Electronic Supplementary Material (ESI) for

Cellular target identification of Withangulatin A using fluorescent analogues and subsequent chemical proteomics

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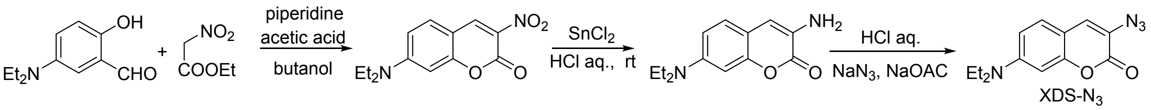
Table of content

1. General methods.

All chemicals were purchased from commercial vendors and used without further purification, unless indicated otherwise. All reactions requiring anhydrous conditions were carried out under argon or nitrogen atmosphere using oven-dried glassware. Reaction progress was monitored by TLC on pre-coated silica plates (Qingdao Huanghai F254nm, 0.25μm) and spots were visualized by UV, iodine or other suitable stains. Column chromatography was performed on silica gel (90e150 mm; Qingdao Marine Chemical Inc.) All NMR spectra (1H-NMR, 13C-NMR) were recorded on Bruker 500 MHz/600 MHz NMR with tetramethylsilane as an internal standard. The following abbreviations were used in reporting spectra, br s (broad singlet), s (singlet), d (doublet), t (triplet), q (quartet), m (multiplet), dd (doublet of doublets). Mass spectra were obtained on a MS Agilent 1100 Series LC/MSD Trap mass spectrometer (ESI-MS) and a Mariner ESI-TOF spectrometer (HRESIMS), respectively. Cell lines were obtained from the Cell Bank of Shanghai Institute 138 of Biochemistry and Cell Biology, Chinese Academy of Sciences (Shanghai, China). MDA-MB-231 and HepG2 cells were cultured in DMEM medium and SK-MEL-28 cells were cultured in RPMI-1640 medium containing 10% heat-inactivated fetal bovine serum. Antibodies against ATF4(D4B8), P-eIF2α (D7D3), BiP (C50B12), CHOP (L63F7), Cleaved PARP (12061) and Tubulin (D71G9) were purchased from CST and SERCA2(DF6240) was purchased from Affinity. The recombinant SERCA2(Ag26307) protein was purchased from Proteintech.

2. Chemistry

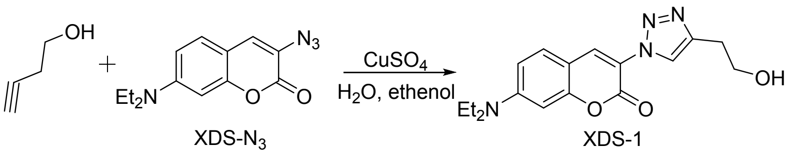
2.1 Synthesis of XDS-N_3



Scheme S1 synthesis of XDS-N_3

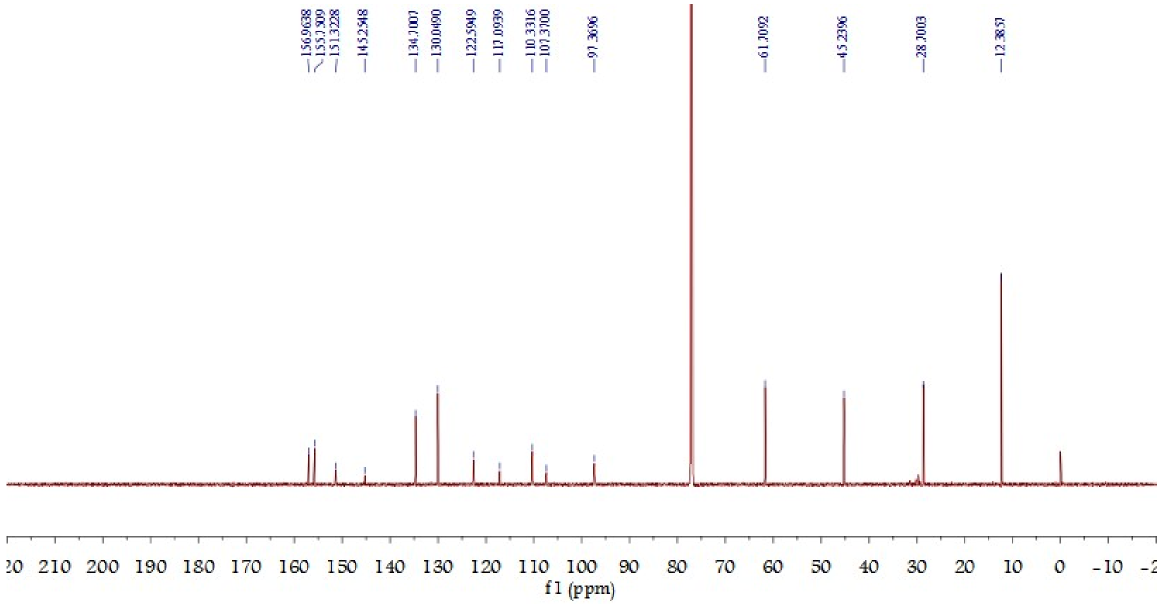
XDS-N_3 was Synthesized according to the previously published procedures.[1] ^{1}H NMR (500 MHz, Chloroform-*d*) δ 7.19 (d, *J* = 8.7 Hz, 1H), 7.10 (s, 1H), 6.59 (dd, *J* = 8.9, 2.4 Hz, 1H), 6.51 (d, *J* = 2.4 Hz, 1H), 3.40 (q, *J* = 7.0 Hz, 4H), 1.20 (t, *J* = 7.1 Hz, 6H).

2.2 Synthesis of XDS-1



Scheme S2 synthesis of XDS-1

(**XDS-1**). Butynol (35 mg, 0.5 mmol) was dissolved in a mixture of water and ethyl alcohol (v/v = 1:1, 6 mL). Then XDS-N_3 (129 mg, 0.5 mmol) and sodium ascorbate (100 µL, 0.1 mmol) of freshly prepared 1 M solution in water was added into the solution, followed by the addition of copper (II) sulfate pentahydrate 7.5 % in water (82.3 µL, 0.025 mmol). The heterogeneous mixture was stirred overnight in the dark at room temperature. The reaction mixture was concentrated in vacuo and purified by column chromatography on silica gel (methylene chloride: methanol = 10:1) to afford 90 mg (55%) of compound XDS-1 as a brown solid.^{1}H NMR (600 MHz, Chloroform-*d*) δ 8.39 (s, 1H), 8.36 (s, 1H), 7.43 (d, *J* = 8.9 Hz, 1H), 6.71 (dd, *J* = 8.9, 2.5 Hz, 1H), 6.59 (d, *J* = 2.4 Hz, 1H), 4.03 (t, *J* = 5.9 Hz, 2H), 3.48 (q, *J* = 7.1 Hz, 4H), 3.06 (t, *J* = 5.9 Hz, 2H), 1.27 (t, *J* = 7.1 Hz, 6H). ^{13}C NMR (151 MHz, Chloroform-*d*) δ 156.96, 155.75, 151.32, 145.25, 134.70, 130.05, 122.59, 117.09, 110.33, 107.37, 97.37, 61.71, 45.24, 29.72, 28.70, 12.39. HRMS-ESI calcd. For $C_{17}H_{20}N_4NaO_3$ [M+Na]$^+$: 351.1428; Found: 351.1432.



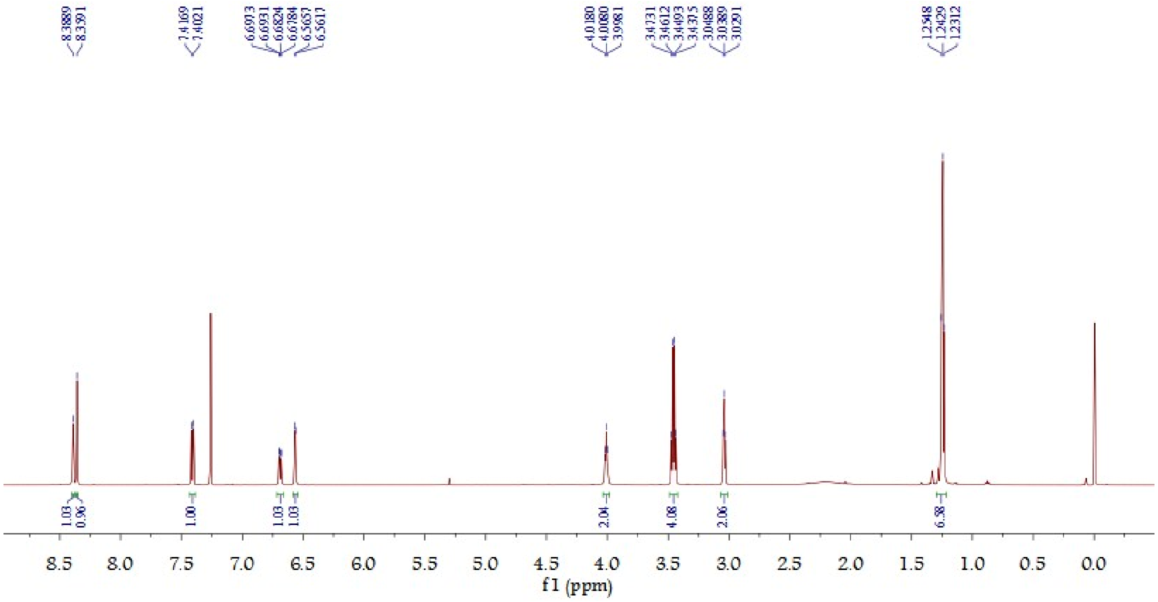
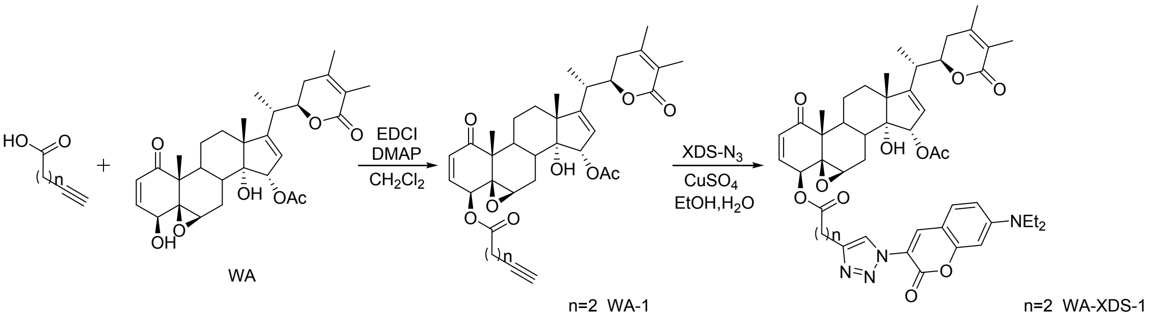


Fig. S1 ^{1}H-NMR and ^{13}C-NMR data of XDS-1

2.3 Synthesis of WA-XDS-1 and WA-XDS-2



n=2 WA-1
n=4 WA-2

n=2 WA-XDS-1
n=4 WA-XDS-2

Scheme S3 synthesis of WA-XDS-1 and WA-XDS-2

(WA-1). 4-Pentynoic acid (20 mg, 0.21 mmol) and EDCI (40 mg, 0.21 mmol) were dissolved in dichlormethane (6 ml), followed by addition of DMAP (26 mg, 0.21 mmol). the solution was cooled to 0 ℃ and stirred for 1 h. Thereafter WA (105 mg, 0.2 mmol) was added and cooling was removed. The mixture was stirred overnight. Then the solvent was removed under reduced pressure and the residue was purified by silica column (grad PE-EtOAc, 20:1-2:1) to give the pure product as a white powder (91 mg, 75%). ^{1}H NMR (600 MHz, Chloroform-*d*) δ 7.07 (dd, *J* = 9.8, 6.0 Hz, 1H), 6.24 (d, *J* = 9.8 Hz, 1H), 5.68 (d, *J* = 2.7 Hz, 1H), 5.22 (d, *J* = 2.7 Hz, 1H), 4.74 (d, *J* = 6.1 Hz, 1H), 4.23 (ddd, *J* = 12.5, 6.8, 3.5 Hz, 1H), 3.35 (br s, 1H), 2.64 – 2.54 (m, 3H), 2.53 – 2.44 (m, 3H), 2.43 – 2.35 (m, 1H), 2.17 (dd, *J* = 17.6, 3.4 Hz, 1H), 1.97 (t, *J* = 2.5 Hz, 1H), 1.93 (s, 3H), 1.93 (s, 3H), 1.86 – 1.80 (m, 5H), 1.77 – 1.61 (m, 4H), 1.45 – 1.35 (m, 5H), 1.11 (d, *J* = 7.0 Hz, 3H), 1.08 (s, 3H). ^{13}C NMR (151 MHz, Chloroform-*d*) δ 201.21, 170.87, 169.55, 166.10, 162.35, 148.45, 140.25, 133.33, 122.21, 120.91, 83.53, 81.92, 81.47, 79.23, 72.23, 69.41, 61.03, 60.14, 52.03, 47.88, 39.51, 37.24, 35.32, 34.40, 33.11, 32.91, 24.40, 21.36, 20.85, 20.46, 17.58, 15.85, 15.61, 14.29, 12.47; HRMS-ESI calcd. For $C_{35}H_{42}NaO_9$ $[M+Na]^+$: 629.2721; Found: 629.2722.

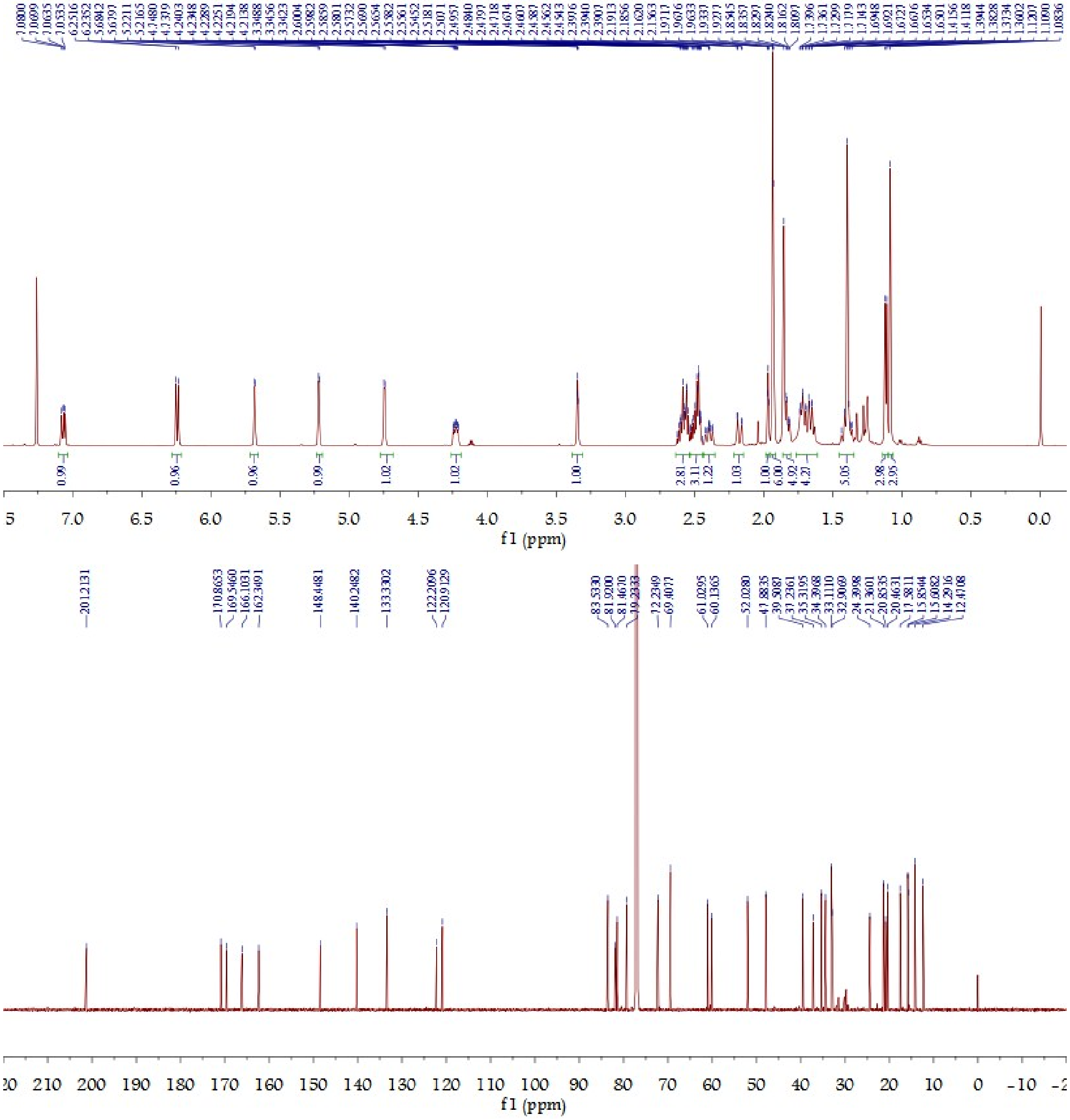
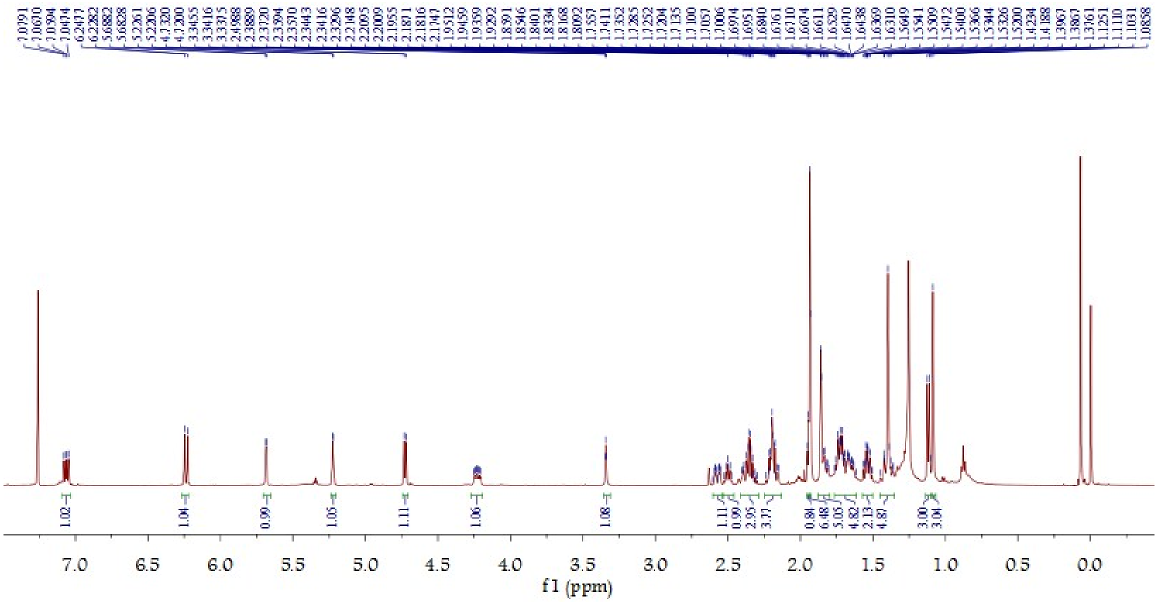


Fig. S2 ^{1}H-NMR and ^{13}C-NMR data of WA-1

(WA-2). By the same general method, 6-Heptynoic acid (27 mg, 0.21 mmol) gave WA-2 (89 mg, 70%) as a light-yellow powder. ^{1}H NMR (500 MHz, Chloroform-*d*) δ 7.06 (dd, *J* = 9.8, 6.0 Hz, 1H), 6.24 (d, *J* = 9.8 Hz, 1H), 5.69 (d, *J* = 2.7 Hz, 1H), 5.22 (d, *J* = 2.8 Hz, 1H), 4.73 (d, *J* = 6.0 Hz, 1H), 4.23 (ddd, *J* = 12.5, 6.7, 3.5 Hz, 1H), 3.34 (br s, 1H), 2.57 (ddd, *J* = 14.9, 3.9, 2.3 Hz, 1H), 2.50 (p, *J* = 7.0 Hz, 1H), 2.41 – 2.29 (m, 3H), 2.25 – 2.13 (m, 4H), 1.95 (t, *J* = 2.5 Hz, 1H), 1.93 (s, 3H), 1.93 (s, 3H), 1.88 – 1.80 (m, 5H), 1.77 – 1.61 (m, 5H), 1.57 – 1.50 (m, 2H), 1.45 – 1.35 (m, 5H), 1.12 (d, *J* = 7.1 Hz, 3H), 1.09 (s, 3H). ^{13}C NMR (126 MHz, Chloroform-*d*) δ 201.36, 172.41, 169.54, 166.06, 162.38, 148.39, 140.58, 133.16, 122.26, 120.97, 83.79, 83.56, 81.51, 79.25, 71.80, 68.75, 61.02, 60.23, 52.06, 47.94, 39.54, 37.28, 35.35, 34.46, 33.52, 32.94, 27.60, 24.45, 23.82, 21.36, 20.92, 20.46, 18.08, 17.58, 15.87, 15.62, 12.48; HRMS-ESI calcd. For $C_{37}H_{46}NaO_9$ $[M+Na]^+$: 657.3034; Found: 657.3046.



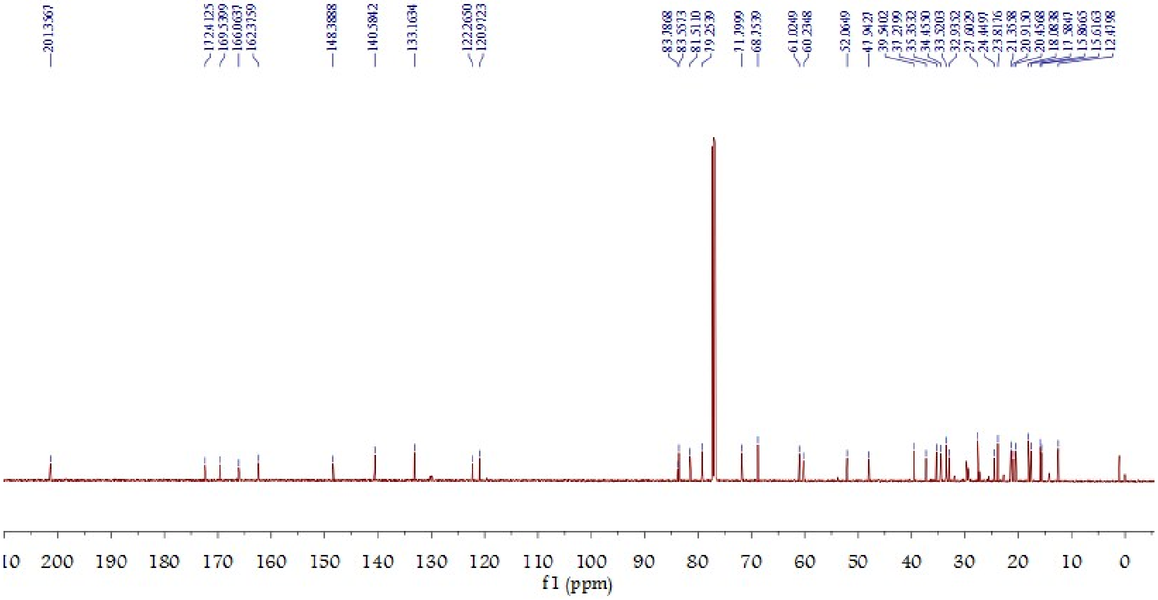
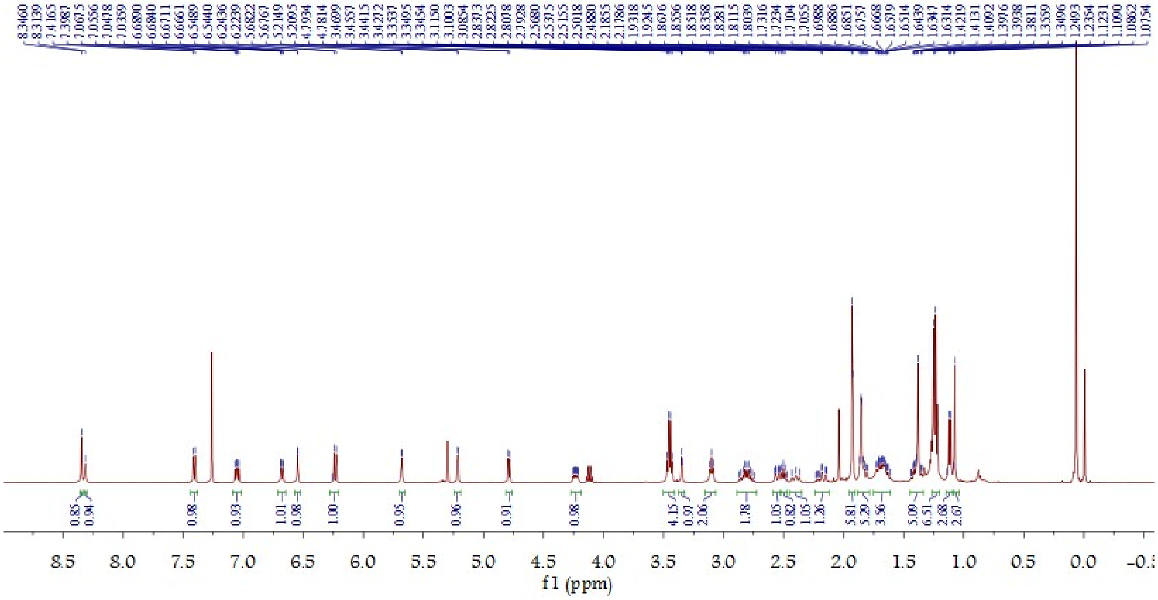


Fig. S3 ^{1}H-NMR and ^{13}C-NMR data of WA-2

(WA-XDS-1). WA-1 (22 mg, 0.036 mmol) was dissolved in a mixture of water and ethyl alcohol (v/v = 1:1, 2 mL). Then XDS-N_3 (9.6 mg, 0.036 mmol) and sodium ascorbate (11 µL, 0.011 mmol) of freshly prepared 1 M solution in water was added into the solution, followed by the addition of copper (II) sulfate pentahydrate 7.5 % in water (9 µL, 0.0028 mmol). The heterogeneous mixture was stirred overnight in the dark at room temperature. The reaction mixture was concentrated in vacuo and purified by column chromatography on silica gel (methylene chloride: methanol = 10:1) to afford 15 mg (48%) of compound WA-XDS-1 as a brown solid. ^{1}H NMR (500 MHz, Chloroform-*d*) δ 8.35 (s, 1H), 8.31 (s, 1H), 7.41 (d, *J* = 8.9 Hz, 1H), 7.05 (dd, *J* = 9.8, 6.0 Hz, 1H), 6.68 (dd, *J* = 9.0, 2.5 Hz, 1H), 6.55 (d, *J* = 2.5 Hz, 1H), 6.23 (d, *J* = 9.8 Hz, 1H), 5.68 (d, *J* = 2.8 Hz, 1H), 5.21 (d, *J* = 2.7 Hz, 1H), 4.79 (d, *J* = 6.0 Hz, 1H), 4.23 (ddd, *J* = 12.6, 6.6, 3.5 Hz, 1H), 3.45 (q, *J* = 7.1 Hz, 4H), 3.35 (br s, 1H), 3.10 (t, *J* = 7.4 Hz, 2H), 2.81 (qt, *J* = 16.1, 7.3 Hz, 2H), 2.55 (dt, *J* = 15.3, 3.1 Hz, 1H), 2.49 (q, *J* = 6.9 Hz, 1H), 2.40 (t, *J* = 15.1 Hz, 1H), 2.23 – 2.12 (m, 1H), 2.04 (s, 1H), 1.93 (s, 3H), 1.93 (s, 3H), 1.89 – 1.78 (m, 5H), 1.68 (m, 4H), 1.38 (s, 5H), 1.29 – 1.21 (t, *J* = 7.1 Hz, 6H), 1.12 (d, *J* = 7.1 Hz, 3H), 1.08 (s, 3H). ^{13}C NMR (151 MHz, Chloroform-*d*) δ 201.37, 171.67, 169.60, 166.13, 162.23, 157.05, 155.77, 151.49, 148.49, 145.63, 140.40, 134.79, 133.18, 130.00, 122.26, 122.18, 120.98, 117.07, 110.02, 107.12, 97.01, 83.55, 81.47, 71.80, 61.20, 60.23, 52.03, 47.83, 44.99, 39.50, 37.24, 35.28, 34.52, 33.62, 32.79, 29.71, 24.42, 21.36, 21.09, 21.04, 20.46, 17.49, 15.84, 12.47, 12.44; HRMS-ESI calcd.For C$_{48}$H$_{57}$N$_4$O$_{11}$ [M+H]$^+$: 865.4018; Found: 865.4052.



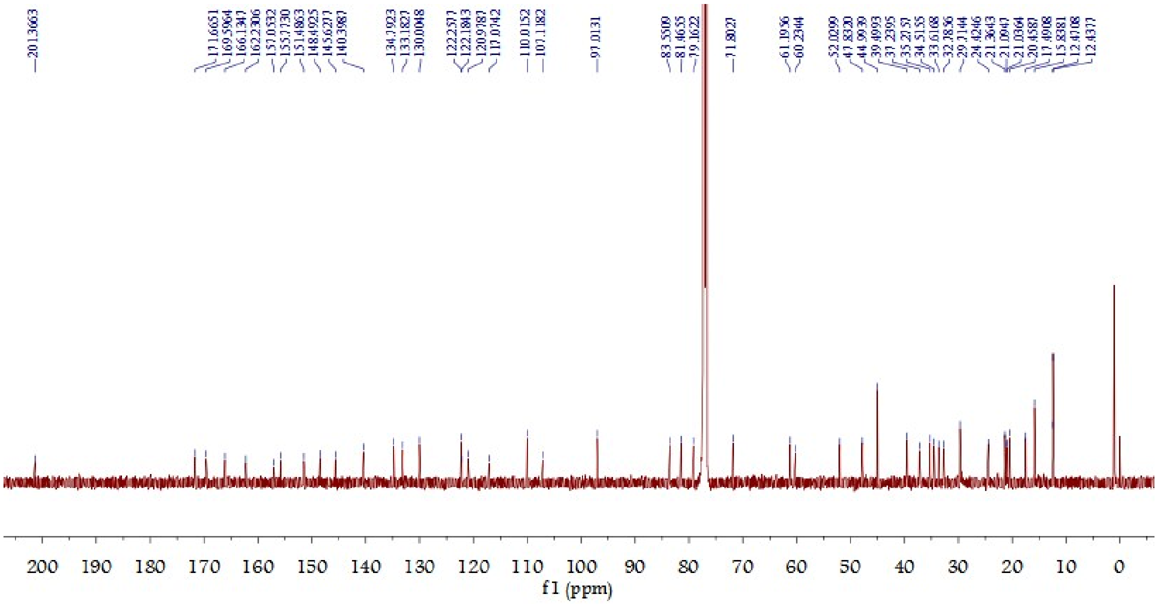


Fig. S4 ^{1}H-NMR and ^{13}C-NMR data of WA-XDS-1

(WA-XDS-2). By the same general method, WA-2 (32 mg, 0.05 mmol) gave WA-XDS-2 (21 mg, 48%) as a brown powder. ^{1}H NMR (600 MHz, Chloroform-*d*) δ 8.36 (s, 1H), 8.35 (s, 1H), 7.40 (d, *J* = 8.8 Hz, 1H), 7.04 (dd, *J* = 9.8, 6.0 Hz, 1H), 6.67 (dd, *J* = 8.9, 2.5 Hz, 1H), 6.55 (d, *J* = 2.5 Hz, 1H), 6.25 (d, *J* = 9.8 Hz, 1H), 5.68 (d, *J* = 2.7 Hz, 1H), 5.23 (d, *J* = 2.7 Hz, 1H), 4.78 (d, *J* = 6.0 Hz, 1H), 4.25 (ddd, *J* = 12.8, 6.3, 3.5 Hz, 1H), 3.45 (q, *J* = 7.2 Hz, 4H), 3.36 (br s, 1H), 2.79 (t, *J* = 7.3 Hz, 2H), 2.58 (dt, *J* = 14.9, 3.0 Hz, 1H), 2.51 (p, *J* = 7.0 Hz, 1H), 2.45 – 2.33 (m, 3H), 2.16 (dd, *J* = 17.6, 3.4 Hz, 1H), 1.93 (s, 3H), 1.93 (s, 3H), 1.85 (m, 5H), 1.79 – 1.57 (m, 8H), 1.39 (m, 5H), 1.23 (t, *J* = 7.1 Hz, 6H), 1.12 (d, *J* = 7.0 Hz, 3H), 1.07 (s, 3H). ^{13}C NMR (151 MHz, Chloroform-*d*) δ 201.58, 172.62, 169.72, 166.36, 162.07, 157.32, 155.83, 151.57, 148.75, 147.71, 140.64, 134.75, 133.29, 130.06, 122.24, 122.00, 121.23, 117.28, 110.16, 107.31, 97.15, 83.77, 81.57, 79.07, 71.65, 61.41, 60.45, 52.21, 48.00, 45.11, 39.70, 37.28, 35.35, 34.76, 33.94, 32.63, 29.83, 28.70, 25.50, 24.64, 24.57, 21.51, 21.12, 20.58, 17.46, 15.93, 12.59, 12.57; HRMS-ESI calcd.For $C_{50}H_{61}N_4O_{11}$ $[M+H]^+$: 893.4331; Found: 893.4341.

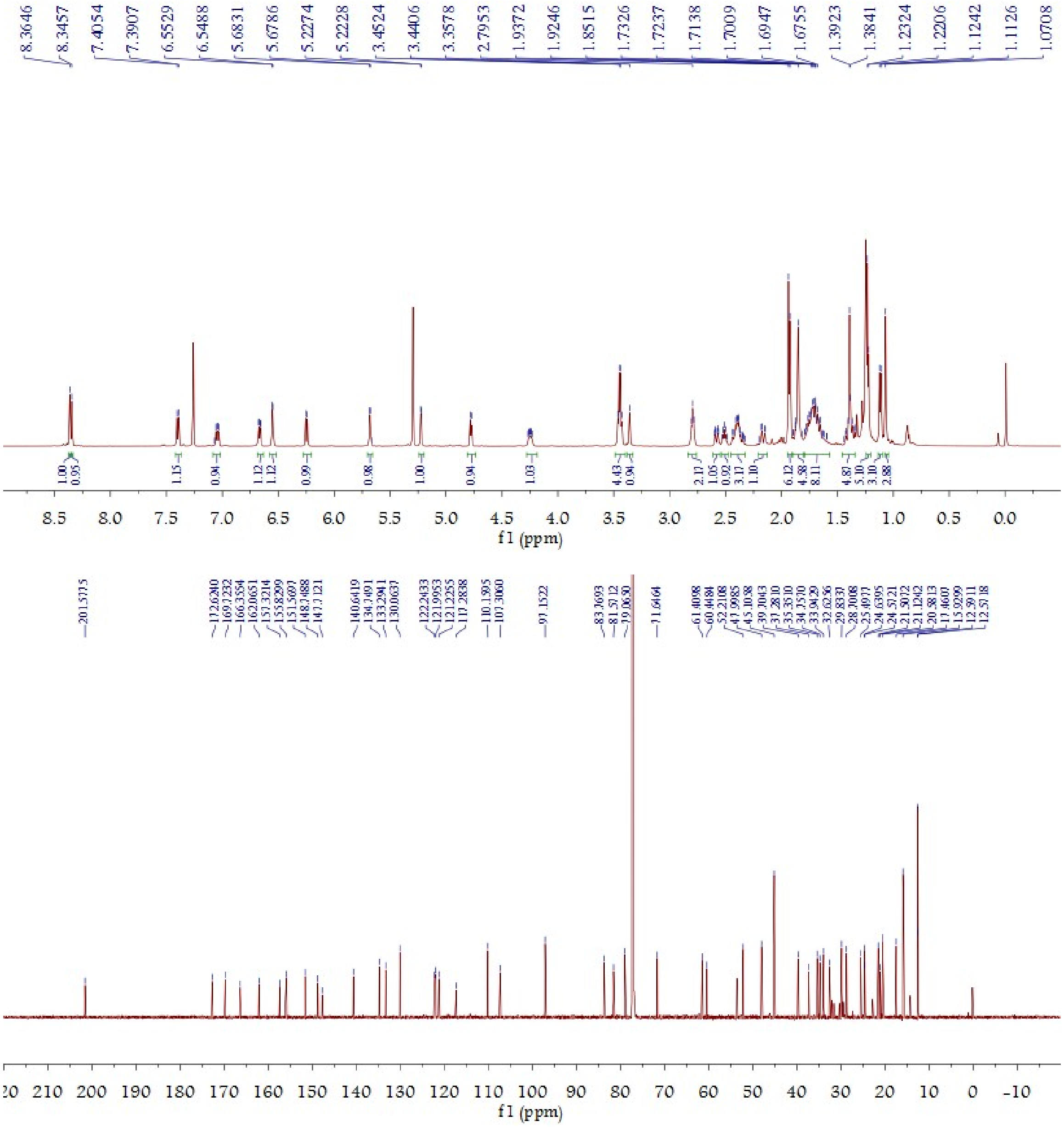
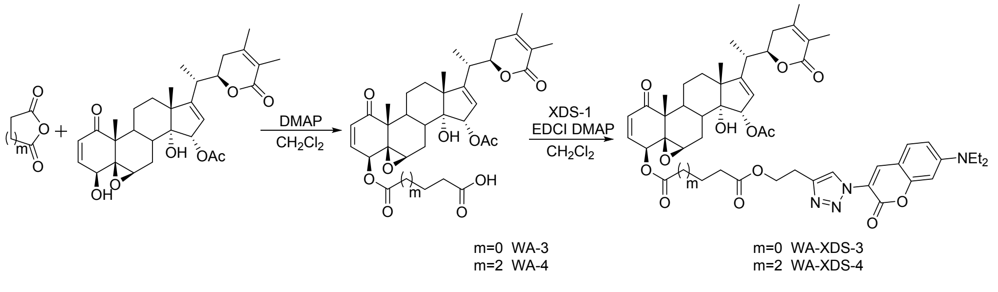


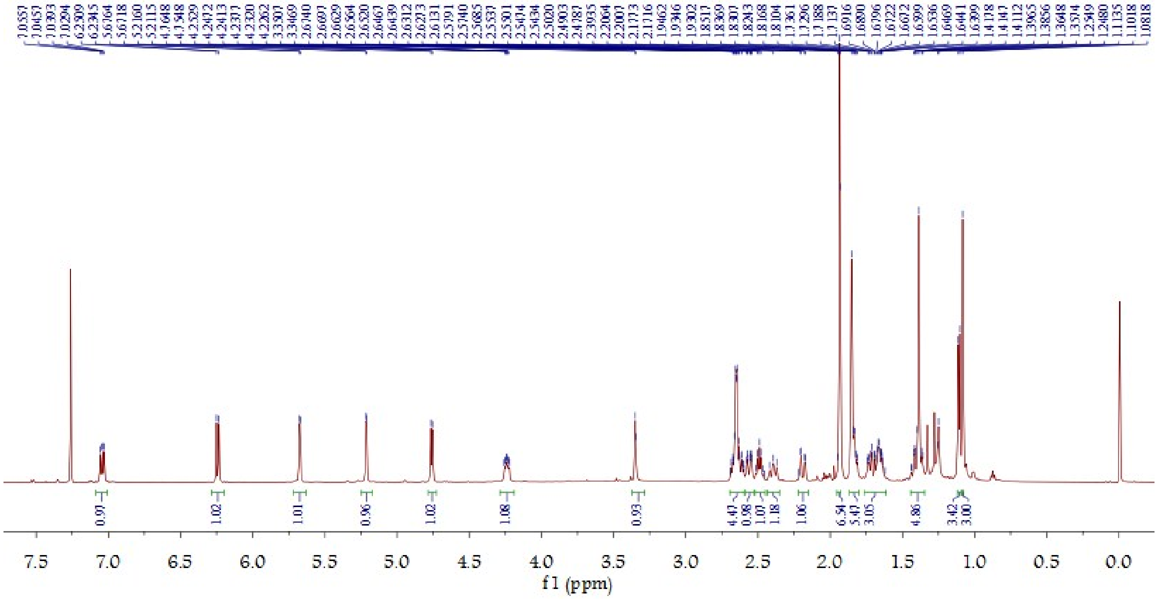
Fig. S5 ^{1}H-NMR and ^{13}C-NMR data of WA-XDS-2

2.4 Synthesis of WA-XDS-3 and WA-XDS-4



Scheme S4 synthesis of WA-XDS-3 and WA-XDS-4

(WA-3). Succinic anhydride (30 mg, 0.3 mmol), DMAP (2 mg 0.02 mmol) and WA (105 mg, 0.2 mmol) were dissolved in dichlormethane (6 ml) and stirred overnight at room temperature. Then the solvent was removed under reduced pressure and the residue was purified by silica column (grad PE-acetone, 10:1-1:2) to give the pure product as a white powder (65 mg, 52%). ^{1}H NMR (600 MHz, Chloroform-*d*) δ 7.04 (dd, *J* = 9.8, 6.0 Hz, 1H), 6.24 (d, *J* = 9.8 Hz, 1H), 5.67 (d, *J* = 2.7 Hz, 1H), 5.21 (d, *J* = 2.7 Hz, 1H), 4.76 (d, *J* = 6.0 Hz, 1H), 4.24 (ddd, *J* = 12.5, 6.9, 3.5 Hz, 1H), 3.35 (br s, 1H), 2.69 – 2.60 (m, 4H), 2.59 – 2.53 (m, 1H), 2.49 (p, *J* = 7.1 Hz, 1H), 2.39 (t, *J* = 15.1 Hz, 1H), 2.19 (dd, *J* = 17.5, 3.4 Hz, 1H), 1.93 (s, 3H), 1.93 (s, 3H), 1.84 (m, 5H), 1.76 – 1.61 (m, 4H), 1.44 – 1.35 (m, 5H), 1.11 (d, *J* = 7.0 Hz, 3H), 1.08 (s, 3H). ^{13}C NMR (151 MHz, Chloroform-*d*) δ 201.40, 175.89, 171.26, 169.65, 166.42, 162.28, 148.73, 140.22, 133.26, 122.14, 120.80, 83.59, 81.51, 79.25, 72.15, 61.16, 60.21, 52.02, 47.87, 39.54, 37.30, 35.35, 34.46, 32.95, 28.90, 28.66, 24.40, 21.38, 20.95, 20.48, 17.65, 15.90, 15.71, 12.45; HRMS-ESI calcd. For $C_{34}H_{42}NaO_{11}$ [M+Na]$^+$: 649.2617; Found: 649.2650.



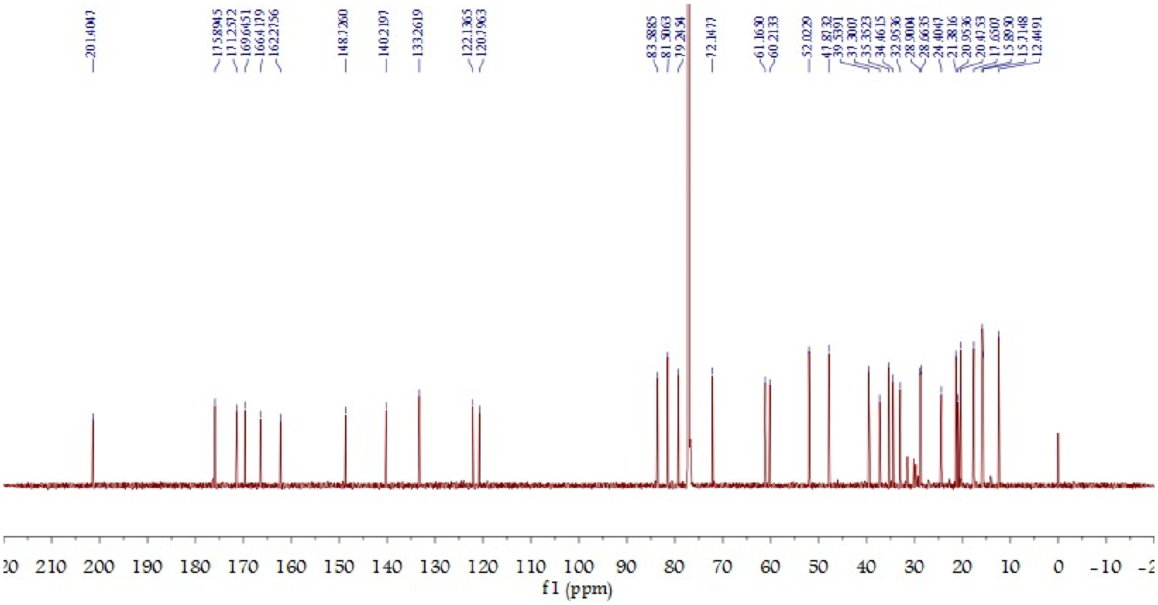


Fig. S6 ^{1}H-NMR and ^{13}C-NMR data of WA-3

(WA-4). By the same general method, Hexanedioic anhydride (38 mg, 0.3 mmol) gave the WA-4 (98 mg, 50%) as a white powder. ^{1}H NMR (500 MHz, Chloroform-*d*) δ 7.05 (dd, *J* = 9.8, 6.0 Hz, 1H), 6.24 (d, *J* = 9.8 Hz, 1H), 5.69 (d, *J* = 2.7 Hz, 1H), 5.22 (d, *J* = 2.7 Hz, 1H), 4.74 (d, *J* = 6.0 Hz, 1H), 4.24 (ddd, *J* = 12.5, 6.9, 3.5 Hz, 1H), 3.35 (br s, 1H), 2.57 (dt, *J* = 15.3, 2.8 Hz, 1H), 2.50 (p, *J* = 7.0 Hz, 1H), 2.36 (m, 5H), 2.23 – 2.16 (m, 1H), 1.93 (s, 3H), 1.93 (s, 3H), 1.85 (m, 5H), 1.76 – 1.61 (m, 8H), 1.47 – 1.33 (m, 5H), 1.12 (d, *J* = 7.1 Hz, 3H), 1.09 (s, 3H). ^{13}C NMR (126 MHz, Chloroform-*d*) δ 201.45, 177.14, 172.29, 169.57, 166.37, 162.31, 148.68, 140.55, 133.16, 122.23, 120.90, 83.56, 81.62, 79.34, 71.76, 61.13, 60.29, 52.06, 47.95, 39.55, 37.35, 35.39, 34.51, 33.67, 33.26, 33.02, 24.44, 24.18, 23.94, 21.35, 20.97, 20.46, 17.65, 15.90, 15.67, 12.45; HRMS-ESI calcd.For $C_{36}H_{46}NaO_{11}$ $[M+Na]^+$: 677.2932; Found: 677.2925.

Fig. S7 ^{1}H-NMR and ^{13}C-NMR data of WA-4

(WA-XDS-3). WA-3 (62.6 mg, 0.1 mmol) and EDCI (30 mg, 0.15 mmol) were dissolved in dichlormethane (6 ml), followed by addition of DMAP (20 mg, 0.15 mmol). the solution was cooled to 0 ℃ and stirred for 1 h. Thereafter XDS-1 (33 mg, 0.1 mmol) was added and cooling was removed. The mixture was stirred overnight. Then the solvent was removed under reduced pressure and the residue was purified by silica column (grad PE-acetone, 20:1-1:2) to give the pure product as a brown powder (39 mg, 42%). ^{1}H NMR (500 MHz, Chloroform-*d*) δ 8.39 (s, 1H), δ 8.36 (s, 1H), 7.40 (d, *J* = 8.9 Hz, 1H), 7.03 (dd, *J* = 9.8, 6.0 Hz, 1H), 6.68 (dd, *J* = 8.9, 2.5 Hz, 1H), 6.55 (d, *J* = 2.4 Hz, 1H), 6.23 (d, *J* = 9.8 Hz, 1H), 5.68 (d, *J* = 2.7 Hz, 1H), 5.21 (d, *J* = 2.7 Hz, 1H), 4.75 (d, *J* = 6.0 Hz, 1H), 4.44 – 4.41 (m, 2H), 4.24 (ddd, *J* = 12.6, 6.5, 3.5 Hz, 1H), 3.45 (q, *J* = 7.1 Hz, 4H), 3.32 (br s, 1H), 3.15 (t, *J* = 6.6 Hz, 2H), 2.69 – 2.58 (m, 4H), 2.55 (dt, *J* = 14.8, 3.1 Hz, 1H), 2.49 (q, *J* = 6.9 Hz, 1H), 2.40 (t, *J* = 15.1 Hz, 1H), 2.22 – 2.18 (m, 1H), 1.93 (s, 3H), 1.93 (s, 3H), 1.87 – 1.80 (m, 5H), 1.67 (m, 4H), 1.42 – 1.34 (m, 5H), 1.23 (t, *J* = 7.1 Hz, 6H), 1.11 (d, *J* = 7.0 Hz, 3H), 1.07 (s, 3H). ^{13}C NMR (151 MHz, Chloroform-*d*) δ 201.30, 171.77, 171.28, 169.59, 166.23, 162.10, 157.06, 155.78, 151.52, 148.62, 143.81, 140.29, 134.72, 133.20, 129.99, 122.77, 122.12, 121.00, 117.01, 110.05, 107.09, 96.99, 83.59, 81.44, 79.07, 72.01, 63.55, 61.14, 60.16, 52.04, 47.82, 45.01, 39.51, 37.22, 35.27, 34.57, 32.70, 29.01, 25.43, 24.41, 21.37, 20.99, 20.46, 17.45, 15.85, 15.75, 12.46, 12.44; HRMS-ESI calcd.For $C_{51}H_{60}N_4NaO_{13}$ $[M+Na]^+$: 959.4049; Found: 959.4085.

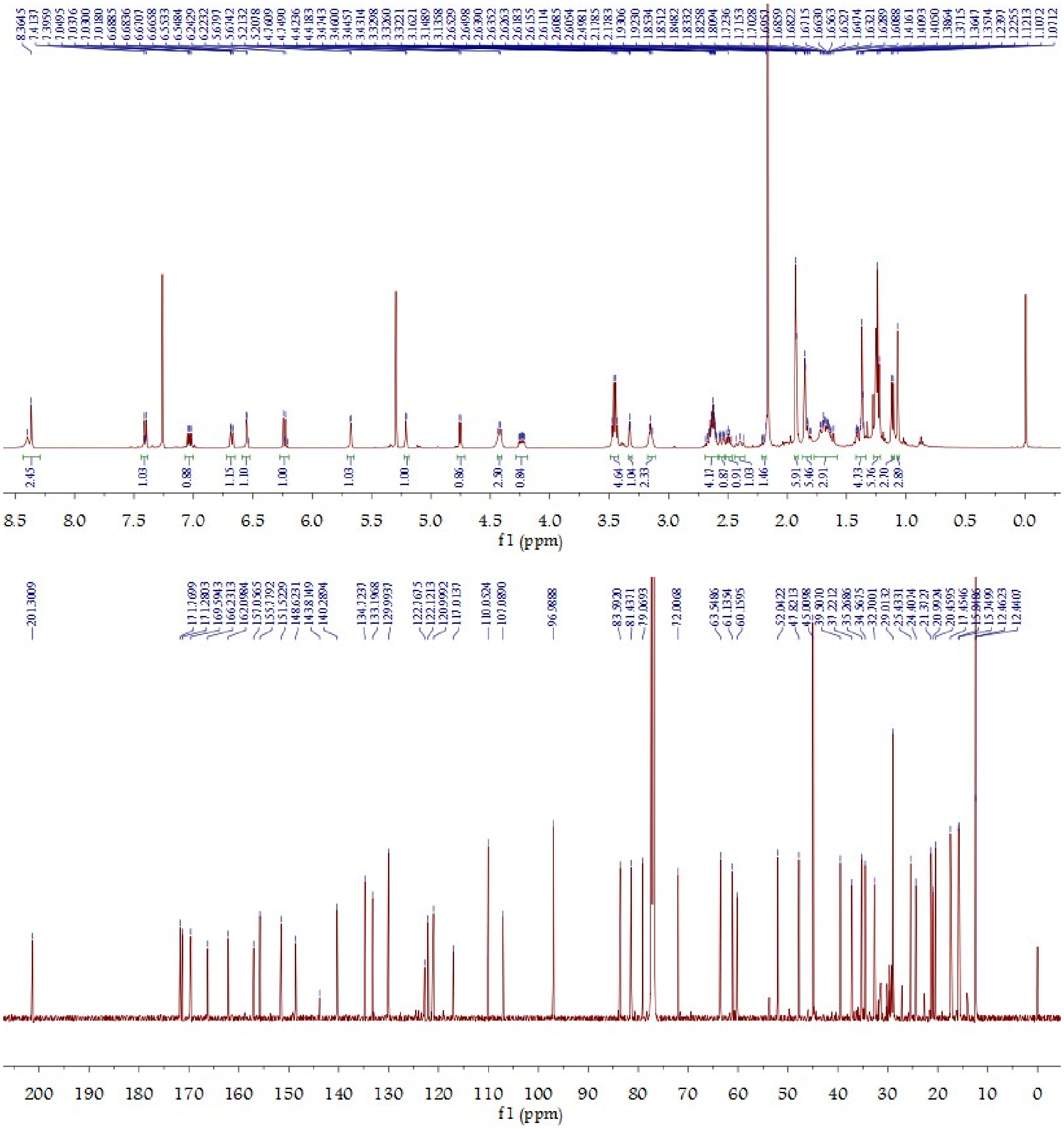
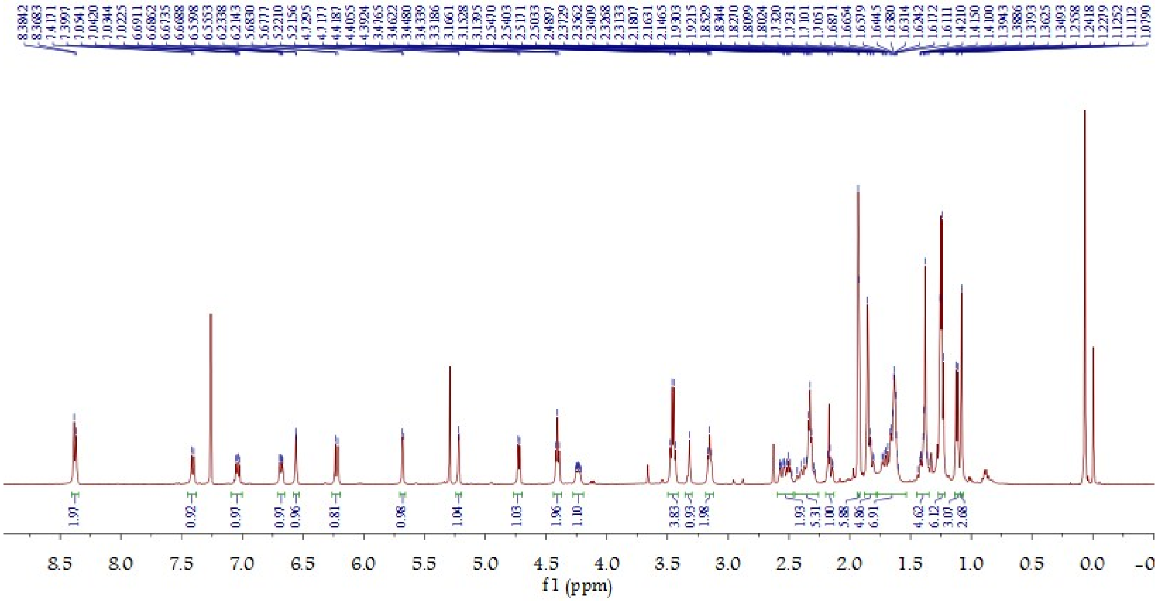


Fig. S8 ^{1}H-NMR and ^{13}C-NMR data of WAXDS-3

(WA-XDS-4). By the same general method, WA-4 (33 mg, 0.05 mmol) gave the WA-XDS-4 (24 mg, 50%) as a brown powder. ^{1}H NMR (500 MHz, Chloroform-*d*) δ 8.38 (s, 1H), 8.37 (s, 1H), 7.41 (d, *J* = 8.7 Hz, 1H), 7.04 (dd, *J* = 9.8, 6.0 Hz, 1H), 6.68 (dd, *J* = 8.7, 2.4 Hz, 1H), 6.56 (d, *J* = 2.2 Hz, 1H), 6.22 (d, *J* = 9.8 Hz, 1H), 5.68 (d, *J* = 2.6 Hz, 1H), 5.22 (d, *J* = 2.7 Hz, 1H), 4.72 (d, *J* = 5.9 Hz, 1H), 4.41 (t, *J* = 6.6 Hz, 2H), 4.24 (ddd, *J* = 12.7, 6.5, 3.2 Hz, 1H), 3.46 (q, *J* = 7.1 Hz, 4H), 3.32 (br s, 1H), 3.15 (t, *J* = 6.6 Hz, 2H), 2.60 – 2.46 (m, 2H), 2.45 – 2.26 (m, 5H), 2.20 – 2.13 (m, 1H), 1.93 (s, 3H), 1.93 (s, 3H), 1.84 (d, *J* = 9.2 Hz, 5H), 1.77 – 1.53 (m, 8H), 1.45 – 1.35 (m, 5H), 1.24 (t, *J* = 7.0 Hz, 6H), 1.12 (d, *J* = 7.0 Hz, 3H), 1.08 (s, 3H). ^{13}C NMR (126 MHz, Chloroform-*d*) δ 201.36, 173.06, 172.32, 169.54, 166.09, 162.19, 156.99, 155.81, 151.52, 148.45, 143.96, 140.56, 134.65, 133.12, 130.02, 122.67, 122.22, 121.09, 117.11, 110.13, 107.20, 97.13, 83.59, 81.49, 79.12, 71.68, 63.08, 61.09, 60.24, 52.09, 47.91, 45.06, 39.55, 37.25, 35.30, 34.58, 33.82, 33.68, 32.76, 25.56, 24.46, 24.27, 24.19, 21.35, 21.00, 20.44, 17.47, 15.86, 15.70, 12.47, 12.46; HRMS-ESI calcd.For $C_{53}H_{64}N_4NaO_{13}$ $[M+Na]^+$: 987.4362; Found: 987.4401.



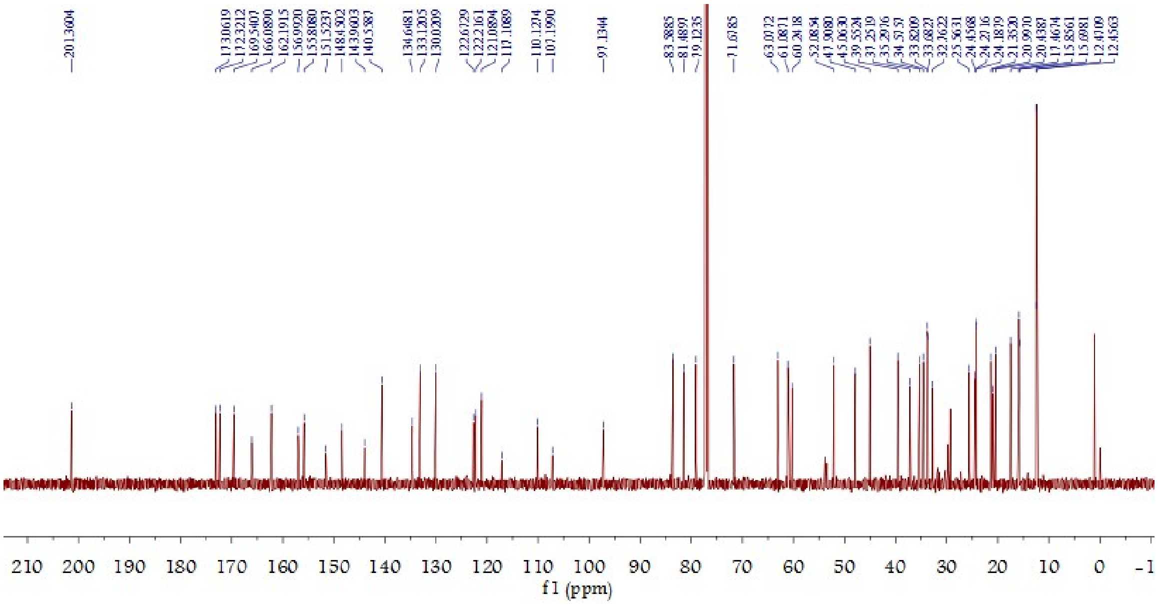


Fig. S9 ^{1}H-NMR and ^{13}C-NMR data of WA-XDS-4

2.5 Measurement of Photophysical Properties

WA-XDS-1/2/3/4 and XDS-1 were dissolved in PBS and dichloromethane (DCM) respectively and make the concentration as 1μM. Then the excitation and emission spectra of these five probes were determined by a Shimadzu FR-6000 luminescence spectrometer

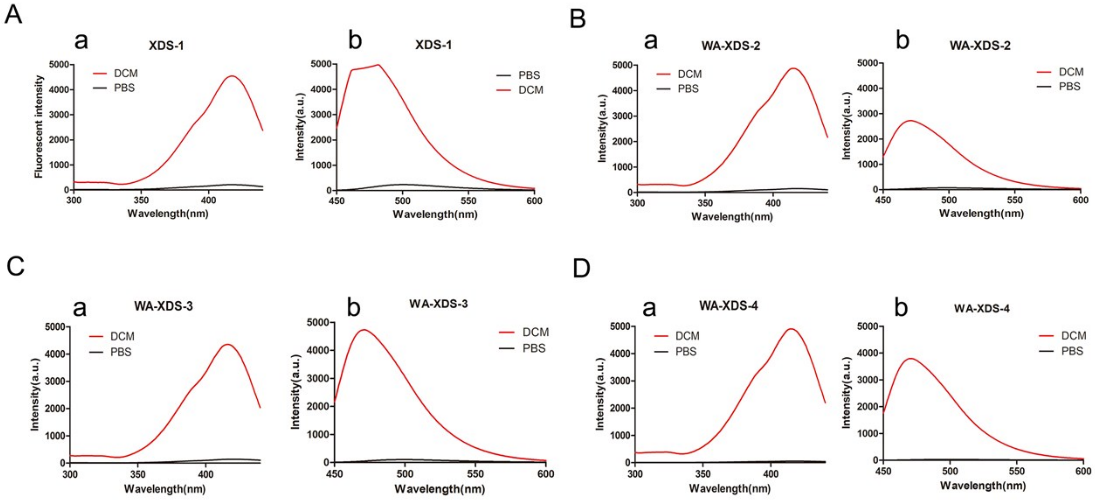


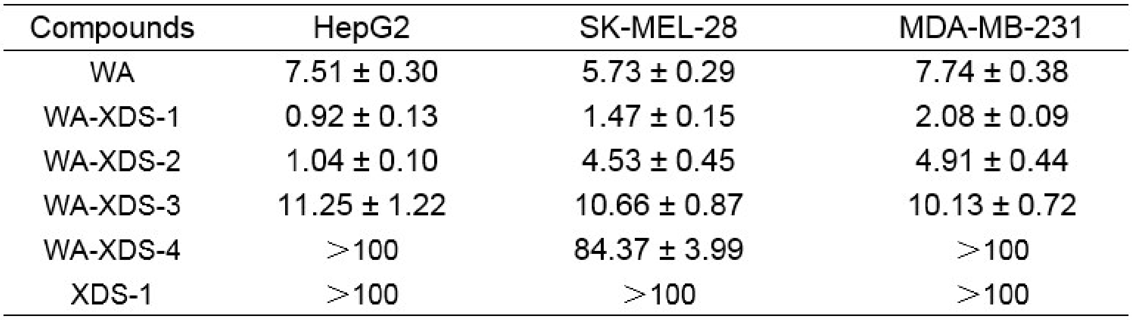
Fig. S10 Excitation (a) and emission (b) spectra of fluorescent probes in dichloromethane and PBS: (A) XDS-1; (B) WA-XDS-2; (C) WA-XDS-3; (D) WA-XDS-4.

3. Biological experiments

3.1 Cell proliferation assay

Cytotoxicity assays were carried out using SK-MEL-28, MDA-MB-231 and HepG2 cells by CCK8 assay. Cells were initially seeded into 96-well plate at a density of 5×10^3 cells/well and incubated for 24 h at 37 ºC in a humidified 5% CO2 incubator. Then WA, XDS-1 and WA-XDS-1/2/3/4 were added to cells with various concentrations and further incubated for 24 h. Then CCK-8 reagent (10 μL) was added to each well and incubated for 2h. Following that, the absorbance was measured at 450 nm with an ELISA reader (SpectraMax Plus384, Molecular Devices, Sunnyvale, CA)

Table S1. IC_{50} Values of XDS-1, WA and its fluorescent analogues On Inhibiting Proliferation of several human cancer cells (μM) [a]



Compounds	HepG2	SK-MEL-28	MDA-MB-231
WA	7.51 ± 0.30	5.73 ± 0.29	7.74 ± 0.38
WA-XDS-1	0.92 ± 0.13	1.47 ± 0.15	2.08 ± 0.09
WA-XDS-2	1.04 ± 0.10	4.53 ± 0.45	4.91 ± 0.44
WA-XDS-3	11.25 ± 1.22	10.66 ± 0.87	10.13 ± 0.72
WA-XDS-4	＞100	84.37 ± 3.99	＞100
XDS-1	＞100	＞100	＞100

[a]IC50 values are the mean of at least three independent assays and are presented as the mean ± SD.

3.2 Fluorescent Cell Staining

For fluorescence observation, MDA-MB-231 cells were seeded into 96-well plate at a density of 1×10^4 cells/well and incubated for 24 h at 37 ºC in a humidified 5% CO2 incubator. Then cells were incubated with fluorescent WA derivatives and XDS-1 that dissolved in DMEM medium for 1h. After incubation, cells were washed with DMEM for three times. Cell imaging was performed with an ImageXpress Micro Confocal analysis.

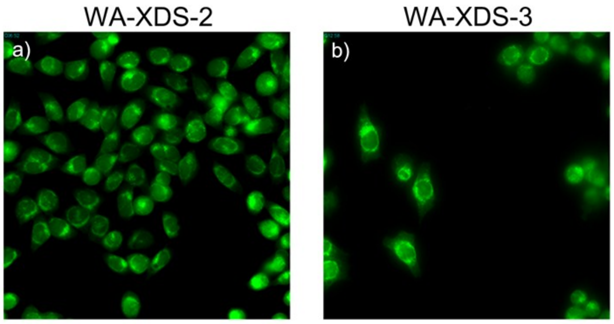


Fig. S11 Uptake of probes in MDA-MB-231 cells: a) 5μM of WA-XDS-2 for 1h; b) 5μM of WA-XDS-3 for 1h

3.3 Subcellular Localization Studies

For co-localization studies, cells were seeded as mentioned above in section 3.2. Briefly, cell were firstly incubated with fluorescent WA derivatives for 1h and then washed with PBS and incubated with mitotracker (YEASEN, China, MitoTracker® Red CMXRos, 100 nM), ER-Tracker Red (BODIPY® TR Glibenclamide, 1μM) or lysotracker (YEASEN, China, LysoTracker Red DND-99 , 50 nM) respectively for another 0.5h. Finally, cells was incubated with reddot (biotium , USA, RedDot™1Far-Red Nuclear Stain) for 5mins. Cell imaging was performed with an ImageXpress Micro Confocal analysis.

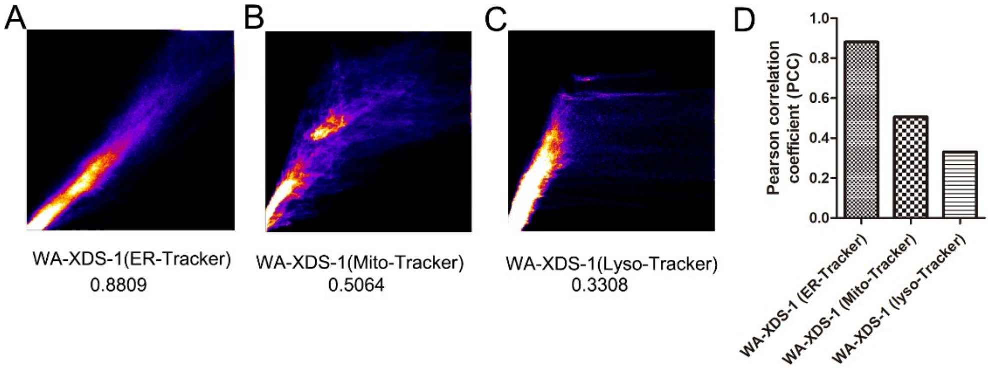


Fig. S12 Pearson correlation coefficient of (A) WA-XDS-1(ER-Tracker); (B) WA-XDS-1(Mito-Tracker); (C) WA-XDS-1(Lyso-Tracker). (D) Overlay of these three Pearson correlation coefficients.

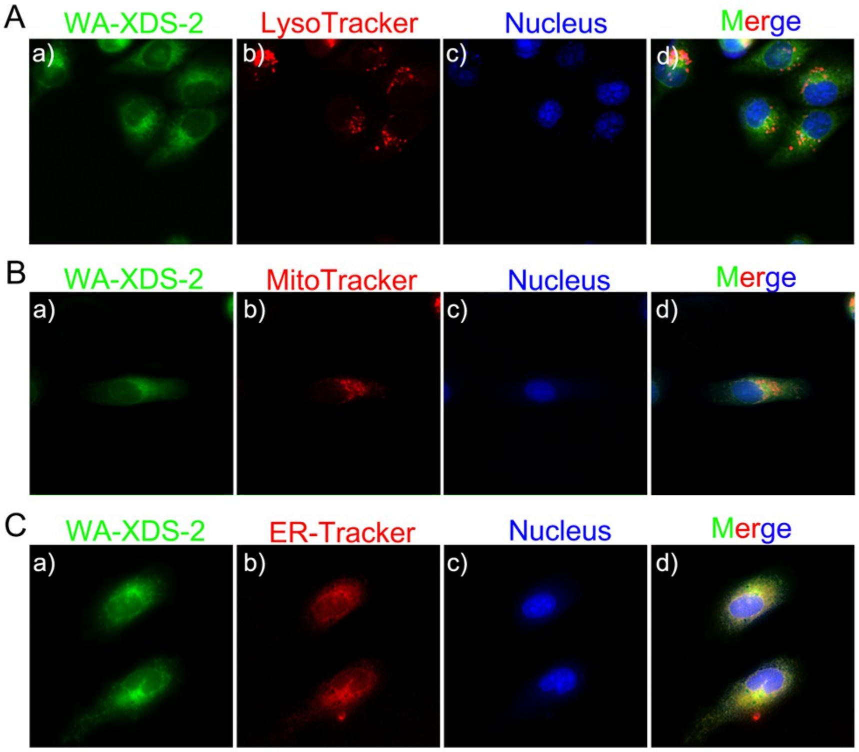


Fig. S13 (A) Co-localization of WA-XDS-2 with LysoTracker in MDA-MB-231 cells: a) 2.5μM of

WA-XDS-2; b) 50nM of LysoTracker; c) reddot d) overlay of three images. (B) Costain of WA-XDS-2 with MitoTracker in MDA-MB-231 cells: a) 2.5μM of WA-XDS-2; b) 100nM of MitoTracker; c) reddot; d) overlay of three images. (C) Costain of WA-XDS-2 with ER-Tracker in MDA-MB-231 cells: a) 2.5μM of WA-XDS-2; b) 1μM of ER-Tracker; c) reddot; d) overlay of three images.

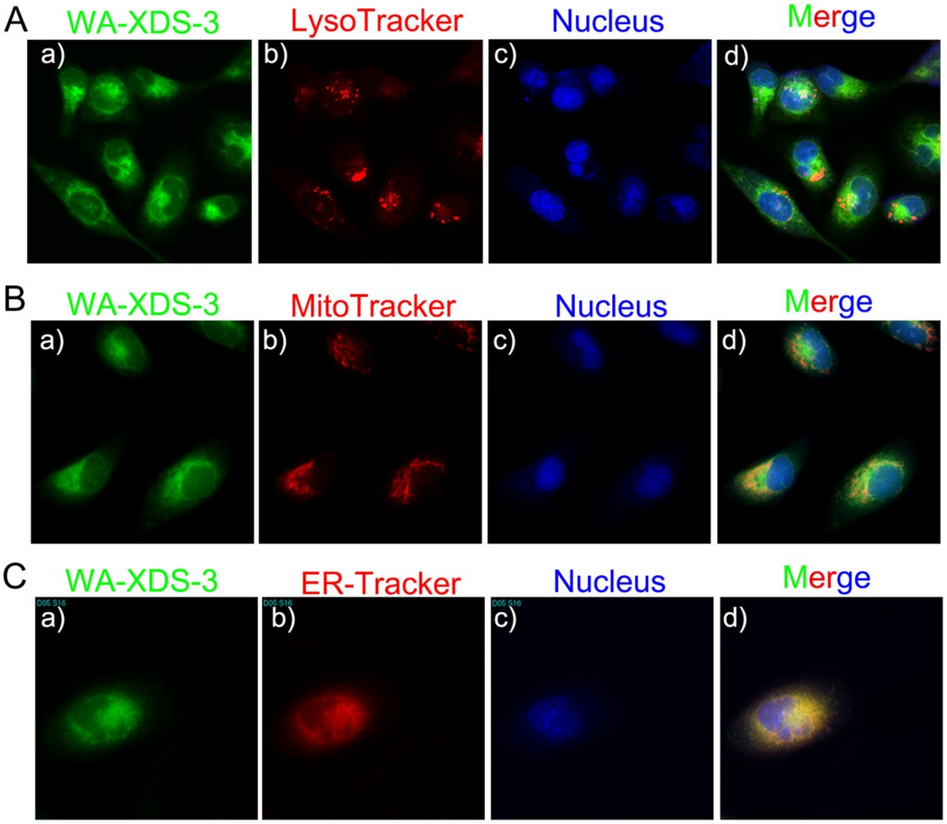


Fig. S14 (A) Co-localization of WA-XDS-3 with LysoTracker in MDA-MB-231 cells: a) 2.5μM of WA-XDS-3; b) 50nM of LysoTracker; c) reddot d) overlay of three images. (B) Costain of WA-XDS-3 with MitoTracker in MDA-MB-231 cells: a) 2.5μM of WA-XDS-3; b) 100nM of MitoTracker; c) reddot; d) overlay of three images. (C) Costain of WA-XDS-3 with ER-Tracker in MDA-MB-231 cells: a) 2.5μM of WA-XDS-3; b) 1μM of ER-Tracker; c) reddot; d) overlay of three images.

3.4 Pull-down assay

Weight out 50mg of Epoxy-activated Sepharose 6B beads and suspend it in distilled water to let it swell to normal size. Dissolve WA to 10mM of NaOH solution and make the concentration of WA as 200μM. Mix the coupling solution containing WA with the medium in a stoppered vessel. Use a shaker in a water bath for 16 hours at 25 °C. Then wash away excess ligand using coupling buffer. The control beads were prepared like the WA-coupled beads without the procedure of coupling with WA. Block the active groups of WA beads and control beads using 1M ethanolamine pH 8.0 overnight at room temperature. The WA-coupled and control beads were finally washed in 3 cycles of alternating low (0.1M acetate buffer, PH=4.0) and high (0.1M tris-HCl buffer, PH=8, containing 0.5M NaCl) PH buffers. Then MDA-MB-231 cells were lysed by scraping the cells in ice-cold lysis buffer (50 mM HEPES pH 8.0, 150 mM NaCl, 0.1 mM EDTA, 0.1% Triton X-100 and complete protease inhibitors) and the cell lysates were added to the WA-coupled beads and incubated overnight at 4 °C. Next, the complex was washed five times with PBS. Finally, one part of the beads was suspended with 2 × loading buffer and boiled to separate the binding protein for WB experiments, the other part of the complex was analyzed by LC-MS/MS to identify the proteins interacted with WA.

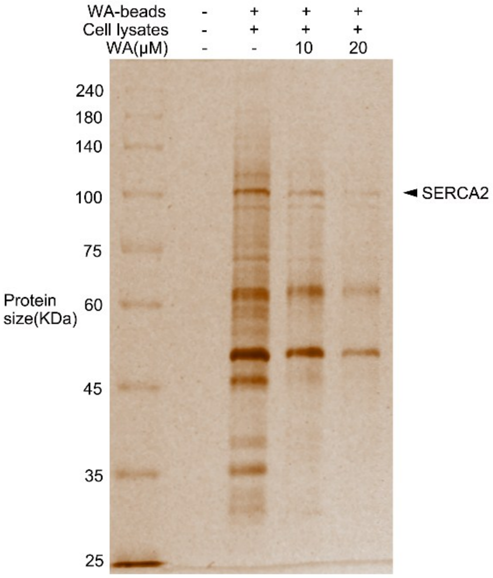


Fig. S15 Proteins interacted with WA was obtained by pull-down experiment and visualized by silver staining

3.5 Immunofluorescence Co-localization Analysis

MDA-MB-231cells were seeded as mentioned above in section 3.2, and then the medium was removed and cells was incubated with fluorescent WA derivatives for 1h, after that cells were washed with PBS for three times and fixed with 4% formaldehyde for 15minutes followed by permeabilizing with 0.2% TritonX-100. Then cells were blocked with 5% BSA (Amresco) for 1 h at room temperature, washed with PBS for three times and incubated with primary antibody against SERCA2 overnight at 4 °C. Next cells were incubated with with dylight 649-conjugated goat anti-rabbit secondary antibody (Abbkine) for 2 h at room temperature. Finally, Nuclei were counter stained with PI for 5minutes. Cell imaging was performed with an ImageXpress Micro Confocal analysis.

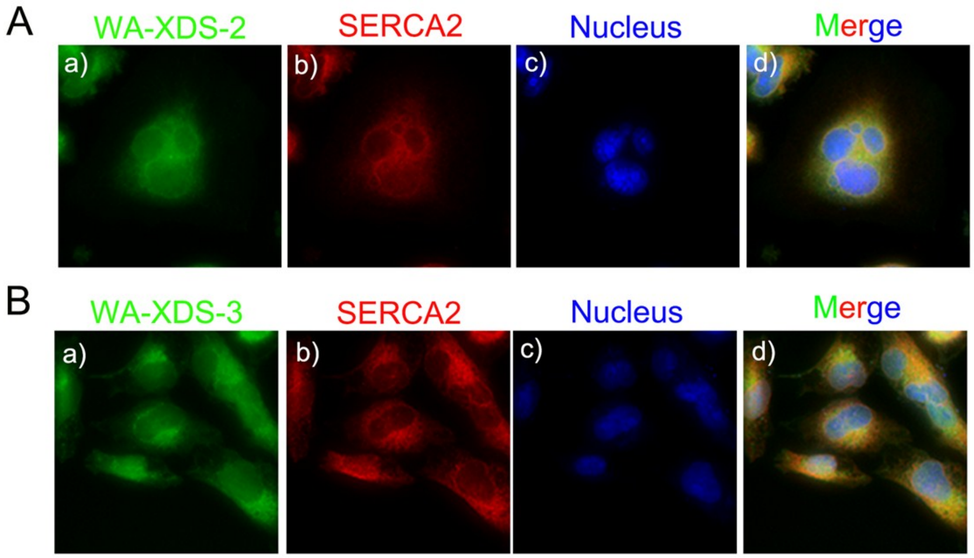


Fig. S16 (A) Immunofluorescence Co-localization of WA-XDS-2 with SERCA2 in MDA-MB-231 cells: a) 2.5μM of WA-XDS-2; b) immunofluorescence against SERCA2; c) 500nM of PI (nuclei specific dye); d) overlay of three images. (B) Immunofluorescence Co-localization of WA-XDS-3 with SERCA2 in MDA-MB-231 cells: a) 2.5μM of WA-XDS-2; b) immunofluorescence against SERCA2; c) 500nM of PI; d) overlay of three images.

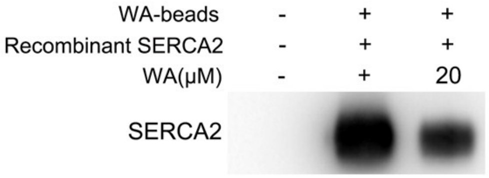


Fig. S17 pull-down experiment of WA with recombinant SERCA2 protein in the absence or presence of 20μM of WA

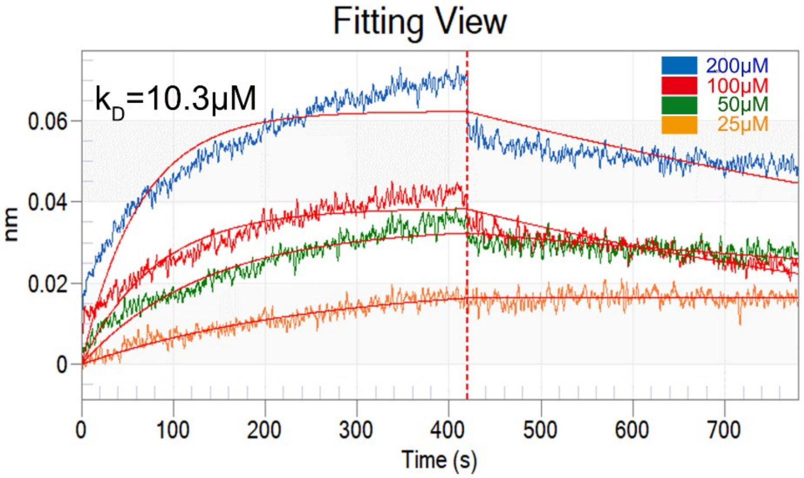


Fig. S18 Biolayer interferometry sensorgrams of the binding of varying concentrations of WA to purified SERCA2 protein.

3.6 LC-MS/MS for target validation

Added 30μg of the beads to 30μL STD buffer and boiled for 5mins to separate the protein and cold to room temperature. Then added 200μL UA buffer (8 M Urea, 150 mM Tris-HCl pH 8.0) and repeated ultrafiltration (Microcon units, 30 kD) for two times. Next 100 μl iodoacetamide (50 mM IAA in UA buffer) was added to block reduced cysteine residues and the samples were incubated for 30 min in darkness. The filters were washed with 100 μl UA buffer three times and then 100 μl 25mM NH_4HCO_3 buffer twice. Finally, the protein suspensions were digested with 4 μg trypsin (Promega) in 40 μl 25mM NH4HCO3 buffer overnight at 37 °C, and the resulting peptides were collected as a filtrate. Each fraction was injected for nanoLC-MS/MS analysis. The peptide mixture was loaded onto a reverse phase trap column (Thermo Scientific Acclaim PepMap100, 100μm*2cm, nanoViper C18) connected to the C18-reversed phase analytical column (Thermo Scientific Easy Column, 10 cm long, 75 μm inner diameter, 3μm resin) in buffer A (0.1% Formic acid) and separated with a linear gradient of buffer B (84% acetonitrile and 0.1% Formic acid) at a flow rate of 300 nl/min controlled by IntelliFlow technology. The 1hour chromatography gradient composed of 0-35% buffer B for 50 min, 35-100% buffer B for 5 min and hold in 100% buffer B for 5 min.

Peptides were then analyzed on a Q Exactive mass spectrometer (Thermo Scientific) that was coupled to Easy nLC (Proxeon Biosystems, now Thermo Fisher Scientific) for 60/120/240 min (determined by project proposal). The mass spectrometer was operated in positive ion mode. MS data was acquired using a data-dependent top10 method dynamically choosing the most abundant precursor ions from the survey scan (300–1800 m/z) for HCD fragmentation. Automatic gain control (AGC) target was set to 3e6, and maximum inject time to 10 ms. Dynamic exclusion duration was 40.0 s. Survey scans were acquired at a resolution of 70,000 at m/z 200 and resolution for HCD spectra was set to 17,500 at m/z 200, and isolation width was 2 m/z. Normalized collision energy was 30 eV and the underfill ratio, which specifies the minimum percentage of the target value likely to be reached at maximum fill time, was defined as 0.1%. The instrument was run with peptide recognition mode enabled.

MS/MS spectra were searched using MASCOT engine (Matrix Science, London, UK; version 2.2) against a nonredundant International Protein Index arabidopsis sequence database v3.85 (released at September 2011; 39679 sequences) from the European Bioinformatics Institute (http://www.ebi.ac.uk/). For protein identification, the following options were used. Peptide mass tolerance=20 ppm, MS/MS tolerance=0.1 Da, Enzyme=Trypsin, Missed cleavage=2, Fixed modification: Carbamidomethyl (C), Variable modification：Oxidation(M)

3.7 Measurement of Ca2+-ATPase (SERCA) activity

MDA-MB-231 cells were incubated various concentrations of WA for 24 h. Then, the cells were washed once with cold saline (0.9% sodium chloride in distilled water) and resuspended with saline. After sonicated for 10 s, SERCA activity of the suspension was measured with Super Microscale

Ca2+-ATPase Detection Kit (A070-4; Nanjing Jiancheng Bioengineering Institute, Nanjing, China) according to the manufacturer's protocols.

3.8 Western Blot Analysis

MDA-MB-231 cells were collected and washed with ice-cold PBS two times before being lysed in radio immunoprecipitation assay (RIPA) lysis buffer. The cell lysates were separated on SDS polyacrylamide gels and transferred to polyvinylidene fluoride membranes (Bio-Rad, Hercules, CA). After blocking nonspecific binding with TBS-T (0.1% tween) containing 5% non-fat milk for 1h at room temperature, the membranes were immunoblotted with the primary antibodies at 4°C overnight. Then the membranes were incubated with HRP-conjugated goat anti-rabbit secondary antibody for 2h at room temperature. The protein bands were detected using the ChemiDOC™ system (Bio-Rad, Hercules, CA) and the densitometry of immunoblots were quantified with Image J software (NIH, Bethesda, MD, USA).

Table S2 Protein identification of WA by LC-MS/MS experiments.

Accession	Description	Score	Coverage	Peptides	PSM	# AAs	MW [kDa]	calc. pI
P04350	Tubulin beta-4A chain OS=Homo sapiens GN=TUBB4A PE=1 SV=2 - [TBB4A_HUMAN]	824.95	47.07	14	31	444	49.6	4.88
H6VRF8	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1 - [H6VRF8_HUMAN]	559.28	28.57	17	26	644	66.0	8.12
P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4 - [EF2_HUMAN]	603.97	29.60	21	25	858	95.3	6.83
Q13509	Tubulin beta-3 chain OS=Homo sapiens GN=TUBB3 PE=1 SV=2 - [TBB3_HUMAN]	533.72	28.89	10	20	450	50.4	4.93
Q92945	Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4 - [FUBP2_HUMAN]	388.87	32.49	17	20	711	73.1	7.30
P78527	DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3 - [PRKDC_HUMAN]	238.04	5.11	18	18	4128	468.8	7.12
P13645	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6 - [K1C10_HUMAN]	376.61	32.02	13	14	584	58.8	5.21
B3KM80	Nucleolin, isoform CRA_c OS=Homo sapiens GN=NCL PE=2 SV=1 - [B3KM80_HUMAN]	324.73	20.90	11	13	536	58.5	4.67
P27816	Microtubule-associated protein 4 OS=Homo sapiens GN=MAP4 PE=1 SV=3 - [MAP4_HUMAN]	194.30	14.06	13	13	1152	120.9	5.43
Q13085	Acetyl-CoA carboxylase 1 OS=Homo sapiens GN=ACACA PE=1 SV=2 - [ACACA_HUMAN]	173.41	5.03	11	12	2346	265.4	6.37
P68104	Elongation factor 1-alpha 1 OS=Homo sapiens GN=EEF1A1 PE=1 SV=1 - [EF1A1_HUMAN]	323.91	27.92	9	12	462	50.1	9.01
F8VPD4	CAD protein OS=Homo sapiens GN=CAD PE=1 SV=1 - [F8VPD4_HUMAN]	197.32	6.52	12	12	2162	235.9	6.55
P30041	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3 - [PRDX6_HUMAN]	258.62	55.36	10	11	224	25.0	6.38
E9PKG1	Protein arginine N-methyltransferase 1 OS=Homo sapiens GN=PRMT1 PE=1 SV=1 - [E9PKG1_HUMAN]	251.66	32.00	10	11	325	37.7	6.15
B7ZLC9	GEMIN5 protein OS=Homo sapiens GN=GEMIN5 PE=2 SV=1 - [B7ZLC9_HUMAN]	87.66	8.03	10	11	1507	168.3	6.62
P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4 - [MYH9_HUMAN]	158.55	6.43	11	11	1960	226.4	5.60
Q86UE4	Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2 - [LYRIC_HUMAN]	133.13	21.65	10	10	582	63.8	9.32
B3KTM6	Ribosomal protein L5, isoform CRA_b OS=Homo sapiens GN=RPL5 PE=2 SV=1 - [B3KTM6_HUMAN]	215.84	34.41	8	10	247	28.0	9.13
P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3 - [G3P_HUMAN]	208.20	28.66	7	10	335	36.0	8.46
B7Z532	cDNA FLJ51028, highly similar to 60 kDa heat shock protein, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B7Z532_HUMAN]	392.11	50.20	9	10	245	26.7	5.22
P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1 - [RL12_HUMAN]	341.58	54.55	6	9	165	17.8	9.42
P05141	ADP/ATP translocase 2 OS=Homo sapiens GN=SLC25A5 PE=1 SV=7 - [ADT2_HUMAN]	169.42	28.86	8	9	298	32.8	9.69
Q5TFE4	5'-nucleotidase domain-containing protein 1 OS=Homo sapiens GN=NT5DC1 PE=1 SV=1 - [NT5D1_HUMAN]	134.05	22.20	8	9	455	51.8	6.35
P23396	40S ribosomal protein S3 OS=Homo sapiens GN=RPS3 PE=1 SV=2 - [RS3_HUMAN]	123.48	36.63	8	9	243	26.7	9.66
A8K4Z4	60S acidic ribosomal protein P0 OS=Homo sapiens PE=2 SV=1 - [A8K4Z4_HUMAN]	253.27	37.85	8	9	317	34.2	5.97
P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4 - [K1C19_HUMAN]	163.95	21.75	9	9	400	44.1	5.14
P18124	60S ribosomal protein L7 OS=Homo sapiens GN=RPL7 PE=1 SV=1 - [RL7_HUMAN]	133.29	24.60	6	8	248	29.2	10.65
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2 - [ROA2_HUMAN]	133.68	16.15	6	8	353	37.4	8.95
F8VTQ5	Heterogeneous nuclear ribonucleoprotein A1 (Fragment) OS=Homo sapiens GN=HNRNPA1 PE=1 SV=1 - [F8VTQ5_HUMAN]	171.06	42.76	6	8	145	16.5	6.64

Q05639	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1 - [EF1A2_HUMAN]	198.52	16.63	7	8	463	50.4	9.03
A0A087WWU8	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=1 SV=1 - [A0A087WWU8_HUMAN]	125.96	29.07	7	8	227	26.4	4.78
P12236	ADP/ATP translocase 3 OS=Homo sapiens GN=SLC25A6 PE=1 SV=4 - [ADT3_HUMAN]	180.25	25.17	7	8	298	32.8	9.74
P07814	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5 - [SYEP_HUMAN]	103.35	6.15	8	8	1512	170.5	7.33
P27348	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1 - [1433T_HUMAN]	145.27	40.82	8	8	245	27.7	4.78
B7Z4V2	cDNA FLJ51907, highly similar to Stress-70 protein, mitochondrial OS=Homo sapiens PE=2 SV=1 - [B7Z4V2_HUMAN]	313.65	16.39	8	8	665	72.4	5.94
P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1 - [AT2A2_HUMAN]	139.80	7.77	7	7	1042	114.7	5.34
9ULT8	E3 ubiquitin-protein ligase HECTD1 OS=Homo sapiens GN=HECTD1 PE=1 SV=3 - [HECD1_HUMAN]	80.89	2.41	7	7	2610	289.2	5.35
P25398	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3 - [RS12_HUMAN]	86.35	46.97	5	7	132	14.5	7.21
P62241	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2 - [RS8_HUMAN]	223.40	37.98	6	7	208	24.2	10.32
P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2 - [HSPB1_HUMAN]	217.12	34.15	6	7	205	22.8	6.40
A6NL76	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=3 - [A6NL76_HUMAN]	94.80	23.62	5	7	254	28.1	6.07
B4DLC0	cDNA FLJ58476, highly similar to Poly(rC)-binding protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DLC0_HUMAN]	137.81	36.21	7	7	301	32.1	7.90
K9J957	Proteasome activator complex subunit 3 OS=Homo sapiens GN=PSME3 PE=1 SV=1 - [K9J957_HUMAN]	167.31	30.74	6	7	231	26.9	5.94
D6RF62	Multifunctional protein ADE2 OS=Homo sapiens GN=PAICS PE=1 SV=1 - [D6RF62_HUMAN]	87.87	28.53	7	7	333	37.1	6.27
B5BU32	Thymidine kinase OS=Homo sapiens GN=TK1 PE=2 SV=1 - [B5BU32_HUMAN]	143.05	28.21	6	7	234	25.4	8.63
Q15654	Thyroid receptor-interacting protein 6 OS=Homo sapiens GN=TRIP6 PE=1 SV=3 - [TRIP6_HUMAN]	36.86	22.06	6	7	476	50.3	7.37
B4E1E0	CTP synthase OS=Homo sapiens PE=2 SV=1 - [B4E1E0_HUMAN]	127.56	21.15	7	7	435	49.7	7.52
Q16576	Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1 - [RBBP7_HUMAN]	123.72	19.29	7	7	425	47.8	5.05
B2RDD7	Protein arginine N-methyltransferase 5 OS=Homo sapiens PE=2 SV=1 - [B2RDD7_HUMAN]	138.37	11.93	7	7	637	72.7	6.29
A8K3C3	T-complex protein 1 subunit delta OS=Homo sapiens PE=2 SV=1 - [A8K3C3_HUMAN]	65.85	11.87	6	7	539	57.9	7.83
Q8TD16	Protein bicaudal D homolog 2 OS=Homo sapiens GN=BICD2 PE=1 SV=1 - [BICD2_HUMAN]	81.17	7.77	6	7	824	93.5	5.44
Q06210	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1 OS=Homo sapiens GN=GFPT1 PE=1 SV=3 - [GFPT1_HUMAN]	115.53	11.59	7	7	699	78.8	7.11
P36578	60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5 - [RL4_HUMAN]	141.32	15.93	6	6	427	47.7	11.06
P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4 - [RL13_HUMAN]	96.86	28.91	6	6	211	24.2	11.65
P46781	40S ribosomal protein S9 OS=Homo sapiens GN=RPS9 PE=1 SV=3 - [RS9_HUMAN]	105.91	22.68	5	6	194	22.6	10.65
Q96AG4	Leucine-rich repeat-containing protein 59 OS=Homo sapiens GN=LRRC59 PE=1 SV=1 - [LRC59_HUMAN]	137.27	19.22	4	6	307	34.9	9.57
Q5RI18	Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens GN=HNRNPU PE=1 SV=9 - [Q5RI18_HUMAN]	116.21	11.30	6	6	602	67.8	9.09
P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3 - [COF1_HUMAN]	48.90	48.19	6	6	166	18.5	8.09
B4DF70	cDNA FLJ60461, highly similar to Peroxiredoxin-2 (EC 1.11.1.15) OS=Homo sapiens PE=2 SV=1 - [B4DF70_HUMAN]	186.32	25.68	5	6	183	20.1	8.78

P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1 - [ATPA_HUMAN]	161.07	13.74	6	6	553	59.7	9.13
P04080	Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2 - [CYTB_HUMAN]	108.40	70.41	4	6	98	11.1	7.56
F5H265	Polyubiquitin-C (Fragment) OS=Homo sapiens GN=UBC PE=1 SV=1 - [F5H265_HUMAN]	126.11	57.72	4	6	149	16.8	6.58
B7Z5C0	cDNA FLJ52352, highly similar to DnaJ homolog subfamily A member 1 OS=Homo sapiens PE=2 SV=1 - [B7Z5C0_HUMAN]	139.86	35.42	6	6	240	27.5	5.94
P30048	Thioredoxin-dependent peroxide reductase, mitochondrial OS=Homo sapiens GN=PRDX3 PE=1 SV=3 - [PRDX3_HUMAN]	156.34	16.02	4	6	256	27.7	7.78
P52597	Heterogeneous nuclear ribonucleoprotein F OS=Homo sapiens GN=HNRNPF PE=1 SV=3 - [HNRPF_HUMAN]	97.93	15.18	5	6	415	45.6	5.58
E9PCY7	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=1 - [E9PCY7_HUMAN]	119.76	13.99	5	6	429	47.1	6.34
P63151	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform OS=Homo sapiens GN=PPP2R2A PE=1 SV=1 - [2ABA_HUMAN]	146.85	13.42	6	6	447	51.7	6.20
Q86X55	Histone-arginine methyltransferase CARM1 OS=Homo sapiens GN=CARM1 PE=1 SV=3 - [CARM1_HUMAN]	165.63	10.86	6	6	608	65.8	6.73
O43252	Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1 OS=Homo sapiens GN=PAPSS1 PE=1 SV=2 - [PAPS1_HUMAN]	72.06	9.13	6	6	624	70.8	6.86
B2R8R5	cDNA, FLJ94025, highly similar to Homo sapiens tripartite motif-containing 28 (TRIM28), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R8R5_HUMAN]	88.03	7.43	5	6	835	88.5	5.77
P22102	Trifunctional purine biosynthetic protein adenosine-3 OS=Homo sapiens GN=GART PE=1 SV=1 - [PUR2_HUMAN]	75.30	7.33	6	6	1010	107.7	6.70
A0A024R1Y2	ATP-citrate synthase OS=Homo sapiens GN=ACLY PE=3 SV=1 - [A0A024R1Y2_HUMAN]	130.68	5.87	6	6	1091	119.7	7.33
Q2NKX8	DNA excision repair protein ERCC-6-like OS=Homo sapiens GN=ERCC6L PE=1 SV=1 - [ERC6L_HUMAN]	123.54	5.68	6	6	1250	141.0	5.31
Q01970	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase beta-3 OS=Homo sapiens GN=PLCB3 PE=1 SV=2 - [PLCB3_HUMAN]	64.19	4.70	5	6	1234	138.7	5.90
C9JXB8	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=1 SV=1 - [C9JXB8_HUMAN]	161.27	36.36	6	6	121	14.4	11.31
F8VVM2	Phosphate carrier protein, mitochondrial OS=Homo sapiens GN=SLC25A3 PE=1 SV=1 - [F8VVM2_HUMAN]	69.45	15.12	5	6	324	36.1	9.26
B3KRM2	Serine/threonine-protein phosphatase OS=Homo sapiens PE=2 SV=1 - [B3KRM2_HUMAN]	114.77	19.09	4	5	309	35.5	5.43
O15269	Serine palmitoyltransferase 1 OS=Homo sapiens GN=SPTLC1 PE=1 SV=1 - [SPTC1_HUMAN]	80.52	10.99	5	5	473	52.7	6.01
Q6IPH7	RPL14 protein OS=Homo sapiens GN=RPL14 PE=1 SV=1 - [Q6IPH7_HUMAN]	144.15	28.64	5	5	220	23.8	10.93
Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2 - [PAIRB_HUMAN]	86.87	14.22	4	5	408	44.9	8.65
P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2 - [RS19_HUMAN]	94.79	28.28	4	5	145	16.1	10.32
A0A087WXM6	60S ribosomal protein L17 (Fragment) OS=Homo sapiens GN=RPL17 PE=3 SV=1 - [A0A087WXM6_HUMAN]	121.58	28.99	4	5	169	19.6	10.04
G3V203	60S ribosomal protein L18 OS=Homo sapiens GN=RPL18 PE=1 SV=1 - [G3V203_HUMAN]	123.40	35.37	5	5	164	18.7	11.59
P61313	60S ribosomal protein L15 OS=Homo sapiens GN=RPL15 PE=1 SV=2 - [RL15_HUMAN]	100.41	21.57	4	5	204	24.1	11.62
H0YEN5	40S ribosomal protein S2 (Fragment) OS=Homo sapiens GN=RPS2 PE=1 SV=1 - [H0YEN5_HUMAN]	96.66	24.10	4	5	195	21.1	9.83
B2R858	cDNA, FLJ93750, Homo sapiens DEAD (Asp-Glu-Ala-Asp) box polypeptide 6 (DDX6), mRNA OS=Homo sapiens PE=2 SV=1 - [B2R858_HUMAN]	100.88	9.53	4	5	472	53.2	8.66

B4DXW6	cDNA FLJ50285, highly similar to Arginyl-tRNA synthetase (EC 6.1.1.19) OS=Homo sapiens PE=2 SV=1 - [B4DXW6_HUMAN]	97.58	12.78	5	5	454	52.3	6.48
A0A0D9SFB3	ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=1 - [A0A0D9SFB3_HUMAN]	91.62	7.97	5	5	640	70.8	7.36
H7BXY3	Putative ATP-dependent RNA helicase DHX30 OS=Homo sapiens GN=DHX30 PE=1 SV=1 - [H7BXY3_HUMAN]	77.59	4.12	5	5	1166	130.5	8.56
A0A0S2Z4Q3	CCHC-type zinc finger nucleic acid binding protein isoform 1 (Fragment) OS=Homo sapiens GN=CNBP PE=2 SV=1 - [A0A0S2Z4Q3_HUMAN]	165.85	32.35	5	5	170	18.7	7.71
D2CVN5	Aryl hydrocarbon receptor-interacting protein AIP722 OS=Homo sapiens GN=AIP PE=4 SV=1 - [D2CVN5_HUMAN]	50.69	21.48	5	5	270	30.8	6.54
P67936	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3 - [TPM4_HUMAN]	102.45	18.55	5	5	248	28.5	4.69
B0AZV0	cDNA, FLJ79540, highly similar to Serine-threonine kinase receptor-associatedprotein OS=Homo sapiens PE=2 SV=1 - [B0AZV0_HUMAN]	24.01	17.58	4	5	256	28.5	4.91
Q96GX9	Methylthioribulose-1-phosphate dehydratase OS=Homo sapiens GN=APIP PE=1 SV=1 - [MTNB_HUMAN]	50.61	17.36	4	5	242	27.1	7.12
Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1 - [DPYL2_HUMAN]	98.27	12.41	5	5	572	62.3	6.38
Q96F86	Enhancer of mRNA-decapping protein 3 OS=Homo sapiens GN=EDC3 PE=1 SV=1 - [EDC3_HUMAN]	24.74	12.40	5	5	508	56.0	7.11
O43353	Receptor-interacting serine/threonine-protein kinase 2 OS=Homo sapiens GN=RIPK2 PE=1 SV=2 - [RIPK2_HUMAN]	52.25	10.37	5	5	540	61.2	7.09
A0A090N8G0	Glycyl-tRNA synthetase OS=Homo sapiens GN=GARS PE=4 SV=1 - [A0A090N8G0_HUMAN]	81.65	9.49	5	5	685	77.5	6.24
B2RD24	cDNA, FLJ96424 OS=Homo sapiens PE=2 SV=1 - [B2RD24_HUMAN]	52.19	8.32	5	5	733	79.6	7.97
A0A0J9YXZ5	Ras GTPase-activating-like protein IQGAP1 OS=Homo sapiens GN=IQGAP1 PE=1 SV=1 - [A0A0J9YXZ5_HUMAN]	67.71	5.21	5	5	1191	135.9	6.14
Q52LW3	Rho GTPase-activating protein 29 OS=Homo sapiens GN=ARHGAP29 PE=1 SV=2 - [RHG29_HUMAN]	47.41	4.20	5	5	1261	142.0	6.74
Q14008	Cytoskeleton-associated protein 5 OS=Homo sapiens GN=CKAP5 PE=1 SV=3 - [CKAP5_HUMAN]	29.06	2.61	5	5	2032	225.4	7.80
O95678	Keratin, type II cytoskeletal 75 OS=Homo sapiens GN=KRT75 PE=1 SV=2 - [K2C75_HUMAN]	113.11	6.35	4	4	551	59.5	7.74
P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1 - [RS6_HUMAN]	125.03	18.88	4	4	249	28.7	10.84
P08779	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV=4 - [K1C16_HUMAN]	79.99	7.40	4	4	473	51.2	5.05
Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4 - [DHX9_HUMAN]	63.46	4.02	4	4	1270	140.9	6.84
P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2 - [RL30_HUMAN]	83.65	41.74	4	4	115	12.8	9.63
P63173	60S ribosomal protein L38 OS=Homo sapiens GN=RPL38 PE=1 SV=2 - [RL38_HUMAN]	99.19	45.71	3	4	70	8.2	10.10
Q8NI62	Ribosomal protein S2 OS=Homo sapiens GN=OK/KNS-cl.6 PE=2 SV=1 - [Q8NI62_HUMAN]	77.36	44.30	3	4	79	8.8	8.00
B5MCP9	40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1 - [B5MCP9_HUMAN]	75.41	32.09	3	4	187	21.3	10.27
D3YTB1	60S ribosomal protein L32 (Fragment) OS=Homo sapiens GN=RPL32 PE=1 SV=1 - [D3YTB1_HUMAN]	115.96	22.56	3	4	133	15.6	11.44
H9E7B8	Cytochrome c oxidase subunit 2 (Fragment) OS=Homo sapiens GN=COX2 PE=3 SV=1 - [H9E7B8_HUMAN]	53.56	4.55	1	4	220	24.8	4.73
P15531	Nucleoside diphosphate kinase A OS=Homo sapiens GN=NME1 PE=1 SV=1 - [NDKA_HUMAN]	79.24	28.29	3	4	152	17.1	6.19
P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3 - [RS18_HUMAN]	72.11	25.00	4	4	152	17.7	10.99

P62266	40S ribosomal protein S23 OS=Homo sapiens GN=RPS23 PE=1 SV=3 - [RS23_HUMAN]	72.35	23.08	3	4	143	15.8	10.49
Q8WW33	Gametocyte-specific factor 1 OS=Homo sapiens GN=GTSF1 PE=1 SV=2 - [GTSF1_HUMAN]	54.62	25.15	4	4	167	19.3	6.51
Q5VVQ1	Translin-associated protein X (Fragment) OS=Homo sapiens GN=TSNAX PE=4 SV=1 - [Q5VVQ1_HUMAN]	56.51	25.15	3	4	163	19.0	7.75
E9PGT1	Translin OS=Homo sapiens GN=TSN PE=1 SV=1 - [E9PGT1_HUMAN]	73.66	24.66	4	4	223	25.6	6.89
P00492	Hypoxanthine-guanine phosphoribosyltransferase OS=Homo sapiens GN=HPRT1 PE=1 SV=2 - [HPRT_HUMAN]	90.34	22.02	4	4	218	24.6	6.68
B4DDF4	Calponin OS=Homo sapiens GN=CNN2 PE=1 SV=1 - [B4DDF4_HUMAN]	110.54	20.47	4	4	298	32.6	6.98
Q9HAV7	GrpE protein homolog 1, mitochondrial OS=Homo sapiens GN=GRPEL1 PE=1 SV=2 - [GRPE1_HUMAN]	60.69	20.28	4	4	217	24.3	8.12
B1AK87	Capping protein (Actin filament) muscle Z-line, beta, isoform CRA_a OS=Homo sapiens GN=CAPZB PE=1 SV=1 - [B1AK87_HUMAN]	100.27	19.62	4	4	260	29.3	6.92
A0A140VJF3	Testicular tissue protein Li 27 OS=Homo sapiens PE=2 SV=1 - [A0A140VJF3_HUMAN]	54.43	17.18	4	4	326	36.9	6.84
Q9UPN1	Serine/threonine-protein phosphatase (Fragment) OS=Homo sapiens GN=PPP1CC PE=3 SV=1 - [Q9UPN1_HUMAN]	37.74	13.95	4	4	294	33.8	5.25
C9IZ80	Basic leucine zipper and W2 domain-containing protein 1 (Fragment) OS=Homo sapiens GN=BZW1 PE=1 SV=1 - [C9IZ80_HUMAN]	102.61	13.27	4	4	294	33.4	7.85
B4DVK5	cDNA FLJ54759, highly similar to DNA replication licensing factor MCM5 OS=Homo sapiens PE=2 SV=1 - [B4DVK5_HUMAN]	28.05	12.86	4	4	412	45.0	8.57
Q5T624	Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=1 - [Q5T624_HUMAN]	36.28	12.56	4	4	422	45.8	4.36
P62140	Serine/threonine-protein phosphatase PP1-beta catalytic subunit OS=Homo sapiens GN=PPP1CB PE=1 SV=3 - [PP1B_HUMAN]	46.86	12.54	4	4	327	37.2	6.19
F5GWF6	T-complex protein 1 subunit beta OS=Homo sapiens GN=CCT2 PE=1 SV=2 - [F5GWF6_HUMAN]	97.68	9.62	4	4	530	56.8	6.44
Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2 - [RCC2_HUMAN]	63.46	9.39	4	4	522	56.0	8.78
P18031	Tyrosine-protein phosphatase non-receptor type 1 OS=Homo sapiens GN=PTPN1 PE=1 SV=1 - [PTN1_HUMAN]	87.67	9.20	4	4	435	49.9	6.27
H3BR35	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A (Fragment) OS=Homo sapiens GN=GSPT1 PE=1 SV=1 - [H3BR35_HUMAN]	62.02	8.63	4	4	475	52.9	5.63
C9JKR2	Albumin, isoform CRA_k OS=Homo sapiens GN=ALB PE=1 SV=1 - [C9JKR2_HUMAN]	77.38	8.39	3	4	417	47.3	6.35
A0A024RDE8	PDZ and LIM domain 5, isoform CRA_c OS=Homo sapiens GN=PDLIM5 PE=4 SV=1 - [A0A024RDE8_HUMAN]	57.42	7.72	4	4	596	63.9	8.21
Q96I24	Far upstream element-binding protein 3 OS=Homo sapiens GN=FUBP3 PE=1 SV=2 - [FUBP3_HUMAN]	53.31	7.52	4	4	572	61.6	8.38
Q53HV2	Chaperonin containing TCP1, subunit 7 (Eta) variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53HV2_HUMAN]	74.56	7.37	4	4	543	59.3	7.65
Q12797	Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3 - [ASPH_HUMAN]	85.12	6.20	4	4	758	85.8	5.01
A0A024R6D1	NIMA (Never in mitosis gene a)-related kinase 9, isoform CRA_a OS=Homo sapiens GN=NEK9 PE=4 SV=1 - [A0A024R6D1_HUMAN]	30.89	5.41	4	4	979	107.1	5.73
A8K5Y7	cDNA FLJ78655, highly similar to Homo sapiens exportin 5 (XPO5), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K5Y7_HUMAN]	88.62	3.74	4	4	1204	136.2	5.90
A0A024R637	TBC1 domain family, member 4, isoform CRA_b OS=Homo sapiens GN=TBC1D4 PE=4 SV=1 - [A0A024R637_HUMAN]	33.64	3.70	4	4	1298	146.5	7.01

I3L3P7	40S ribosomal protein S15a OS=Homo sapiens GN=RPS15A PE=1 SV=1 - [I3L3P7_HUMAN]	70.84	22.00	2	3	100	11.5	10.15
F8WD59	40S ribosomal protein SA (Fragment) OS=Homo sapiens GN=RPSA PE=1 SV=2 - [F8WD59_HUMAN]	132.30	34.48	3	3	116	12.6	9.41
M0QZC5	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=1 - [M0QZC5_HUMAN]	39.42	21.19	3	3	118	14.0	10.32
P62750	60S ribosomal protein L23a OS=Homo sapiens GN=RPL23A PE=1 SV=1 - [RL23A_HUMAN]	81.27	18.59	3	3	156	17.7	10.45
I6L965	KRT18 protein (Fragment) OS=Homo sapiens GN=KRT18 PE=2 SV=1 - [I6L965_HUMAN]	101.65	7.26	3	3	372	42.1	5.10
Q58FF6	Putative heat shock protein HSP 90-beta 4 OS=Homo sapiens GN=HSP90AB4P PE=5 SV=1 - [H90B4_HUMAN]	68.12	6.53	3	3	505	58.2	4.73
B4DEI3	cDNA FLJ57715, highly similar to Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens PE=2 SV=1 - [B4DEI3_HUMAN]	46.41	18.59	3	3	156	16.7	9.39
P67809	Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3 - [YBOX1_HUMAN]	60.36	13.27	3	3	324	35.9	9.88
P46783	40S ribosomal protein S10 OS=Homo sapiens GN=RPS10 PE=1 SV=1 - [RS10_HUMAN]	77.99	14.55	2	3	165	18.9	10.15
Q7Z417	Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens GN=NUFIP2 PE=1 SV=1 - [NUFP2_HUMAN]	50.61	4.60	3	3	695	76.1	8.70
E4W6B6	RPL27/NME2 fusion protein (Fragment) OS=Homo sapiens GN=RPL27 PE=2 SV=1 - [E4W6B6_HUMAN]	61.79	31.75	3	3	126	14.2	10.46
J3KPD9	NME1-NME2 readthrough OS=Homo sapiens GN=NME1-NME2 PE=1 SV=1 - [J3KPD9_HUMAN]	64.80	25.89	3	3	197	22.4	9.54
E5RJR5	S-phase kinase-associated protein 1 OS=Homo sapiens GN=SKP1 PE=1 SV=1 - [E5RJR5_HUMAN]	107.48	20.86	3	3	163	18.7	4.70
E9PKT8	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens GN=NAP1L4 PE=1 SV=1 - [E9PKT8_HUMAN]	59.60	18.34	3	3	169	19.1	5.03
H0YAF8	Receptor of-activated protein C kinase 1 (Fragment) OS=Homo sapiens GN=RACK1 PE=1 SV=1 - [H0YAF8_HUMAN]	58.52	12.12	2	3	198	22.0	6.33
Q9Y3I0	tRNA-splicing ligase RtcB homolog OS=Homo sapiens GN=RTCB PE=1 SV=1 - [RTCB_HUMAN]	56.19	5.94	3	3	505	55.2	7.23
D3DWL0	Plectin 1, intermediate filament binding protein 500kDa, isoform CRA_b OS=Homo sapiens GN=PLEC1 PE=4 SV=1 - [D3DWL0_HUMAN]	68.82	1.85	3	3	2105	234.0	5.91
K7EPR5	cAMP-dependent protein kinase type I-alpha regulatory subunit (Fragment) OS=Homo sapiens GN=PRKAR1A PE=1 SV=8 - [K7EPR5_HUMAN]	37.75	57.78	2	3	45	5.1	5.91
C9JYQ9	60S ribosomal protein L22-like 1 OS=Homo sapiens GN=RPL22L1 PE=1 SV=1 - [C9JYQ9_HUMAN]	94.72	35.54	3	3	121	14.5	9.38
E9PMW7	Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=1 SV=1 - [E9PMW7_HUMAN]	65.74	34.62	3	3	130	14.2	7.52
C9K025	60S ribosomal protein L35a (Fragment) OS=Homo sapiens GN=RPL35A PE=1 SV=1 - [C9K025_HUMAN]	60.53	31.91	3	3	94	10.6	10.71
P26447	Protein S100-A4 OS=Homo sapiens GN=S100A4 PE=1 SV=1 - [S10A4_HUMAN]	27.80	26.73	3	3	101	11.7	6.11
I3NI03	Protein disulfide-isomerase (Fragment) OS=Homo sapiens GN=P4HB PE=1 SV=1 - [I3NI03_HUMAN]	66.04	26.51	3	3	166	18.5	6.11
A0A087WUV8	Basigin OS=Homo sapiens GN=BSG PE=1 SV=1 - [A0A087WUV8_HUMAN]	74.21	25.93	3	3	189	20.5	6.68
P40616	ADP-ribosylation factor-like protein 1 OS=Homo sapiens GN=ARL1 PE=1 SV=1 - [ARL1_HUMAN]	110.68	18.23	3	3	181	20.4	5.72
F5H0E2	4F2 cell-surface antigen heavy chain (Fragment) OS=Homo sapiens GN=SLC3A2 PE=1 SV=1 - [F5H0E2_HUMAN]	37.85	17.93	3	3	145	15.7	5.06
B2RDE8	cDNA, FLJ96580, highly similar to Homo sapiens hepatoma-derived growth factor (high-mobility group protein 1-like) (HDGF), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDE8_HUMAN]	42.21	17.92	3	3	240	26.8	4.67

G3V1D4	Lin-7 homolog C (C. elegans), isoform CRA_b OS=Homo sapiens GN=LIN7C PE=1 SV=1 - [G3V1D4_HUMAN]	83.44	16.76	3	3	173	19.2	9.07
Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1 - [PSME1_HUMAN]	86.14	14.06	3	3	249	28.7	6.02
P25788	Proteasome subunit alpha type-3 OS=Homo sapiens GN=PSMA3 PE=1 SV=2 - [PSA3_HUMAN]	56.94	11.37	3	3	255	28.4	5.33
P35249	Replication factor C subunit 4 OS=Homo sapiens GN=RFC4 PE=1 SV=2 - [RFC4_HUMAN]	48.25	11.29	3	3	363	39.7	8.02
B3KN49	cDNA FLJ13562 fis, clone PLACE1008080, highly similar to Homo sapiens hexamethylene bis-acetamide inducible 1 (HEXIM1), mRNA OS=Homo sapiens PE=2 SV=1 - [B3KN49_HUMAN]	56.12	10.86	3	3	359	40.6	4.89
B4DE94	cDNA FLJ57707, highly similar to Ketosamine-3-kinase (EC 2.7.1.-) OS=Homo sapiens PE=2 SV=1 - [B4DE94_HUMAN]	44.56	10.28	3	3	282	31.4	8.05
Q9UHR4	Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1 OS=Homo sapiens GN=BAIAP2L1 PE=1 SV=2 - [BI2L1_HUMAN]	72.30	8.02	3	3	511	56.8	8.68
Q9UBB4	Ataxin-10 OS=Homo sapiens GN=ATXN10 PE=1 SV=1 - [ATX10_HUMAN]	30.19	8.00	3	3	475	53.5	5.25
B3KRR1	cDNA FLJ34725 fis, clone MESAN2005958, highly similar to RNA-binding protein Luc7-like 2 OS=Homo sapiens PE=2 SV=1 - [B3KRR1_HUMAN]	64.36	7.67	3	3	339	40.5	10.14
A0A024QZJ7	Coiled-coil domain containing 6, isoform CRA_a OS=Homo sapiens GN=CCDC6 PE=4 SV=1 - [A0A024QZJ7_HUMAN]	29.94	7.59	3	3	474	53.3	7.34
P42166	Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2 - [LAP2A_HUMAN]	62.72	5.48	3	3	694	75.4	7.66
P11488	Guanine nucleotide-binding protein G(t) subunit alpha-1 OS=Homo sapiens GN=GNAT1 PE=1 SV=5 - [GNAT1_HUMAN]	58.72	5.43	2	3	350	40.0	5.62
Q13151	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1 - [ROA0_HUMAN]	82.43	7.21	2	3	305	30.8	9.29
B4DSE4	cDNA FLJ54056, highly similar to Splicing factor 1 OS=Homo sapiens PE=2 SV=1 - [B4DSE4_HUMAN]	60.03	7.08	3	3	452	48.6	9.77
Q53EZ4	Centrosomal protein of 55 kDa OS=Homo sapiens GN=CEP55 PE=1 SV=3 - [CEP55_HUMAN]	97.59	6.68	3	3	464	54.1	7.01
B4DUR8	T-complex protein 1 subunit gamma OS=Homo sapiens GN=CCT3 PE=1 SV=1 - [B4DUR8_HUMAN]	56.28	6.40	3	3	500	55.6	5.64
P61619	Protein transport protein Sec61 subunit alpha isoform 1 OS=Homo sapiens GN=SEC61A1 PE=1 SV=2 - [S61A1_HUMAN]	39.52	6.30	3	3	476	52.2	8.06
Q15758	Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2 - [AAAT_HUMAN]	86.67	5.91	3	3	541	56.6	5.48
H7BXI1	Extended synaptotagmin-2 (Fragment) OS=Homo sapiens GN=ESYT2 PE=1 SV=1 - [H7BXI1_HUMAN]	33.77	4.07	3	3	884	97.9	8.57
Q8TC07	TBC1 domain family member 15 OS=Homo sapiens GN=TBC1D15 PE=1 SV=2 - [TBC15_HUMAN]	88.59	4.05	3	3	691	79.4	5.67
O95373	Importin-7 OS=Homo sapiens GN=IPO7 PE=1 SV=1 - [IPO7_HUMAN]	40.64	3.56	3	3	1038	119.4	4.82
A0A0U1RR39	E3 ubiquitin-protein ligase CBL OS=Homo sapiens GN=CBL PE=1 SV=1 - [A0A0U1RR39_HUMAN]	44.14	3.36	3	3	862	95.0	6.40
Q59HA5	Cyclin G-associated kinase variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59HA5_HUMAN]	55.76	2.84	3	3	1196	130.7	5.74
A8K6V3	cDNA FLJ78677, highly similar to Homo sapiens splicing factor 3b, subunit 3, 130kDa (SF3B3), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6V3_HUMAN]	56.96	2.71	3	3	1217	135.5	5.21
A8K8U1	cDNA FLJ77762, highly similar to Homo sapiens cullin-associated and neddylation-dissociated 1 (CAND1), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K8U1_HUMAN]	55.11	2.36	3	3	1230	136.2	5.83
A0A024RAL3	Zinc finger, FYVE domain containing 16, isoform CRA_a OS=Homo sapiens GN=ZFYVE16 PE=4 SV=1 -	49.67	2.08	3	3	1539	168.7	4.82

	[A0A024RAL3_HUMAN]							
E9PEM5	Lipopolysaccharide-responsive and beige-like anchor protein OS=Homo sapiens GN=LRBA PE=1 SV=1 - [E9PEM5_HUMAN]	43.75	1.48	3	3	2575	286.8	5.52
Q6FG99	RPLP1 protein OS=Homo sapiens GN=RPLP1 PE=2 SV=1 - [Q6FG99_HUMAN]	124.81	29.82	2	2	114	11.6	4.37
A0A087X0X3	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=1 - [A0A087X0X3_HUMAN]	26.05	3.15	2	2	730	77.5	8.78
P49458	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2 - [SRP09_HUMAN]	73.77	23.26	2	2	86	10.1	7.97
H0YLP6	60S ribosomal protein L28 OS=Homo sapiens GN=RPL28 PE=1 SV=1 - [H0YLP6_HUMAN]	52.35	13.48	2	2	89	9.7	10.36
F8WBR5	Calmodulin-2 OS=Homo sapiens GN=CALM2 PE=1 SV=1 - [F8WBR5_HUMAN]	46.32	26.15	2	2	65	7.4	4.01
P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2 - [RL22_HUMAN]	65.26	30.47	2	2	128	14.8	9.19
D6RBD7	Eukaryotic translation elongation factor 1 epsilon-1 OS=Homo sapiens GN=EEF1E1 PE=4 SV=1 - [D6RBD7_HUMAN]	61.50	14.00	2	2	150	16.7	8.12
E7ETK0	40S ribosomal protein S24 OS=Homo sapiens GN=RPS24 PE=1 SV=1 - [E7ETK0_HUMAN]	60.50	19.85	2	2	131	15.2	10.89
Q53F35	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53F35_HUMAN]	69.33	9.60	2	2	250	28.7	4.06
P31930	Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3 - [QCR1_HUMAN]	21.39	5.83	2	2	480	52.6	6.37
Q5VU77	Ubiquitin-associated protein 2-like (Fragment) OS=Homo sapiens GN=UBAP2L PE=1 SV=1 - [Q5VU77_HUMAN]	60.77	7.71	2	2	350	37.9	6.74
B4DKM5	cDNA FLJ60120, highly similar to Voltage-dependent anion-selective channel protein 2 OS=Homo sapiens PE=2 SV=1 - [B4DKM5_HUMAN]	46.34	7.06	2	2	255	27.5	5.47
B4E043	KH domain containing, RNA binding, signal transduction associated 1, isoform CRA_b OS=Homo sapiens GN=KHDRBS1 PE=2 SV=1 - [B4E043_HUMAN]	60.07	6.63	2	2	347	38.7	6.47
Q96T67	TOB3 OS=Homo sapiens PE=2 SV=1 - [Q96T67_HUMAN]	43.21	3.11	2	2	578	65.1	9.33
Q14694	Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2 - [UBP10_HUMAN]	45.05	2.76	2	2	798	87.1	5.31
F8VWU4	Ras-related protein Rab-5C (Fragment) OS=Homo sapiens GN=RAB5C PE=1 SV=8 - [F8VWU4_HUMAN]	63.35	24.18	2	2	91	9.9	8.00
A0A087X2D0	Serine/arginine-rich-splicing factor 3 OS=Homo sapiens GN=SRSF3 PE=1 SV=1 - [A0A087X2D0_HUMAN]	24.78	23.16	2	2	95	10.3	5.14
P08708	40S ribosomal protein S17 OS=Homo sapiens GN=RPS17 PE=1 SV=2 - [RS17_HUMAN]	55.69	22.96	2	2	135	15.5	9.85
Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3 - [H2A1H_HUMAN]	0.00	21.88	2	2	128	13.9	10.89
A0A0D9SFA8	Mitochondrial glutamate carrier 1 (Fragment) OS=Homo sapiens GN=SLC25A22 PE=1 SV=1 - [A0A0D9SFA8_HUMAN]	30.39	21.65	2	2	97	10.6	9.45
Q8N5K1	CDGSH iron-sulfur domain-containing protein 2 OS=Homo sapiens GN=CISD2 PE=1 SV=1 - [CISD2_HUMAN]	0.00	21.48	2	2	135	15.3	9.61
H0YFC6	GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=1 SV=1 - [H0YFC6_HUMAN]	36.26	21.36	2	2	103	11.7	10.33
P10599	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 - [THIO_HUMAN]	112.28	20.95	2	2	105	11.7	4.92
M0QZN2	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=1 - [M0QZN2_HUMAN]	106.92	17.91	2	2	134	14.8	8.48
E5RJ41	Catenin alpha-1 (Fragment) OS=Homo sapiens	29.09	17.39	2	2	161	17.5	9.35

	GN=CTNNA1 PE=1 SV=1 - [E5RJ41_HUMAN]							
Q9P0N4	HSPC245 OS=Homo sapiens PE=2 SV=1 - [Q9P0N4_HUMAN]	40.53	16.13	2	2	124	14.1	4.73
K7EPJ1	Ubiquitin-conjugating enzyme E2 S (Fragment) OS=Homo sapiens GN=UBE2S PE=1 SV=1 - [K7EPJ1_HUMAN]	0.00	15.69	2	2	204	22.4	6.29
P42766	60S ribosomal protein L35 OS=Homo sapiens GN=RPL35 PE=1 SV=2 - [RL35_HUMAN]	38.55	15.45	2	2	123	14.5	11.05
P62318	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1 - [SMD3_HUMAN]	30.94	15.08	2	2	126	13.9	10.32
Q96AH2	Similar to mannose-6-phosphate receptor (Cation dependent) (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q96AH2_HUMAN]	18.24	14.88	2	2	168	18.8	5.19
B5BU08	U2 small nuclear RNA auxillary factor 1 isoform a OS=Homo sapiens GN=U2AF1 PE=2 SV=1 - [B5BU08_HUMAN]	75.11	12.92	2	2	240	27.9	8.54
J3QLN6	Eukaryotic initiation factor 4A-I (Fragment) OS=Homo sapiens GN=EIF4A1 PE=1 SV=1 - [J3QLN6_HUMAN]	53.52	12.88	2	2	163	18.0	7.85
B1AH78	Ras-related C3 botulinum toxin substrate 2 (Fragment) OS=Homo sapiens GN=RAC2 PE=1 SV=1 - [B1AH78_HUMAN]	58.99	12.65	2	2	166	18.5	6.54
P24534	Elongation factor 1-beta OS=Homo sapiens GN=EEF1B2 PE=1 SV=3 - [EF1B_HUMAN]	122.77	12.44	2	2	225	24.7	4.67
A8KA83	cDNA FLJ78586, highly similar to Homo sapiens VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa (VAPA), mRNA OS=Homo sapiens PE=1 SV=1 - [A8KA83_HUMAN]	36.74	12.40	2	2	242	27.3	8.62
F5H617	Reticulon (Fragment) OS=Homo sapiens GN=RTN3 PE=1 SV=1 - [F5H617_HUMAN]	32.29	8.65	2	2	185	19.9	8.63
C9JZG1	Eukaryotic translation initiation factor 3 subunit B (Fragment) OS=Homo sapiens GN=EIF3B PE=1 SV=1 - [C9JZG1_HUMAN]	44.28	8.61	2	2	302	33.4	4.36
B2RDZ9	cDNA, FLJ96850 OS=Homo sapiens PE=2 SV=1 - [B2RDZ9_HUMAN]	31.35	8.59	2	2	291	31.9	5.27
J3KNF4	Copper chaperone for superoxide dismutase OS=Homo sapiens GN=CCS PE=1 SV=1 - [J3KNF4_HUMAN]	39.25	8.24	2	2	255	27.1	5.90
B4DHC4	cDNA FLJ51843, highly similar to 14-3-3 protein gamma OS=Homo sapiens PE=2 SV=1 - [B4DHC4_HUMAN]	66.76	8.00	2	2	225	25.6	4.92
Q53GL1	Nicotinamide-nucleotide adenylyltransferase (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q53GL1_HUMAN]	38.47	7.89	2	2	279	31.9	8.87
P50402	Emerin OS=Homo sapiens GN=EMD PE=1 SV=1 - [EMD_HUMAN]	39.58	7.87	2	2	254	29.0	5.50
Q75MT5	Putative uncharacterized protein RFC2 OS=Homo sapiens GN=RFC2 PE=2 SV=1 - [Q75MT5_HUMAN]	50.04	7.81	2	2	320	35.2	5.54
H9E778	Cytochrome c oxidase subunit 1 OS=Homo sapiens GN=COX1 PE=3 SV=1 - [H9E778_HUMAN]	0.00	7.80	1	2	513	56.9	6.57
Q52LJ0	Protein FAM98B OS=Homo sapiens GN=FAM98B PE=1 SV=1 - [FA98B_HUMAN]	0.00	7.27	2	2	330	37.2	6.29
B4DKE6	cDNA FLJ60629, highly similar to Replication factor C subunit 3 OS=Homo sapiens PE=2 SV=1 - [B4DKE6_HUMAN]	35.52	7.21	2	2	305	34.8	8.59
Q9BQA1	Methylosome protein 50 OS=Homo sapiens GN=WDR77 PE=1 SV=1 - [MEP50_HUMAN]	56.85	7.02	2	2	342	36.7	5.17
Q2TAM5	RELA protein OS=Homo sapiens GN=RELA PE=1 SV=1 - [Q2TAM5_HUMAN]	45.64	6.90	2	2	377	42.8	8.37
Q9BZX2	Uridine-cytidine kinase 2 OS=Homo sapiens GN=UCK2 PE=1 SV=1 - [UCK2_HUMAN]	66.96	6.90	2	2	261	29.3	6.70
Q1RMG2	Adenosylhomocysteinase OS=Homo sapiens GN=AHCY PE=2 SV=1 - [Q1RMG2_HUMAN]	31.96	6.54	2	2	306	33.8	6.61
A0A024R837	Haloacid dehalogenase-like hydrolase domain containing 3, isoform CRA_a OS=Homo sapiens GN=HDHD3 PE=4 SV=1 - [A0A024R837_HUMAN]	42.21	6.37	2	2	251	28.1	6.58

Q96GM8	Target of EGR1 protein 1 OS=Homo sapiens GN=TOE1 PE=1 SV=1 - [TOE1_HUMAN]	20.14	6.27	2	2	510	56.5	7.18
Q5HYL6	Putative uncharacterized protein DKFZp686E1899 OS=Homo sapiens GN=DKFZp686E1899 PE=2 SV=1 - [Q5HYL6_HUMAN]	0.00	6.25	2	2	352	39.5	5.19
P53007	Tricarboxylate transport protein, mitochondrial OS=Homo sapiens GN=SLC25A1 PE=1 SV=2 - [TXTP_HUMAN]	44.47	6.11	2	2	311	34.0	9.89
Q01804	OTU domain-containing protein 4 OS=Homo sapiens GN=OTUD4 PE=1 SV=4 - [OTUD4_HUMAN]	27.00	2.42	2	2	1114	124.0	6.71
Q9Y6A5	Transforming acidic coiled-coil-containing protein 3 OS=Homo sapiens GN=TACC3 PE=1 SV=1 - [TACC3_HUMAN]	67.23	2.39	2	2	838	90.3	5.05
A8K5D9	cDNA FLJ77424, highly similar to Homo sapiens anillin, actin binding protein (scraps homolog, Drosophila), mRNA OS=Homo sapiens PE=2 SV=1 - [A8K5D9_HUMAN]	44.39	2.21	2	2	1086	119.8	8.22
Q9NYF8	Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=1 SV=2 - [BCLF1_HUMAN]	33.44	2.17	2	2	920	106.1	9.98
A8K940	cDNA FLJ77630, highly similar to Homo sapiens BPY2 interacting protein 1, mRNA OS=Homo sapiens PE=1 SV=1 - [A8K940_HUMAN]	66.31	2.17	2	2	1059	112.2	7.30
G5E9A6	Ubiquitin carboxyl-terminal hydrolase 11 OS=Homo sapiens GN=USP11 PE=1 SV=1 - [G5E9A6_HUMAN]	54.08	2.17	2	2	920	105.0	5.33
B2R5U1	cDNA, FLJ92620, highly similar to Homo sapiens staphylococcal nuclease domain containing 1 (SND1),mRNA OS=Homo sapiens PE=2 SV=1 - [B2R5U1_HUMAN]	30.90	2.03	2	2	885	99.6	6.96
P35568	Insulin receptor substrate 1 OS=Homo sapiens GN=IRS1 PE=1 SV=1 - [IRS1_HUMAN]	30.15	2.01	2	2	1242	131.5	8.54
H0YN14	Importin-4 OS=Homo sapiens GN=IPO4 PE=1 SV=1 - [H0YN14_HUMAN]	71.72	1.98	2	2	911	101.4	5.05
A0A0A6YY96	Iron-responsive element-binding protein 2 OS=Homo sapiens GN=IREB2 PE=1 SV=1 - [A0A0A6YY96_HUMAN]	43.70	1.97	2	2	963	105.0	7.05
A0A0G2JNZ2	Protein scribble homolog OS=Homo sapiens GN=SCRIB PE=1 SV=1 - [A0A0G2JNZ2_HUMAN]	38.68	1.35	2	2	1630	174.8	5.07
Q14669	E3 ubiquitin-protein ligase TRIP12 OS=Homo sapiens GN=TRIP12 PE=1 SV=1 - [TRIPC_HUMAN]	26.69	1.26	2	2	1992	220.3	8.48
P42704	Leucine-rich PPR motif-containing protein, mitochondrial OS=Homo sapiens GN=LRPPRC PE=1 SV=3 - [LPPRC_HUMAN]	29.60	1.00	2	2	1394	157.8	6.13
A0A1U9X987	PRRC2A OS=Homo sapiens PE=4 SV=1 - [A0A1U9X987_HUMAN]	43.63	0.98	2	2	2153	228.4	9.45
Q8TCJ2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE=1 SV=1 - [STT3B_HUMAN]	38.91	0.97	1	2	826	93.6	8.91
Q9Y490	Talin-1 OS=Homo sapiens GN=TLN1 PE=1 SV=3 - [TLN1_HUMAN]	46.50	0.91	2	2	2541	269.6	6.07
B4DHR1	cDNA FLJ53009, highly similar to Calreticulin OS=Homo sapiens PE=2 SV=1 - [B4DHR1_HUMAN]	0.00	5.66	1	1	212	24.3	5.11
B4DLZ4	cDNA FLJ57528, highly similar to Dihydropyrimidinase-related protein 3 OS=Homo sapiens PE=2 SV=1 - [B4DLZ4_HUMAN]	41.80	5.61	1	1	196	21.1	9.58
H0YAP0	Zinc finger C2HC domain-containing protein 1A (Fragment) OS=Homo sapiens GN=ZC2HC1A PE=1 SV=1 - [H0YAP0_HUMAN]	25.37	5.58	1	1	197	20.9	9.86
H0YJ21	Cytoplasmic dynein 1 heavy chain 1 (Fragment) OS=Homo sapiens GN=DYNC1H1 PE=1 SV=1 - [H0YJ21_HUMAN]	25.81	5.56	1	1	180	21.0	7.25
C9JKY3	Epithelial cell adhesion molecule (Fragment) OS=Homo sapiens GN=EPCAM PE=1 SV=1 - [C9JKY3_HUMAN]	20.35	5.53	1	1	199	20.9	9.28
B7Z6D9	cDNA FLJ52750, highly similar to Rho guanine nucleotide exchange factor 7 OS=Homo sapiens PE=2 SV=1 - [B7Z6D9_HUMAN]	0.00	5.52	1	1	181	20.2	6.19

H7C0F9	Leucine-rich repeat and calponin homology domain-containing protein 3 (Fragment) OS=Homo sapiens GN=LRCH3 PE=1 SV=1 - [H7C0F9_HUMAN]	27.60	5.52	1	1	181	20.0	7.66
H0UI83	Proteasome subunit alpha type OS=Homo sapiens GN=hCG_41772 PE=3 SV=1 - [H0UI83_HUMAN]	28.79	5.42	1	1	166	18.2	8.57
A8MU58	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2 OS=Homo sapiens GN=AIMP2 PE=1 SV=2 - [A8MU58_HUMAN]	0.00	5.37	1	1	242	26.7	8.07
E9PH64	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 OS=Homo sapiens GN=NDUFB9 PE=1 SV=1 - [E9PH64_HUMAN]	19.47	5.36	1	1	168	20.4	7.88
Q9H2R8	CGI16-iso OS=Homo sapiens PE=2 SV=1 - [Q9H2R8_HUMAN]	20.42	5.29	1	1	189	21.6	7.50
H0YBR5	Eukaryotic translation initiation factor 3 subunit E (Fragment) OS=Homo sapiens GN=EIF3E PE=1 SV=1 - [H0YBR5_HUMAN]	39.09	5.26	1	1	171	20.2	5.16
B1AMX7	TNF receptor-associated factor 2 (Fragment) OS=Homo sapiens GN=TRAF2 PE=1 SV=8 - [B1AMX7_HUMAN]	35.83	5.26	1	1	171	18.6	7.21
K7EJ49	Kelch-like ECH-associated protein 1 (Fragment) OS=Homo sapiens GN=KEAP1 PE=1 SV=1 - [K7EJ49_HUMAN]	0.00	5.19	1	1	212	23.4	5.96
H0YL43	Reticulocalbin-2 (Fragment) OS=Homo sapiens GN=RCN2 PE=1 SV=1 - [H0YL43_HUMAN]	35.29	5.16	1	1	155	17.7	4.59
H0YA24	Pleiotropic regulator 1 (Fragment) OS=Homo sapiens GN=PLRG1 PE=1 SV=1 - [H0YA24_HUMAN]	0.00	5.13	1	1	156	17.4	9.54
B4DTS5	cDNA FLJ58882, highly similar to 26S proteasome non-ATPase regulatory subunit 11 OS=Homo sapiens PE=2 SV=1 - [B4DTS5_HUMAN]	29.18	5.10	1	1	314	35.1	6.92
F8VS10	Spermatogenesis-associated serine-rich protein 2 OS=Homo sapiens GN=SPATS2 PE=1 SV=1 - [F8VS10_HUMAN]	0.00	5.08	1	1	295	32.5	7.39
Q96BK8	C8orf30A protein (Fragment) OS=Homo sapiens GN=C8orf30A PE=2 SV=1 - [Q96BK8_HUMAN]	0.00	5.08	1	1	256	28.8	5.22
D6R9P3	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=1 SV=1 - [D6R9P3_HUMAN]	52.17	5.00	1	1	280	30.3	7.91
P49721	Proteasome subunit beta type-2 OS=Homo sapiens GN=PSMB2 PE=1 SV=1 - [PSB2_HUMAN]	0.00	4.98	1	1	201	22.8	7.02
E9PH82	Protein FAM98A OS=Homo sapiens GN=FAM98A PE=1 SV=1 - [E9PH82_HUMAN]	46.10	4.81	1	1	312	34.4	8.28
B4DR67	cDNA FLJ56758, highly similar to Dolichyl-phosphate beta-glucosyltransferase (EC 2.4.1.117) OS=Homo sapiens PE=2 SV=1 - [B4DR67_HUMAN]	23.48	4.78	1	1	230	25.3	9.06
Q86T96	E3 ubiquitin-protein ligase RNF180 OS=Homo sapiens GN=RNF180 PE=2 SV=2 - [RN180_HUMAN]	0.00	4.73	1	1	592	68.2	8.56
Q969E8	Pre-rRNA-processing protein TSR2 homolog OS=Homo sapiens GN=TSR2 PE=1 SV=1 - [TSR2_HUMAN]	26.81	4.71	1	1	191	20.9	4.39
A6NE76	Cullin-4B (Fragment) OS=Homo sapiens GN=CUL4B PE=1 SV=2 - [A6NE76_HUMAN]	42.67	4.70	1	1	234	27.9	5.41
H7C3X0	Protein O-GlcNAcase (Fragment) OS=Homo sapiens GN=MGEA5 PE=1 SV=1 - [H7C3X0_HUMAN]	37.54	4.69	1	1	256	29.7	7.01
E9PIB2	Gasdermin-D (Fragment) OS=Homo sapiens GN=GSDMD PE=1 SV=1 - [E9PIB2_HUMAN]	19.71	4.69	1	1	277	30.8	9.04
H7C2Y7	Unconventional myosin-Ib (Fragment) OS=Homo sapiens GN=MYO1B PE=1 SV=1 - [H7C2Y7_HUMAN]	26.42	4.69	1	1	192	21.8	8.46
A0A140TA73	Beta-2-syntrophin (Fragment) OS=Homo sapiens GN=SNTB2 PE=1 SV=1 - [A0A140TA73_HUMAN]	46.29	4.66	1	1	193	19.4	10.21
E9PMD4	FACT complex subunit SSRP1 (Fragment) OS=Homo sapiens GN=SSRP1 PE=1 SV=2 - [E9PMD4_HUMAN]	30.80	4.62	1	1	173	19.8	5.57
Q59G63	Phosphoribosyl pyrophosphate amidotransferase proprotein variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59G63_HUMAN]	33.75	4.61	1	1	217	24.5	8.92
Q7Z7A3	Cytoplasmic tRNA 2-thiolation protein 1 OS=Homo sapiens GN=CTU1 PE=1 SV=1 - [CTU1_HUMAN]	33.21	4.60	1	1	348	36.4	9.20

H0YB26	Copine-3 (Fragment) OS=Homo sapiens GN=CPNE3 PE=1 SV=1 - [H0YB26_HUMAN]	18.74	4.58	1	1	262	29.4	5.74
B4DUX0	cDNA FLJ60167, highly similar to Cytosolic acyl coenzyme A thioester hydrolase(EC 3.1.2.2) OS=Homo sapiens PE=2 SV=1 - [B4DUX0_HUMAN]	53.43	4.53	1	1	265	29.6	7.85
F5GZ03	T-complex protein 1 subunit alpha (Fragment) OS=Homo sapiens GN=TCP1 PE=1 SV=1 - [F5GZ03_HUMAN]	62.78	4.52	1	1	221	24.1	7.05
Q9BVV7	Mitochondrial import inner membrane translocase subunit Tim21 OS=Homo sapiens GN=TIMM21 PE=1 SV=1 - [TIM21_HUMAN]	38.09	4.44	1	1	248	28.2	9.70
H7C0V0	m-AAA protease-interacting protein 1, mitochondrial (Fragment) OS=Homo sapiens GN=MAIP1 PE=1 SV=1 - [H7C0V0_HUMAN]	0.00	4.44	1	1	225	25.1	9.07
Q5JXM0	Putative uncharacterized protein DKFZp564C0482 OS=Homo sapiens GN=DKFZp564C0482 PE=4 SV=1 - [Q5JXM0_HUMAN]	25.67	4.44	1	1	248	27.1	5.53
G3V4M9	Inositol 1,3,4-triphosphate 5/6 kinase, isoform CRA_c OS=Homo sapiens GN=ITPK1 PE=1 SV=1 - [G3V4M9_HUMAN]	0.00	4.41	1	1	295	31.7	5.74
A0A087WWI6	DDB1- and CUL4-associated factor 7 (Fragment) OS=Homo sapiens GN=DCAF7 PE=1 SV=6 - [A0A087WWI6_HUMAN]	34.76	4.37	1	1	206	23.4	5.99
H7C3L4	TRAF family member-associated NF-kappa-B activator (Fragment) OS=Homo sapiens GN=TANK PE=1 SV=1 - [H7C3L4_HUMAN]	31.54	4.36	1	1	275	30.6	5.94
A0A1W2PRL9	Transcription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1 PE=1 SV=1 - [A0A1W2PRL9_HUMAN]	30.11	4.29	1	1	280	31.6	8.53
P41227	N-alpha-acetyltransferase 10 OS=Homo sapiens GN=NAA10 PE=1 SV=1 - [NAA10_HUMAN]	26.06	4.26	1	1	235	26.4	5.64
A3KFJ1	Aurora kinase A (Fragment) OS=Homo sapiens GN=AURKA PE=1 SV=8 - [A3KFJ1_HUMAN]	22.18	4.26	1	1	188	21.0	9.96
Q7L294	SAPS3 protein (Fragment) OS=Homo sapiens GN=SAPS3 PE=2 SV=1 - [Q7L294_HUMAN]	22.78	4.17	1	1	336	36.2	4.17
B4DEX8	S-adenosylmethionine synthase OS=Homo sapiens GN=MAT2A PE=2 SV=1 - [B4DEX8_HUMAN]	49.98	4.14	1	1	362	39.7	6.04
Q9NT62	Ubiquitin-like-conjugating enzyme ATG3 OS=Homo sapiens GN=ATG3 PE=1 SV=1 - [ATG3_HUMAN]	53.48	4.14	1	1	314	35.8	4.74
Q96SP2	cDNA FLJ14726 fis, clone NT2RP3001727, highly similar to Rattus norvegicus implantation-associated protein (IAG2) mRNA OS=Homo sapiens PE=2 SV=1 - [Q96SP2_HUMAN]	0.00	4.13	1	1	218	24.4	9.07
Q8TBT6	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q8TBT6_HUMAN]	17.15	4.13	1	1	315	34.5	8.87
A0A0S2Z476	Proteasome 26S subunit non-ATPase 12 isoform 2 OS=Homo sapiens GN=PSMD12 PE=2 SV=1 - [A0A0S2Z476_HUMAN]	62.45	4.11	1	1	316	36.6	7.56
Q9NPD3	Exosome complex component RRP41 OS=Homo sapiens GN=EXOSC4 PE=1 SV=3 - [EXOS4_HUMAN]	0.00	4.08	1	1	245	26.4	6.52
B3KXN9	cDNA FLJ45793 fis, clone NT2RI2009233 OS=Homo sapiens PE=2 SV=1 - [B3KXN9_HUMAN]	61.45	4.07	1	1	270	29.8	6.04
E9PJT3	Splicing factor 3B subunit 2 (Fragment) OS=Homo sapiens GN=SF3B2 PE=1 SV=1 - [E9PJT3_HUMAN]	42.94	4.03	1	1	273	29.1	5.66
F8W787	Cathepsin D (Fragment) OS=Homo sapiens GN=CTSD PE=1 SV=1 - [F8W787_HUMAN]	0.00	4.02	1	1	199	21.5	5.80
D6RHI7	Cyclin-H OS=Homo sapiens GN=CCNH PE=1 SV=1 - [D6RHI7_HUMAN]	0.00	4.02	1	1	249	28.9	5.92
Q9C004	Protein sprouty homolog 4 OS=Homo sapiens GN=SPRY4 PE=1 SV=2 - [SPY4_HUMAN]	29.39	4.01	1	1	299	32.5	7.88
H3BT22	Origin recognition complex subunit 6 OS=Homo sapiens GN=ORC6 PE=1 SV=1 - [H3BT22_HUMAN]	0.00	3.94	1	1	203	22.8	8.48
D3DVA3	Misato homolog 1 (Drosophila), isoform CRA_a OS=Homo sapiens GN=MSTO1 PE=4 SV=1 - [D3DVA3_HUMAN]	37.36	3.88	1	1	309	34.3	6.40

E9PNW8	Fatty acyl-CoA reductase (Fragment) OS=Homo sapiens GN=FAR1 PE=1 SV=1 - [E9PNW8_HUMAN]	38.97	3.88	1	1	335	37.5	6.92
B7Z4Z4	cDNA FLJ51918, highly similar to Peroxisomal membrane protein PEX14 OS=Homo sapiens PE=2 SV=1 - [B7Z4Z4_HUMAN]	28.84	3.83	1	1	313	34.2	4.84
O43819	Protein SCO2 homolog, mitochondrial OS=Homo sapiens GN=SCO2 PE=1 SV=3 - [SCO2_HUMAN]	26.09	3.76	1	1	266	29.8	8.85
C9J057	Asparagine synthetase [glutamine-hydrolyzing] (Fragment) OS=Homo sapiens GN=ASNS PE=1 SV=8 - [C9J057_HUMAN]	0.00	3.74	1	1	214	24.3	7.44
P20618	Proteasome subunit beta type-1 OS=Homo sapiens GN=PSMB1 PE=1 SV=2 - [PSB1_HUMAN]	31.44	3.73	1	1	241	26.5	8.13
B7ZA10	cDNA, FLJ79024, highly similar to Arfaptin-1 OS=Homo sapiens PE=2 SV=1 - [B7ZA10_HUMAN]	35.94	3.72	1	1	296	33.7	8.43
B4DU21	cDNA FLJ58352, highly similar to Ectonucleoside triphosphate diphosphohydrolase 4 (EC 3.6.1.6) OS=Homo sapiens PE=2 SV=1 - [B4DU21_HUMAN]	0.00	3.70	1	1	541	61.6	7.65
Q5HYC5	Putative uncharacterized protein DKFZp686L08115 (Fragment) OS=Homo sapiens GN=DKFZp686L08115 PE=4 SV=1 - [Q5HYC5_HUMAN]	34.32	3.63	1	1	248	27.6	9.54
B4DUM2	cDNA FLJ53891, highly similar to Adenylosuccinate lyase (EC 4.3.2.2) OS=Homo sapiens PE=2 SV=1 - [B4DUM2_HUMAN]	28.05	3.62	1	1	304	34.5	7.08
P09923	Intestinal-type alkaline phosphatase OS=Homo sapiens GN=ALPI PE=1 SV=2 - [PPBI_HUMAN]	44.21	3.60	1	1	528	56.8	5.86
Q5H919	HIV Tat-specific factor 1 (Fragment) OS=Homo sapiens GN=HTATSF1 PE=1 SV=1 - [Q5H919_HUMAN]	39.45	3.59	1	1	223	25.2	4.65
B2RB99	cDNA, FLJ95387 OS=Homo sapiens PE=2 SV=1 - [B2RB99_HUMAN]	25.21	3.59	1	1	306	33.8	8.59
B4DMT5	Eukaryotic translation initiation factor 3 subunit F OS=Homo sapiens GN=EIF3F PE=2 SV=1 - [B4DMT5_HUMAN]	26.55	3.58	1	1	307	33.2	5.59
B1AL69	Hsp90 co-chaperone Cdc37-like 1 OS=Homo sapiens GN=CDC37L1 PE=1 SV=1 - [B1AL69_HUMAN]	0.00	3.57	1	1	308	35.6	5.71
Q59H15	SAM domain-and HD domain-containing protein 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59H15_HUMAN]	38.17	3.57	1	1	336	38.2	6.37
B3KXD6	Pescadillo homolog OS=Homo sapiens GN=PES1 PE=1 SV=1 - [B3KXD6_HUMAN]	25.79	3.56	1	1	449	51.4	5.20
A0A024R755	Calumenin, isoform CRA_a OS=Homo sapiens GN=CALU PE=4 SV=1 - [A0A024R755_HUMAN]	24.15	3.49	1	1	315	37.1	4.59
Q9UG64	Putative uncharacterized protein DKFZp586I1223 (Fragment) OS=Homo sapiens GN=DKFZp586I1223 PE=2 SV=1 - [Q9UG64_HUMAN]	0.00	3.48	1	1	316	35.2	6.67
Q15181	Inorganic pyrophosphatase OS=Homo sapiens GN=PPA1 PE=1 SV=2 - [IPYR_HUMAN]	45.82	3.46	1	1	289	32.6	5.86
H3BTU3	Transcription factor 25 (Fragment) OS=Homo sapiens GN=TCF25 PE=1 SV=1 - [H3BTU3_HUMAN]	35.51	3.40	1	1	265	29.7	5.92
Q15293	Reticulocalbin-1 OS=Homo sapiens GN=RCN1 PE=1 SV=1 - [RCN1_HUMAN]	0.00	3.32	1	1	331	38.9	5.00
Q6PK21	OGFR protein OS=Homo sapiens PE=2 SV=1 - [Q6PK21_HUMAN]	32.56	3.31	1	1	513	54.1	6.14
F8VS07	LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1 - [F8VS07_HUMAN]	0.00	3.29	1	1	456	51.1	5.49
B7Z2V6	cDNA FLJ53889, highly similar to Vacuolar ATP synthase catalytic subunit A, ubiquitous isoform (EC 3.6.3.14) OS=Homo sapiens PE=2 SV=1 - [B7Z2V6_HUMAN]	0.00	3.29	1	1	334	37.7	5.41
B4DJI1	cDNA FLJ52549, highly similar to L-lactate dehydrogenase A chain (EC 1.1.1.27) OS=Homo sapiens PE=2 SV=1 - [B4DJI1_HUMAN]	68.91	3.28	1	1	305	33.6	8.46
Q16698	2,4-dienoyl-CoA reductase, mitochondrial OS=Homo sapiens GN=DECR1 PE=1 SV=1 - [DECR_HUMAN]	50.00	3.28	1	1	335	36.0	9.28
K7ENG2	Splicing factor U2AF 65 kDa subunit OS=Homo sapiens GN=U2AF2 PE=1 SV=1 - [K7ENG2_HUMAN]	45.46	3.26	1	1	307	33.9	5.03

A0A1W2PQS1	26S protease regulatory subunit 7 OS=Homo sapiens GN=PSMC2 PE=1 SV=1 - [A0A1W2PQS1_HUMAN]	38.82	3.25	1	1	400	44.8	6.60
B4YAH7	ALDH2 (Fragment) OS=Homo sapiens GN=ALDH2 PE=3 SV=1 - [B4YAH7_HUMAN]	52.30	3.24	1	1	247	26.6	5.90
L0R5B4	Alternative protein HNRNPUL1 OS=Homo sapiens GN=HNRNPUL1 PE=4 SV=1 - [L0R5B4_HUMAN]	40.72	3.16	1	1	285	29.2	8.63
A8K6D4	cDNA FLJ77769, highly similar to Homo sapiens NAD kinase, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K6D4_HUMAN]	0.00	3.14	1	1	446	49.2	6.64
B4E3A3	cDNA FLJ53283, highly similar to N(2),N(2)-dimethylguanosine tRNAmethyltransferase (EC 2.1.1.32) OS=Homo sapiens PE=2 SV=1 - [B4E3A3_HUMAN]	28.71	3.11	1	1	354	39.0	8.47
Q9Y570	Protein phosphatase methylesterase 1 OS=Homo sapiens GN=PPME1 PE=1 SV=3 - [PPME1_HUMAN]	24.00	3.11	1	1	386	42.3	5.97
A0A024QZV0	HCG1811539, isoform CRA_b OS=Homo sapiens GN=hCG_1811539 PE=3 SV=1 - [A0A024QZV0_HUMAN]	48.06	3.09	1	1	324	36.2	5.47
Q9GZL7	Ribosome biogenesis protein WDR12 OS=Homo sapiens GN=WDR12 PE=1 SV=2 - [WDR12_HUMAN]	17.84	3.07	1	1	423	47.7	5.90
Q96K98	cDNA FLJ14414 fis, clone HEMBA1004847, highly similar to SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN OS=Homo sapiens PE=2 SV=1 - [Q96K98_HUMAN]	31.05	3.06	1	1	327	37.2	6.11
P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2 - [LDHB_HUMAN]	39.43	2.99	1	1	334	36.6	6.05
Q8WVX6	WAPAL protein OS=Homo sapiens GN=WAPAL PE=1 SV=1 - [Q8WVX6_HUMAN]	76.31	2.99	1	1	402	45.5	5.08
B4DV67	cDNA FLJ58284, moderately similar to Probable transcription factor PML OS=Homo sapiens PE=2 SV=1 - [B4DV67_HUMAN]	19.71	2.96	1	1	405	43.9	6.89
B3KM60	cDNA FLJ10367 fis, clone NT2RM2001424, highly similar to Heterogeneous nuclear ribonucleoprotein U-like protein 1 OS=Homo sapiens PE=2 SV=1 - [B3KM60_HUMAN]	24.62	2.95	1	1	339	37.1	9.00
H7BY36	RNA-binding protein EWS (Fragment) OS=Homo sapiens GN=EWSR1 PE=1 SV=1 - [H7BY36_HUMAN]	38.32	2.92	1	1	308	32.2	9.82
Q8WWH5	Probable tRNA pseudouridine synthase 1 OS=Homo sapiens GN=TRUB1 PE=1 SV=1 - [TRUB1_HUMAN]	30.40	2.87	1	1	349	37.2	8.25
A8K0T9	cDNA FLJ75422, highly similar to Homo sapiens capping protein (actin filament) muscle Z-line, alpha 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K0T9_HUMAN]	44.51	2.80	1	1	286	32.9	5.69
B7Z4A4	cDNA FLJ53058, highly similar to Legumain (EC 3.4.22.34) OS=Homo sapiens PE=2 SV=1 - [B7Z4A4_HUMAN]	35.10	2.76	1	1	398	45.6	6.96
Q96CS3	FAS-associated factor 2 OS=Homo sapiens GN=FAF2 PE=1 SV=2 - [FAF2_HUMAN]	44.31	2.70	1	1	445	52.6	5.62
Q14181	DNA polymerase alpha subunit B OS=Homo sapiens GN=POLA2 PE=1 SV=2 - [DPOA2_HUMAN]	0.00	2.68	1	1	598	65.9	5.24
B4DW90	cDNA FLJ58737, highly similar to Splicing factor 3A subunit 3 OS=Homo sapiens PE=2 SV=1 - [B4DW90_HUMAN]	25.41	2.68	1	1	448	52.4	5.27
Q8IX90	Spindle and kinetochore-associated protein 3 OS=Homo sapiens GN=SKA3 PE=1 SV=2 - [SKA3_HUMAN]	0.00	2.67	1	1	412	46.3	5.11
A8K3S0	cDNA FLJ76127, highly similar to Homo sapiens replication factor C (activator 1) 5, 36.5kDa (RFC5), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K3S0_HUMAN]	47.64	2.65	1	1	340	38.4	7.20
D6RJ96	Heat shock 70 kDa protein 4L (Fragment) OS=Homo sapiens GN=HSPA4L PE=1 SV=1 - [D6RJ96_HUMAN]	36.05	2.64	1	1	531	59.2	6.54
B1APR7	Eyes absent homolog OS=Homo sapiens GN=EYA3 PE=1 SV=1 - [B1APR7_HUMAN]	37.83	2.64	1	1	416	45.5	5.85
I3L0K7	Heat shock protein 75 kDa, mitochondrial OS=Homo sapiens GN=TRAP1 PE=1 SV=1 - [I3L0K7_HUMAN]	34.16	2.63	1	1	495	57.2	7.59

A0A024RC87	Ribonuclease/angiogenin inhibitor 1, isoform CRA_a OS=Homo sapiens GN=RNH1 PE=4 SV=1 - [A0A024RC87_HUMAN]	48.68	2.63	1	1	456	49.4	4.84
B8ZZZ7	DNA polymerase-transactivated protein 6, isoform CRA_b OS=Homo sapiens GN=SPATS2L PE=1 SV=1 - [B8ZZZ7_HUMAN]	40.16	2.61	1	1	498	54.9	9.73
Q7Z5D5	Medulloblastoma antigen MU-MB-2.50 (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q7Z5D5_HUMAN]	39.08	2.60	1	1	384	43.7	5.50
O95801	Tetratricopeptide repeat protein 4 OS=Homo sapiens GN=TTC4 PE=1 SV=3 - [TTC4_HUMAN]	51.71	2.58	1	1	387	44.7	5.60
C9JRJ5	LIM domain-containing protein 1 OS=Homo sapiens GN=LIMD1 PE=1 SV=1 - [C9JRJ5_HUMAN]	25.20	2.58	1	1	620	65.5	7.46
B4DF60	cDNA FLJ55960, highly similar to Protein transport protein Sec23A OS=Homo sapiens PE=2 SV=1 - [B4DF60_HUMAN]	57.81	2.56	1	1	663	74.2	7.68
Q59H27	Hydroxysteroid (17-beta) dehydrogenase 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59H27_HUMAN]	34.92	2.55	1	1	471	51.1	8.02
F6T1Q0	2',5'-phosphodiesterase 12 OS=Homo sapiens GN=PDE12 PE=1 SV=1 - [F6T1Q0_HUMAN]	26.74	2.54	1	1	472	52.1	7.84
E5RIM3	Phospholipase A-2-activating protein OS=Homo sapiens GN=PLAA PE=1 SV=1 - [E5RIM3_HUMAN]	37.68	2.46	1	1	609	66.7	5.97
B4E0F9	cDNA FLJ60383, highly similar to Ubiquitin-like PHD and RING fingerdomain-containing protein 1 (EC 6.3.2.-) OS=Homo sapiens PE=2 SV=1 - [B4E0F9_HUMAN]	49.91	2.45	1	1	408	45.5	9.31
O95817	BAG family molecular chaperone regulator 3 OS=Homo sapiens GN=BAG3 PE=1 SV=3 - [BAG3_HUMAN]	63.53	2.43	1	1	575	61.6	6.95
Q9BSY0	PTDSS1 protein (Fragment) OS=Homo sapiens GN=PTDSS1 PE=2 SV=2 - [Q9BSY0_HUMAN]	22.63	2.42	1	1	331	38.6	8.73
Q8TCT9	Minor histocompatibility antigen H13 OS=Homo sapiens GN=HM13 PE=1 SV=1 - [HM13_HUMAN]	40.67	2.39	1	1	377	41.5	6.43
P43686	26S proteasome regulatory subunit 6B OS=Homo sapiens GN=PSMC4 PE=1 SV=2 - [PRS6B_HUMAN]	38.85	2.39	1	1	418	47.3	5.21
B2RDT8	cDNA, FLJ96764, highly similar to Homo sapiens sorting nexin 8 (SNX8), mRNA OS=Homo sapiens PE=2 SV=1 - [B2RDT8_HUMAN]	0.00	2.37	1	1	465	52.6	7.39
A0A024QZR3	Protein pelota homolog OS=Homo sapiens GN=hCG_2002731 PE=3 SV=1 - [A0A024QZR3_HUMAN]	0.00	2.34	1	1	385	43.3	6.34
Q59H67	Hepatoma-derived growth factor-related protein 2 isoform 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1 - [Q59H67_HUMAN]	0.00	2.33	1	1	472	51.7	8.85
P00390	Glutathione reductase, mitochondrial OS=Homo sapiens GN=GSR PE=1 SV=2 - [GSHR_HUMAN]	52.52	2.30	1	1	522	56.2	8.50
Q6UXN9	WD repeat-containing protein 82 OS=Homo sapiens GN=WDR82 PE=1 SV=1 - [WDR82_HUMAN]	48.94	2.24	1	1	313	35.1	7.69
Q7L0Y3	Mitochondrial ribonuclease P protein 1 OS=Homo sapiens GN=TRMT10C PE=1 SV=2 - [MRRP1_HUMAN]	0.00	2.23	1	1	403	47.3	9.36
Q69YN2	CWF19-like protein 1 OS=Homo sapiens GN=CWF19L1 PE=1 SV=2 - [C19L1_HUMAN]	27.55	2.23	1	1	538	60.6	7.24
B4E164	cDNA FLJ56613, highly similar to Serine/threonine-protein kinase TBK1 (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1 - [B4E164_HUMAN]	19.27	2.22	1	1	496	57.0	6.77
D3DVQ1	Leucine zipper-EF-hand containing transmembrane protein 1, isoform CRA_a OS=Homo sapiens GN=LETM1 PE=4 SV=1 - [D3DVQ1_HUMAN]	22.14	2.15	1	1	559	63.5	5.24
A0A1B0GV49	Alpha-aminoadipic semialdehyde dehydrogenase OS=Homo sapiens GN=ALDH7A1 PE=1 SV=1 - [A0A1B0GV49_HUMAN]	0.00	2.12	1	1	472	50.9	7.64
Q9ULC5	Long-chain-fatty-acid--CoA ligase 5 OS=Homo sapiens GN=ACSL5 PE=1 SV=1 - [ACSL5_HUMAN]	0.00	2.05	1	1	683	75.9	6.92
P62191	26S proteasome regulatory subunit 4 OS=Homo sapiens GN=PSMC1 PE=1 SV=1 - [PRS4_HUMAN]	34.62	2.05	1	1	440	49.2	6.21

B7Z592	cDNA FLJ61635, highly similar to Homo sapiens likely ortholog of mouse immediate early response, erythropoietin 4 (LEREPO4), mRNA OS=Homo sapiens PE=2 SV=1 - [B7Z592_HUMAN]	33.97	2.04	1	1	392	44.9	7.87
B3KM27	cDNA FLJ10093 fis, clone HEMBA1002363, highly similar to Structural maintenance of chromosome 2-like 1 protein (Fragment) OS=Homo sapiens PE=2 SV=1 - [B3KM27_HUMAN]	0.00	2.04	1	1	489	55.9	6.52
A0A087WZK9	Eukaryotic translation initiation factor 3 subunit H OS=Homo sapiens GN=EIF3H PE=1 SV=1 - [A0A087WZK9_HUMAN]	38.50	2.01	1	1	349	39.6	6.39
A0A0J9YYL3	Poly(U)-binding-splicing factor PUF60 (Fragment) OS=Homo sapiens GN=PUF60 PE=1 SV=1 - [A0A0J9YYL3_HUMAN]	37.19	1.98	1	1	505	54.6	5.34
A0A024R3M0	Signal recognition particle receptor ('docking protein'), isoform CRA_a OS=Homo sapiens GN=SRPR PE=4 SV=1 - [A0A024R3M0_HUMAN]	43.22	1.93	1	1	414	44.4	8.19
A0A172Q398	CUB domain-containing protein 1 (Fragment) OS=Homo sapiens GN=CDCP1 PE=2 SV=1 - [A0A172Q398_HUMAN]	33.10	1.88	1	1	637	71.6	8.15
Q8IZW8	Tensin-4 OS=Homo sapiens GN=TNS4 PE=1 SV=3 - [TENS4_HUMAN]	26.74	1.82	1	1	715	76.7	7.34
A0A087WW43	Inter-alpha-trypsin inhibitor heavy chain H3 OS=Homo sapiens GN=ITIH3 PE=1 SV=1 - [A0A087WW43_HUMAN]	59.00	1.79	1	1	670	75.0	5.86
O95831	Apoptosis-inducing factor 1, mitochondrial OS=Homo sapiens GN=AIFM1 PE=1 SV=1 - [AIFM1_HUMAN]	39.35	1.79	1	1	613	66.9	8.95
B3KQH4	cDNA FLJ90464 fis, clone NT2RP3002281, highly similar to RNA-binding protein 12 OS=Homo sapiens PE=2 SV=1 - [B3KQH4_HUMAN]	22.72	1.76	1	1	568	59.1	8.51
Q32Q67	DNM1L protein (Fragment) OS=Homo sapiens GN=DNM1L PE=2 SV=1 - [Q32Q67_HUMAN]	0.00	1.74	1	1	575	64.1	8.22
B3KTP7	cDNA FLJ38566 fis, clone HCHON2005118, highly similar to Collagen alpha-1(XV) chain OS=Homo sapiens PE=2 SV=1 - [B3KTP7_HUMAN]	50.04	1.74	1	1	745	75.3	4.31
B4DXI9	cDNA FLJ55940, highly similar to Transcription intermediary factor 1-gamma OS=Homo sapiens PE=2 SV=1 - [B4DXI9_HUMAN]	27.28	1.74	1	1	633	70.1	6.79
B4DJ85	cDNA FLJ60587, highly similar to Glomulin OS=Homo sapiens PE=2 SV=1 - [B4DJ85_HUMAN]	42.45	1.72	1	1	580	66.7	5.31
B3KMX1	cDNA FLJ12848 fis, clone NT2RP2003391, highly similar to Transportin-3 OS=Homo sapiens PE=2 SV=1 - [B3KMX1_HUMAN]	27.02	1.67	1	1	480	53.9	6.47
P61221	ATP-binding cassette sub-family E member 1 OS=Homo sapiens GN=ABCE1 PE=1 SV=1 - [ABCE1_HUMAN]	0.00	1.67	1	1	599	67.3	8.34
B4DRU9	cDNA FLJ57179, highly similar to Homo sapiens ATP-binding cassette, sub-family F (GCN20), member 3 (ABCF3), mRNA OS=Homo sapiens PE=2 SV=1 - [B4DRU9_HUMAN]	20.97	1.65	1	1	668	75.5	7.18
Q2NL82	Pre-rRNA-processing protein TSR1 homolog OS=Homo sapiens GN=TSR1 PE=1 SV=1 - [TSR1_HUMAN]	0.00	1.62	1	1	804	91.8	7.42
B7Z842	cDNA FLJ52374, highly similar to Ubiquitin carboxyl-terminal hydrolase 7 (EC 3.1.2.15) OS=Homo sapiens PE=2 SV=1 - [B7Z842_HUMAN]	38.68	1.57	1	1	509	58.5	6.06
D3DQF6	POU domain, class 4, transcription factor 3, isoform CRA_a OS=Homo sapiens GN=POU4F3 PE=4 SV=1 - [D3DQF6_HUMAN]	67.65	1.56	1	1	771	84.1	9.83
Q4ZG57	DNA helicase (Fragment) OS=Homo sapiens GN=MCM6 PE=3 SV=1 - [Q4ZG57_HUMAN]	26.51	1.53	1	1	785	88.9	5.60
A2I829	NF-kappaB repressing factor (Fragment) OS=Homo sapiens GN=NKRF PE=2 SV=1 - [A2I829_HUMAN]	0.00	1.50	1	1	599	67.4	8.87
C9J6B6	Eukaryotic translation initiation factor 4 gamma 1 (Fragment) OS=Homo sapiens GN=EIF4G1 PE=1 SV=1 - [C9J6B6_HUMAN]	50.63	1.45	1	1	757	82.4	4.83
A0A0G2JR96	Cytoplasmic FMR1-interacting protein 1 (Fragment)	33.62	1.39	1	1	862	100.2	6.44

	OS=Homo sapiens GN=CYFIP1 PE=1 SV=4 - [A0A0G2JR96_HUMAN]							
Q6UWE0	E3 ubiquitin-protein ligase LRSAM1 OS=Homo sapiens GN=LRSAM1 PE=1 SV=1 - [LRSM1_HUMAN]	33.46	1.38	1	1	723	83.5	5.94
A8K9U6	cDNA FLJ76121, highly similar to Homo sapiens zinc finger CCCH-type, antiviral 1 (ZC3HAV1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1 - [A8K9U6_HUMAN]	0.00	1.33	1	1	902	101.4	8.35
Q08J23	tRNA (cytosine(34)-C(5))-methyltransferase OS=Homo sapiens GN=NSUN2 PE=1 SV=2 - [NSUN2_HUMAN]	33.97	1.30	1	1	767	86.4	6.77
H9KVB3	Otogelin OS=Homo sapiens GN=OTOG PE=4 SV=2 - [H9KVB3_HUMAN]	0.00	1.30	1	1	2913	313.2	5.77
B4E091	cDNA FLJ55438, highly similar to Splicing factor 3 subunit 1 OS=Homo sapiens PE=2 SV=1 - [B4E091_HUMAN]	43.24	1.30	1	1	690	77.4	5.16
H7BYN4	Kinesin-like protein OS=Homo sapiens GN=KIF23 PE=1 SV=1 - [H7BYN4_HUMAN]	0.00	1.26	1	1	952	109.1	8.57
Q9NZB2	Constitutive coactivator of PPAR-gamma-like protein 1 OS=Homo sapiens GN=FAM120A PE=1 SV=2 - [F120A_HUMAN]	0.00	1.25	1	1	1118	121.8	8.88
Q9BR63	FARSB protein (Fragment) OS=Homo sapiens GN=FARSB PE=2 SV=2 - [Q9BR63_HUMAN]	0.00	1.20	1	1	585	65.7	6.84
E5KLK2	Mitochondrial dynamin-like 120 kDa protein OS=Homo sapiens GN=OPA1 PE=3 SV=1 - [E5KLK2_HUMAN]	34.26	1.19	1	1	924	107.5	7.99
A0A1W2PQ15	Ankyrin repeat domain-containing protein 17 OS=Homo sapiens GN=ANKRD17 PE=1 SV=1 - [A0A1W2PQ15_HUMAN]	26.98	1.16	1	1	1123	117.9	4.84
B3KSS1	cDNA FLJ36845 fis, clone ASTRO2013050, weakly similar to UBIQUITIN-ACTIVATING ENZYME E1 OS=Homo sapiens PE=2 SV=1 - [B3KSS1_HUMAN]	26.09	1.13	1	1	800	90.0	6.51
H0YDK8	Pumilio homolog 1 (Fragment) OS=Homo sapiens GN=PUM1 PE=1 SV=1 - [H0YDK8_HUMAN]	36.74	1.11	1	1	900	95.7	7.62
O95487	Protein transport protein Sec24B OS=Homo sapiens GN=SEC24B PE=1 SV=2 - [SC24B_HUMAN]	38.10	1.10	1	1	1268	137.3	6.67
B4E216	cDNA FLJ57339, highly similar to Complement C3 OS=Homo sapiens PE=2 SV=1 - [B4E216_HUMAN]	54.10	1.09	1	1	1098	122.5	6.93
B4DIW2	cDNA FLJ54035, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1 - [B4DIW2_HUMAN]	18.96	1.08	1	1	830	93.9	5.87
H0Y785	Ankyrin repeat and KH domain-containing protein 1 (Fragment) OS=Homo sapiens GN=ANKHD1 PE=1 SV=1 - [H0Y785_HUMAN]	0.00	1.07	1	1	1024	107.8	9.45
D3DTH7	Myosin IC, isoform CRA_a OS=Homo sapiens GN=MYO1C PE=3 SV=1 - [D3DTH7_HUMAN]	34.42	1.04	1	1	862	98.9	9.42
E9PKN0	Pre-mRNA cleavage complex 2 protein Pcf11 (Fragment) OS=Homo sapiens GN=PCF11 PE=1 SV=1 - [E9PKN0_HUMAN]	0.00	1.02	1	1	784	88.9	9.85
H0YD14	Myoferlin (Fragment) OS=Homo sapiens GN=MYOF PE=1 SV=1 - [H0YD14_HUMAN]	30.52	0.93	1	1	1177	134.7	6.39
O60566	Mitotic checkpoint serine/threonine-protein kinase BUB1 beta OS=Homo sapiens GN=BUB1B PE=1 SV=3 - [BUB1B_HUMAN]	0.00	0.86	1	1	1050	119.5	5.27
Q9H3U1	Protein unc-45 homolog A OS=Homo sapiens GN=UNC45A PE=1 SV=1 - [UN45A_HUMAN]	0.00	0.85	1	1	944	103.0	6.07
A4FUT8	JMJD1B protein (Fragment) OS=Homo sapiens GN=JMJD1B PE=2 SV=1 - [A4FUT8_HUMAN]	20.52	0.84	1	1	1551	168.9	7.52
A0A024R972	Laminin, gamma 1 (Formerly LAMB2), isoform CRA_a OS=Homo sapiens GN=LAMC1 PE=4 SV=1 - [A0A024R972_HUMAN]	23.59	0.83	1	1	1573	173.9	5.05
Q2PNX9	Phosphatidic acid-preferring phospholipase A1 OS=Homo sapiens PE=2 SV=1 - [Q2PNX9_HUMAN]	41.42	0.81	1	1	745	83.1	5.83
P53621	Coatomer subunit alpha OS=Homo sapiens GN=COPA PE=1 SV=2 - [COPA_HUMAN]	35.53	0.74	1	1	1224	138.3	7.66
Q6WKZ4	Rab11 family-interacting protein 1 OS=Homo sapiens GN=RAB11FIP1 PE=1 SV=3 - [RFIP1_HUMAN]	38.34	0.62	1	1	1283	137.1	5.43

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