2	8
Mucin-16 OS=Homo sapiens GN=MUC16 PE=1 SV=2	MUC16_HUMAN-DECOY	?	1	0	3
Thyroid receptor-interacting protein 11 OS=Homo sapiens GN=TRIP11 PE=1 SV=3	TRIPB_HUMAN	228 kDa	1	0	4
40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	RS11_HUMAN	18 kDa	1	2	4
E3 ubiquitin-protein ligase TRIM21 OS=Homo sapiens GN=TRIM21 PE=1 SV=1	RO52_HUMAN	54 kDa	1	3	1
Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	FUBP2_HUMAN	73 kDa	1	3	3

Leucine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=LARS PE=1 SV=2	SYLC_HUMAN	134 kDa	1	5	2
Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1	AT1B3_HUMAN	32 kDa	1	2	3
Nodal modulator 1 OS=Homo sapiens GN=NOMO1 PE=1 SV=5	NOMO1_HUMAN (+2)	134 kDa	1	2	2
Polyhomeotic-like protein 2 OS=Homo sapiens GN=PHC2 PE=1 SV=1	PHC2_HUMAN	91 kDa	1	2	0
Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1	KINH_HUMAN	110 kDa	1	2	2
DnaJ homolog subfamily C member 7 OS=Homo sapiens GN=DNAJC7 PE=1 SV=2	DNJC7_HUMAN	56 kDa	1	3	1
Calpastatin OS=Homo sapiens GN=CAST PE=1 SV=4	ICAL_HUMAN	77 kDa	1	2	1
Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3	PRDX3_HUMAN	28 kDa	1	3	2
40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3	RS9_HUMAN	23 kDa	1	1	2
Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	PSME1_HUMAN	29 kDa	1	2	3
Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial OS=Homo sapiens GN=PDHA1 PE=1 SV=3	ODPA_HUMAN	43 kDa	1	3	2
Ubiquilin-1 OS=Homo sapiens GN=UBQLN1 PE=1 SV=2	UBQL1_HUMAN	63 kDa	1	3	3
Elongator complex protein 1 OS=Homo sapiens GN=IKBKAP PE=1 SV=3	ELP1_HUMAN	150 kDa	1	3	4
Very-long-chain enoyl-CoA reductase OS=Homo sapiens GN=TECR PE=1 SV=1	TECR_HUMAN	36 kDa	1	2	2
Uncharacterized protein C2orf47, mitochondrial OS=Homo sapiens GN=C2orf47 PE=1 SV=1	CB047_HUMAN	33 kDa	1	2	2
Transmembrane protein 33 OS=Homo sapiens GN=TMEM33 PE=1 SV=2	TMM33_HUMAN	28 kDa	1	2	2
Mitochondrial carrier homolog 2 OS=Homo sapiens GN=MTCH2 PE=1 SV=1	MTCH2_HUMAN	33 kDa	1	2	1
Eukaryotic translation initiation factor 3 subunit B OS=Homo sapiens GN=EIF3B PE=1 SV=3	EIF3B_HUMAN	92 kDa	1	3	2
Transmembrane 9 superfamily member 3 OS=Homo sapiens GN=TM9SF3 PE=1 SV=2	TM9S3_HUMAN	68 kDa	1	2	2

Pyridoxal-dependent decarboxylase domain-containing protein 1 OS=Homo sapiens GN=PDXDC1 PE=1 SV=2	PDXD1_HUMAN	87 kDa	1	1	3
GTPase-activating protein and VPS9 domain-containing protein 1 OS=Homo sapiens GN=GAPVD1 PE=1 SV=2	GAPD1_HUMAN	165 kDa	1	2	1
Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens GN=FKBP8 PE=1 SV=2	FKBP8_HUMAN	45 kDa	1	2	1
Glutathione S-transferase kappa 1 OS=Homo sapiens GN=GSTK1 PE=1 SV=3	GSTK1_HUMAN	25 kDa	1	3	2
Mitochondrial dicarboxylate carrier OS=Homo sapiens GN=SLC25A10 PE=1 SV=2	DIC_HUMAN	31 kDa	1	2	3
Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1	STRAP_HUMAN	38 kDa	1	2	2
Folate receptor alpha OS=Homo sapiens GN=FOLR1 PE=1 SV=3	FOLR1_HUMAN	30 kDa	1	2	2
26S protease regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2	PRS6B_HUMAN	47 kDa	1	3	1
Histone acetyltransferase type B catalytic subunit OS=Homo sapiens GN=HAT1 PE=1 SV=1	HAT1_HUMAN	50 kDa	1	3	1
NAD(P)H dehydrogenase [quinone] 1 OS=Homo sapiens GN=NQO1 PE=1 SV=1	NQO1_HUMAN	31 kDa	1	1	2
Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3	MPRI_HUMAN	274 kDa	1	1	3
UDP-glucose 6-dehydrogenase OS=Homo sapiens GN=UGDH PE=1 SV=1	UGDH_HUMAN	55 kDa	1	2	1
Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	PROF1_HUMAN	15 kDa	1	2	1
Multidrug resistance-associated protein 1 OS=Homo sapiens GN=ABCC1 PE=1 SV=3	MRP1_HUMAN	172 kDa	1	1	2
CDP-diacylglycerol--inositol 3-phosphatidyltransferase OS=Homo sapiens GN=CDIPT PE=1 SV=1	CDIPT_HUMAN	24 kDa	1	2	1
Probable ubiquitin carboxyl-terminal hydrolase FAF-X OS=Homo sapiens GN=USP9X PE=1 SV=3	USP9X_HUMAN	292 kDa	1	2	1
Protein jagunal homolog 1 OS=Homo sapiens GN=JAGN1 PE=1 SV=1	JAGN1_HUMAN	21 kDa	1	1	2
Probable glutathione peroxidase 8 OS=Homo sapiens GN=GPX8 PE=1 SV=2	GPX8_HUMAN	24 kDa	1	2	2
Proteasome subunit alpha type-7 OS=Homo sapiens GN=PSMA7 PE=1 SV=1	PSA7_HUMAN	28 kDa	1	3	1

Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	MIF_HUMAN	12 kDa	1	2	2
40S ribosomal protein S13 OS=Homo sapiens GN=RPS13 PE=1 SV=2	RS13_HUMAN	17 kDa	1	2	1
Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4	MYO1C_HUMAN	122 kDa	1	1	2
N-acetylgalactosaminyltransferase 7 OS=Homo sapiens GN=GALNT7 PE=1 SV=1	GALT7_HUMAN	75 kDa	1	2	1
Non-specific lipid-transfer protein OS=Homo sapiens GN=SCP2 PE=1 SV=2	NLTP_HUMAN	59 kDa	1	1	2
Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2	LYRIC_HUMAN	64 kDa	1	2	1
26S proteasome non-ATPase regulatory subunit 7 OS=Homo sapiens GN=PSMD7 PE=1 SV=2	PSMD7_HUMAN	37 kDa	1	3	1
Ornithine aminotransferase, mitochondrial OS=Homo sapiens GN=OAT PE=1 SV=1	OAT_HUMAN	49 kDa	1	0	2
Importin-11 OS=Homo sapiens GN=IPO11 PE=1 SV=1	IPO11_HUMAN	113 kDa	1	0	2
Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3	CKAP5_HUMAN	226 kDa	1	2	0
Cytoplasmic dynein 2 heavy chain 1 OS=Homo sapiens GN=DYNC2H1 PE=1 SV=4	DYHC2_HUMAN	493 kDa	1	0	2
Sodium-coupled neutral amino acid transporter 2 OS=Homo sapiens GN=SLC38A2 PE=1 SV=2	S38A2_HUMAN	56 kDa	1	2	1
Trypsin-3 OS=Homo sapiens GN=PRSS3 PE=1 SV=2	TRY3_HUMAN	33 kDa	1	2	1
GTP-binding protein SAR1a OS=Homo sapiens GN=SAR1A PE=1 SV=1	SAR1A_HUMAN (+1)	22 kDa	1	2	1
Integrin alpha-5 OS=Homo sapiens GN=ITGA5 PE=1 SV=2	ITA5_HUMAN	115 kDa	1	1	2
Polyadenylate-binding protein 4 OS=Homo sapiens GN=PABPC4 PE=1 SV=1	PABP4_HUMAN	71 kDa	1	1	2
3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase OS=Homo sapiens GN=EBP PE=1 SV=3	EBP_HUMAN	26 kDa	1	1	2
Peptidyl-prolyl cis-trans isomerase FKBP11 OS=Homo sapiens GN=FKBP11 PE=1 SV=1	FKB11_HUMAN	22 kDa	1	1	2
40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1	RS24_HUMAN	15 kDa	1	2	1

Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2	SRP09_HUMAN	10 kDa	1	2	1
cGMP-inhibited 3',5'-cyclic phosphodiesterase A OS=Homo sapiens GN=PDE3A PE=1 SV=3	PDE3A_HUMAN	125 kDa	1	2	1
Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1	SGTA_HUMAN	34 kDa	1	2	1
Membrane-associated progesterone receptor component 1 OS=Homo sapiens GN=PGRMC1 PE=1 SV=3	PGRC1_HUMAN	22 kDa	1	3	1
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial OS=Homo sapiens GN=ECH1 PE=1 SV=2	ECH1_HUMAN	36 kDa	1	2	1
26S proteasome non-ATPase regulatory subunit 14 OS=Homo sapiens GN=PSMD14 PE=1 SV=1	PSDE_HUMAN	35 kDa	1	2	1
Exportin-7 OS=Homo sapiens GN=XPO7 PE=1 SV=3	XPO7_HUMAN	124 kDa	1	2	1
UPF0568 protein C14orf166 OS=Homo sapiens GN=C14orf166 PE=1 SV=1	CN166_HUMAN	28 kDa	1	2	0
26S protease regulatory subunit 10B OS=Homo sapiens GN=PSMC6 PE=1 SV=1	PRS10_HUMAN	44 kDa	1	3	0
Growth factor receptor-bound protein 2 OS=Homo sapiens GN=GRB2 PE=1 SV=1	GRB2_HUMAN	25 kDa	1	2	0
2-oxoglutarate dehydrogenase, mitochondrial OS=Homo sapiens GN=OGDH PE=1 SV=3	ODO1_HUMAN (+1)	116 kDa	1	2	0
Lanosterol synthase OS=Homo sapiens GN=LSS PE=1 SV=1	ERG7_HUMAN	83 kDa	1	2	0
Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1	DDX5_HUMAN	69 kDa	1	2	0
Aladin OS=Homo sapiens GN=AAAS PE=1 SV=1	AAAS_HUMAN	60 kDa	1	0	2
Histone deacetylase 4 OS=Homo sapiens GN=HDAC4 PE=1 SV=3	HDAC4_HUMAN	119 kDa	0	0	123
Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4	MACF1_HUMAN	838 kDa	0	3	0
Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5 OS=Homo sapiens GN=MACF1 PE=1 SV=4	MACF1_HUMAN-DECOY	?	0	4	1
Dynein heavy chain 5, axonemal OS=Homo sapiens GN=DNAH5 PE=1 SV=3	DYH5_HUMAN	529 kDa	0	3	1
Structural maintenance of chromosomes protein 5 OS=Homo sapiens GN=SMC5	SMC5_HUMA	129 kDa	0	0	5

PE=1 SV=2	N				
Serine/threonine-protein kinase SMG1 OS=Homo sapiens GN=SMG1 PE=1 SV=3	SMG1_HUMAN	410 kDa	0	2	0
Histone-lysine N-methyltransferase ASH1L OS=Homo sapiens GN=ASH1L PE=1 SV=2	ASH1L_HUMAN	333 kDa	0	1	2
26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens GN=PSMD11 PE=1 SV=3	PSD11_HUMAN	47 kDa	0	3	0
Ankyrin repeat domain-containing protein 26 OS=Homo sapiens GN=ANKRD26 PE=1 SV=3	ANR26_HUMAN	196 kDa	0	0	2
Rho guanine nucleotide exchange factor 17 OS=Homo sapiens GN=ARHGEF17 PE=1 SV=1	ARHGH_HUMAN	222 kDa	0	0	6
Cardiomyopathy-associated protein 5 OS=Homo sapiens GN=CMYA5 PE=1 SV=3	CMYA5_HUMAN-DECOY	?	0	0	2
Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	LMNA_HUMAN	74 kDa	0	2	3
Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	COPB_HUMAN	107 kDa	0	2	2
Long-chain-fatty-acid--CoA ligase 4 OS=Homo sapiens GN=ACSL4 PE=1 SV=2	ACSL4_HUMAN	79 kDa	0	2	3
Nebulin OS=Homo sapiens GN=NEB PE=1 SV=4	NEBU_HUMAN	773 kDa	0	2	1
E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=1 SV=3	RN213_HUMAN-DECOY	?	0	0	2
Calmin OS=Homo sapiens GN=CLMN PE=1 SV=1	CLMN_HUMAN-DECOY	?	0	2	0
Triple functional domain protein OS=Homo sapiens GN=TRIO PE=1 SV=2	TRIO_HUMAN	347 kDa	0	0	3
60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2	RL38_HUMAN	8 kDa	0	2	0
Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	TERA_HUMAN	89 kDa	0	2	3
Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=4	U2AF2_HUMAN	54 kDa	0	2	2
Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	LEG1_HUMAN	15 kDa	0	3	2
Electron transfer flavoprotein subunit alpha, mitochondrial OS=Homo sapiens GN=ETFA PE=1 SV=1	ETFA_HUMAN	35 kDa	0	2	1

DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3	MCM3_HUMAN	91 kDa	0	2	2
Vacuolar protein sorting-associated protein 13B OS=Homo sapiens GN=VPS13B PE=1 SV=2	VP13B_HUMAN-DECOY	?	0	2	0
Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2	H13_HUMAN	22 kDa	0	4	0
Mucin-19 OS=Homo sapiens GN=MUC19 PE=1 SV=2	MUC19_HUMAN-DECOY	?	0	2	0
CAAX prenyl protease 1 homolog OS=Homo sapiens GN=ZMPSTE24 PE=1 SV=2	FACE1_HUMAN	55 kDa	0	2	0
Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	SET_HUMAN	33 kDa	0	1	2
Transmembrane and coiled-coil domain-containing protein 1 OS=Homo sapiens GN=TMCO1 PE=1 SV=1	TMCO1_HUMAN	21 kDa	0	3	1
Tyrosine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=YARS PE=1 SV=4	SYYC_HUMAN	59 kDa	0	1	3
60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	RL10_HUMAN	25 kDa	0	1	3
Proteasome assembly chaperone 1 OS=Homo sapiens GN=PSMG1 PE=1 SV=1	PSMG1_HUMAN	33 kDa	0	1	2
Eukaryotic translation initiation factor 4 gamma 2 OS=Homo sapiens GN=EIF4G2 PE=1 SV=1	IF4G2_HUMAN	102 kDa	0	2	1
Epididymis-specific alpha-mannosidase OS=Homo sapiens GN=MAN2B2 PE=1 SV=4	MA2B2_HUMAN-DECOY	?	0	1	2
Ubiquitin carboxyl-terminal hydrolase 34 OS=Homo sapiens GN=USP34 PE=1 SV=2	UBP34_HUMAN-DECOY	?	0	1	2
Apolipoprotein B-100 OS=Homo sapiens GN=APOB PE=1 SV=2	APOB_HUMAN	516 kDa	0	0	2
Ubiquitin carboxyl-terminal hydrolase 40 OS=Homo sapiens GN=USP40 PE=2 SV=3	UBP40_HUMAN	140 kDa	0	0	2
Hemicentin-1 OS=Homo sapiens GN=HMCN1 PE=1 SV=2	HMCN1_HUMAN	613 kDa	0	0	2
Short transient receptor potential channel 5 OS=Homo sapiens GN=TRPC5 PE=1 SV=1	TRPC5_HUMAN-DECOY	?	0	0	3
Acyl-coenzyme A thioesterase 9, mitochondrial OS=Homo sapiens GN=ACOT9 PE=1 SV=2	ACOT9_HUMAN	50 kDa	0	2	0
RAC-alpha serine/threonine-protein kinase OS=Homo sapiens GN=AKT1 PE=1 SV=2	AKT1_HUMAN	56 kDa	0	0	2
FRAS1-related extracellular matrix protein 2 OS=Homo sapiens GN=FREM2 PE=1	FREM2_HUM	351 kDa	0	2	0

SV=2	AN				
Emerin OS=Homo sapiens GN=EMD PE=1 SV=1	EMD_HUMAN	29 kDa	0	2	1
Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	K1C18_HUMAN	48 kDa	0	1	3
2-aminoethanethiol dioxygenase OS=Homo sapiens GN=ADO PE=1 SV=2	AEDO_HUMAN	30 kDa	0	2	1
Guanine nucleotide-binding protein G(k) subunit alpha OS=Homo sapiens GN=GNAI3 PE=1 SV=3	GNAI3_HUMAN	41 kDa	0	3	4
Retinol dehydrogenase 10 OS=Homo sapiens GN=RDH10 PE=1 SV=1	RDH10_HUMAN	38 kDa	0	1	2
Hydroxymethylglutaryl-CoA synthase, cytoplasmic OS=Homo sapiens GN=HMGCS1 PE=1 SV=2	HMCS1_HUMAN	57 kDa	0	2	1
Uridine 5'-monophosphate synthase OS=Homo sapiens GN=UMPS PE=1 SV=1	UMPS_HUMAN	52 kDa	0	2	1
Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2	LAP2A_HUMAN	75 kDa	0	2	1
Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	CATD_HUMAN	45 kDa	0	2	1
EMILIN-2 OS=Homo sapiens GN=EMILIN2 PE=1 SV=3	EMIL2_HUMAN	116 kDa	0	2	0
Ras-related protein Rab-9A OS=Homo sapiens GN=RAB9A PE=1 SV=1	RAB9A_HUMAN	23 kDa	0	2	0
Cyclin-dependent kinase 13 OS=Homo sapiens GN=CDK13 PE=1 SV=2	CDK13_HUMAN	165 kDa	0	3	1
Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4	NONO_HUMAN	54 kDa	0	3	0
ATPase ASNA1 OS=Homo sapiens GN=ASNA1 PE=1 SV=2	ASNA_HUMAN	39 kDa	0	3	0
Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1 OS=Homo sapiens GN=GBF1 PE=1 SV=2	GBF1_HUMAN	206 kDa	0	2	0
Glucocorticoid receptor OS=Homo sapiens GN=NR3C1 PE=1 SV=1	GCR_HUMAN	86 kDa	0	0	3
Signal transducer and activator of transcription 5A OS=Homo sapiens GN=STAT5A PE=1 SV=1	STA5A_HUMAN	91 kDa	0	2	0
Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens GN=ATP1B1 PE=1 SV=1	AT1B1_HUMAN	35 kDa	0	2	0

Aldehyde dehydrogenase family 16 member A1 OS=Homo sapiens GN=ALDH16A1 PE=1 SV=2	A16A1_HUMAN-DECOY	?	0	3	0
Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	HORN_HUMAN	282 kDa	0	2	0
E3 ubiquitin-protein ligase RBBP6 OS=Homo sapiens GN=RBBP6 PE=1 SV=1	RBBP6_HUMAN	202 kDa	0	0	2
Structural maintenance of chromosomes protein 4 OS=Homo sapiens GN=SMC4 PE=1 SV=2	SMC4_HUMAN	147 kDa	0	3	0
Mucin-19 OS=Homo sapiens GN=MUC19 PE=1 SV=2	MUC19_HUMAN	598 kDa	0	2	0
Bloom syndrome protein OS=Homo sapiens GN=BLM PE=1 SV=1	BLM_HUMAN	159 kDa	0	0	2
Matrix-remodeling-associated protein 5 OS=Homo sapiens GN=MXRA5 PE=2 SV=3	MXRA5_HUMAN-DECOY	?	0	0	2
Zinc finger protein 36, C3H1 type-like 2 OS=Homo sapiens GN=ZFP36L2 PE=1 SV=3	TISD_HUMAN-DECOY	?	0	2	0
DNA polymerase zeta catalytic subunit OS=Homo sapiens GN=REV3L PE=1 SV=2	DPOLZ_HUMAN	353 kDa	0	2	0
A disintegrin and metalloproteinase with thrombospondin motifs 9 OS=Homo sapiens GN=ADAMTS9 PE=1 SV=4	ATS9_HUMAN-DECOY	?	0	0	2
Nucleolar protein 6 OS=Homo sapiens GN=NOL6 PE=1 SV=2	NOL6_HUMAN-DECOY	?	0	2	0
A-kinase anchor protein 12 OS=Homo sapiens GN=AKAP12 PE=1 SV=4	AKA12_HUMAN	191 kDa	0	2	0
Mitochondrial import receptor subunit TOM22 homolog OS=Homo sapiens GN=TOMM22 PE=1 SV=3	TOM22_HUMAN	16 kDa	0	2	0
Protein S100-A10 OS=Homo sapiens GN=S100A10 PE=1 SV=2	S10AA_HUMAN	11 kDa	0	2	0
Suppressor of G2 allele of SKP1 homolog OS=Homo sapiens GN=SUGT1 PE=1 SV=3	SUGT1_HUMAN	41 kDa	0	2	0
Hepatocyte growth factor receptor OS=Homo sapiens GN=MET PE=1 SV=4	MET_HUMAN	156 kDa	0	2	0
ATP-binding cassette sub-family B member 7, mitochondrial OS=Homo sapiens GN=ABCB7 PE=1 SV=2	ABCB7_HUMAN	83 kDa	0	2	0
Thymidylate kinase OS=Homo sapiens GN=DTYMK PE=1 SV=4	KTHY_HUMAN	24 kDa	0	2	0
Cytoplasmic dynein 1 heavy chain 1 OS=Homo sapiens GN=DYNC1H1 PE=1 SV=5	DYHC1_HUM	?	0	0	2

	AN-DECOY				
Mediator of RNA polymerase II transcription subunit 23 OS=Homo sapiens GN=MED23 PE=1 SV=2	MED23_HUMAN	156 kDa	0	2	0
Retrotransposon-derived protein PEG10 OS=Homo sapiens GN=PEG10 PE=1 SV=2	PEG10_HUMAN	80 kDa	0	2	0
Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2	DYN2_HUMAN	98 kDa	0	2	0
General transcription factor II-I OS=Homo sapiens GN=GTF2I PE=1 SV=2	GTF2I_HUMAN	112 kDa	0	0	3
Protein NRDE2 homolog OS=Homo sapiens GN=NRDE2 PE=1 SV=3	NRDE2_HUMAN-DECOY	?	0	0	2
Carboxypeptidase A2 OS=Homo sapiens GN=CPA2 PE=1 SV=3	CBPA2_HUMAN-DECOY	?	0	0	2
Keratin, type II cuticular Hb5 OS=Homo sapiens GN=KRT85 PE=1 SV=1	KRT85_HUMAN	56 kDa	0	2	0
Nuclear receptor-binding factor 2 OS=Homo sapiens GN=NRBF2 PE=1 SV=1	NRBF2_HUMAN	32 kDa	0	2	0
FH2 domain-containing protein 1 OS=Homo sapiens GN=FHDC1 PE=1 SV=2	FHDC1_HUMAN	125 kDa	0	2	0
Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	TNPO1_HUMAN-DECOY	?	0	0	2
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5 OS=Homo sapiens GN=SMARCA5 PE=1 SV=1	SMCA5_HUMAN-DECOY	?	0	2	0
Probable ATP-dependent RNA helicase DDX60 OS=Homo sapiens GN=DDX60 PE=1 SV=3	DDX60_HUMAN-DECOY	?	0	2	0
N-alpha-acetyltransferase 35, NatC auxiliary subunit OS=Homo sapiens GN=NAA35 PE=1 SV=1	NAA35_HUMAN-DECOY	?	0	0	2

SI Table 2: Mass spectrometry analysis of PHP4 enriched HeLa cell lysates

Protein	spectral counts	spectral counts
TBL1X	17	0
KDM1A	17	0
RCOR1	11	0
MTA2	10	0
GSE1	9	0
MIER1	9	0
NCOR1	23	3
RBBP4	7	1
HDAC8	7	1
RBBP7	6	1
HDAC6	6	1
TTC38	6	0
HDAC2	15	3
CHD4	5	0
NCOR2	42	9
HDAC1	13	3
GNPI1	8	2
HM20B	4	0
RCOR3	4	0
HDAC3	7	2

[a]Soluble protein fraction was enriched on streptavidin resin preincubated with PHP4 and in the absence (sample 1) or presence (sample 2) of probe PHP2 as a competitor. The table contains the top 20 proteins identified and ranked by fold change of spectral counts between the two samples. Where no spectral counts were identified a value of 1 was used to calculate a fold change.

References

1. R. Neelarapu, D. L. Holzle, S. Velaparthi, H. Bai, M. Brunsteiner, S. Y. Blond and P. A. Petukhov, *J Med Chem*, 2011, **54**, 4350-4364.
2. K. Huber, G. Doyon, J. Plaks, E. Fyne, J. W. Mellors and N. Sluis-Cremer, *J. Biol. Chem.*, 2011, **286**, 22211-22218.
3. C. M. Salisbury and B. F. Cravatt, *Proc. Natl. Acad. Sci. USA*, 2007, **104**, 1171-1176.
4. C. M. Salisbury and B. F. Cravatt, *J. Am. Chem. Soc.*, 2008, **130**, 2184-2194.
5. J. E. Bradner, N. West, M. L. Grachan, E. F. Greenberg, S. J. Haggarty, T. Warnow and R. Mazitschek, *Nat Chem Biol*, 2010, **6**, 238-243.
6. H. S. Tae, J. Hines, A. R. Schneekloth and C. M. Crews, *Org Lett*, 2010, **12**, 4308-4311.
7. M. Lobera, K. P. Madauss, D. T. Pohlhaus, Q. G. Wright, M. Trocha, D. R. Schmidt, E. Baloglu, R. P. Trump, M. S. Head, G. A. Hofmann, M. Murray-Thompson, B. Schwartz, S. Chakravorty, Z. Wu, P. K. Mander, L. Kruidenier, R. A. Reid, W. Burkhart, B. J. Turunen, J. X. Rong, C. Wagner, M. B. Moyer, C. Wells, X. Hong, J. T. Moore, J. D. Williams, D. Soler, S. Ghosh and M. A. Nolan, *Nat Chem Biol*, 2013, **9**, 319-325.