

## **Supporting Information**

### **An OGA-resistant Probe Allow Specific Visualization and Accurate Identification of *O*-GlcNAc-modified Proteins in Cells**

Jing Li,<sup>\*,†,‡,§,#</sup> Jiajia Wang,<sup>†,§,#</sup> Liuqing Wen,<sup>‡</sup> He Zhu,<sup>‡</sup> Shanshan Li,<sup>‡</sup> Kenneth Huang,<sup>‡</sup> Kuan Jiang,<sup>†</sup> Xu Li,<sup>‡</sup> Cheng Ma,<sup>‡</sup> Jingyao Qu,<sup>‡</sup> Aishwarya Parameswaran,<sup>‡</sup> Jing Song,<sup>‡</sup> Wei Zhao,<sup>†</sup> Peng George Wang<sup>\*,†,‡</sup>

<sup>†</sup>State Key Laboratory of Medicinal Chemical Biology, College of Pharmacy and Tianjin Key Laboratory of Molecular Drug Research, Nankai University, Haihe Education Park, 38 Tongyan Road, Tianjin 300353, People's Republic of China

<sup>§</sup>School of Food and Drug, Luoyang Normal University, Luoyang, People's Republic of China

<sup>‡</sup>Department of Chemistry and Center of Diagnostics & Therapeutics, Georgia State University, 50 Decatur St SE, Atlanta, GA 30303, United States

## **Table of contents**

### **I. Supplementary schemes and figures**

**Figure S1.** HPLC detection for the OGA hydrolysis of *O*-GlcNAc-peptide and *O*-4dGlcNAc-peptide.

**Figure S2.** SDS-PAGE of purified WT-OGA and mutant D285A-OGA.

**Scheme S1.** Synthesis of Ac<sub>3</sub>4dGlcNAz and 4dGlcNAz.

**Figure S3.** UDP-4dGlcNAz processed by human GalNAc salvage pathway *in Vitro*.

**Figure S4.** Concentration-dependent labeling of **5**

**Figure S5.** Time-dependent labeling of **5**

### **II. Materials and methods**

### **III. References**

### **IV. NMR spectra of compounds**

### **V. Supplementary Tables**

**Table S1.** Enzymatic characterization of human WT-OGA and mutant D285A-OGA.

**Table S2.** Cytotoxicity of **5** in HEK293 cells.

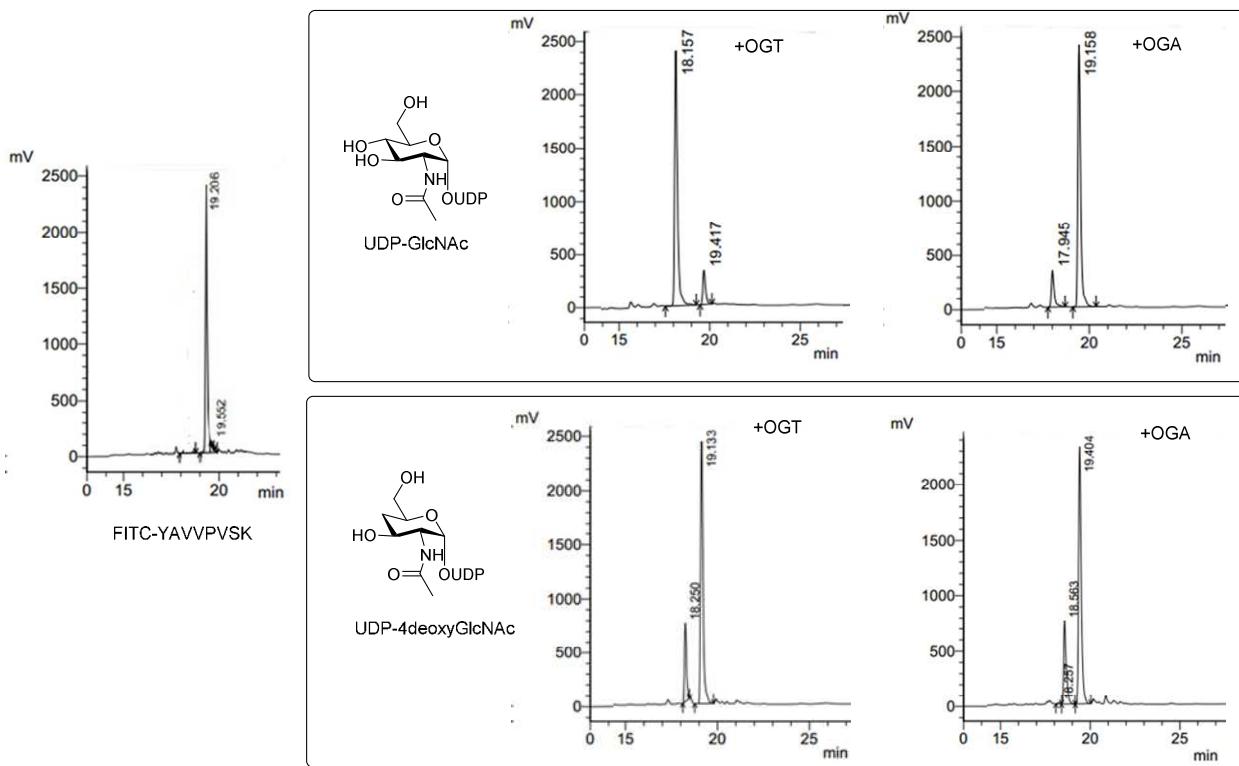
**Table S3.** Proteins identified from HEK293 cells treated with Ac<sub>3</sub>4dGlcNAz.

**Table S4.** Proteins identified from HEK293 cells treated with Ac<sub>4</sub>GlcNAz.

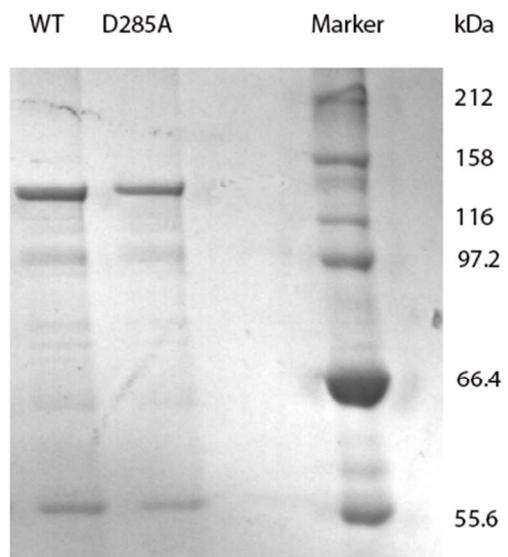
**Table S5.** Proteins identified from HEK293 cells treated with Ac<sub>4</sub>GalNAz.

**Table S6.** Nups identified from Ac<sub>3</sub>4dGlcNAz, Ac<sub>4</sub>GalNAz and Ac<sub>3</sub>6AzGlcNAc.

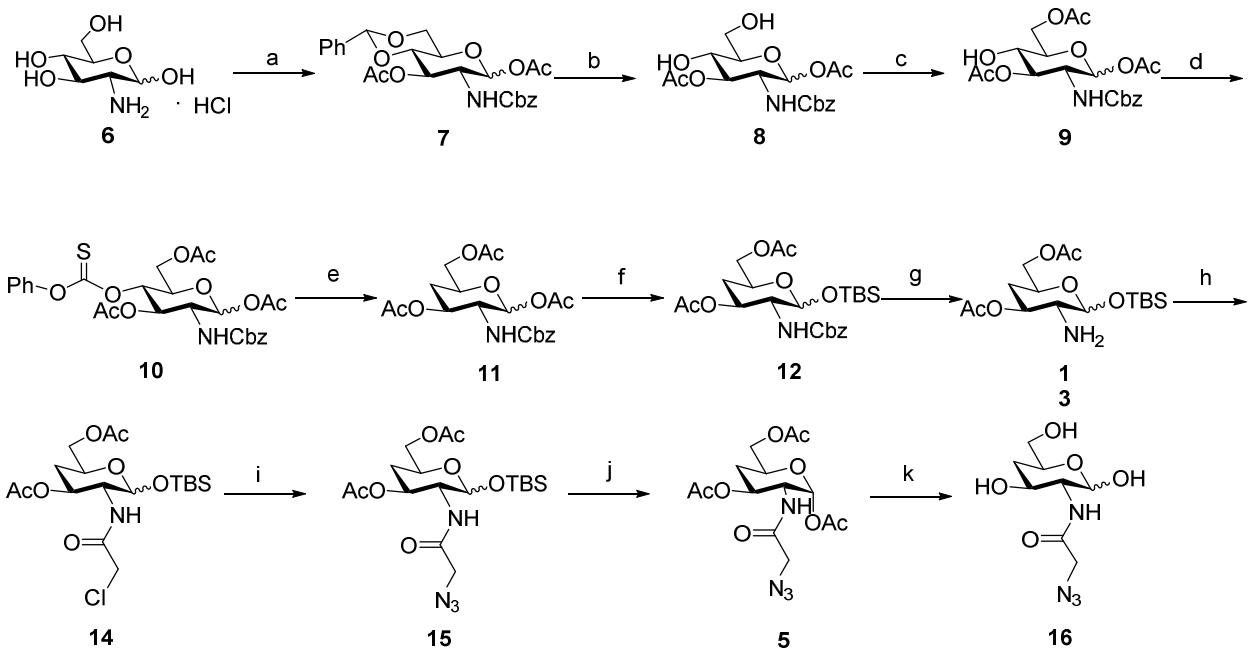
## I. Supplementary schemes and figures



**Figure S1.** HPLC detection for the OGA hydrolysis of *O*-GlcNAc-peptide and *O*-4dGlcNAc-peptide. Upper: For UDP-GlcNAc assay, peptide (FITC-YAVVPVSK) was first reacted with OGT and produced glycopeptide with *O*-GlcNAc, then inactivated OGT, add OGA in the reaction. OGA can hydrolyze *O*-GlcNAc from glycopeptide efficiently. Bottom: For UDP-4dGlcNAc assay, peptide (FITC-YAVVPVSK) was first reacted with OGT and produced glycopeptide with *O*-4dGlcNAc, then inactivated OGT, add OGA in the reaction. OGA cannot hydrolyze *O*-4dGlcNAc from glycopeptide.

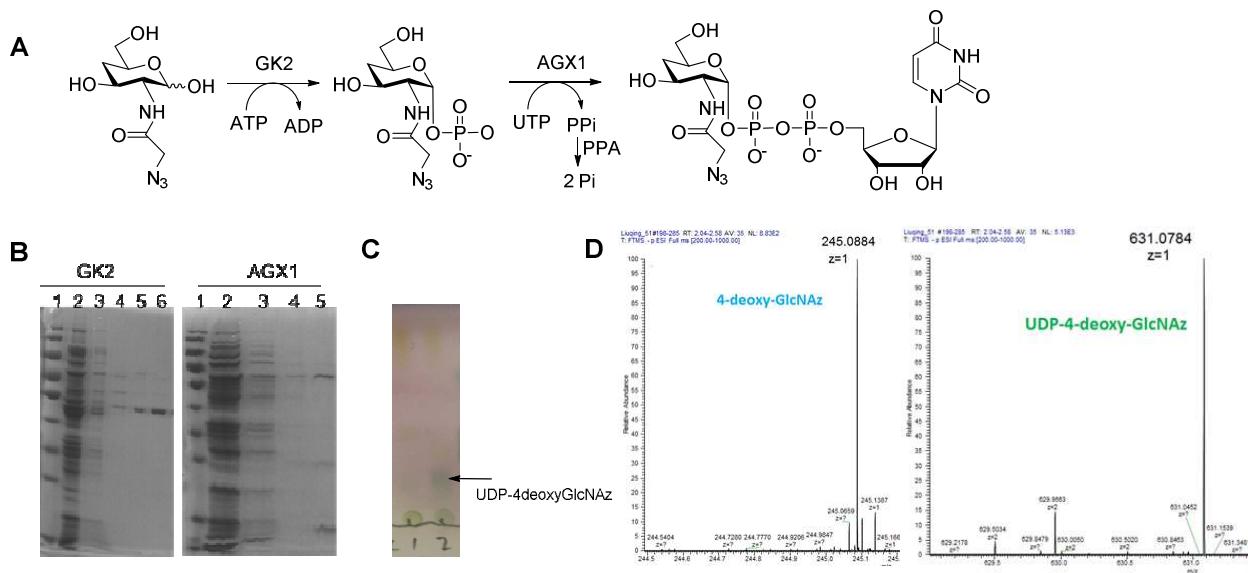


**Figure S2.** SDS-PAGE of purified WT-OGA and mutant D285A-OGA.



**Scheme S1.** Synthesis of Ac<sub>3</sub>4dGlcNAz and 4dGlcNAz.

Reagent: (a) i) CbzCl, NaHCO<sub>3</sub>; ii) PhCH(OCH<sub>3</sub>)<sub>2</sub>, CSA, DMF; iii) Ac<sub>2</sub>O, Pyridine; 48.8% over three steps; (b) 80% HOAc, 66.4%; (c) AcCl, pyridine, CH<sub>2</sub>Cl<sub>2</sub>, 78.4%; (d) Phenyl chlorothionocarbonate, DMAP, CH<sub>3</sub>CN, 79.7%; (e) AIBN, Bu<sub>3</sub>SnH, Toluene, 75%; (f) i) NH<sub>3</sub>, THF/MeOH; ii) TBSCl, imidazole, DMF, 62.5%; (g) H<sub>2</sub>, 20% Pd(OH)<sub>2</sub>, 97.7%; (h) Chloroacetic anhydride, Pyridine, 82.3%; (i) NaN<sub>3</sub>, DMF, 80.4%; (j) i) TBAF, HOAc, THF; (ii) Ac<sub>2</sub>O, pyridine, 76.6%; (k) MeONa, MeOH, 56.1%.



**Figure S3.** UDP-4dGlcNAz processed by human GalNAc salvage pathway *in vitro*. (A) Human GalNAc salvage pathway; (B) Expression GK2 and AGX1 in *E. coli* BL21. Lane 1, marker; lane 2, total protein; lane 3, flow through; lane 4, washing; lane 5, elution; lane 6, concentration. (C) TLC detection of UDP-4dGlcNAc. (D) The MS confirmation of UDP-4dGlcNAz (MW = 631) and 4dGlcNAz (MW = 245).

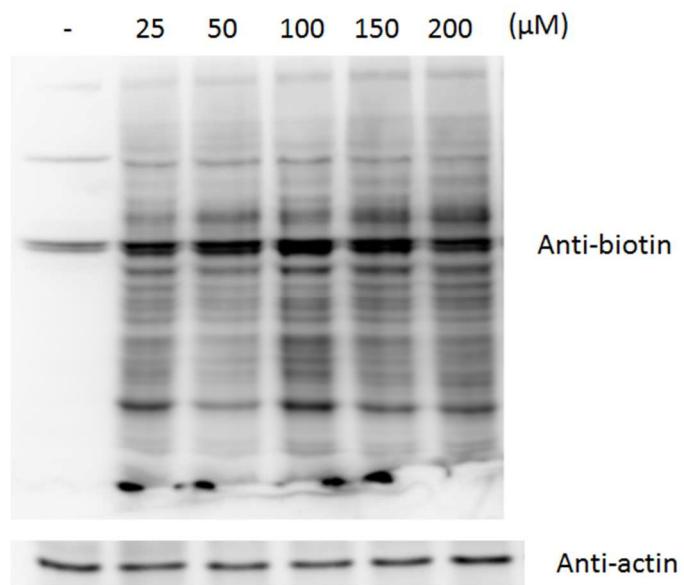


Figure S4. PC3 cells were treated with varying concentrations of Ac<sub>3</sub>4dGlcNAz, followed by CuAAC and analysis by Western blot.

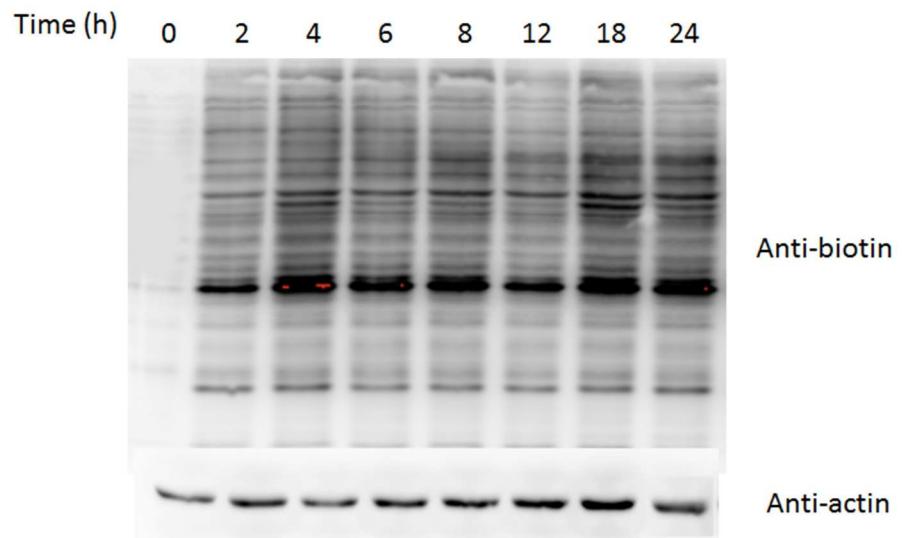


Figure S5. PC3 cells were treated with 100  $\mu$ M Ac<sub>3</sub>dGlcNAz for the indicated times, followed by CuAAC and analysis by Western blot.

## II. Materials and methods

### Materials and Reagents

All reagents used for chemical synthesis were purchased from Sigma-Aldrich, Alfa Aesar, EMD Millipore and Thermo Fisher Scientific unless otherwise specified and used with further purification. Ac4GlcNAc, Ac4GlcNAz, Ac4GalNAz and Diazo-Biotin-Alkyne were purchased from Click Chemistry Tools. UDP-GlcNAc and UDP-4 deoxyGlcNAc were kindly provided by Dr. Xi Chen group.<sup>1</sup> All cell culture reagents were purchased from Gibco. DIBO-Biotin, Alexa Fluor 488-conjugated streptavidin, Image-iTTM LIVE Plasma Membrane and Nuclear Labeling Kit (I34406) and all Immunoblotting materials were purchased from Life Technologies. Streptavidin HRP antibody (ab7403), anti-Nup62 antibody Mab 414 (ab24609), anti-EGFR (ab52894), anti-HSP 90 (ab13492), and anti-H3 (EPR17899) were purchased from Abcam. Sequencing grade modified trypsin was purchased from Promega Corporation. All anhydrous reactions were performed under argon or nitrogen atmosphere. Thin-layer chromatography (TLC) was performed on silica gel GF254 plates with detection using short wave UV light ( $\lambda = 254$  nm) and staining with 10% phosphomolybdic acid in EtOH or a p-anisaldehyde solution (EtOH / p-anisaldehyde / AcOH / H<sub>2</sub>SO<sub>4</sub>, 135:5:4:1.5), followed by heating on a hotplate. Flash chromatography was performed with silica gel (100 - 200 mesh) with EtOAc and petroleum ether or EtOAc (or CH<sub>2</sub>Cl<sub>2</sub>) and MeOH as eluent. <sup>1</sup>H and <sup>13</sup>C NMR spectra were recorded on a Bruker AV 400 spectrometer at 400 MHz (<sup>1</sup>H NMR) and 100 MHz (<sup>13</sup>C NMR), using CDCl<sub>3</sub> or CD<sub>3</sub>OD as solvents. Coupling constants are reported in Hertz. High-resolution mass spectra (HRMS) were obtained on a Varian QFT-ESI mass spectrometer.

### Synthesis of Ac<sub>3</sub>4dGlcNAz and 4dGlcNAz

#### **1,3-Di-O-Acetyl-4,6-O-Benzylidene-2-Benzylloxycarbonylamino-2-Deoxy-D-Glucopyranose (7)**

To the solution of commercially available glucosamine hydrochloride **6** (10.0 g, 46.3 mmol) and sodium bicarbonate (11.7 g, 140.2 mmol) was dissolved in 200 mL water and cooled at ice bath, then benzyl carbonochloridate (7 mL, 51.0 mmol) was added dropwise and the reaction was then stirred for 8 h at room temperature. Upon completion, the mixture was acidified with 1 M HCl until the pH ~ 1, then the resulting crude was filtered and washed with 2 × 100 mL water, the white solid was dried under reduced pressure at 40 °C to afford crude 2-benzylloxycarbonylamino-2-deoxy-D-glucopyranose as white solid and used without further purification (12.8 g, 88.2%).

To the solution of intermediate above (9.0 g, 28.7 mmol) and camphorsulfonic acid (673.7 mg, 2.9 mmol) in DMF, benzaldehyde dimethyl acetal was added dropwise and the mixture was stirred at room temperature overnight under an argon atmosphere. TLC analysis showed that most of the starting material was consumed and the reaction was quenched by the addition of 5 mL Et<sub>3</sub>N. The reaction was concentrated under reduced pressure and the crude product was dissolved in 100 mL pyridine at 0 °C and acetic anhydride (8.4 mL, 89.3 mmol) was added dropwise, the reaction was allowed to warm to room temperature and stirred for another 5h. TLC indicated that complete

conversion of starting material to a major product (Petroleum ether/EtOAc, 1:1,  $R_f = 0.73$ ), the mixture was concentrated in vacuo and the crude product was extracted with 300 mL EtOAc and washed with 50 mL 1M HCl, 100 mL saturated sodium bicarbonate and 100 mL saturated brine successively. The organic layer was dried with anhydrous sodium sulfate and concentrated under decreased pressure affords the crude product which was purified by column chromatography to afford compound **2** as a white solid (6.8 g, 48.8%).  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.35 (m,  $J = 6.4$  Hz, 10H), 6.17 (s, 1H), 5.51 (d,  $J = 11.2$  Hz, 1H), 5.34 (t,  $J = 10.0$  Hz, 1H), 5.03-5.15 (m, 4H), 4.35-4.27 (m, 1H), 4.17-4.22(m, 1H), 3.92 (t,  $J = 9.2$  Hz, 1H), 3.76 (t,  $J = 9.6$  Hz, 2H), 2.14 (s, 3H), 1.97 (s, 3H).  $^{13}\text{C}$  (100 MHz,  $\text{CDCl}_3$ )  $\delta$  171.38, 169.14, 155.86, 136.76, 136.02, 129.25, 128.61, 128.55, 128.36, 128.30, 128.18, 128.01, 126.17, 101.62, 91.41, 78.57, 69.68, 68.59, 67.27, 64.91, 53.51, 20.95, 20.73. HRMS (ESI):  $m/z$  [M+NH<sub>4</sub>]<sup>+</sup> calculated for  $\text{C}_{25}\text{H}_{27}\text{NO}_9$ : 503.2030, found: 503.2028.

### **1,3-Di-O-Acetyl-2-Benzylloxycarbonylamino-2-Deoxy-D-Glucopyranose (8)**

Compound **7** (6.8 g, 14.01 mmol) was dissolved in 150 mL 80% AcOH and stirred at 60 °C overnight, TLC analysis showed complete conversion of starting material to a major product (Petroleum ether / EtOAc, 1:3,  $R_f = 0.31$ ) and the solvent was removed by vacuum. The resulting crude mixture was dissolved in  $\text{CH}_2\text{Cl}_2$  and brought to a neutral pH by the addition of saturated aqueous  $\text{NaHCO}_3$  and subsequently extracted with  $\text{CH}_2\text{Cl}_2$ , the organic layer was washed with saturated brine and dried over sodium sulfate, filtered and concentrated. The crude mixture was purified by column chromatography to afford the pure product **3** as white solid (3.7 g, 66.4%).  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.38-7.29 (m, 5H), 6.16 (d,  $J = 3.6$  Hz, 1H), 5.20-5.09 (m, 3H), 5.02 (d,  $J = 12.0$  Hz, 1H), 4.15-4.02 (m, 1H), 3.87 (t,  $J = 9.6$  Hz, 1H), 3.82 (s, 2H), 3.70 (d,  $J = 10.0$  Hz, 1H), 2.13 (s, 3H), 1.99 (s, 3H).  $^{13}\text{C}$  (100 MHz,  $\text{CDCl}_3$ )  $\delta$  172.10, 169.48, 156.03, 135.97, 128.60, 128.53, 128.36, 128.16, 91.26, 73.73, 73.22, 67.78, 67.25, 61.18, 52.89, 20.98, 20.80; HRMS (ESI):  $m/z$  [M+NH<sub>4</sub>]<sup>+</sup> calculated for  $\text{C}_{18}\text{H}_{23}\text{NO}_9$ : 415.1717, found: 415.1715.

### **1,3,6-Tri-O-Acetyl-2-Benzylloxycarbonylamino-2-Deoxy-D-Glucopyranose (9)**

Compound **8** (3.7 g, 9.3 mmol) was dissolved in dry  $\text{CH}_2\text{Cl}_2$  and pyridine (1.1 mL, 13.9 mmol) was added and the reaction was stirred at -10 °C under argon for 20 min, then acetyl chloride (0.73 mL, 10.2 mmol) was added dropwise and the reaction was stirred at this temperature for 6 h. TLC analysis showed that starting material was consumed completely (Petroleum ether/EtOAc, 1:1,  $R_f = 0.37$ ), the reaction was concentrated in vacuo and purified by column chromatography to afford the pure product **4** as colorless oil (3.2 g, 78.4%).  $^1\text{H}$  NMR (400 MHz,  $\text{CDCl}_3$ )  $\delta$  7.40-7.31 (m, 5H), 6.17 (d,  $J = 3.6$  Hz, 1H), 5.18-4.99 (m, 4H), 4.54 (dd,  $J = 12.4, 3.5$  Hz, 1H), 4.19 (dd,  $J = 12.4, 1.6$  Hz, 1H), 4.10 (td,  $J = 10.4, 3.6$  Hz, 1H), 3.84 (d,  $J = 10.0$  Hz, 1H), 3.62 (t,  $J = 9.6$  Hz, 1H), 2.14 (s, 2H), 2.12 (s, 3H), 1.99 (s, 2H).  $^{13}\text{C}$  NMR (100 MHz,  $\text{CDCl}_3$ )  $\delta$  172.02, 171.90, 169.02, 155.83, 136.00, 128.59, 128.36, 128.20, 91.13, 72.68, 72.14, 67.98, 67.22, 62.55, 52.77, 20.96, 20.84, 20.77; HRMS (ESI):  $m/z$  [M+NH<sub>4</sub>]<sup>+</sup> calculated for  $\text{C}_{20}\text{H}_{25}\text{NO}_{10}$ : 457.1822, found: 457.1822.

### **1,3,6-Tri-O-Acetyl-2-Benzylloxycarbonylamino-2-Deoxy-4-O-(Phenoxythiocarbonyl)-D-Glucopyranose (10)**

A mixture of compound **9** (3.2 g, 7.2 mmol) and dimethylaminopyridine (1.3 g, 10.8 mmol) were dissolved in anhydrous CH<sub>3</sub>CN (30 mL) and stirred at ice bath under argon, then phenyl chlorothionocarbonate (1.2 mL, 9.5 mmol) was added dropwise and the reaction was warmed to room temperature slowly and stirred for another 6h. The reaction was monitored by TLC (Petroleum ether / EtOAc, 2:1, R<sub>f</sub>= 0.46) and quenched with methanol (1 mL). The mixture was diluted with ethyl acetate (150 mL) and washed with 1 M HCl (25 mL), saturated sodium bicarbonate (50 mL), brine (50 mL) and dried over anhydrous sodium sulfate, the organic layer was concentrated and purified by column chromatography to afford the product **5** as white solid (3.3 g, 79.7%). <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ 7.46-7.31 (m, 8H), 7.04 (d, J = 7.6 Hz, 2H), 6.25 (d, J = 3.6 Hz, 1H), 5.84 (t, J = 9.6 Hz, 1H), 5.48-5.40 (m, 1H), 5.10 (dd, J = 42.8, 12.0 Hz, 2H), 5.00 (d, J = 9.6 Hz, 1H), 4.40 (dd, J = 12.8, 3.6 Hz, 1H), 4.32 (td, J = 10.4, 3.6 Hz, 1H), 4.23-4.12 (m, 2H), 2.19 (s, 3H), 2.08 (s, 3H), 1.97 (s, 3H). <sup>13</sup>C NMR (100 MHz, CDCl<sub>3</sub>) δ 194.24, 171.15, 170.60, 168.69, 155.65, 153.37, 135.89, 129.72, 128.63, 128.44, 128.30, 126.93, 121.61, 90.73, 76.68, 70.74, 69.34, 67.41, 61.35, 52.77, 20.99, 20.96, 20.69; HRMS (ESI): m/z [M+NH<sub>4</sub>]<sup>+</sup> calculated for C<sub>27</sub>H<sub>29</sub>NO<sub>11</sub>S: 593.1805, found: 593.1793.

### **1,3,6-Tri-O-Acetyl-2-Benzylloxycarbonylamino-2,4-Dideoxy-D-Glucopyranose (11)**

A solution of compound **10** (3.3 g, 5.7 mmol) and recrystallization 2,2-azobisisobutyronitrile (74.8 mg, 0.4 mmol) in anhydrous toluene (40 mL) at room temperature under argon atmosphere, Tributyltin Hydride (1.7 mL, 6.3 mmol) was added dropwise and the reaction was heated to 80 °C slowly and stirred at this condition continually until the starting material was completed as determined by TLC (Petroleum ether / EtOAc, 2:1, R<sub>f</sub> = 0.22). The reaction was concentrated in vacuo and purified by column chromatography to afford the product **6** as white solid (1.8 g, 75%). <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ 7.39–7.31 (m, 5H), 6.22 (d, J = 3.6 Hz, 1H), 5.15 (d, J = 12.4 Hz, 2H), 5.03 (d, J = 12.4 Hz, 1H), 4.83 (d, J = 9.6 Hz, 1H), 4.17-4.03 (m, 4H), 2.17-2.06 (m, 7H), 1.97 (s, 3H), 1.72 (q, J = 11.6 Hz, 1H). <sup>13</sup>C NMR (100 MHz, CDCl<sub>3</sub>) δ 171.12, 170.75, 169.02, 155.81, 136.08, 128.59, 128.34, 128.24, 92.02, 67.89, 67.69, 67.18, 65.29, 53.25, 32.63, 21.00, 20.89, 20.79; HRMS (ESI): m/z [M+NH<sub>4</sub>]<sup>+</sup> calculated for C<sub>20</sub>H<sub>25</sub>NO<sub>9</sub>: 441.1873, found: 441.1867.

### **1-O-(Tert-butyldimethylsilyl)-3,6-Di-O-Acetyl-2-Benzylloxycarbonylamino-2,4-Dideoxy-D-Glucopyranose (12)**

At 0 °C, Compound **11** (1.8 g, 4.2 mmol) in THF / MeOH = 7:3 (20 mL) was bubbled with ammonia till saturation, the reaction was monitored by TLC (Petroleum ether / EtOAc, 1:1, R<sub>f</sub> = 0.50). After completion of the reaction, the mixture was concentrated in vacuo to get the crude product which was used without further purification. Tert-butyldimethylsilyl chloride (1.27 g, 8.4 mmol) was added to the intermediate compound and imidazole (714 mg, 10.5 mmol) in anhydrous DMF (15 mL) at 0 °C, TLC analysis showed that complete conversion of the starting material to a major product (Petroleum ether/EtOAc, 2:1, R<sub>f</sub> = 0.53), the mixture was concentrated and extracted with ethyl acetate (50 mL) and washed with 1 M HCl (15 mL), saturated sodium bicarbonate(20 mL), brine (20 mL)and dried over anhydrous sodium sulfate, the organic layer was concentrated and purified by column chromatography to afford the product **7** as white solid (1.3 g, 62.5%). <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>) δ 7.32 (s, 5H),

5.05 (s, 2H), 4.82 (d,  $J$  = 8.4 Hz, 1H), 4.62 (s, 1H), 4.14 (dd,  $J$  = 11.6, 6.8 Hz, 1H), 3.99 (dd,  $J$  = 11.6, 4.0 Hz, 1H), 3.72-3.70 (m, 1H), 3.48-3.46 (d,  $J$  = 8.4 Hz, 1H), 2.05 (s, 1H), 2.01 (dd,  $J$  = 5.2, 1.2 Hz, 1H), 1.97 (s, 3H), 1.53 (dd,  $J$  = 11.6 Hz, 1H), 0.86 (s, 9H), 0.06 (d,  $J$  = 12.8 Hz, 6H).  $^{13}\text{C}$  NMR (100 MHz,  $\text{CDCl}_3$ )  $\delta$  170.87, 170.74, 136.44, 128.48, 128.09, 96.73, 69.95, 69.34, 66.75, 65.62, 58.57, 33.13, 25.57, 20.98, 20.79, 17.96, -4.25, -5.36; HRMS (ESI):  $m/z$  [M+H] $^+$  calculated for  $\text{C}_{24}\text{H}_{37}\text{NO}_8\text{Si}$ : 496.2366, found: 496.2368.

### **1-O-(Tert-butyldimethylsilyl)-3,6-Di-O-Acetyl-2-Amino-2,4-Dideoxy-D-Glucopyranose (13)**

A solution of compound **12** (1.3 g, 2.6 mmol) in ethyl acetate (5 mL) was hydrogenated in the presence of 20%  $\text{Pd}(\text{OH})_2$  on charcoal at room temperature for 2 h. The reaction was monitored by TLC (Petroleum ether / EtOAc, 1:2,  $R_f$  = 0.05), then the catalyst was filtered off through Celite and the filtrate was concentrated in vacuo to afford the product **8** as colorless oil (850 mg, 97.7%).  $^1\text{H}$  NMR (400 MHz, )  $\delta$  4.72-4.67 (m, 1H), 4.41 (d,  $J$  = 7.6 Hz, 1H), 4.12 (dd,  $J$  = 11.6, 7.2 Hz, 1H), 4.02 (dd,  $J$  = 11.6, 4.0 Hz, 1H), 3.74-3.69 (m, 1H), 2.73 (dd,  $J$  = 10.0, 7.6 Hz, 1H), 2.09 (dd,  $J$  = 2.0, 5.2 Hz, 1H), 2.06 (s, 3H), 2.03 (s, 3H), 1.39 (dd,  $J$  = 12.0 Hz, 23.6 Hz, 1H), 0.89 (s, 9H), 0.11 (d,  $J$  = 1.6 Hz, 6H).  $^{13}\text{C}$  NMR (100 MHz,  $\text{CDCl}_3$ )  $\delta$  170.71, 170.62, 98.97, 73.71, 69.50, 65.74, 58.07, 32.40, 25.75, 21.15, 20.79, 18.04, -4.09, -5.17; HRMS (ESI):  $m/z$  [M+H] $^+$  calculated for  $\text{C}_{16}\text{H}_{31}\text{NO}_6\text{Si}$ : 362.1999, found: 362.2001.

### **1-O-(Tert-butyldimethylsilyl)-3,6-Di-O-Acetyl-2-Chloroacetamido-2,4-Dideoxy-D-Glucopyranose (14)**

Chloroacetic anhydride (804 mg, 4.6 mmol) was added to the solution of compound **13** (850 mg, 2.3 mmol) in pyridine (10 mL) and the resulting mixture was stirred at room temperature for 5 h. TLC analysis showed complete conversion of the starting material to a major product (Petroleum ether / EtOAc, 2:1,  $R_f$  = 0.33). The mixture was concentrated and diluted with ethyl acetate (50 mL) and washed with water (20 mL), saturated sodium bicarbonate (20 mL), brine (20 mL). The organic phase was separated and dried over anhydrous sodium sulfate, the organic layer was concentrated and the residue was purified by column chromatography to afford the product **9** as white solid (824 mg, 82.3%).  $^1\text{H}$  NMR (400 MHz, )  $\delta$  6.51 (d,  $J$  = 8.8 Hz, 1H), 5.16-5.09 (m, 1H), 4.73 (d,  $J$  = 8.0 Hz, 1H), 4.15 (dd,  $J$  = 12.0, 7.6 Hz, 2H), 4.09 (dd,  $J$  = 12.0, 7.6 Hz, 2H), 3.99 (s, 2H), 3.79-3.72 (m, 2H), 2.08 (m, 1H), 2.06 (s, 3H), 1.96 (s, 3H), 1.57 (dd,  $J$  = 12.0, 24.0 Hz, 1H), 0.86 (s, 9H), 0.08 (d,  $J$  = 8.4 Hz, 6H).  $^{13}\text{C}$  NMR (100 MHz,  $\text{CDCl}_3$ )  $\delta$  170.84, 170.72, 166.03, 96.15, 77.38, 77.06, 76.74, 69.66, 69.46, 65.55, 57.52, 42.57, 33.06, 25.53, 21.02, 20.79, 17.89, -4.18, -5.36. HRMS (ESI):  $m/z$  [M+H] $^+$  calculated for  $\text{C}_{18}\text{H}_{32}\text{ClNO}_7\text{Si}$ : 438.1715, found: 438.1703.

### **1-O-(Tert-butyldimethylsilyl)-3,6-Di-O-Acetyl-2-Azidoacetamido-2,4-Dideoxy-D-Glucopyranose (15)**

The solution of compound **14** (824 mg, 1.8 mmol) and sodium azide (244 mg, 3.76 mmol) in anhydrous DMF (10 mL) was stirred at 70 °C overnight, TLC analysis indicated that the starting material was consumed completely (Petroleum ether / EtOAc, 2:1,  $R_f$  = 0.22). The reaction was concentrated and purified by column chromatography to afford the product **15** as a white solid (672.5 mg, 80.4%).  $^1\text{H}$  NMR (400 MHz, )  $\delta$  6.44 (d,  $J$  = 9.2 Hz, 1H), 5.10-5.03 (m, 1H), 4.70 (d,  $J$  = 8.0 Hz, 1H), 4.13-4.05 (m, 2H), 3.87 (d,  $J$  = 2.4 Hz, 2H), 3.76-3.70 (m, 2H), 2.03-2.00 (m, 7H), 1.52 (dd,  $J$  = 23.6, 12.0 Hz, 1H), 0.83 (s, 9H), 0.05 (d,  $J$  = 8.0 Hz, 6H).  $^{13}\text{C}$  NMR (100 MHz,  $\text{CDCl}_3$ )  $\delta$  170.86,

170.73, 166.77, 96.19, 69.82, 69.39, 65.57, 57.04, 52.76, 33.01, 25.51, 21.01, 20.76, 17.88, -4.17, -5.38; HRMS (ESI):  $m/z$  [M+Na]<sup>+</sup> calculated for C<sub>18</sub>H<sub>32</sub>N<sub>4</sub>O<sub>7</sub>Si: 467.1938, found: 467.1937.

### **1,3,6-Tri-O-Acetyl-2-Azidoacetamido-2,4-Dideoxy-D-Glucopyranose (5)**

To a solution of compound **15** (672.5 mg, 1.5 mmol) in THF (5 mL) at room temperature, was added a solution of TBAF (1.8 mL of a 1M sol. in THF, 1.8 mmol) and acetic acid (130  $\mu$ L, 2.3 mmol). The reaction was stirred for 6 h and TLC analysis showed complete conversion of the starting material to a major product (Petroleum ether / EtOAc, 1:1, R<sub>f</sub>=0.16). The reaction was concentrated and diluted with ethyl acetate (30 mL) and washed with 1 M HCl (2×10 mL), saturated sodium bicarbonate(10 mL), brine (10 mL), the organic phase was dried over anhydrous sodium sulfate and concentrated by oil pump. The crude product was dissolved in pyridine (10 mL) without further purification, acetyl anhydride (0.28 mL, 3.0 mmol) was added and the mixture was stirred at room temperature for 4h. TLC analysis indicated the starting material was consumed completely (Petroleum ether / EtOAc, 1:1, R<sub>f</sub>=0.28), the reaction was concentrated and diluted with ethyl acetate (30 mL) and washed with 1M HCl (10 mL), saturated sodium bicarbonate(10 mL), brine (10 mL). The organic phase was separated and dried over anhydrous sodium sulfate, the organic layer was concentrated and purified by column chromatography to afford the target product **5** as a colorless oil (427.8 mg, 76.6%). <sup>1</sup>H NMR (400 MHz, CDCl<sub>3</sub>)  $\delta$  6.40 (d,  $J$  = 8.8 Hz, 1H), 6.22 (d,  $J$  = 3.6 Hz, 1H), 5.27-5.20 (m, 1H), 4.35-4.27 (m, 1H), 4.19-4.09 (m, 3H), 3.95 (s, 2H), 2.18 (s, 3H), 2.15-2.08 (m, 7H), 1.77 (dd,  $J$  = 24.0, 12.0 Hz, 1H). <sup>13</sup>C NMR (100 MHz, CDCl<sub>3</sub>)  $\delta$  171.33, 170.73, 169.06, 166.99, 91.41, 67.77, 67.36, 65.23, 52.45, 51.67, 32.51, 21.01, 20.97, 20.77; HRMS (ESI):  $m/z$  [M+NH<sub>4</sub>]<sup>+</sup> calculated for C<sub>14</sub>H<sub>20</sub>N<sub>4</sub>O<sub>8</sub>: 390.1625, found: 390.1619.

### **2-Azidoacetamido-2,4-Dideoxy-D-Glucopyranose (16)**

To the solution of **5** (50 mg, 0.13 mmol) in 5 mL dry methanol, catalytic amount CH<sub>3</sub>ONa was added and the pH was adjusted to 9 - 10, the mixture was stirred at room temperature for 5 h. TLC analysis showed that starting material was consumed completely (CH<sub>2</sub>Cl<sub>2</sub> / CH<sub>3</sub>OH, 5:1, R<sub>f</sub> = 0.55), then neutralized with Amberlite IR-120 (H<sup>+</sup> form) and filtered. The filtrate was concentrated in vacuo and purified by column chromatography to afford the product **16** as colorless oil (18.5 mg, 56.1%). <sup>1</sup>H NMR (400 MHz, CD<sub>3</sub>OD)  $\delta$  5.15 (d,  $J$  = 3.4 Hz, 1H), 4.09-4.05 (m, 1H), 3.94-3.90 (m, 3H), 3.60-3.58 (m, 1H), 3.55 (d,  $J$  = 4.8 Hz, 2H), 2.02-1.97 (m, 1H), 1.44 (m, 1H); <sup>13</sup>C NMR (100 MHz, CD<sub>3</sub>OD)  $\delta$  169.20, 91.70, 72.63, 68.04, 65.52, 64.46, 51.51, 35.96. HRMS (ESI):  $m/z$  [M-H]<sup>-</sup> calculated for C<sub>8</sub>H<sub>13</sub>N<sub>4</sub>O<sub>5</sub>: 245.0886, found: 245.0884.

### **Site-directed mutagenesis of the hOGA recombinant protein**

Site-directed mutagenesis was performed using the Quickchange Site-Directed Mutagenesis Kit (Stratagene) following the manufacturer's protocol. The plasmid pET28a-OGA was used as a template, and the mutagenic primer sequences were as following, forward: 5'-CTGGGATAACATTGATGCTAATGCTTATGATCAGAACAGACTG-3'; reverse: 5'-CAGTCTCTTGATCATAAGCATTAGCATGAATGTTATCCAG-3'. The insertion of each mutation gene was further confirmed by restriction mapping and sequencing.

### **Expression, purification and enzymatic assay of GK2, AGX1, OGT and OGA**

The expression of human GalNAc Kinase 2 (GK2) and human UDP-GalNAc pyrophosphorylase (AGX1) from *E. coli* were carried out as previously described.<sup>2</sup> One-pot two-enzyme system (4dGlcNAz was incubated overnight at 37 °C with GK2 and AGX1 in the presence of ATP and UTP. ATP served as phosphate donor for GK2 while UTP as nucleotide donor for AGX1) was used to produce of UDP-4dGlcNAz.

Plasmids pET28a-fOGA containing human OGA and pET24b-ncOGT containing human OGT were kindly provided by Dr. Hart from Johns Hopkins University and Dr. Suzanne Walker from Harvard Medical School respectively. The expression, purification and activity assay procedures were carried out as previously described.<sup>3</sup> In brief, peptide (FITC-YAVVPVSK) was incubated in the presence of OGT, UDP-4dGlcNAc or UDP-GlcNAc in Tris buffer, pH 7.5 containing 12.5 mM MgCl<sub>2</sub>, and 1 mM 2-mercaptoethanol for 4 h at 37 °C. After that, the reaction was heated at 65 °C for 10 min to inactivate OGT, followed by incubation with OGA for 2 h at 37 °C. All reactions were then quenched by the addition of an equal volume of methanol and analyzed by HPLC. HPLC was carried out using an Ultimate HPLC with connected Famos Autosampler (LC Packings, Amsterdam, Netherlands). Samples were loaded onto a guard column (300 μm ID × 5 cm C18 PepMap) in the injection loop, and washed with 0.1% formic acid at 40 μL/min for 2 min using a Switchos pump (LC Packings). Peptides were then separated on an analytical column (75 μm ID × 15 cm C18 PepMap) at a flow rate of 200 nL/min with a gradient from 5% to 40% buffer B (80% acetonitrile / 0.1% formic acid) over a period of 32 min.

For fluorescence detection of OGA activity was as following. The reaction system (50μL, pH 6.5) contained 50 mM NaH<sub>2</sub>PO<sub>4</sub>, 100 mM NaCl, 0.1% BSA, fluorescent substrate 4-methylumbelliferyl 2-acetamido-2-deoxy-β-D-glucopyranoside (concentrations used: 0.15625, 0.3125, 0.625, 1.25, 2.5, 5.0 mM), and 2 μL of purified OGA (10 μg/ μL). Reactions were incubated at 37 °C for 10 min and terminated by the addition of 150 μL of quenching buffer (200 mM glycine, pH 10.8). The assay solution was then transferred into a 96-well plate and the fluorescence was measured on a microplate reader (excitation, 368 nm; emission, 450 nm).

### **Enzymatic synthesis of UDP-4dGlcNAc**

GK2, AGX1 and PPA were prepared as previously reported.<sup>1</sup> To a solution of 10 ml reaction system, 50 mg of 4dGlcNAc, 165 mg of ATP, 176 mg of UTP, 50 mM of Tris-HCl buffer (pH 7.5), 5 mM of Mg<sup>2+</sup>, 2 mg of GK2, 1 mg of AGX1, and 100 ug of PPA were added. PPA was used to improve the conversion ratio. The reaction was carefully carried at 37°C to allow the formation of UDP-4dGlcNAc. The reaction was monitored by TLC (EtOAc/MeOH/H<sub>2</sub>O/HOAc=5:2:1.4:0.4). Finally the product was purified by Bio-Gel P-2 column and confirmed by LC-MS.

### **Cell culture and metabolic labeling**

HEK293, HeLa, PC-3 and NIH3T3 cells were maintained in 5% CO<sub>2</sub> at 37 °C, and grown in DMEM with 4.5 mg/mL glucose supplemented with 10% fetal bovine serum, 0.1% antibiotics antimycotic solution (100 ×). Media

containing Ac<sub>4</sub>GlcNAc, Ac<sub>4</sub>GlcNAz, Ac<sub>4</sub>GalNAz, Ac<sub>3</sub>4dGlcNAz (1,000 × stock in DMSO) at 100 μM concentration, or DMSO vehicle was added as indicated when cells were maintained approximately 80% confluence.

### Cytotoxicity Assay<sup>4</sup>

HEK293, HeLa, PC-3 and NIH3T3 cells were seeded at a density of 40,000 cells per well into 96-well plates and incubated overnight. The cells were then treated with varying concentrations of Ac<sub>3</sub>4dGlcNAz at 37 °C in 5% CO<sub>2</sub> for 24 h. Then 20 μL of 3-(4,5 dimethylthiazol-2-yl)-2,5-diphenyl-tetrazoliumbromide (MTT, Sigma Aldrich) solution (5 mg/mL in PBS) was added to each well and incubated for 4 h at 37 °C. After removal of the media, MTT formazan was dissolved in 150 μL of dimethylsulfoxide (DMSO) and monitored using a microplate reader at a wavelength of 570 nM.

### Azide–Alkyne cycloaddition *in vitro*

As previously described,<sup>5</sup> cell lysates or the reaction samples were incubated with DIBO-biotin (10 μM) or diazo-biotin-alkyne cocktail in dark at room temperature for 1 h. The newly click chemistry cocktail, containing 100 μM diazo-biotin-alkyne, 1 mM tris (2-carboxyethyl) phosphine hydrochloride (TCEP), 100 μM tris [(1-benzyl-1-H-1,2,3- triazol-4-yl) methyl] amine (TBTA) and 1 mM CuSO<sub>4</sub>·5H<sub>2</sub>O was made according to the previous report.<sup>5</sup> After reaction, 5 × volume of ice cold methanol was added and placed at -20°C for 2 h to precipitate proteins. The reactions were then centrifuged at 10000 g for 10 min at 4°C. The supernatant was removed, and the pellet was allowed to air-dry for 15 min and dissolved in 50 μL 4% SDS buffer (4% SDS, 150 mM NaCl, 50 mM TEA, pH 7.4). The mixture was sonicated in a bath sonicator to ensure complete dissolution, and 50 μL of 2 × SDS free loading buffer (20% glycerol, 0.2% bromophenol blue, 1.4% β-mercaptoethanol, pH 6.8) was then added. The samples were boiled for 5 min at 97 °C, and 20 μg of protein was loaded per lane for SDS-PAGE separation.

### Azide labeling and immunofluorescence assays

PC-3 cells (50,000 cells) were grown on coverslips in the presence of Ac<sub>4</sub>GlcNAz, Ac<sub>4</sub>GalNAz, Ac<sub>3</sub>4dGlcNAz (1,000 × stock in DMSO) at 50 μM concentration, and DMSO vehicle for 2 days to metabolically incorporate corresponding *N*-azido acetyl-GlcNAc derivatives into their glycoproteins. Cells bearing azides were treated with DIBO-Biotin (10 μM) in labeling buffer (PBS, pH 7.4 containing 1% FBS) for 1 h at room temperature, followed by fixation with formaldehyde (3.7% in PBS) for 15 min at room temperature. Cells were washed four times and permeabilized for 10 min at room temperature with Triton X-100 (0.2%) in PBS. The cells were washed four times with PBS buffer and incubated with Alexa Fluor 488-conjugated streptavidin (10 μg/mL; Molecular Probes) for 1 h at room temperature. Cells were washed three times with PBS and mounted with PermaFluor (Thermo Electron Corp.) before imaging. Initial analysis was performed on a Zeiss AxioPlan2 fluorescent microscope. Confocal images were acquired on an Olympus FV-1000 laser scanning confocal microscope using a 60 × (N.A. 1.42) oil objective. Stacks of optical sections were collected in the z dimensions. The step size, based on the calculated

optimum for each objective, was between 0.25 and 0.5  $\mu$ m. Subsequently, each stack was collapsed into a single image (zprojection). Analysis was performed offline using ImageJ 1.39f software (National Institutes of Health, U.S.) and Adobe Photoshop CS3 Extended Version 10.0 (Adobe Systems Inc.), whereby all images were treated equally.

To examine the distribution of azide labeling proteins in living cells, HeLa cells were grown overnight to 60–80% confluence on sterile MatTek (Ashland, MA) glass-bottom culture dishes. These cells were washed three times with PBS and incubated 10 min (at 37 °C, 5% CO<sub>2</sub>) with Alexa Fluor 488-conjugated streptavidin (10  $\mu$ g/mL; Molecular Probes) for 1 h at room temperature and then with the Image-iT kit (Life Technologies) comprising the Alexa Fluor 594 conjugate of wheat germ agglutinin (WGA-AF 594) at 5  $\mu$ g/ mL to label the outer face of the plasma membranes red and 2  $\mu$ g/mL of Hoechst 33342 to label double-stranded DNA and nuclei blue. The cells were then washed three times with PBS. A culture dish was then placed on the stage of a Leica TCP SP8 MP inverted spectral confocal microscope equipped with 405 nm and tunable white light lasers. The excitation/emission band-pass wavelengths used to detect Hoechst 33342, Alexa Fluor 488 and Alexa Fluor 594 WGA were set to 405/415-470, 488/495-519 nm and 594/610-680 nm, respectively. Microscopy was performed on a Olympus VHY-700 inverted microscope equipped with a 4 $\times$  eyepiece and a 25 $\times$  numerical aperture objective lens. A 175-W Xenon lamp housed in a Sutter DG4 illuminator linked to the microscope by an optical fiber assured shuttering and illumination. SLIDEBOOK software (Intelligent Imaging Solutions) was used to control the microscope and the camera. Image stacks spaced 0.5  $\mu$ m apart were acquired by using a CoolSNAP HQ charged-coupled device camera (Roper Scientific). The image stacks were digitally deconvolved using the Adobe Photoshop software 7.0 and single z-plane images are shown. All image acquisition and processing was performed under identical conditions for test and control samples.

### **Immunoprecipitation of NUP62<sup>6</sup>**

HEK293 cells were treated with 100  $\mu$ M Ac<sub>4</sub>GalNAz, Ac<sub>3</sub>4dGlcNAz (1,000  $\times$  stock in DMSO) or DMSO and allowed to incubate for 18 h. After that cells were washed with PBS, trypsinized and pelleted. Cold lysis buffer (50 mM Tris, pH 7.4 / 100 mM NaCl / 2 mM EDTA/1 mM PMSF / 1% SDS) was added and the mixture and heated at 96 °C for 5 min after which the cells were sonicated for 5 mins and then centrifuged at 4°C for 10 min at 10,000 g. The supernatant was collected and the protein concentration was determined by BCA assay (Pierce, Thermo Scientific). Total cell lysate (1.5 mg) was diluted as necessary to a final volume of 1 mL with 1% NP-40 buffer with Complete Mini, EDTA-free Protease Inhibitor Cocktail Tablets (Thermo Scientific). The solution was mixed and centrifuged, after which mAb 414 bound to protein-A/G Sepharose was added to the supernatant. The mixture was gently rocked for 2 h after which the protein A/G beads were collected by centrifugation at 2,000 g for 2 min at 4 °C and washed extensively with cold PBS. The buffer was removed, and aliquots of the immunoprecipitated Nup62 from cells were treated with click reaction as described above. Samples were analyzed for the azide and Nup62 by Western blot.

### **Immunoprecipitation of GlyCAM-IgG labeling<sup>7</sup>**

HEK293 cells were treated with 100  $\mu$ M Ac<sub>4</sub>GalNAz, Ac<sub>4</sub>GlcNAz, Ac<sub>3</sub>4dGlcNAz (1000  $\times$  stock in DMSO) or DMSO and allowed to incubate 24 h. After that, the media from each sample was collected by centrifugation at 3,000 g for 10 min at 4 °C to remove cell debris. The supernatant (1 mL) was incubated with 50  $\mu$ L recombinant protein G sepharose beads (Invitrogen) in 100 mM TEA, pH 8.0 overnight. Beads were collected by centrifugation at 2,000g for 2 min at 4 °C. Beads were washed 3 times with 1 mL 100 mM TEA pH 8.0. GlyCAM-IgG were eluted by addition of 50  $\mu$ L 4% SDS buffer (4% SDS, 150 mM NaCl, 50 mM TEA, pH 7.4) and boiling for 5 min at 97 °C. Protein concentration was determined by BCA assay (Thermo Scientific). Final SDS concentration was diluted to 0.5% by addition of 50 mM TEA, pH 7.4. The appropriate amount of click chemistry cocktail was added and the reaction was allowed to proceed for 1 h, after which 4 $\times$  loading buffer (200 mM Tris-HCl, 4% SDS, 40% glycerol, 0.4% bromophenol blue, 1.4%  $\beta$ -mercaptoethanol, pH 6.8) was added. Samples were boiled for 5 min at 97 °C, and 20  $\mu$ g proteins were loaded for SDS-PAGE and Western blot analysis.

### Western blotting

Proteins were separated by SDS-PAGE before being transferred to PVDF membrane (Bio-Rad) using standard Western blotting procedures. All Western blots were blocked in TBST (0.1% Tween-20, 150 mM NaCl, 10 mM Tris, pH 8.0) containing 3% BSA for 2 h at RT. The blots were then incubated with the appropriate primary antibody in blocking buffer at 4 °C overnight. The anti-MAb414 antibody was used at 1 : 2,000 dilution for detection of Nup62. The streptavidin-HRP antibody was used at 1 : 12,000. The blots were then washed three times in TBST for 10 min and incubated with the horseradish peroxidase (HRP)-conjugated secondary antibody for 2 h in blocking buffer at RT. HRP-conjugated anti-mouse (Abcam) were used at 1:5,000 dilution. After being washed three more times with TBST for 10 min, the blots were developed using ECL reagents (Bio-Rad) and the ChemiDoc XRS+ molecular imager (Bio-Rad).

### Biotin enrichment and on-bead trypsin lysis<sup>5</sup>

NIH3T3 cell pellets labeled with 100  $\mu$ M Ac<sub>4</sub>GalNAz, Ac<sub>3</sub>4dGlcNAz or Ac<sub>4</sub>GlcNAc were resuspended in 200  $\mu$ L H<sub>2</sub>O, 60  $\mu$ L PMSF in H<sub>2</sub>O (250 mM), and 500  $\mu$ L of 0.05% SDS buffer (0.05% SDS, 10 mM TEA pH 7.4, 150 mM NaCl) with Complete Mini protease inhibitor cocktail (Roche Biosciences). The cells were incubated on ice for 30 min with the addition of 8  $\mu$ L Benzonase (Sigma). 4% SDS buffer (2,000  $\mu$ L) was added, and the cells were briefly sonicated in a bath sonicator followed by centrifugation (20 000g for 10 min at 15°C). Soluble protein concentration was normalized by BCA assay (Pierce, Thermo Scientific) to 1 mg/mL, and 10 mg total proteins were subjected to the appropriate amount of click chemistry cocktail containing Diazo-Biotin-Alkyne (10 mM, Click Chemistry Tools) for 1 h, after which 10 volumes of ice-cold MeOH were added. Precipitation proceeded 2 h at -20 °C. Precipitated proteins were centrifuged at 5,200g for 30 min at 0 °C and washed 3 times with 40 mL ice-cold MeOH, with resuspension of the pellet each time. The pellet was then air-dried for 1 h. To capture the biotinylated proteins by streptavidin beads, the air-dried protein pellet was resuspended in 2 mL of resuspension buffer (6 M urea, 2 M

thiourea, 10 mM HEPES, pH 8.0) by bath sonication. To cap cysteine residues, 100  $\mu$ L freshly made TCEP (200 mM stock solution, Thermo) was then added and the mixture was incubated for 30 min, followed by 40  $\mu$ L freshly prepared iodoacetamide (1 M stock solution, Sigma) and incubation for another 30 min in dark. Streptavidin beads (250  $\mu$ L of a 50% slurry per sample, Thermo) were washed twice with 1 mL PBS and once with 1 mL resuspension buffer, followed by resuspension in 200  $\mu$ L resuspension buffer. Each sample was combined with streptavidin beads and incubated on a rotator for 2 h. These mixtures were then transferred to Mini Bio-Spin columns (Bio-Rad) and placed on a vacuum manifold. Captured proteins were then washed with agitation five times with 10 mL resuspension buffer, five times with 10 mL 1% SDS in PBS, thirty times with 1 mL PBS (vacuum applied between each wash), and five times with 1 mL 2 M urea in PBS (vacuum applied between each wash). Beads were then resuspended in 1 mL 2 M urea in PBS, transferred to screw-top tubes, and pelleted by centrifugation at 2,000 g for 2 min. At this time, 800  $\mu$ L supernatant was removed, leaving a volume of 200  $\mu$ L. 2  $\mu$ L CaCl<sub>2</sub> (200 mM stock, 1 mM final concentration) and 2  $\mu$ L 1 mg/mL sequence grade trypsin (Promega) was added and incubated at 37 °C for 18 h. The resulting mixtures of tryptic peptides and beads were transferred to Mini Bio-Spin columns (Bio-Rad) and the eluent was collected by centrifugation at 1,000 g for 2 min. Any remaining peptides were eluted by the addition of 100  $\mu$ L 25 mM ammonium bicarbonate followed by centrifugation immediately as above. The tryptic peptides were then applied to C18 spin columns (Pierce) according to manufacturer's instructions, eluted with 70% acetonitrile in H<sub>2</sub>O, and concentrated to dry on a SpeedVac.

### **LC–MS/MS Analysis**

Peptides were desalted using C18 ZipTip (Millipore). Nano RP HPLC-MS experiments were performed on an LTQ-Orbitrap Elite mass spectrometer (Thermo Fisher) equipped with EASY-spray source and nano-LC UltiMate 3000 high performance liquid chromatography system (Thermo Fisher). Briefly, EASY-Spray PepMap C18 Column (75  $\mu$ m id  $\times$  15 cm, 3  $\mu$ m) was used for separation. Separation was achieved with a linear gradient from 3% to 40% buffer B for 40 min at a flow rate of 300 nL/min (mobile phase A: 1.95% ACN, 97.95% H<sub>2</sub>O, 0.1% FA; mobile phase B: 79.95% ACN, 19.95% H<sub>2</sub>O, 0.1% FA). LTQ-Orbitrap Elite mass spectrometer was operated in the data-dependent mode. A full-scan survey MS experiment (*m/z* range from 400 to 1,600; automatic gain control target, 1,000,000 ions; resolution at 400 *m/z*, 60,000; maximum ion accumulation time, 500 ms) was acquired by the Orbitrap mass spectrometer, and ten most intense ions were fragmented via collision-induced dissociation (CID). The other conditions used were: capillary temperature of 200 °C, collision energy of 35 eV.

### **Data Analysis**

The raw file was searched using pFind 2.1 software<sup>8</sup> against Uniprot-Swiss HUMAN.fasta (2015\_09 Release, 20,196 reviewed entries). Searching parameters were used as follows: fixed modification, carbamidomethyl (Cys); variable modifications, deamination (Asn) and oxidation (Met). Trypsin was selected as the enzyme, and two missed cleavages were allowed. The mass tolerance for the precursor ions and the fragment ions was set to 20 ppm and 0.8

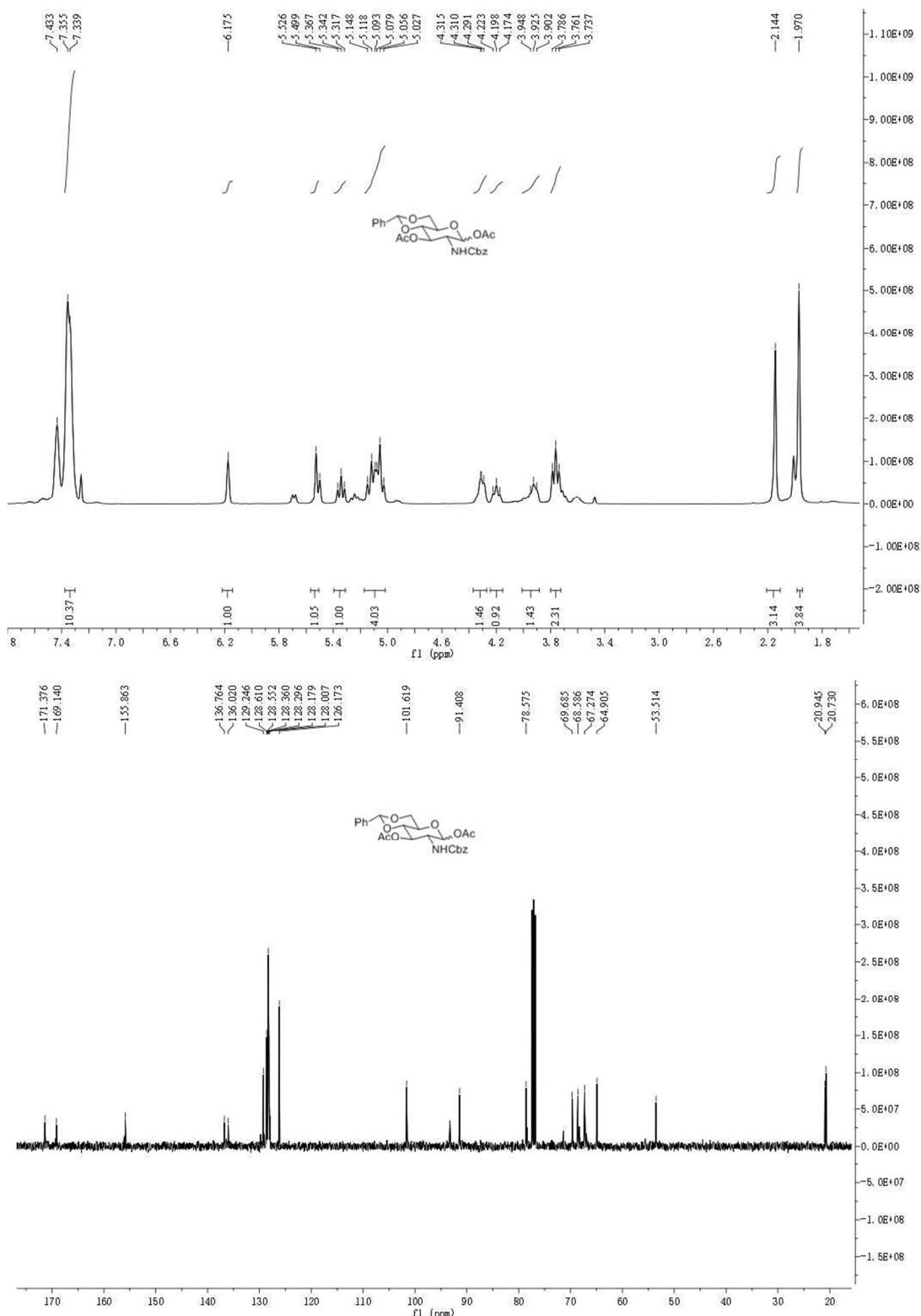
Da, respectively. A false discovery rate (FDR) of 1% was applied to all data sets at the peptide level. Furthermore, pBuild 2.0 was used to remove redundant protein entries and integrate the related proteins into a single group entry. Labeled proteins were identified as those that met the following threshold criteria<sup>5</sup>: 1) Proteins must have been identified by at least 1 unique peptide in each of the three data sets and a total of 3 spectral counts in the sum of three replicate data sets. 2) The sum of spectral counts of the Ac<sub>3</sub>4dGlcNAz and Ac<sub>4</sub>GalNAz treated samples must be 3-times greater than those in the control group sample CK. 3) The number of spectral counts in the Ac<sub>3</sub>4dGlcNAz and Ac<sub>4</sub>GalNAz treated sample compared to the control must be statistically significant ( $p < 0.05$ , t-test). Following the criteria above, subcellular localization of the identified proteins was performed in the Ingenuity Pathways Analysis (IPA) software (Redwood City, CA, USA) and Mammalian Protein Localization Database (<http://locate.imb.uq.edu.au/>). Previous reported *O*-GlcNAc-modified proteins data were consisted of large-scale proteomic techniques including elimination-addition chemistry<sup>9</sup>, *O*-GlcNAc-specific antibodies methods<sup>10</sup>, metabolic chemical reporters<sup>5, 11</sup>, enzymatic extension<sup>12</sup> and dbOGAP<sup>13</sup> (<http://cbsb.lombardi.georgetown.edu/hulab/OGAP.html>).

### III References

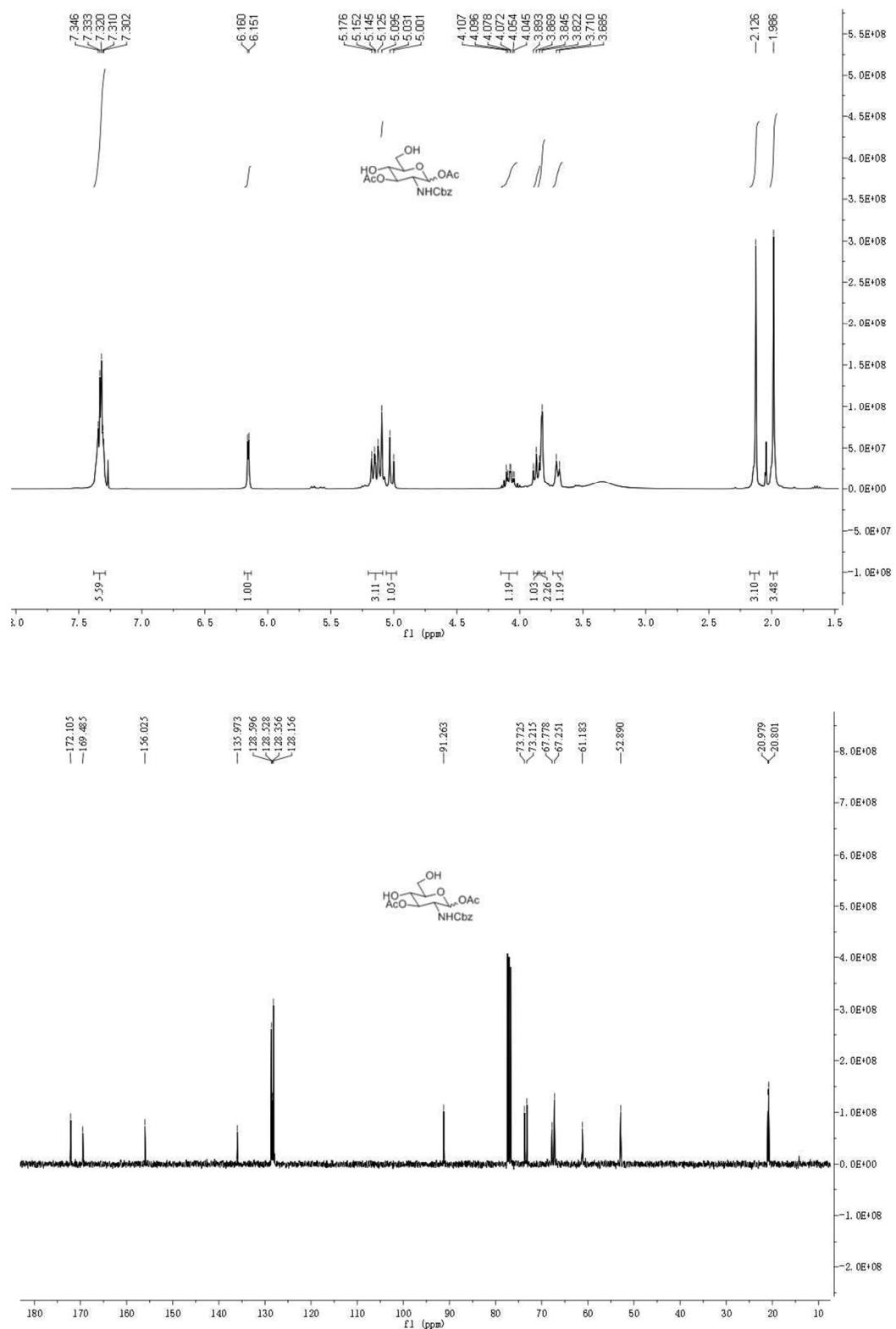
1. Cai, L.; Guan, W.; Kitaoka, M.; Shen, J.; Xia, C.; Chen, W.; Wang, P. G., A chemoenzymatic route to N-acetylglucosamine-1-phosphate analogues: substrate specificity investigations of N-acetylhexosamine 1-kinase. *Chem. Commun. (Camb)* **2009**, (20), 2944-6.
2. Pouilly, S.; Bourgeaux, V.; Piller, F.; Piller, V., Evaluation of analogues of GalNAc as substrates for enzymes of the mammalian GalNAc salvage pathway. *ACS Chem. Biol.* **2012**, 7 (4), 753-60.
3. (a) Gross, B. J.; Kraybill, B. C.; Walker, S., Discovery of O-GlcNAc transferase inhibitors. *J. Am. Chem. Soc.* **2005**, 127 (42), 14588-9; (b) Li, J.; Huang, C. L.; Zhang, L. W.; Lin, L.; Li, Z. H.; Zhang, F. W.; Wang, P., Isoforms of human O-GlcNAcase show distinct catalytic efficiencies. *Biochemistry (Mosc)* **2010**, 75 (7), 938-43.
4. Li, Z.; Li, T.; Dai, S.; Xie, X.; Ma, X.; Zhao, W.; Zhang, W.; Li, J.; Wang, P. G., New insights into the pharmacological chaperone activity of c2-substituted glucoimidazoles for the treatment of Gaucher disease. *Chem. biochem* **2013**, 14 (10), 1239-47.
5. Chuh, K. N.; Zaro, B. W.; Piller, F.; Piller, V.; Pratt, M. R., Changes in metabolic chemical reporter structure yield a selective probe of O-GlcNAc modification. *J. Am. Chem. Soc.* **2014**, 136 (35), 12283-95.
6. Vocadlo, D. J.; Hang, H. C.; Kim, E. J.; Hanover, J. A.; Bertozzi, C. R., A chemical approach for identifying O-GlcNAc-modified proteins in cells. *Proc. Natl. Acad. Sci. U. S. A.* **2003**, 100 (16), 9116-21.
7. Zaro, B. W.; Yang, Y. Y.; Hang, H. C.; Pratt, M. R., Chemical reporters for fluorescent detection and identification of O-GlcNAc-modified proteins reveal glycosylation of the ubiquitin ligase NEDD4-1. *Proc. Natl. Acad. Sci. U. S. A.* **2011**, 108 (20), 8146-51.
8. Li, D.; Fu, Y.; Sun, R.; Ling, C. X.; Wei, Y.; Zhou, H.; Zeng, R.; Yang, Q.; He, S.; Gao, W., pFind: a novel database-searching software system for automated peptide and protein identification via tandem mass spectrometry. *Bioinformatics* **2005**, 21 (13), 3049-50.
9. Nandi, A.; Sprung, R.; Barma, D. K.; Zhao, Y.; Kim, S. C.; Falck, J. R.; Zhao, Y., Global identification of O-GlcNAc-modified proteins. *Anal. Chem.* **2006**, 78 (2), 452-8.
10. Teo, C. F.; Ingale, S.; Wolfert, M. A.; Elsayed, G. A.; Not, L. G.; Chatham, J. C.; Wells, L.; Boons, G. J., Glycopeptide-specific monoclonal antibodies suggest new roles for O-GlcNAc. *Nat. Chem. Biol.* **2010**, 6 (5), 338-43.
11. (a) Hahne, H.; Sobotzki, N.; Nyberg, T.; Helm, D.; Borodkin, V. S.; van Aalten, D. M.; Agnew, B.; Kuster, B., Proteome wide purification and identification of O-GlcNAc-modified proteins using click chemistry and mass spectrometry. *J. Proteome Res.* **2013**, 12 (2), 927-36; (b) Yu, S. H.; Boyce, M.; Wands, A. M.; Bond, M. R.; Bertozzi, C. R.; Kohler, J. J., Metabolic labeling enables selective photocrosslinking of O-GlcNAc-modified proteins to their binding partners. *Proc. Natl. Acad. Sci. U. S. A.* **2012**, 109 (13), 4834-9.
12. (a) Clark, P. M.; Dweck, J. F.; Mason, D. E.; Hart, C. R.; Buck, S. B.; Peters, E. C.; Agnew, B. J.; Hsieh-Wilson, L. C., Direct in-gel fluorescence detection and cellular imaging of O-GlcNAc-modified proteins. *J. Am. Chem. Soc.* **2008**, 130 (35), 11576-7; (b) Khidekel, N.; Ficarro, S. B.; Clark, P. M.; Bryan, M. C.; Swaney, D. L.; Rexach, J. E.; Sun, Y. E.; Coon, J. J.; Peters, E. C.; Hsieh-Wilson, L. C., Probing the dynamics of O-GlcNAc glycosylation in the brain using quantitative proteomics. *Nat. Chem. Biol.* **2007**, 3 (6), 339-48.
13. Wang, J.; Torii, M.; Liu, H.; Hart, G. W.; Hu, Z. Z. *BMC Bioinformatics* **2011**, 12, 91.

## IV NMR spectra of compounds

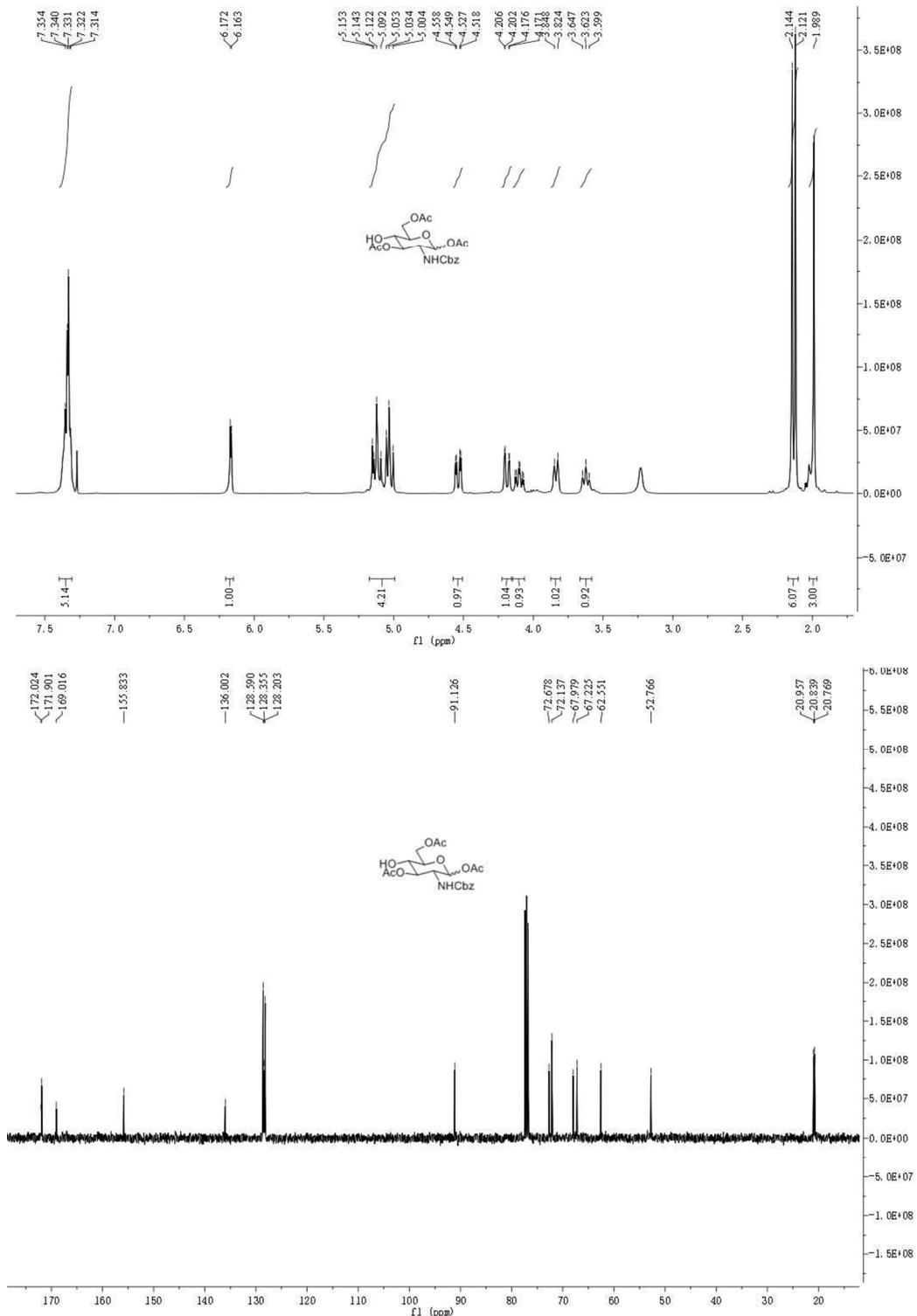
### 1,3-Di-O-Acetyl-4,6-O-Benzylidene-2-Benzylloxycarbonylamino-2-Deoxy-D-Glucopyranose (7)



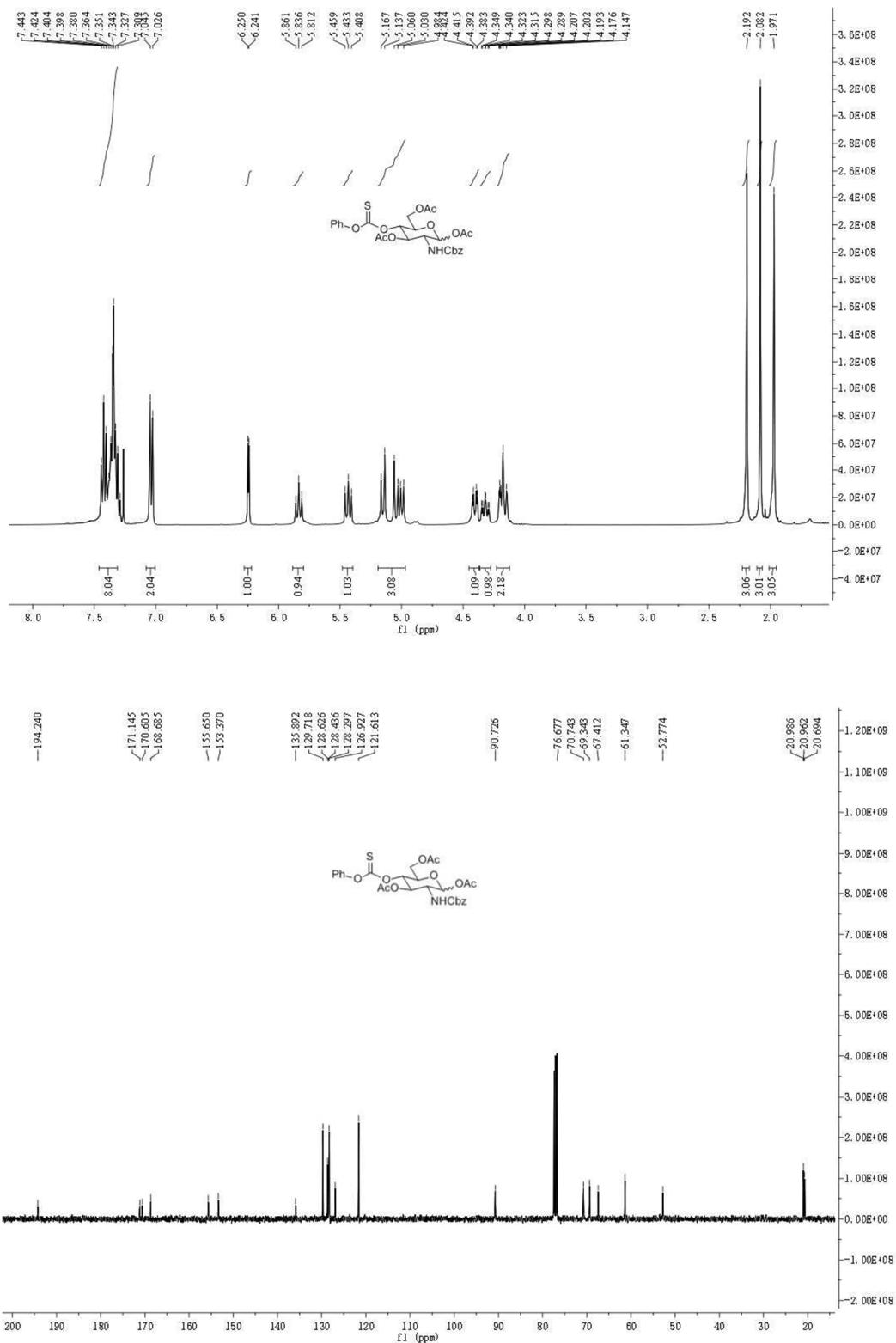
**1,3-Di-O-Acetyl-2-Benzylloxycarbonylamino-2-Deoxy-D-Glucopyranose (8)**



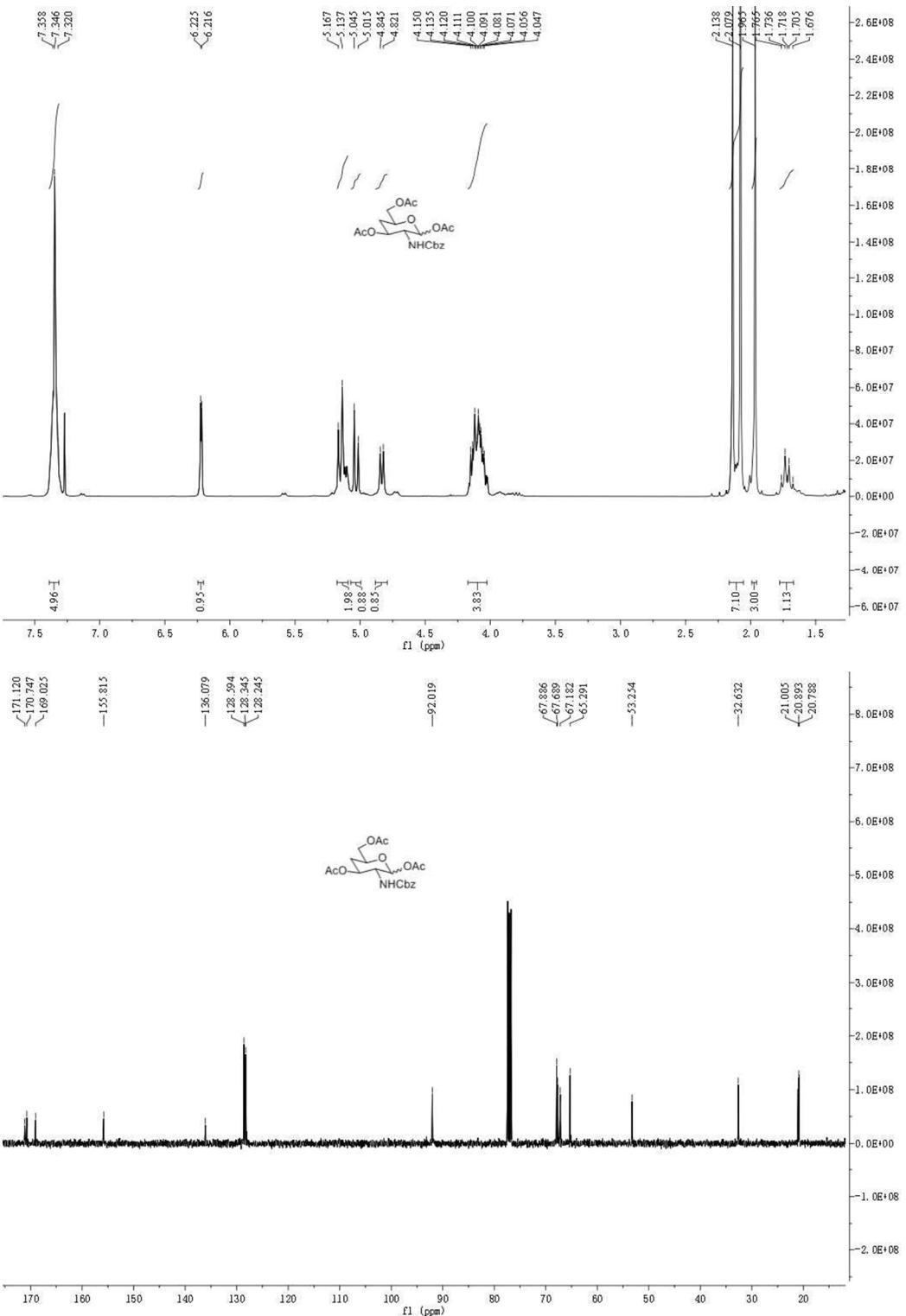
**1,3,6-Tri-O-Acetyl-2-Benzylloxycarbonylamino-2-Deoxy-D-Glucopyranose (9)**



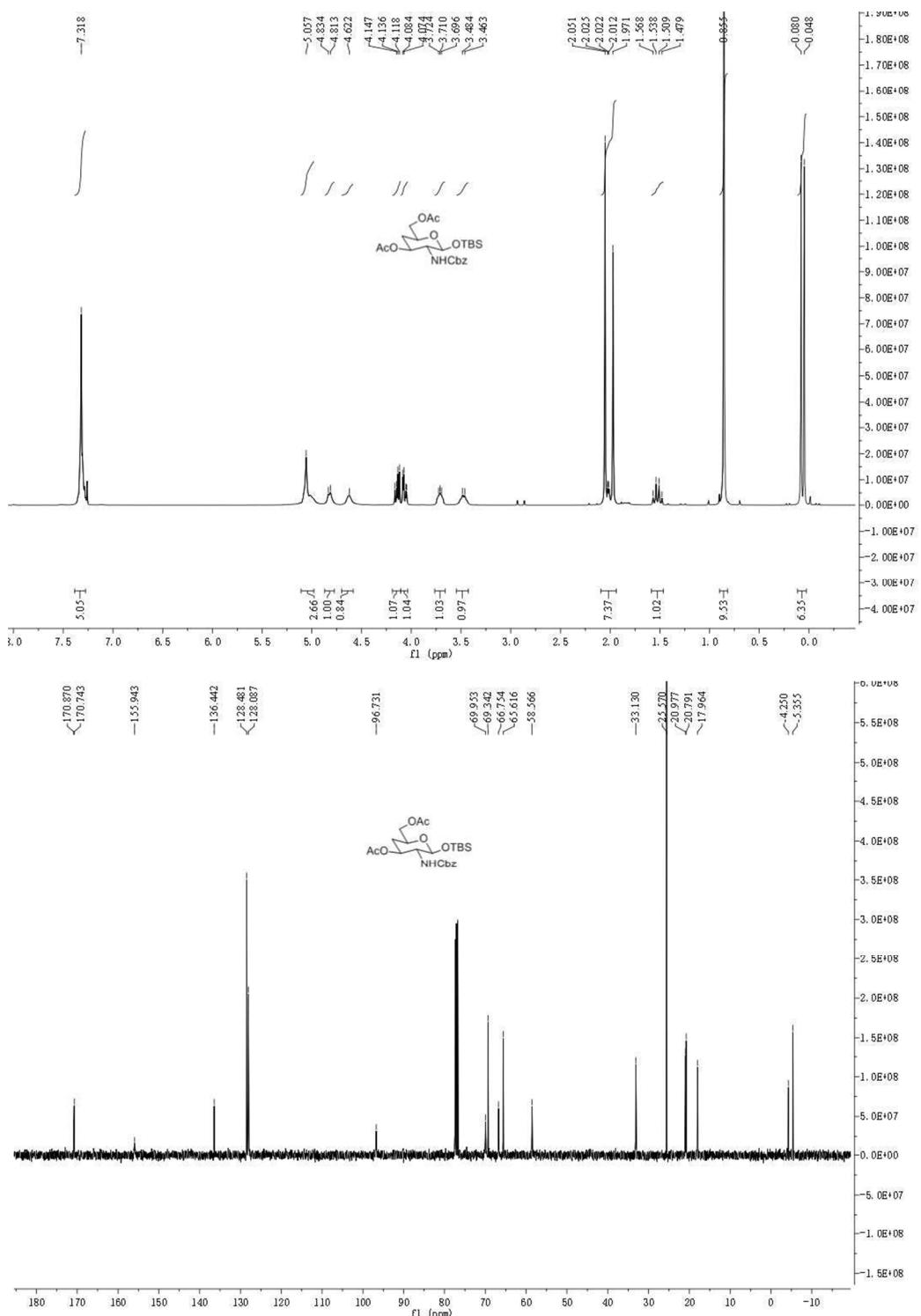
**1,3,6-Tri-O-Acetyl-2-Benzylloxycarbonylamino-2-Deoxy-4-O-(Phenoxythiocarbonyl)-D-Glucopyranose (10)**



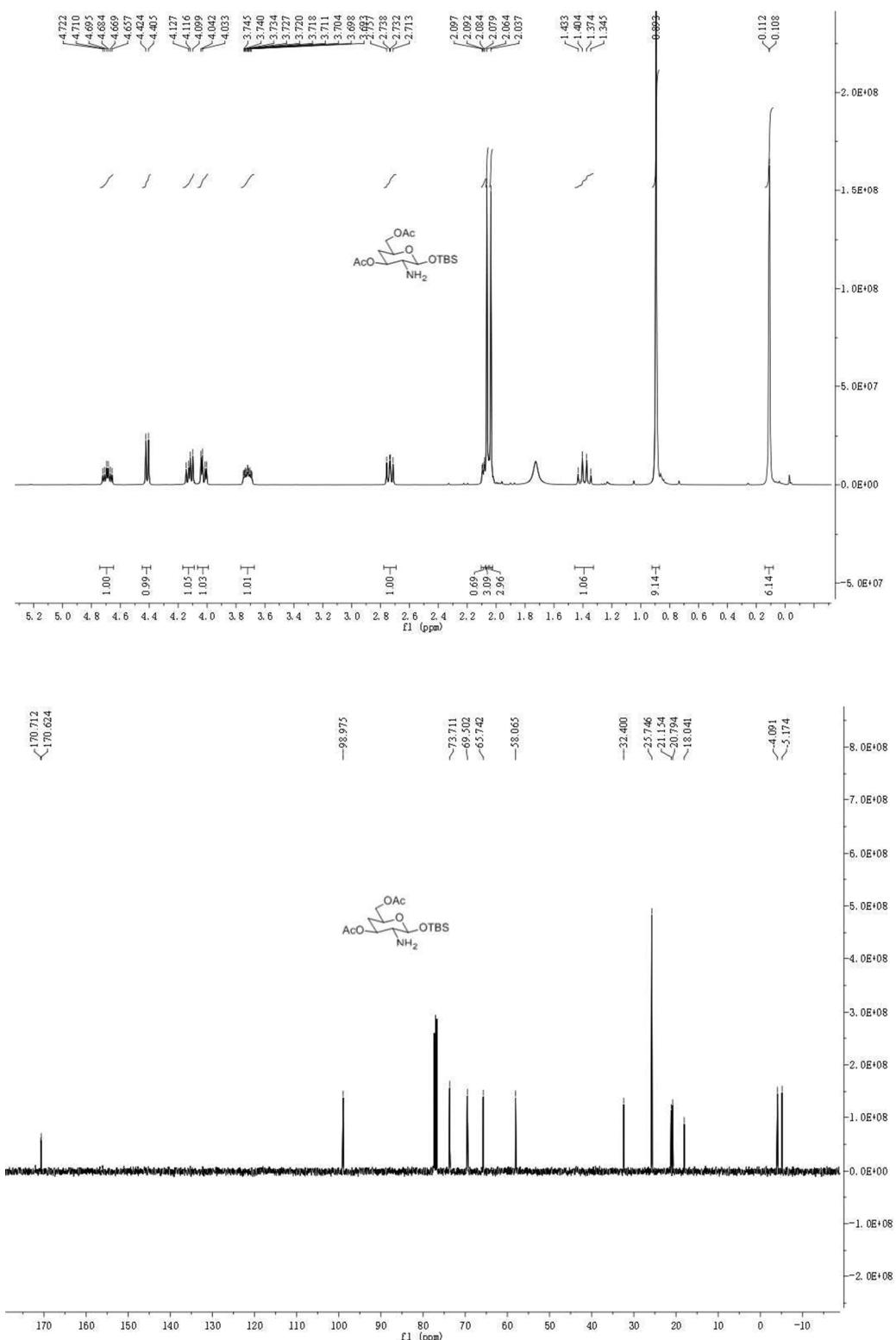
### 1,3,6-Tri-O-Acetyl-2-Benzylloxycarbonylamino-2,4-Dideoxy-D-Glucopyranose (11)



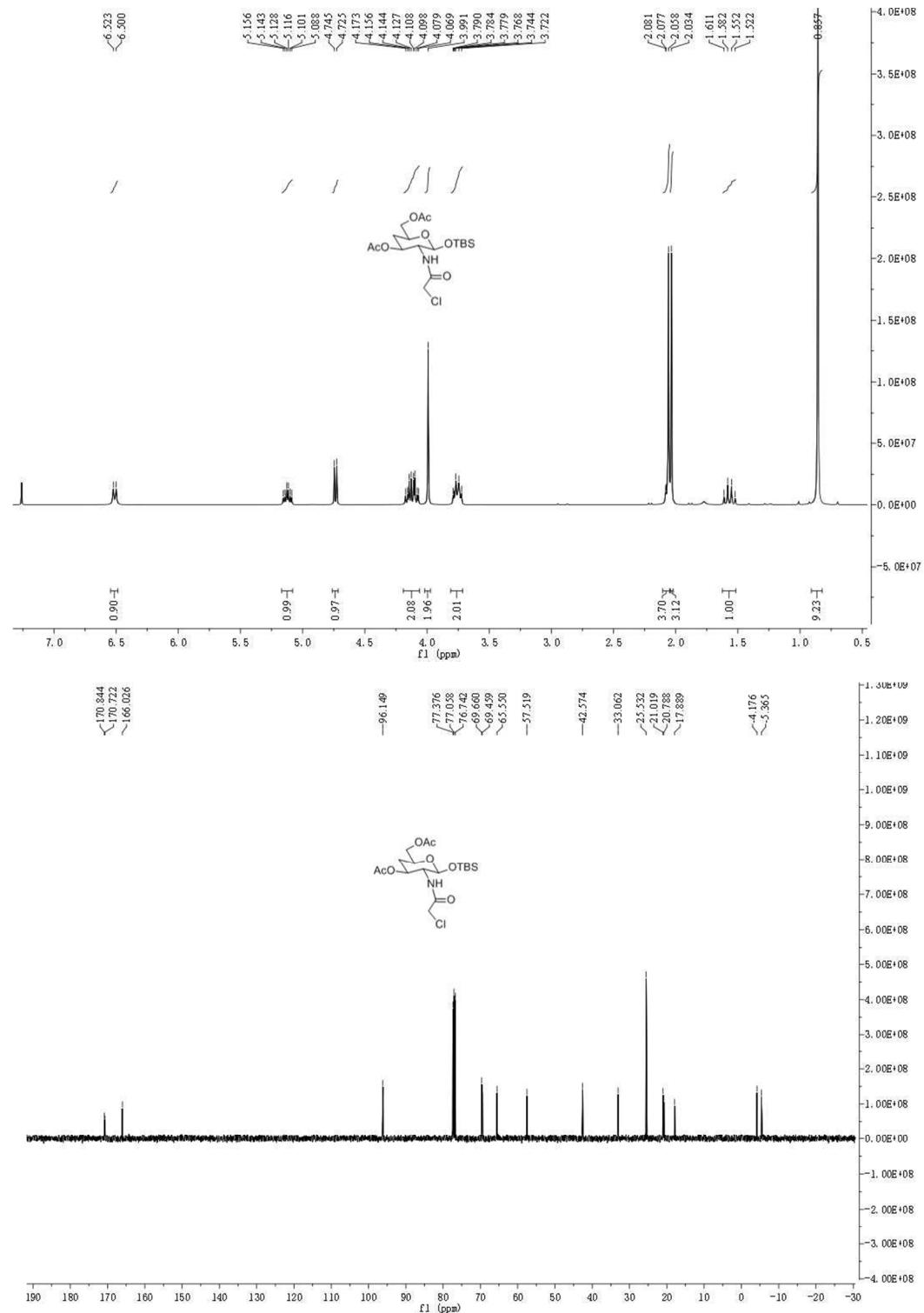
**1-O-(Tert-butyldimethylsilyl)-3,6-Di-O-Acetyl-2-Benzylloxycarbonylamino-2,4-Dideoxy-D-Glucopyranose (12)**



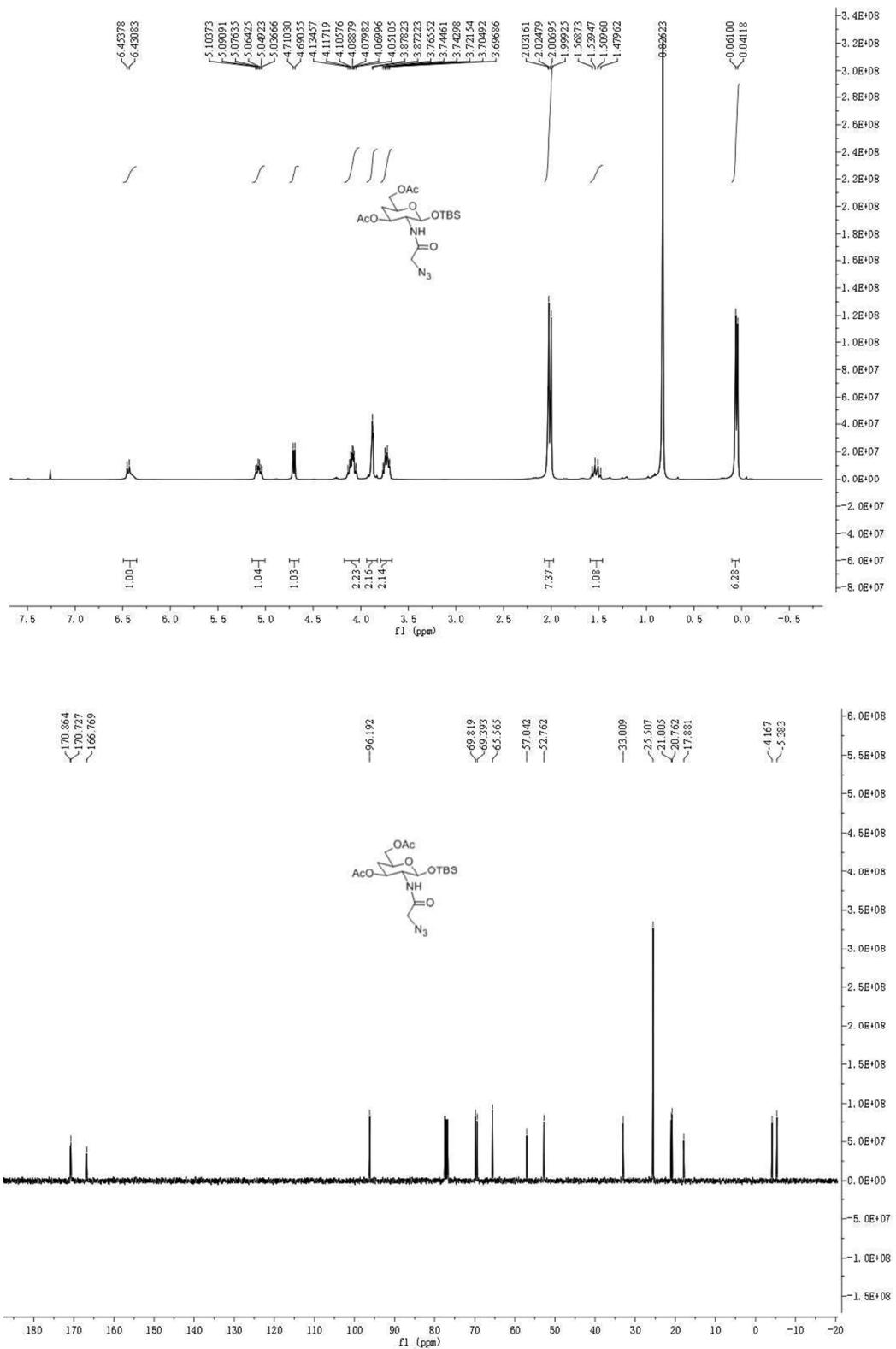
**1-O-(Tert-butyldimethylsilyl)-3,6-Di-O-Acetyl-2-Amino-2,4-Dideoxy-D-Glucopyranose (13)**



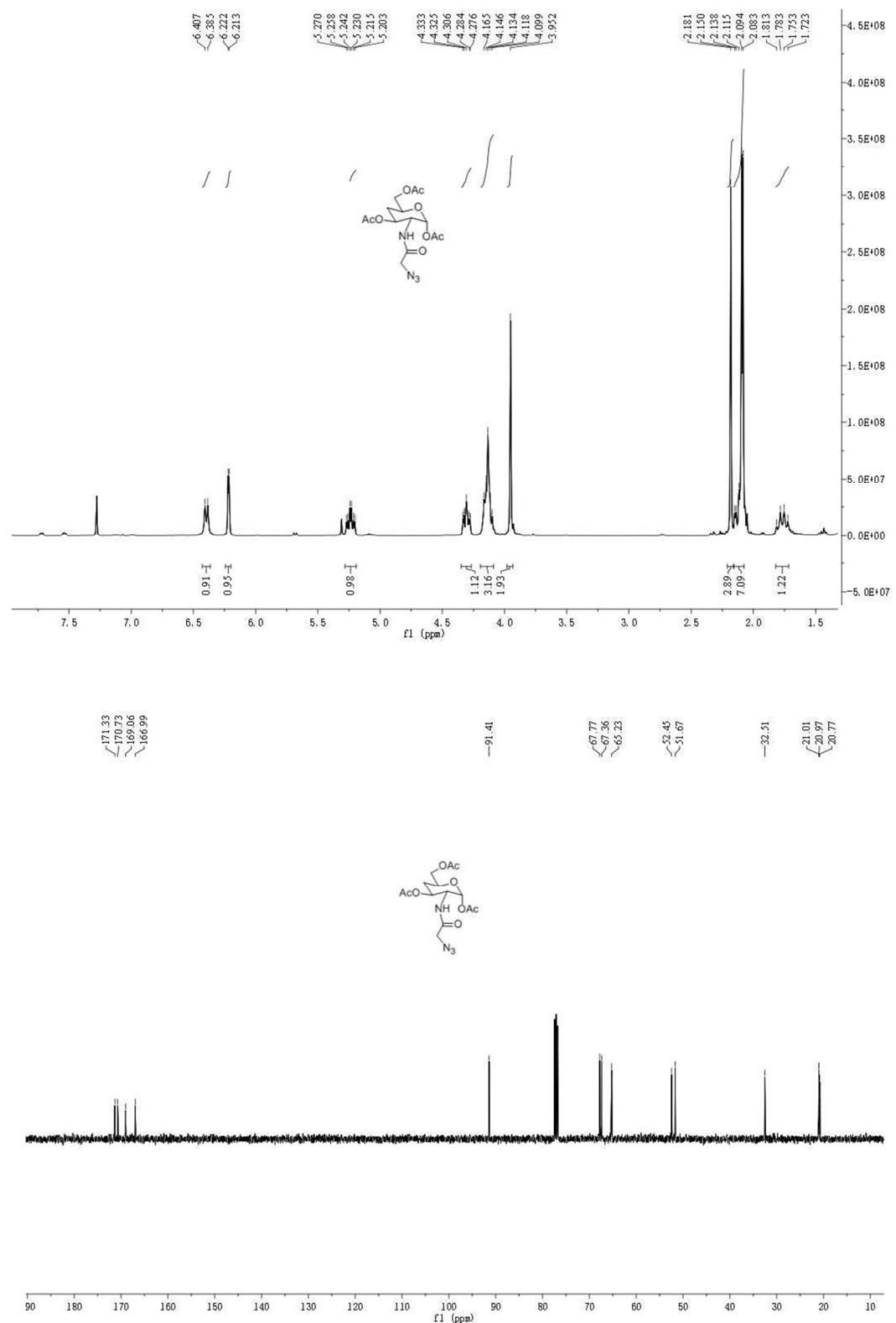
### **1-O-(Tert-butylidemethylsilyl)-3,6-Di-O-Acetyl-2-Chloroacetamido-2,4-Dideoxy-D-Glucopyranose (14)**



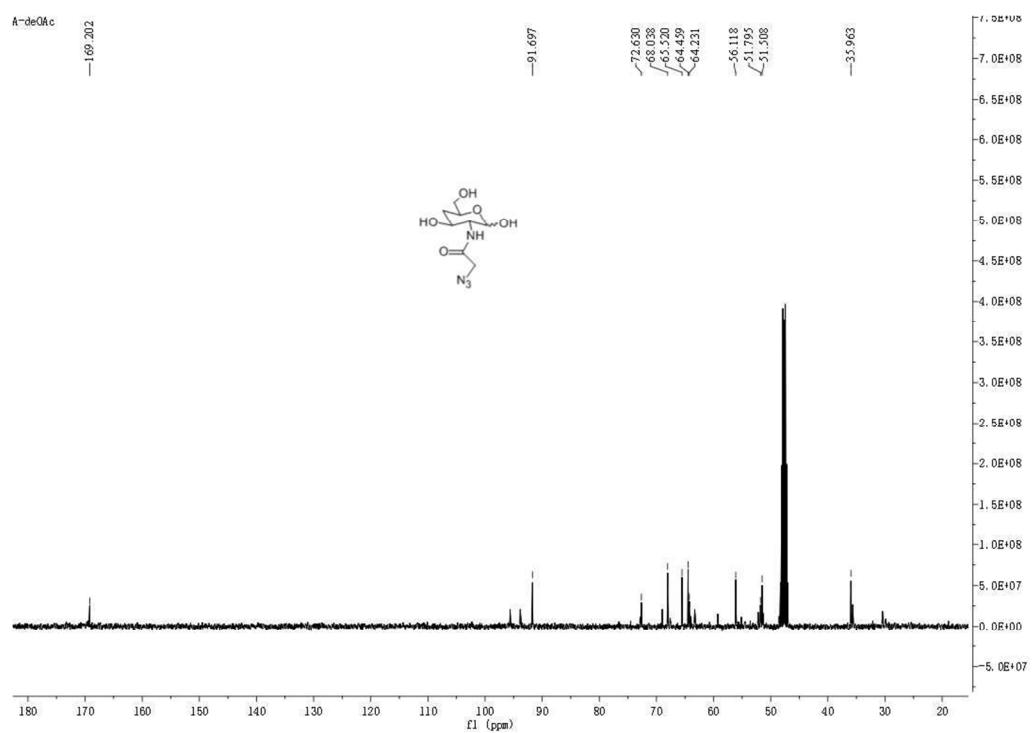
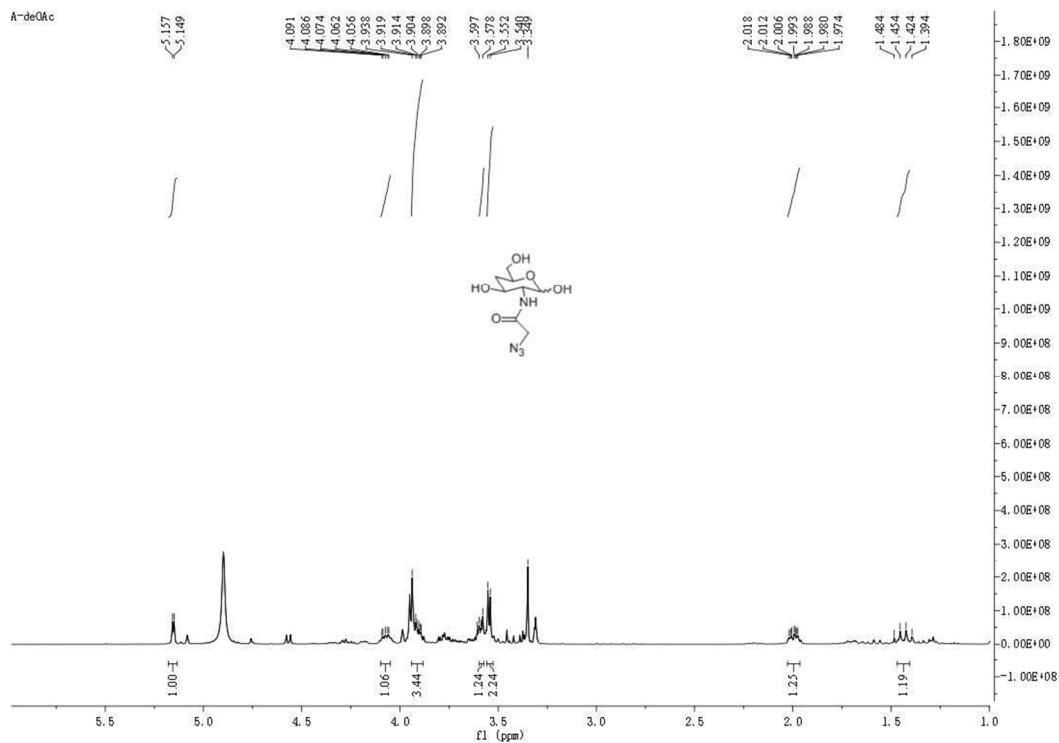
**1-O-(Tert-butyldimethylsilyl)-3,6-Di-O-Acetyl-2-Azidoacetamido-2,4-Dideoxy-D-Glucopyranose (15)**



### 1,3,6-Tri-O-Acetyl-2-Azidoacetamido-2,4-Dideoxy-D-Glucopyranose (5)



## **2-Azidoacetamido-2,4-Dideoxy-D-Glucopyranose (16)**



## V Supplementary Tables

**Table S1.** Enzymatic characterization of human WT-OGA and mutant D285A-OGA.

Type	$K_m$ (mM)	$V_{max}$ ( $\mu\text{mol}/\text{min}\cdot\text{mg}$ )	$k_{cat}$ ( $\text{s}^{-1}$ )	$k_{cat}/K_m$ ( $\text{s}^{-1}\text{M}^{-1}$ )
WT	$1.3 \pm 0.06$	$1.13 \pm 0.05$	$0.79 \pm 0.07$	606
D285A	$2.42 \pm 0.1$	$0.017 \pm 0.006$	$0.01 \pm 0.0006$	5

**Table S2.** Cytotoxicity of 5 in HEK293 cells.

Compound	% Inhibition		
	HEK293	PC3	HeLa
DMSO	-	-	-
5 (25 µM)	-	-	-
5 (50 µM)	-	-	-
5 (100 µM)	0.1 ± 0.01	-	0.1 ± 0.01
5 (150 µM)	6 ± 0.2	5 ± 0.1	7 ± 0.3
5 (200 µM)	15 ± 0.3	13 ± 0.2	15 ± 0.3

**Mean of three independent triplicate experiments.**

**Table S3.** Proteins identified from HEK293 cells treated with **5** ( $\text{Ac}_3\text{dGlcNAz}$ ) indicated the proteins identified in previous reports).

ID	Gene	Description	Location	5 ( $\text{Ac}_3\text{dGlcNAz}$ )								t-test	Reference		
				Spectral counts											
				Exp. 1		Exp. 2		Exp. 3		Sum					
ID	Gene	Description	Location	-	+	-	+	-	+	10	3.171E-02				
A6NEC2	LOC440434	aminopeptidase puromycin sensitive pseudogene	Cytoplasm	0	5	0	3	0	2	10	3.171E-02				
A6NHG4	DDTL	D-dopachrome tautomerase-like	Cytoplasm	0	1	0	1	0	2	4	2.860E-02				
A6NHL2	TUBAL3	tubulin, alpha-like 3	Cytoplasm	0	6	0	2	0	3	11	4.637E-02				
O00154	ACOT7	acyl-CoA thioesterase 7	Cytoplasm	0	1	0	2	0	3	6	3.709E-02	11a			
O00170	AIP	aryl hydrocarbon receptor interacting protein	Cytoplasm	0	1	0	1	0	1	3	0.000E+00				
O00629	KPNA4	karyopherin alpha 4 (importin alpha 3)	Cytoplasm	0	2	0	2	0	1	5	1.887E-02	11a			
O14964	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	Cytoplasm	0	6	0	6	0	6	29	0.000E+00				
O14974	PPP1R12A	protein phosphatase 1, regulatory subunit 12A	Cytoplasm	0	12	0	11	0	18	41	1.232E-02	10,12a,13			
O15164	TRIM24	tripartite motif containing 24	Cytoplasm	0	2	0	3	0	3	8	7.634E-03				
O15294	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase	Cytoplasm	0	4	0	4	0	3	11	4.082E-03	10,13,11a			
O15405	TOX3	TOX high mobility group box family member 3	Cytoplasm	0	2	0	2	0	3	7	9.902E-03				
O43432	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	Cytoplasm	0	4	0	4	0	5	13	2.933E-03				
O43765	SGTA	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	Cytoplasm	0	3	0	4	0	3	10	4.926E-03				
O43896	KIF1C	kinesin family member 1C	Cytoplasm	0	1	0	2	0	1	4	2.860E-02				
O60318	MCM3AP	minichromosome maintenance complex component 3 associated protein	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	11a			
O60502	MGEA5	meningioma expressed antigen 5 (hyaluronidase)	Cytoplasm	0	8	0	7	0	2	17	4.630E-02	13,11a			
O60518	RANBP6	RAN binding protein 6	Cytoplasm	0	1	0	2	0	2	5	1.887E-02				
O75369	FLNB	filamin B, beta	Cytoplasm	0	1	0	1	0	2	4	2.860E-02	11a			
O75390	CS	citrate synthase	Cytoplasm	0	4	0	5	0	3	12	1.010E-02				
O75534	CSDE1	cold shock domain containing E1, RNA-binding	Cytoplasm	0	4	0	1	0	4	9	4.773E-02	10,13			
O75886	STAM2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	Cytoplasm	0	7	0	6	0	11	24	1.729E-02				
O75928	PIAS2	protein inhibitor of activated STAT, 2	Cytoplasm	0	1	0	1	0	2	4	2.860E-02				

O94888	UBXN7	UBX domain protein 7	Cytoplasm	0	1	0	1	0	3	6	6.481E-02	11a
O95429	BAG4	BCL2-associated athanogene 4	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	
O95486	SEC24A	SEC24 homolog A, COPII coat complex component	Cytoplasm	0	11	0	10	0	16	37	1.095E-02	
O95487	SEC24B	SEC24 homolog B, COPII coat complex component	Cytoplasm	0	13	0	11	0	17	41	8.126E-03	11a
O95628	CNOT4	CCR4-NOT transcription complex, subunit 4	Cytoplasm	0	3	0	2	0	3	13	7.634E-03	
O95677	EYA4	EYA transcriptional coactivator and phosphatase 4	Cytoplasm	0	3	0	4	0	2	9	1.755E-02	
O95678	KRT75	keratin 75, type II	Cytoplasm	0	1	0	1	0	2	4	2.860E-02	
P00492	HPRT1	hypoxanthine phosphoribosyltransferase 1	Cytoplasm	0	4	0	4	0	6	14	9.902E-03	10,13
P05412	JUN	jun proto-oncogene	Cytoplasm	0	1	0	1	0	1	5	0.000E+00	13
P05783	KRT18	keratin 18, type I	Cytoplasm	0	6	0	8	0	8	22	4.082E-03	13
P05787	KRT8	keratin 8, type II	Cytoplasm	0	3	0	3	0	3	9	0.000E+00	13
P08243	ASNS	asparagine synthetase (glutamine-hydrolyzing)	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	
P09493	TPM1	tropomyosin 1 (alpha)	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	
P09960	LTA4H	leukotriene A4 hydrolase	Cytoplasm	0	3	0	4	0	3	17	4.926E-03	9,13
P10155	TROVE2	TROVE domain family, member 2	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	11a
P13489	RNH1	ribonuclease/angiogenin inhibitor 1	Cytoplasm	0	1	0	3	0	3	7	3.641E-02	11a
P15313	ATP6V1B1	ATPase, H <sup>+</sup> transporting, lysosomal 56/58kDa, V1 subunit B1	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	
P17980	PSMC3	proteasome 26S subunit, ATPase 3	Cytoplasm	0	1	0	1	0	1	5	0.000E+00	11a
P18085	ARF4	ADP-ribosylation factor 4	Cytoplasm	0	2	0	3	0	4	9	1.755E-02	
P20618	PSMB1	proteasome subunit beta 1	Cytoplasm	0	2	0	1	0	3	6	3.709E-02	
P22061	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase	Cytoplasm	0	2	0	2	0	2	6	0.000E+00	11a
P23381	WARS	tryptophanyl-tRNA synthetase	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	9,13,11a
P23921	RRM1	ribonucleotide reductase M1	Cytoplasm	0	3	0	3	0	1	7	3.641E-02	9,13,11a
P24752	ACAT1	acetyl-CoA acetyltransferase 1	Cytoplasm	0	5	0	4	0	5	14	2.532E-03	11a
P25325	MPST	mercaptopyruvate sulfurtransferase	Cytoplasm	0	2	0	2	0	2	10	0.000E+00	11a
P26583	HMGGB2	high mobility group box 2	Cytoplasm	0	1	0	1	0	1	5	0.000E+00	11a
P26641	EEF1G	eukaryotic translation elongation factor 1 gamma	Cytoplasm	0	7	0	8	0	4	19	1.709E-02	9,13,11a
P27708	CAD	carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase	Cytoplasm	0	3	0	5	0	4	26	1.010E-02	9,13,11a
P28340	POLD1	polymerase (DNA directed), delta 1, catalytic subunit	Cytoplasm	0	1	0	1	0	1	5	0.000E+00	
P30041	PRDX6	peroxiredoxin 6	Cytoplasm	0	8	0	7	0	14	29	2.376E-02	11a
P30046	DDT	D-dopachrome tautomerase	Cytoplasm	0	3	0	3	0	4	10	4.926E-03	

P30048	PRDX3	peroxiredoxin 3	Cytoplasm	0	5	0	2	0	6	13	3.453E-02	11a
P30154	PPP2R1B	protein phosphatase 2, regulatory subunit A, beta	Cytoplasm	0	4	0	4	0	5	13	2.933E-03	
P30520	ADSS	adenylosuccinate synthase	Cytoplasm	0	2	0	1	0	2	7	1.887E-02	11a
P31153	MAT2A	methionine adenosyltransferase II, alpha	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	
P32969	RPL9	ribosomal protein L9	Cytoplasm	0	1	0	2	0	3	6	3.709E-02	10,13
P35080	PFN2	profilin 2	Cytoplasm	0	1	0	1	0	2	4	2.860E-02	11a
P40429	RPL13A	ribosomal protein L13a	Cytoplasm	0	1	0	1	0	2	4	2.860E-02	13
P41250	GARS	glycyl-tRNA synthetase	Cytoplasm	0	4	0	4	0	8	16	2.860E-02	13,11a
P46109	CRKL	v-crk avian sarcoma virus CT10 oncogene homolog-like	Cytoplasm	0	4	0	3	0	6	13	1.951E-02	11a
P46781	RPS9	ribosomal protein S9	Cytoplasm	0	3	0	2	0	3	12	7.634E-03	13
P47755	CAPZA2	capping protein (actin filament) muscle Z-line, alpha 2	Cytoplasm	0	1	0	1	0	1	5	0.000E+00	
P47756	CAPZB	capping protein (actin filament) muscle Z-line, beta	Cytoplasm	0	2	0	3	0	5	10	3.171E-02	12a,13
P48147	PREP	prolyl endopeptidase	Cytoplasm	0	24	0	20	0	20	49	1.942E-03	
P49589	CARS	cysteinyl-tRNA synthetase	Cytoplasm	0	3	0	3	0	1	7	3.641E-02	11a
P49590	HARS2	histidyl-tRNA synthetase 2, mitochondrial	Cytoplasm	0	3	0	3	0	3	9	0.000E+00	
P49591	SARS	seryl-tRNA synthetase	Cytoplasm	0	2	0	2	0	2	6	0.000E+00	
P52907	CAPZA1	capping protein (actin filament) muscle Z-line, alpha 1	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	
P53396	ACLY	ATP citrate lyase	Cytoplasm	0	11	0	9	0	14	34	8.021E-03	13,11a
P58546	MTPN	myotrophin	Cytoplasm	0	1	0	1	0	2	4	2.860E-02	
P60981	DSTN	destrin (actin depolymerizing factor)	Cytoplasm	0	3	0	1	0	3	7	3.641E-02	11a
P61081	UBE2M	ubiquitin-conjugating enzyme E2M	Cytoplasm	0	2	0	1	0	2	5	1.887E-02	11a
P61289	PSME3	proteasome activator subunit 3	Cytoplasm	0	2	0	3	0	2	7	9.902E-03	11a
P62136	PPP1CA	protein phosphatase 1, catalytic subunit, alpha isozyme	Cytoplasm	0	5	0	4	0	4	10	2.933E-03	
P62195	PSMC5	proteasome 26S subunit, ATPase 5	Cytoplasm	0	1	0	2	0	3	6	3.709E-02	
P63208	SKP1	S-phase kinase-associated protein 1	Cytoplasm	0	2	0	1	0	1	4	2.860E-02	11a
P67936	TPM4	tropomyosin 4	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	11a
P68036	UBE2L3	ubiquitin-conjugating enzyme E2L 3	Cytoplasm	0	1	0	1	0	1	5	0.000E+00	
P83916	CBX1	chromobox homolog 1	Cytoplasm	0	1	0	1	0	2	4	2.860E-02	
Q01518	CAP1	CAP, adenylate cyclase-associated protein 1 (yeast)	Cytoplasm	0	2	0	2	0	5	10	4.773E-02	
Q01813	PFKP	phosphofructokinase, platelet	Cytoplasm	0	6	0	4	0	4	14	9.902E-03	
Q02543	RPL18A	ribosomal protein L18a	Cytoplasm	0	4	0	4	0	2	9	1.887E-02	10,13

Q06124	PTPN11	protein tyrosine phosphatase, non-receptor type 11	Cytoplasm	0	1	0	2	0	1	4	2.860E-02	13,11a
Q06210	GFPT1	glutamine-fructose-6-phosphate transaminase 1	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	11a
Q06413	MEF2C	myocyte enhancer factor 2C	Cytoplasm	0	2	0	2	0	1	5	1.887E-02	
Q06787	FMR1	fragile X mental retardation 1	Cytoplasm	0	3	0	2	0	1	6	3.709E-02	11a
Q12756	KIF1A	kinesin family member 1A	Cytoplasm	0	1	0	2	0	1	4	2.860E-02	
Q12904	AIMP1	aminoacyl tRNA synthetase complex-interacting multifunctional protein 1	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	
Q13485	SMAD4	SMAD family member 4	Cytoplasm	0	1	0	1	0	1	9	0.000E+00	
Q13546	RIPK1	receptor (TNFRSF)-interacting serine-threonine kinase 1	Cytoplasm	0	2	0	2	0	1	5	1.887E-02	11a
Q14117	DPYS	Dihydropyrimidinase	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	
Q14152	EIF3A	eukaryotic translation initiation factor 3, subunit A	Cytoplasm	0	1	0	1	0	2	4	2.860E-02	
Q14671	PUM1	pumilio RNA-binding family member 1	Cytoplasm	1	6	1	6	2	11	23	2.079E-02	
Q14687	GSE1	Gse1 coiled-coil protein	cytoplasm	0	1	0	1	0	2	7	2.860E-02	
Q14847	LASP1	LIM and SH3 protein 1	Cytoplasm	0	1	0	1	0	2	4	2.860E-02	
Q15185	PTGES3	prostaglandin E synthase 3 (cytosolic)	Cytoplasm	0	1	0	3	0	2	6	3.709E-02	
Q15645	TRIP13	thyroid hormone receptor interactor 13	Cytoplasm	0	2	0	3	0	1	6	3.709E-02	11a
Q15691	MAPRE1	microtubule-associated protein, RP/EB family, member 1	Cytoplasm	0	2	0	1	0	1	4	2.860E-02	9,13
Q15717	ELAVL1	ELAV like RNA binding protein 1	Cytoplasm	0	3	0	3	0	4	16	4.926E-03	10,13,11a
Q16204	CCDC6	coiled-coil domain containing 6	Cytoplasm	0	1	0	1	0	2	4	2.860E-02	11a
Q16543	CDC37	cell division cycle 37	Cytoplasm	0	6	0	4	0	9	19	2.441E-02	11a
Q16637	SMN1	Survival motor neuron protein	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	11a
Q58FF3	HSP90B2P	heat shock protein 90kDa beta (Grp94), member 2, pseudogene	Cytoplasm	0	1	0	2	0	2	5	1.887E-02	
Q58FG0	HSP90AA5P	heat shock protein 90kDa alpha (cytosolic), class A member 5, pseudogene	Cytoplasm	0	3	0	4	0	4	11	4.082E-03	
Q5T6F2	UBAP2	ubiquitin associated protein 2	Cytoplasm	0	4	0	5	0	5	21	2.532E-03	13,11a
Q659C4	LARP1B	La ribonucleoprotein domain family, member 1B	Cytoplasm	0	2	0	2	0	2	6	0.000E+00	11a
Q66K74	MAP1S	microtubule-associated protein 1S	Cytoplasm	0	1	0	2	0	2	7	1.887E-02	11a
Q6P2E9	EDC4	enhancer of mRNA decapping 4	Cytoplasm	0	5	0	5	0	5	25	0.000E+00	11a
Q6UVJ0	SASS6	SAS-6 centriolar assembly protein	Cytoplasm	0	2	0	1	0	3	6	3.709E-02	11a
Q6ZSR9	AAK1	AP2 associated kinase 1	Cytoplasm	0	2	0	3	0	1	6	3.709E-02	11a
Q7Z3K3	POGZ	pogo transposable element with ZNF domain	Cytoplasm	0	12	0	12	0	9	33	4.082E-03	13,11a
Q7Z4Q2	HEATR3	HEAT repeat containing 3	cytoplasm	0	3	0	3	0	1	7	3.641E-02	11a

Q7Z4W1	DCXR	dicarbonyl/L-xylulose reductase	Cytoplasm	0	1	0	2	0	1	5	2.860E-02	
Q7Z6Z7	HUWE1	HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase	Cytoplasm	0	1	0	1	0	1	13	0.000E+00	11a
Q86YP4	GATAD2A	GATA zinc finger domain containing 2A	Cytoplasm	0	9	0	10	0	20	39	3.293E-02	11a
Q8IWZ3	ANKHD1/AN KHD1- EIF4EBP3	ankyrin repeat and KH domain containing 1	Cytoplasm	0	3	0	4	0	3	36	4.926E-03	11a
Q8IY67	RAVER1	ribonucleoprotein, PTB-binding 1	Cytoplasm	0	1	0	1	0	2	6	2.860E-02	11a
Q8IYB5	SMAP1	small ArfGAP 1	Cytoplasm	0	1	0	1	0	2	7	2.860E-02	
Q8ND56	LSM14A	LSM14A mRNA processing body assembly factor	Cytoplasm	0	1	0	1	0	1	5	0.000E+00	11a
Q8NEM7	SUPT20H	SPT20 homolog, SAGA complex component	cytoplasm	0	1	0	1	0	1	3	0.000E+00	
Q8NHV4	NEDD1	neural precursor cell expressed, developmentally down-regulated 1	Cytoplasm	0	1	0	1	0	2	4	2.860E-02	
Q8TF68	ZNF384	zinc finger protein 384	Cytoplasm	0	2	0	1	0	2	9	1.887E-02	
Q8WU79	SMAP2	small ArfGAP2	Cytoplasm	0	4	0	2	0	2	14	2.860E-02	
Q8WXI9	GATAD2B	GATA zinc finger domain containing 2B	Cytoplasm	0	8	0	10	0	17	35	2.529E-02	13,11a
Q92552	MRPS27	mitochondrial ribosomal protein S27	cytoplasm	0	1	0	1	0	2	4	2.860E-02	
Q92615	LARP4B	La ribonucleoprotein domain family, member 4B	Cytoplasm	0	2	0	1	0	2	10	1.887E-02	11a
Q92879	CELF1	CUGBP, Elav-like family member 1	Cytoplasm	0	2	0	2	0	4	9	2.860E-02	11a
Q92973	TNPO1	transportin 1	Cytoplasm	0	2	0	2	0	3	7	9.902E-03	11b,11a
Q96D71	REPS1	RALBP1 associated Eps domain containing 1	cytoplasm	0	2	0	3	0	2	13	9.902E-03	
Q96F45	ZNF503	zinc finger protein 503	Cytoplasm	0	1	0	1	0	1	5	0.000E+00	11a
Q96J92	WNK4	WNK lysine deficient protein kinase 4	Cytoplasm	0	2	0	1	0	4	7	5.904E-02	
Q96KB5	PBK	PDZ binding kinase	Cytoplasm	0	2	0	1	0	1	4	2.860E-02	11a
Q96PK6	RBM14	RNA binding motif protein 14	Cytoplasm	2	10	1	10	4	20	40	2.428E-02	13,11a
Q96RN5	MED15	mediator complex subunit 15	Cytoplasm	0	4	0	5	0	8	17	2.108E-02	11a
Q96SI9	STRBP	spermatid perinuclear RNA binding protein	Cytoplasm	0	1	0	1	0	1	5	0.000E+00	11a
Q99666	RGPD5	RANBP2-like and GRIP domain-containing protein 5/6	Cytoplasm	0	1	0	1	0	1	5	0.000E+00	
Q99816	TSG101	tumor susceptibility 101	Cytoplasm	0	2	0	1	0	3	6	3.709E-02	11a
Q9BUP0	EFHD1	EF-hand domain family, member D1	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	
Q9BWD1	ACAT2	acetyl-CoA acetyltransferase 2	Cytoplasm	0	1	0	2	0	2	11	1.887E-02	
Q9BXW7	CECR5	cat eye syndrome chromosome region, candidate 5	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	
Q9C0B0	UNK	unkempt family zinc finger	Cytoplasm	0	1	0	2	0	2	10	1.887E-02	11a

Q9H115	NAPB	N-ethylmaleimide-sensitive factor attachment protein, beta	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	
Q9H3U1	UNC45A	unc-45 myosin chaperone A	cytoplasm	0	7	0	6	0	4	17	1.169E-02	11a
Q9H4A3	WNK1	WNK lysine deficient protein kinase 1	Cytoplasm	0	6	0	6	0	8	37	4.926E-03	10,13
Q9H6Z4	RANBP3	RAN binding protein 3	Cytoplasm	0	1	0	1	0	2	5	2.860E-02	
Q9NQ88	TIGAR	TP53 induced glycolysis regulatory phosphatase	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	11a
Q9NQW7	XPNPEP1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	Cytoplasm	0	1	0	1	0	2	4	2.860E-02	
Q9NSK0	KLC4	kinesin light chain 4	Cytoplasm	0	2	0	1	0	1	4	2.860E-02	11a
Q9NUQ3	TXLNG	taxilin gamma	Cytoplasm	0	1	0	1	0	2	6	2.860E-02	11a
Q9NYJ8	TAB2	TGF-beta activated kinase 1/MAP3K7 binding protein 2	Cytoplasm	0	1	0	2	0	3	6	3.709E-02	
Q9UBT2	UBA2	ubiquitin-like modifier activating enzyme 2	Cytoplasm	0	4	0	6	0	2	12	3.709E-02	
Q9UGR2	ZC3H7B	zinc finger CCCH-type containing 7B	Cytoplasm	0	2	0	3	0	1	6	3.709E-02	
Q9UIU6	SIX4	SIX homeobox 4	cytoplasm	0	3	0	4	0	4	11	4.082E-03	11a
Q9UL15	BAG5	BCL2-associated athanogene 5	Cytoplasm	0	4	0	4	0	2	10	1.887E-02	11a
Q9ULV4	CORO1C	coronin, actin binding protein, 1C	Cytoplasm	0	1	0	4	0	2	7	5.904E-02	9,13
Q9UMX0	UBQLN1	ubiquilin 1	Cytoplasm	0	7	0	7	0	8	58	1.030E-03	
Q9Y371	SH3GLB1	SH3-domain GRB2-like endophilin B1	Cytoplasm	0	1	0	1	0	2	6	2.860E-02	11a
Q9Y520	PRRC2C	proline-rich coiled-coil 2C	Cytoplasm	0	8	0	8	0	16	32	2.860E-02	10,13,11a
Q9Y5A9	YTHDF2	YTH N(6)-methyladenosine RNA binding protein 2	Cytoplasm	0	5	0	5	0	11	21	3.641E-02	11a
Q9Y6G9	DYNC1LI1	dynein, cytoplasmic 1, light intermediate chain 1	Cytoplasm	0	1	0	1	0	1	3	0.000E+00	11a
Q9Y6M1	IGF2BP2	insulin-like growth factor 2 mRNA binding protein 2	Cytoplasm	0	2	0	2	0	1	5	1.887E-02	
P51148	RAB5C	RAB5C, member RAS oncogene family	Cytoplasm-Endosome	0	3	0	2	0	1	6	3.709E-02	11a
O00429	DNM1L	dynamin 1-like	Cytoplasm-ER	0	9	0	9	0	10	28	6.365E-04	
O94979	SEC31A	SEC31 homolog A, COPII coat complex component	Cytoplasm-ER	0	14	0	10	0	15	56	6.764E-03	10,13,11a
P53992	SEC24C	SEC24 homolog C, COPII coat complex component	Cytoplasm-ER	2	14	5	14	7	16	44	4.926E-03	10,13
Q9Y6Y8	SEC23IP	SEC23 interacting protein	Cytoplasm-ER	0	13	0	12	0	11	36	1.153E-03	10,13,11a
P55786	NPEPPS	aminopeptidase puromycin sensitive	Cytoplasm-Golgi	0	12	0	8	0	7	27	1.381E-02	11a
Q13492	PICALM	phosphatidylinositol binding clathrin assembly protein	Cytoplasm-Golgi	0	14	0	15	0	16	45	7.391E-04	
Q14677	CLINT1	clathrin interactor 1	Cytoplasm-Golgi	0	11	0	11	0	19	41	1.801E-02	11a
Q16891	IMMT	inner membrane protein, mitochondrial	Cytoplasm-mitochondria	0	2	0	3	0	4	9	1.755E-02	
Q9Y305	ACOT9	acyl-CoA thioesterase 9	Cytoplasm-mitochondria	0	2	0	1	0	1	4	2.860E-02	

P04181	OAT	ornithine aminotransferase	Cytoplasm-mitochondria	0	7	0	6	0	13	26	2.906E-02	11a
P11498	PC	pyruvate carboxylase	Cytoplasm-mitochondria	0	15	0	18	0	22	55	6.006E-03	
P33316	DUT	deoxyuridine triphosphatase	Cytoplasm-mitochondria	0	2	0	2	0	4	8	2.860E-02	11a
P36776	LONP1	Ion peptidase 1, mitochondrial	Cytoplasm-mitochondria	0	2	0	1	0	1	4	2.860E-02	
P42126	ECI1	enoyl-CoA delta isomerase 1	Cytoplasm-mitochondria	0	3	0	2	0	5	10	3.171E-02	
P51649	ALDH5A1	aldehyde dehydrogenase 5 family, member A1	Cytoplasm-mitochondria	0	1	0	1	0	1	5	0.000E+00	
Q00059	TFAM	transcription factor A, mitochondrial	Cytoplasm-mitochondria	0	2	0	1	0	1	4	2.860E-02	
Q5TC12	ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1	Cytoplasm-mitochondria	0	1	0	2	0	1	4	2.860E-02	11a
Q7Z434	MAVS	mitochondrial antiviral signaling protein	Cytoplasm-mitochondria	0	2	0	2	0	3	7	9.902E-03	11a
Q9Y277	VDAC3	voltage-dependent anion channel 3	Cytoplasm-mitochondria	0	4	0	2	0	5	11	2.664E-02	11a
O60641	SNAP91	synaptosomal-associated protein, 91kDa	Cytoplasm-Membrane	0	1	0	2	0	3	6	3.709E-02	12a
P07951	TPM2	tropomyosin 2 (beta)	Cytoplasm-Membrane	0	1	0	1	0	1	3	0.000E+00	
P56134	ATP5J2	ATP synthase, H <sup>+</sup> transporting, mitochondrial Fo complex, subunit F2	Cytoplasm-Membrane	0	2	0	2	0	2	6	0.000E+00	
P78417	GSTO1	glutathione S-transferase omega 1	Cytoplasm-Membrane	0	1	0	1	0	2	6	2.860E-02	13
P84085	ARF5	ADP-ribosylation factor 5	Cytoplasm-Membrane	0	3	0	4	0	7	14	3.019E-02	
Q00005	PPP2R2B	protein phosphatase 2, regulatory subunit B, beta	Cytoplasm-Membrane	0	2	0	2	0	1	5	1.887E-02	
Q13283	G3BP1	GTPase activating protein (SH3 domain) binding protein 1	Cytoplasm-Membrane	0	1	0	2	0	2	5	1.887E-02	10,13
Q14444	CAPRIN1	cell cycle associated protein 1	Cytoplasm-Membrane	1	8	1	10	2	12	30	5.098E-03	10,13,11a
Q15758	SLC1A5	solute carrier family 1 (neutral amino acid transporter), member 5	Cytoplasm-Membrane	0	1	0	2	0	2	7	1.887E-02	
Q9UM54	MYO6	myosin VI	Cytoplasm-Membrane	0	3	0	3	0	1	7	3.641E-02	
P14174	MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	Extracellular Space	0	2	0	1	0	2	11	1.887E-02	11a

Q15437	SEC23B	Sec23 homolog B, COPII coat complex component	Extracellular Space	0	1	0	2	0	1	4	2.860E-02	10
Q96NM4	TOX2	TOX high mobility group box family member 2	Extracellular Space	0	1	0	1	0	2	4	2.860E-02	
A5YKK6	CNOT1	CCR4-NOT transcription complex, subunit 1	Nucleus	0	2	0	2	0	1	6	1.887E-02	11a
A6NDG6	PGP	phosphoglycolate phosphatase	Nucleus	0	2	0	2	0	2	6	0.000E+00	11a
A6NHR9	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	Nucleus	0	2	0	1	0	1	4	2.860E-02	11a
A6NMV6	ANXA2P2	annexin A2 pseudogene 2	Nucleus	0	3	0	4	0	1	8	4.709E-02	
A8CG34	POM121/PO M121C	POM121 transmembrane nucleoporin	Nucleus	0	3	0	2	0	5	10	3.171E-02	
A8MYZ6	FOXO6	forkhead box O6	Nucleus	0	1	0	1	0	1	3	0.000E+00	
O00217	NDUFS8	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)	Nucleus	0	1	0	1	0	1	3	0.000E+00	
O00268	TAF4	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	Nucleus	0	5	0	8	0	8	21	9.902E-03	13
O00303	EIF3F	eukaryotic translation initiation factor 3, subunit F	Nucleus	0	3	0	1	0	3	7	3.641E-02	
O14497	ARID1A	AT rich interactive domain 1A (SWI-like)	Nucleus	0	4	0	4	0	5	24	2.933E-03	10,13,11a
O14715	RGPD4 (includes others)	RANBP2-like and GRIP domain containing 5	Nucleus	0	1	0	1	0	1	5	0.000E+00	
O14770	MEIS2	Meis homeobox 2	Nucleus	0	2	0	2	0	1	5	1.887E-02	
O14776	TCERG1	transcription elongation regulator 1	Nucleus	0	5	0	5	0	5	29	0.000E+00	10,13,11a
O14979	HNRNPDL	heterogeneous nuclear ribonucleoprotein D-like	Nucleus	0	4	0	3	0	4	11	4.082E-03	10,13
O14980	XPO1	exportin 1	Nucleus	0	7	0	8	0	6	21	3.367E-03	11b,11a
O14983	ATP2A1	ATPase, Ca++ transporting, cardiac muscle, fast twitch 1	Nucleus	0	2	0	2	0	1	5	1.887E-02	
O15047	SETD1A	SET domain containing 1A	Nucleus	0	2	0	2	0	2	10	0.000E+00	10,13,11a
O15504	NUPL2	nucleoporin like 2	Nucleus	0	1	0	1	0	1	3	0.000E+00	
O43143	DHX15	DEAH (Asp-Glu-Ala-His) box helicase 15	Nucleus	0	11	0	9	0	6	26	1.349E-02	13,11a
O43524	FOXO3	forkhead box O3	Nucleus	0	3	0	4	0	3	10	4.926E-03	11a
O43670	ZNF207	zinc finger protein 207	Nucleus	0	3	0	4	0	7	14	3.019E-02	10,13
O43823	AKAP8	A kinase (PRKA) anchor protein 8	Nucleus	0	3	0	2	0	3	8	7.634E-03	
O60333	KIF1B	kinesin family member 1B	Nucleus	0	1	0	2	0	1	4	2.860E-02	
O60664	PLIN3	perilipin 3	Nucleus	0	1	0	1	0	1	3	0.000E+00	11a
O75179	ANKRD17	ankyrin repeat domain 17	Nucleus	0	3	0	5	0	4	29	1.010E-02	13,11a

O75376	NCOR1	nuclear receptor corepressor 1	Nucleus	0	4	0	7	0	7	18	1.334E-02	13,11a
O75400	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A	Nucleus	0	1	0	2	0	2	6	1.887E-02	11a
O75643	SNRNP200	small nuclear ribonucleoprotein 200kDa (U5)	Nucleus	0	5	0	3	0	3	10	1.575E-02	11a
O75694	NUP155	nucleoporin 155kDa	Nucleus	0	2	0	3	0	3	8	7.634E-03	11a
O75909	CCNK	cyclin K	Nucleus	0	2	0	2	0	3	7	9.902E-03	13
O75925	PIAS1	protein inhibitor of activated STAT, 1	Nucleus	0	3	0	4	0	2	9	1.755E-02	
O94842	TOX4	TOX high mobility group box family member 4	Nucleus	0	5	0	4	0	6	15	6.536E-03	
O94900	TOX	thymocyte selection-associated high mobility group box	Nucleus	0	1	0	1	0	1	3	0.000E+00	
O95104	SCAF4	SR-related CTD-associated factor 4	Nucleus	0	2	0	1	0	2	9	1.887E-02	
O95336	PGLS	6-phosphogluconolactonase	Nucleus	0	1	0	2	0	4	7	5.904E-02	11a
P00491	PNP	purine nucleoside phosphorylase	Nucleus	0	8	0	5	0	10	23	1.705E-02	11a
P02545	LMNA	lamin A/C	Nucleus	0	2	0	1	0	2	6	1.887E-02	13,11a
P04150	NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	Nucleus	0	1	0	2	0	1	4	2.860E-02	
P04632	CAPNS1	calpain, small subunit 1	Nucleus	0	1	0	1	0	1	3	0.000E+00	11a
P05198	EIF2S1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	Nucleus	0	2	0	1	0	3	6	3.709E-02	
P05455	SSB	Sjogren syndrome antigen B (autoantigen La)	Nucleus	0	4	0	4	0	6	14	9.902E-03	
P07355	ANXA2	annexin A2	Nucleus	0	3	0	4	0	1	8	4.709E-02	9,13,11a
P08047	SP1	Sp1 transcription factor	Nucleus	0	5	0	5	0	6	17	1.942E-03	10,13
P09086	POU2F2	POU class 2 homeobox 2	Nucleus	0	2	0	2	0	3	11	9.902E-03	
P10515	DLAT	dihydrolipoamide S-acetyltransferase	Nucleus	0	2	0	1	0	2	5	1.887E-02	
P11388	TOP2A	topoisomerase (DNA) II alpha	Nucleus	0	10	0	7	0	5	22	1.854E-02	
P13010	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)	Nucleus	0	14	0	13	0	13	40	3.122E-04	13,11a
P14859	POU2F1	POU class 2 homeobox 1	Nucleus	0	5	0	5	0	6	28	1.942E-03	10,13,11a
P17812	CTPS1	CTP synthase 1	Nucleus	0	7	0	4	0	2	13	4.822E-02	11a
P18124	RPL7	ribosomal protein L7	Nucleus	0	2	0	2	0	2	6	0.000E+00	
P19525	EIF2AK2	eukaryotic translation initiation factor 2-alpha kinase 2	Nucleus	0	1	0	1	0	2	6	2.860E-02	11a
P20265	POU3F2	POU class 3 homeobox 2	Nucleus	0	1	0	1	0	1	3	0.000E+00	
P21281	ATP6V1B2	ATPase, 2	Nucleus	0	1	0	1	0	1	5	0.000E+00	
P22234	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	Nucleus	0	7	0	5	0	7	19	5.450E-03	10,13,11a

P22681	CBL	Cbl proto-oncogene, E3 ubiquitin protein ligase	Nucleus	0	6	0	5	0	5	12	1.942E-03	11a
P23246	SFPQ	splicing factor proline/glutamine-rich	Nucleus	0	1	0	1	0	2	6	2.860E-02	10,13,11a
P23511	NFYA	nuclear transcription factor Y, alpha	Nucleus	0	1	0	1	0	2	10	2.860E-02	11a
P24539	ATP5F1	ATP synthase, H <sup>+</sup> transporting, mitochondrial Fo complex, subunit B1	Nucleus	0	1	0	1	0	1	3	0.000E+00	
P26368	U2AF2	U2 small nuclear RNA auxiliary factor 2	Nucleus	0	4	0	2	0	3	19	1.755E-02	
P26599	PTBP1	polypyrimidine tract binding protein 1	Nucleus	0	2	0	2	0	1	6	1.887E-02	10,13,11a
P27540	ARNT	aryl hydrocarbon receptor nuclear translocator	Nucleus	0	2	0	2	0	3	7	9.902E-03	
P27635	RPL10	ribosomal protein L10	Nucleus	0	1	0	2	0	2	5	1.887E-02	10,13
P27816	MAP4	microtubule-associated protein 4	Nucleus	0	2	0	2	0	3	7	9.902E-03	10,13,11a
P28066	PSMAS5	proteasome subunit alpha 5	Nucleus	0	2	0	1	0	1	4	2.860E-02	13,11a
P29558	RBMS1	RNA binding motif, single stranded interacting protein 1	Nucleus	0	1	0	1	0	2	4	2.860E-02	
P30044	PRDX5	peroxiredoxin 5	Nucleus	0	2	0	2	0	1	5	1.887E-02	11a
P33991	MCM4	minichromosome maintenance complex component 4	Nucleus	0	6	0	5	0	2	13	3.453E-02	
P33992	MCM5	minichromosome maintenance complex component 5	Nucleus	0	4	0	8	0	8	13	1.887E-02	
P35609	ACTN2	actinin, alpha 2	Nucleus	0	2	0	4	0	2	8	2.860E-02	
P35637	FUS	FUS RNA binding protein	Nucleus	0	5	0	4	0	5	24	2.532E-03	
P35658	NUP214	nucleoporin 214kDa	Nucleus	0	19	0	13	0	15	74	6.220E-03	10,11b,13, 11a
P35659	DEK	DEK proto-oncogene	Nucleus	0	3	0	4	0	5	12	1.010E-02	11a
P36551	CPOX	coproporphyrinogen oxidase	Nucleus	0	2	0	1	0	1	4	2.860E-02	11a
P36873	PPP1CC	protein phosphatase 1, catalytic subunit, gamma isozyme	Nucleus	0	4	0	4	0	2	9	1.887E-02	
P37198	NUP62	nucleoporin 62kDa	Nucleus	1	12	1	10	2	18	40	1.440E-02	10,13,11a
P38432	COIL	coilin	Nucleus	0	1	0	1	0	2	6	2.860E-02	11a
P38919	EIF4A3	eukaryotic translation initiation factor 4A3	Nucleus	0	3	0	2	0	1	6	3.709E-02	
P40938	RFC3	replication factor C (activator 1) 3, 38kDa	Nucleus	0	2	0	1	0	1	4	2.860E-02	11a
P41219	PRPH	peripherin	Nucleus	0	2	0	3	0	2	7	9.902E-03	
P42166	TMPO	thymopoietin	Nucleus	0	6	0	8	0	13	27	2.478E-02	11a
P42167	TMPO	thymopoietin	Nucleus	0	5	0	4	0	4	13	2.933E-03	
P43487	RANBP1	RAN binding protein 1	Nucleus	0	2	0	2	0	4	8	2.860E-02	10,13,11a
P46776	RPL27A	ribosomal protein L27a	Nucleus	0	1	0	2	0	3	6	3.709E-02	10,13

P46940	IQGAP1	IQ motif containing GTPase activating protein 1	Nucleus	0	3	0	3	0	2	8	7.634E-03	9,13,11a
P49137	MAPKAPK2	mitogen-activated protein kinase-activated protein kinase 2	Nucleus	0	1	0	1	0	2	4	2.860E-02	
P49458	SRP9	signal recognition particle 9kDa	Nucleus	0	1	0	1	0	2	4	2.860E-02	10,13,11a
P49750	YLPM1	YLP motif containing 1	Nucleus	0	2	0	2	0	3	14	9.902E-03	10,13,11a
P49756	RBM25	RNA binding motif protein 25	Nucleus	0	6	0	6	0	4	16	7.634E-03	11a
P49790	NUP153	nucleoporin 153kDa	Nucleus	0	15	0	17	0	16	73	6.498E-04	10,11b,13, 11a
P49792	RANBP2	RAN binding protein 2	Nucleus	0	10	0	11	0	21	42	2.877E-02	11b,13,11a
P49848	TAF6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa	Nucleus	0	3	0	2	0	3	8	7.634E-03	
P49916	LIG3	ligase III, DNA, ATP-dependent	Nucleus	0	2	0	3	0	3	8	7.634E-03	
P50914	RPL14	ribosomal protein L14	Nucleus	0	1	0	1	0	1	3	0.000E+00	
P51532	SMARCA4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	Nucleus	0	2	0	3	0	2	7	9.902E-03	
P51610	HCFC1	host cell factor C1	Nucleus	0	24	0	27	0	46	97	2.125E-02	13
P52594	AGFG1	ArfGAP with FG repeats 1	Nucleus	0	5	0	4	0	5	29	2.532E-03	10,13,11a
P52597	HNRNPF	heterogeneous nuclear ribonucleoprotein F	Nucleus	0	1	0	1	0	2	6	2.860E-02	11a
P52655	GTF2A1	general transcription factor IIA, 1, 19/37kDa	Nucleus	0	1	0	1	0	2	4	2.860E-02	11a
P52732	KIF11	kinesin family member 11	Nucleus	0	3	0	4	0	2	9	1.755E-02	11a
P52948	NUP98	nucleoporin 98kDa	Nucleus	0	16	0	14	0	17	47	1.577E-03	10,13,11a
P53007	SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	Nucleus	0	4	0	3	0	1	8	4.709E-02	
P54727	RAD23B	RAD23 homolog B, nucleotide excision repair protein	Nucleus	0	13	0	9	0	24	46	3.796E-02	12a,11a
P55010	EIF5	eukaryotic translation initiation factor 5	Nucleus	0	1	0	3	0	4	8	4.709E-02	
P55060	CSE1L	CSE1 chromosome segregation 1-like (yeast)	Nucleus	0	21	0	22	0	20	48	3.775E-04	13,11a
P55265	ADAR	adenosine deaminase, RNA-specific	Nucleus	0	5	0	4	0	3	12	1.010E-02	
P56545	CTBP2	C-terminal binding protein 2	Nucleus	0	2	0	1	0	2	7	1.887E-02	
P60953	CDC42	cell division cycle 42	Nucleus	0	1	0	2	0	2	7	1.887E-02	

P61586	RHOA	ras homolog family member A	Nucleus	0	1	0	1	0	2	4	2.860E-02	
P62266	RPS23	ribosomal protein S23	Nucleus	0	1	0	1	0	1	3	0.000E+00	9,13
P62318	SNRPD3	small nuclear ribonucleoprotein D3 polypeptide 18kDa	Nucleus	0	1	0	2	0	2	7	1.887E-02	10,13
P62333	PSMC6	proteasome 26S subunit, ATPase 6	Nucleus	0	3	0	4	0	5	12	1.010E-02	
P62714	PPP2CB	protein phosphatase 2, catalytic subunit, beta isozyme	Nucleus	0	3	0	1	0	2	6	3.709E-02	
P68400	CSNK2A1	casein kinase 2, alpha 1 polypeptide	Nucleus	0	3	0	4	0	7	14	3.019E-02	
P68431	HIST1H3A	Histone H3.1	Nucleus	0	2	0	1	0	2	7	1.887E-02	13
P78364	PHC1	polyhomeotic homolog 1 (Drosophila)	Nucleus	0	2	0	2	0	2	6	0.000E+00	
P78406	RAE1	ribonucleic acid export 1	Nucleus	0	1	0	2	0	2	8	1.887E-02	10,13,11a
P81877	SSBP2	single-stranded DNA binding protein 2	Nucleus	0	1	0	1	0	2	4	2.860E-02	
P84243	H3F3A	Histone H3.3	Nucleus	0	2	0	1	0	2	7	1.887E-02	
P85037	FOXK1	forkhead box K1	Nucleus	0	3	0	3	0	4	15	4.926E-03	11a
P98082	DAB2	Dab, mitogen-responsive phosphoprotein, homolog 2 (Drosophila)	Nucleus	0	1	0	1	0	1	3	0.000E+00	
Q01085	TIAL1	TIA1 cytotoxic granule-associated RNA binding protein-like 1	Nucleus	0	1	0	1	0	2	7	2.860E-02	
Q01167	FOXK2	forkhead box K2	Nucleus	0	2	0	1	0	2	7	1.887E-02	11a
Q01844	EWSR1	EWS RNA-binding protein 1	Nucleus	0	2	0	2	0	1	6	1.887E-02	13,11a
Q02078	MEF2A	myocyte enhancer factor 2A	Nucleus	0	2	0	3	0	2	7	9.902E-03	
Q02880	TOP2B	topoisomerase (DNA) II beta	Nucleus	0	5	0	7	0	5	13	6.780E-03	
Q03164	KMT2A	lysine (K)-specific methyltransferase 2A	Nucleus	0	2	0	2	0	3	7	9.902E-03	10,13,11a
Q04206	RELA	v-rel avian reticuloendotheliosis viral oncogene homolog A	Nucleus	0	2	0	1	0	2	5	1.887E-02	13
Q04637	EIF4G1	eukaryotic translation initiation factor 4 gamma, 1	Nucleus	0	2	0	1	0	2	6	1.887E-02	9,13
Q04726	TLE3	transducin-like enhancer of split 3	Nucleus	0	1	0	1	0	1	11	0.000E+00	
Q04864	REL	v-rel avian reticuloendotheliosis viral oncogene homolog	Nucleus	0	2	0	1	0	1	4	2.860E-02	
Q06323	PSME1	proteasome activator subunit 1	Nucleus	0	2	0	3	0	2	7	9.902E-03	11a
Q07021	C1QBP	complement component 1, q subcomponent binding protein	Nucleus	0	3	0	2	0	5	10	3.171E-02	
Q07955	SRSF1	serine/arginine-rich splicing factor 1	Nucleus	0	2	0	3	0	1	6	3.709E-02	11a
Q08J23	NSUN2	NOP2/Sun RNA methyltransferase family, member 2	Nucleus	0	2	0	3	0	6	11	4.637E-02	11a
Q09161	NCBP1	nuclear cap binding protein subunit 1, 80kDa	Nucleus	0	1	0	1	0	1	3	0.000E+00	11a
Q09472	EP300	E1A binding protein p300	Nucleus	0	2	0	4	0	3	16	1.755E-02	
Q12778	FOXO1	forkhead box O1	Nucleus	0	4	0	3	0	1	8	4.709E-02	13,11a
Q12874	SF3A3	splicing factor 3a, subunit 3, 60kDa	Nucleus	0	2	0	2	0	4	8	2.860E-02	11a

Q12948	FOXC1	forkhead box C1	Nucleus	0	5	0	5	0	5	15	0.000E+00	
Q13111	CHAF1A	chromatin assembly factor 1, subunit A (p150)	Nucleus	0	1	0	1	0	1	3	0.000E+00	11a
Q13185	CBX3	chromobox homolog 3	Nucleus	0	3	0	4	0	6	13	1.951E-02	
Q13330	MTA1	metastasis associated 1	Nucleus	0	1	0	1	0	2	4	2.860E-02	
Q13618	CUL3	cullin 3	Nucleus	0	1	0	1	0	1	3	0.000E+00	
Q13619	CUL4A	cullin 4A	Nucleus	0	4	0	4	0	2	9	1.887E-02	
Q13620	CUL4B	cullin 4B	Nucleus	0	10	0	12	0	6	28	1.695E-02	
Q14008	CKAP5	cytoskeleton associated protein 5	Nucleus	0	4	0	4	0	3	11	4.082E-03	11a
Q14157	UBAP2L	ubiquitin associated protein 2-like	Nucleus	0	15	0	12	0	13	75	2.173E-03	10,12a,13,1 1a
Q14194	CRMP1	collapsin response mediator protein 1	Nucleus	0	2	0	2	0	3	7	9.902E-03	
Q14657	LAGE3	L antigen family, member 3	Nucleus	0	3	0	3	0	1	7	3.641E-02	
Q14686	NCOA6	nuclear receptor coactivator 6	Nucleus	0	2	0	1	0	3	6	3.709E-02	11a
Q14739	LBRY	lamin B receptor	Nucleus	0	2	0	1	0	1	4	2.860E-02	
Q14814	MEF2D	myocyte enhancer factor 2D	Nucleus	0	2	0	2	0	1	5	1.887E-02	13
Q15003	NCAPH	non-SMC condensin I complex, subunit H	Nucleus	0	5	0	6	0	2	13	3.453E-02	11a
Q15021	NCAPD2	non-SMC condensin I complex, subunit D2	Nucleus	0	2	0	2	0	1	5	1.887E-02	
Q15102	PAFAH1B3	platelet-activating factor acetylhydrolase 1b, catalytic subunit 3 (29kDa)	Nucleus	0	1	0	1	0	1	3	0.000E+00	
Q15424	SAFB	scaffold attachment factor B	Nucleus	0	2	0	1	0	2	5	1.887E-02	11a
Q15428	SF3A2	splicing factor 3a, subunit 2, 66kDa	Nucleus	0	3	0	2	0	6	11	4.637E-02	
Q15459	SF3A1	splicing factor 3a, subunit 1, 120kDa	Nucleus	0	17	0	20	0	23	84	3.708E-03	11a
Q15532	SS18	synovial sarcoma translocation, chromosome 18	Nucleus	0	1	0	2	0	1	4	2.860E-02	
Q15596	NCOA2	nuclear receptor coactivator 2	Nucleus	0	3	0	3	0	5	11	1.575E-02	11a
Q15637	SF1	splicing factor 1	Nucleus	0	1	0	2	0	2	6	1.887E-02	10,13,11a
Q15648	MED1	mediator complex subunit 1	Nucleus	0	3	0	5	0	7	15	2.471E-02	
Q15652	JMJD1C	jumonji domain containing 1C	Nucleus	0	1	0	2	0	2	5	1.887E-02	
Q15750	TAB1	TGF-beta activated kinase 1/MAP3K7 binding protein 1	Nucleus	0	4	0	4	0	5	18	2.933E-03	
Q15788	NCOA1	nuclear receptor coactivator 1	Nucleus	0	3	0	3	0	2	8	7.634E-03	
Q15813	TBCE	tubulin folding cofactor E	Nucleus	0	1	0	2	0	2	5	1.887E-02	11a
Q15942	ZYX	zyxin	Nucleus	0	6	0	4	0	5	27	6.536E-03	
Q16181	SEPT7	septin 7	Nucleus	0	1	0	3	0	3	7	3.641E-02	12a

Q16576	RBBP7	retinoblastoma binding protein 7	Nucleus	0	6	0	6	0	5	17	1.721E-03
Q16594	TAF9	TAF9 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 32kDa	Nucleus	0	2	0	2	0	2	6	0.000E+00
Q16656	NRF1	nuclear respiratory factor 1	Nucleus	0	4	0	2	0	4	10	1.887E-02
Q16695	HIST3H3	histone cluster 3, H3	Nucleus	0	2	0	1	0	2	7	1.887E-02
Q53ET0	CRTC2	CREB regulated transcription coactivator 2	Nucleus	0	1	0	1	0	2	5	2.860E-02
Q5T8P6	RBM26	RNA binding motif protein 26	Nucleus	0	8	0	11	0	18	37	2.657E-02
Q5VT52	RPRD2	regulation of nuclear pre-mRNA domain containing 2	Nucleus	0	1	0	2	0	2	20	1.887E-02
Q5VZL5	ZMYM4	zinc finger, MYM-type 4	Nucleus	0	3	0	2	0	1	6	3.709E-02
Q66LE6	PPP2R2D	protein phosphatase 2, regulatory subunit B, delta	Nucleus	0	2	0	2	0	1	5	1.887E-02
Q6NVV1	RPL13AP3	ribosomal protein L13a pseudogene 3	Nucleus	0	1	0	1	0	2	4	2.860E-02
Q6NXT2	H3F3C	H3 histone, family 3C	Nucleus	0	2	0	1	0	2	7	1.887E-02
Q6P3W7	SCYL2	SCY1-like, kinase-like 2	Nucleus	0	6	0	6	0	10	22	1.575E-02
Q6PJ7	ZC3H14	zinc finger CCCH-type containing 14	Nucleus	0	2	0	3	0	3	16	7.634E-03
Q6UN15	FIP1L1	factor interacting with PAPOLA and CPSF1	Nucleus	0	2	0	3	0	6	11	4.637E-02
Q6UU9	CRTC1	CREB regulated transcription coactivator 1	Nucleus	0	3	0	3	0	3	9	0.000E+00
Q6VMQ6	ATF7IP	activating transcription factor 7 interacting protein	Nucleus	0	3	0	5	0	8	16	3.343E-02
Q6W2J9	BCOR	BCL6 corepressor	Nucleus	0	2	0	2	0	2	6	0.000E+00
Q6XE24	RBMS3	RNA binding motif, single stranded interacting protein 3	Nucleus	0	1	0	1	0	2	4	2.860E-02
Q6ZRS2	SRCAP	Snf2-related CREBBP activator protein	Nucleus	0	1	0	2	0	2	7	1.887E-02
Q71DI3	HIST2H3A	Histone H3.2	Nucleus	0	2	0	1	0	2	7	1.887E-02
Q7LBC6	KDM3B	lysine (K)-specific demethylase 3B	Nucleus	0	8	0	7	0	8	41	9.425E-04
Q7Z3B4	NUP54	nucleoporin 54kDa	Nucleus	0	12	0	10	0	25	47	3.975E-02
Q7Z417	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	Nucleus	0	6	0	5	0	8	19	9.422E-03
Q7Z589	C11orf30	chromosome 11 open reading frame 30	Nucleus	0	1	0	3	0	4	8	4.709E-02
Q7Z5J4	RAI1	retinoic acid induced 1	Nucleus	1	3	1	3	1	3	9	0.000E+00
Q7Z5L9	IRF2BP2	interferon regulatory factor 2 binding protein 2	Nucleus	0	1	0	1	0	2	6	2.860E-02
Q7Z739	YTHDF3	YTH N(6)-methyladenosine RNA binding protein 3	Nucleus	0	9	0	9	0	18	36	2.860E-02
Q7Z7K6	CENPV	centromere protein V	Nucleus	0	1	0	1	0	1	3	0.000E+00
Q86SX6	GLRX5	glutaredoxin 5	Nucleus	0	1	0	1	0	2	4	2.860E-02
Q86UK7	ZNF598	zinc finger protein 598	Nucleus	0	2	0	2	0	3	11	9.902E-03

Q86X55	CARM1	coactivator-associated arginine methyltransferase 1	Nucleus	0	2	0	3	0	3	15	7.634E-03	10,12a,13,1 1a
Q86XP3	DDX42	DEAD (Asp-Glu-Ala-Asp) box helicase 42	Nucleus	0	3	0	1	0	4	8	4.709E-02	
Q8IU81	IRF2BP1	interferon regulatory factor 2 binding protein 1	Nucleus	0	2	0	1	0	2	8	1.887E-02	
Q8IVH2	FOXP4	forkhead box P4	Nucleus	0	2	0	3	0	1	6	3.709E-02	
Q8IVW6	ARID3B	AT rich interactive domain 3B (BRIGHT-like)	Nucleus	0	3	0	2	0	4	9	1.755E-02	11a
Q8IX12	CCAR1	cell division cycle and apoptosis regulator 1	Nucleus	0	9	0	13	0	12	34	5.530E-03	10,13,11a
Q8N3X1	FNBP4	formin binding protein 4	Nucleus	0	5	0	3	0	5	13	1.143E-02	
Q8N684	CPSF7	cleavage and polyadenylation specific factor 7, 59kDa	Nucleus	0	2	0	3	0	4	9	1.755E-02	
Q8NCW5	APOA1BP	apolipoprotein A-I binding protein	Nucleus	0	1	0	1	0	2	7	2.860E-02	
Q8ND24	RNF214	ring finger protein 214	Nucleus	0	1	0	2	0	2	5	1.887E-02	11a
Q8NDX5	PHC3	polyhomeotic homolog 3 (Drosophila)	Nucleus	0	2	0	2	0	3	7	9.902E-03	10,13
Q8NEV1	CSNK2A1	casein kinase 2, alpha 1 polypeptide	Nucleus	0	2	0	3	0	4	9	1.755E-02	
Q8NEZ2	VPS37A	vacuolar protein sorting 37 homolog A (S. cerevisiae)	Nucleus	0	2	0	2	0	3	13	9.902E-03	
Q8NF64	ZMIZ2	zinc finger, MIZ-type containing 2	Nucleus	0	1	0	1	0	2	4	2.860E-02	
Q8NI36	WDR36	WD repeat domain 36	Nucleus	0	1	0	1	0	1	3	0.000E+00	
Q8TAQ2	SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	Nucleus	0	4	0	4	0	5	22	2.933E-03	
Q8TB72	PUM2	pumilio RNA-binding family member 2	Nucleus	0	1	0	2	0	2	6	1.887E-02	
Q8TEQ6	GEMIN5	gem (nuclear organelle) associated protein 5	Nucleus	0	2	0	2	0	4	8	2.860E-02	
Q8WU90	ZC3H15	zinc finger CCCH-type containing 15	Nucleus	0	1	0	1	0	1	3	0.000E+00	11a
Q8WWK9	CKAP2	cytoskeleton associated protein 2	Nucleus	0	2	0	2	0	2	6	0.000E+00	
Q8WWM7	ATXN2L	ataxin 2-like	Nucleus	0	9	0	10	0	23	42	4.498E-02	13,11a
Q8WXF0	SRSF12	serine/arginine-rich splicing factor 12	Nucleus	0	1	0	2	0	1	4	2.860E-02	11a
Q92599	SEPT8	septin 8	Nucleus	0	1	0	1	0	1	3	0.000E+00	
Q92688	ANP32B	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	Nucleus	0	1	0	1	0	1	3	0.000E+00	

Q92734	TFG	TRK-fused gene	Nucleus	0	5	0	7	0	14	26	4.323E-02	11a
Q92783	STAM	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	Nucleus	0	9	0	8	0	14	31	1.539E-02	
Q92793	CREBBP	CREB binding protein	Nucleus	0	3	0	4	0	4	19	4.082E-03	13
Q92804	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	Nucleus	0	2	0	1	0	3	6	3.709E-02	11a
Q92922	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	Nucleus	0	3	0	3	0	5	14	1.575E-02	
Q93052	LPP	LIM domain containing preferred translocation partner in lipoma	Nucleus	0	5	0	4	0	7	16	1.314E-02	11a
Q96BD5	PHF21A	PHD finger protein 21A	Nucleus	0	1	0	1	0	1	3	0.000E+00	
Q96C19	EFHD2	EF-hand domain family, member D2	Nucleus	0	1	0	1	0	1	3	0.000E+00	11a
Q96CN7	ISOC1	isochorismatase domain containing 1	Nucleus	0	1	0	1	0	1	3	0.000E+00	
Q96HA1	POM121/PO M121C	POM121 transmembrane nucleoporin	Nucleus	0	3	0	2	0	5	10	3.171E-02	13
Q96HC4	PDLIM5	PDZ and LIM domain 5	Nucleus	0	5	0	4	0	6	20	6.536E-03	11a
Q96I24	FUBP3	far upstream element (FUSE) binding protein 3	Nucleus	0	8	0	8	0	17	33	3.350E-02	11a
Q96JM3	CHAMP1	chromosome alignment maintaining phosphoprotein 1	Nucleus	0	2	0	1	0	3	6	3.709E-02	11a
Q96KR1	ZFR	zinc finger RNA binding protein	Nucleus	0	2	0	2	0	1	6	1.887E-02	10,13
Q96RK0	CIC	capicua transcriptional repressor	Nucleus	0	1	0	1	0	1	5	0.000E+00	10,13
Q96ST3	SIN3A	SIN3 transcription regulator family member A	Nucleus	0	5	0	8	0	5	18	1.334E-02	11a
Q96T58	SPEN	spen family transcriptional repressor	Nucleus	0	4	0	3	0	4	23	4.082E-03	13,11a
Q99497	PARK7	parkinson protein 7	Nucleus	0	1	0	1	0	1	3	0.000E+00	11a
Q99504	EYA3	EYA transcriptional coactivator and phosphatase 3	Nucleus	0	5	0	7	0	2	14	4.240E-02	11a
Q99700	ATXN2	ataxin 2	Nucleus	0	5	0	7	0	5	30	6.780E-03	10,13
Q99829	CPNE1	copine I	Nucleus	0	6	0	6	0	2	14	3.641E-02	
Q99856	ARID3A	AT rich interactive domain 3A (BRIGHT-like)	Nucleus	0	3	0	3	0	4	10	4.926E-03	
Q99873	PRMT1	protein arginine methyltransferase 1	Nucleus	0	5	0	3	0	2	10	3.171E-02	9,11a
Q99958	FOXC2	forkhead box C2	Nucleus	0	4	0	5	0	3	12	1.010E-02	
Q99961	SH3GL1	SH3-domain GRB2-like 1	Nucleus	0	2	0	1	0	1	4	2.860E-02	
Q9BPX3	NCAPG	non-SMC condensin I complex, subunit G	Nucleus	0	2	0	4	0	2	7	2.860E-02	11a
Q9BQ04	RBM4B	RNA binding motif protein 4B	Nucleus	0	5	0	4	0	6	15	6.536E-03	
Q9BQ52	ELAC2	elaC ribonuclease Z 2	Nucleus	0	3	0	1	0	3	7	3.641E-02	
Q9BQA1	WDR77	WD repeat domain 77	Nucleus	0	4	0	4	0	8	16	2.860E-02	11a

Q9BSD7	NTPCR	nucleoside-triphosphatase, cancer-related	Nucleus	0	1	0	1	0	2	4	2.860E-02	
Q9BTC0	DIDO1	death inducer-obliterator 1	Nucleus	0	1	0	1	0	2	6	2.860E-02	10,13,11a
Q9BUJ2	HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	Nucleus	0	8	0	5	0	10	23	1.705E-02	
Q9BVL2	NUP58	nucleoporin 58kDa	Nucleus	0	7	0	9	0	19	35	4.403E-02	11a
Q9BVP2	GNL3	guanine nucleotide binding protein-like 3 (nucleolar)	Nucleus	0	2	0	3	0	3	14	7.634E-03	11a
Q9BWF3	RBM4	RNA binding motif protein 4	Nucleus	0	6	0	6	0	10	22	1.575E-02	11a
Q9BWG4	SSBP4	single stranded DNA binding protein 4	Nucleus	0	1	0	1	0	1	3	0.000E+00	
Q9BWW4	SSBP3	single stranded DNA binding protein 3	Nucleus	0	1	0	1	0	2	4	2.860E-02	
Q9BYG3	NIFK	nucleolar protein interacting with the FHA domain of MKI67	Nucleus	0	2	0	2	0	2	6	0.000E+00	11a
Q9BYJ9	YTHDF1	YTH N(6)-methyladenosine RNA binding protein 1	Nucleus	0	7	0	6	0	14	27	3.504E-02	10,13
Q9BZA5	TXLNGY	taxilin gamma pseudogene, Y-linked	Nucleus	0	1	0	1	0	2	4	2.860E-02	
Q9H0C2	SLC25A31	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	Nucleus	0	2	0	3	0	1	6	3.709E-02	
Q9H0E3	SAP130	Sin3A-associated protein, 130kDa	Nucleus	0	2	0	4	0	4	10	1.887E-02	13
Q9H0E9	BRD8	bromodomain containing 8	Nucleus	0	1	0	1	0	2	4	2.860E-02	
Q9H0U4	RAB1B	RAB1B, member RAS oncogene family	Nucleus	0	2	0	1	0	1	6	2.860E-02	
Q9H1B7	IRF2BPL	interferon regulatory factor 2 binding protein-like	Nucleus	0	4	0	5	0	10	19	3.809E-02	11a
Q9H2F5	EPC1	enhancer of polycomb homolog 1 (Drosophila)	Nucleus	0	2	0	1	0	3	6	3.709E-02	
Q9H334	FOXP1	forkhead box P1	Nucleus	0	1	0	2	0	2	5	1.887E-02	11a
Q9H3S7	PTPN23	protein tyrosine phosphatase, non-receptor type 23	Nucleus	0	10	0	9	0	9	28	6.365E-04	
Q9H7N4	SCAF1	SR-related CTD-associated factor 1	Nucleus	0	4	0	1	0	2	7	5.904E-02	11a
Q9HB07	C12orf10	chromosome 12 open reading frame 10	Nucleus	0	4	0	2	0	4	10	1.887E-02	
Q9HB71	CACYBP	calcyclin binding protein	Nucleus	0	2	0	3	0	3	15	7.634E-03	11a
Q9HBM6	TAF9B	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	Nucleus	0	2	0	2	0	3	7	9.902E-03	
Q9HC38	GLOD4	glyoxalase domain containing 4	Nucleus	0	2	0	3	0	6	11	4.637E-02	11a
Q9NTZ6	RBM12	RNA binding motif protein 12	Nucleus	0	11	0	11	0	13	51	1.625E-03	11a
Q9NXV6	CDKN2AIP	CDKN2A interacting protein	Nucleus	0	3	0	4	0	4	17	4.082E-03	13,11a
Q9NYV4	CDK12	cyclin-dependent kinase 12	Nucleus	0	2	0	3	0	3	12	7.634E-03	10,13
Q9NZL9	MAT2B	methionine adenosyltransferase II, beta	Nucleus	0	1	0	1	0	2	4	2.860E-02	
Q9NZN8	CNOT2	CCR4-NOT transcription complex, subunit 2	Nucleus	0	3	0	5	0	6	14	1.695E-02	
Q9P2N5	RBM27	RNA binding motif protein 27	Nucleus	0	8	0	7	0	8	35	9.425E-04	10,13,11a

Q9UBV8	PEF1	penta-EF-hand domain containing 1	Nucleus	0	2	0	2	0	3	7	9.902E-03	11a
Q9UHD9	UBQLN2	ubiquilin 2	Nucleus	0	9	0	10	0	11	60	1.658E-03	
Q9UHR5	SAP30BP	SAP30 binding protein	Nucleus	0	6	0	7	0	11	24	1.729E-02	13,11a
Q9UHX1	PUF60	poly-U binding splicing factor 60kDa	Nucleus	0	9	0	10	0	10	52	5.935E-04	11a
Q9UJZ1	STOML2	stomatin (EPB72)-like 2	Nucleus	0	3	0	4	0	5	12	1.010E-02	11a
Q9UKD1	GMEB2	glucocorticoid modulatory element binding protein 2	Nucleus	0	1	0	2	0	1	4	2.860E-02	13
Q9UKI9	POU2F3	POU class 2 homeobox 3	Nucleus	0	2	0	2	0	3	11	9.902E-03	
Q9UKN8	GTF3C4	general transcription factor IIIC, polypeptide 4, 90kDa	Nucleus	0	2	0	2	0	1	5	1.887E-02	11a
Q9UKY1	ZHX1	zinc fingers and homeoboxes 1	Nucleus	0	4	0	2	0	6	12	3.709E-02	13,11a
Q9ULJ6	ZMIZ1	zinc finger, MIZ-type containing 1	Nucleus	0	1	0	1	0	1	3	0.000E+00	
Q9ULM3	YEATS2	YEATS domain containing 2	Nucleus	0	1	0	1	0	2	5	2.860E-02	10,11a
Q9ULT8	HECTD1	HECT domain containing E3 ubiquitin protein ligase 1	Nucleus	0	2	0	2	0	1	5	1.887E-02	11a
Q9ULU4	ZMYND8	zinc finger, MYND-type containing 8	Nucleus	0	2	0	2	0	4	8	2.860E-02	11a
Q9ULX6	AKAP8L	A kinase (PRKA) anchor protein 8-like	Nucleus	0	3	0	1	0	3	7	3.641E-02	11a
Q9UPN9	TRIM33	tripartite motif containing 33	Nucleus	0	6	0	5	0	11	22	2.924E-02	11a
Q9UPQ9	TNRC6B	trinucleotide repeat containing 6B	Nucleus	0	2	0	1	0	2	5	1.887E-02	
Q9UPT8	ZC3H4	zinc finger CCCH-type containing 4	Nucleus	0	1	0	1	0	1	3	0.000E+00	11a
Q9UQ35	SRRM2	serine/arginine repetitive matrix 2	Nucleus	0	5	0	6	0	6	30	1.721E-03	13,11a
Q9UQR0	SCML2	sex comb on midleg-like 2 ( <i>Drosophila</i> )	Nucleus	0	2	0	1	0	3	6	3.709E-02	
Q9Y2X3	NOP58	NOP58 ribonucleoprotein	Nucleus	0	10	0	8	0	5	23	1.705E-02	11a
Q9Y2X9	ZNF281	zinc finger protein 281	Nucleus	0	6	0	5	0	12	23	3.628E-02	13,11a
Q9Y2Z0	SUGT1	SGT1 homolog, MIS12 kinetochore complex assembly cochaperone	Nucleus	0	2	0	1	0	2	7	1.887E-02	11a
Q9Y383	LUC7L2	LUC7-like 2 pre-mRNA splicing factor	Nucleus	0	1	0	1	0	1	3	0.000E+00	11a
Q9Y3B4	SF3B6	splicing factor 3b, subunit 6, 14kDa	Nucleus	0	1	0	2	0	2	5	1.887E-02	11a
Q9Y467	SALL2	spalt-like transcription factor 2	Nucleus	0	1	0	1	0	2	5	2.860E-02	
Q9Y5B9	SUPT16H	SPT16 homolog, facilitates chromatin remodeling subunit	Nucleus	0	2	0	2	0	2	6	0.000E+00	11a
Q9Y5V3	MAGED1	melanoma antigen family D1	Nucleus	0	1	0	1	0	1	3	0.000E+00	
P17655	CAPN2	calpain 2, (m/II) large subunit	Plasma Membrane	0	4	0	4	0	2	9	1.887E-02	
P23284	PPIB	peptidylprolyl isomerase B (cyclophilin B)	Plasma Membrane	0	3	0	3	0	2	8	7.634E-03	11a
P63010	AP2B1	adaptor-related protein complex 2, beta 1 subunit	Plasma	0	14	0	14	0	34	62	4.510E-02	12a



Membrane

**Table S4.** Proteins identified from HEK293 cells treated with 1(Ac<sub>4</sub>GlcNAz) ( indicated the proteins identified in previous reports).

ID	Gene	Description	Location	1(Ac <sub>4</sub> GlcNAz )								t-test	Previous identification		
				Spectral counts											
				Exp. 1	Exp. 2	Exp. 3	Sum	-	+	-	+				
A0AVT1	UBA6 MOP4 UBE1L2	Ubiquitin-like modifier-activating enzyme 6	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a			
000170	AIP	aryl hydrocarbon receptor interacting protein	Cytoplasm	0	1	0	1	0	1	3	0.00E+00				
000203	AP3B1 ADTB3A	AP-3 complex subunit beta-1	Cytoplasm	0	2	0	2	0	2	6	0.00E+00				
014920	IKBKB IKKB	Inhibitor of nuclear factor kappa-B kinase subunit beta	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	12a, 13			
014974	PPP1R12A	protein phosphatase 1, regulatory subunit 12A	Cytoplasm	0	2	0	3	0	3	8	1.32E-03	10, 12a, 13			
015013	ARHGEF10 KIAA0294	Rho guanine nucleotide exchange factor 10	Cytoplasm	0	1	0	1	0	1	3	0.00E+00				
015042	U2SURP KIAA0332 SR140	U2 snRNP-associated SURP motif-containing protein	Cytoplasm	1	4	1	3	1	3	10	2.19E-03	11a			
015111	CHUK IKKA TCF16	Inhibitor of nuclear factor kappa-B kinase subunit alpha	Cytoplasm	0	1	0	2	0	1	4	1.61E-02				
043396	TXNL1 TRP32 TXL TXNL	Thioredoxin-like protein 1	Cytoplasm	0	1	0	1	0	1	3	0.00E+00				
043432	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	Cytoplasm	0	3	0	4	0	3	10	5.62E-04				
043847	NRDC NRD1	Nardilysin	Cytoplasm	0	2	0	2	0	2	6	0.00E+00				
060231	DHX16 DBP2 DDX16 KIAA0577	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	Cytoplasm	0	1	0	1	0	1	3	0.00E+00				
060282	KIF5C KIAA0531 NKHC2	Kinesin heavy chain isoform 5C	Cytoplasm	0	2	0	1	0	1	4	1.61E-02				
060313	OPA1 KIAA0567	Dynamin-like 120 kDa protein, mitochondrial	Cytoplasm	0	1	0	1	0	1	3	0.00E+00				
060343	TBC1D4 AS160	TBC1 domain family member 4	Cytoplasm	0	1	0	1	0	1	3	0.00E+00				

KIAA0603														
					Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
075037	KIF21B KIAA0449	Kinesin-like protein KIF21B			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
075475	PSIP1 DFS70 LEDGF PSIP2	PC4 and SFRS1-interacting protein			Cytoplasm	0	2	0	2	0	2	6	0.00E+00	11a
075489	NDUFS3	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial			Cytoplasm	0	5	0	5	0	5	15	0.00E+00	
075534	CSDE1	cold shock domain containing E1, RNA-binding			Cytoplasm	0	2	0	2	0	2	6	0.00E+00	10, 12a, 13
075688	PPM1B PP2CB	Protein phosphatase 1B			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
075821	EIF3G EIF3S4	Eukaryotic translation initiation factor 3 subunit G (eIF3g)			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	10, 11a, 12a, 13
094832	MYO1D KIAA0727	Unconventional myosin-Id			Cytoplasm	0	2	0	3	0	1	6	2.57E-02	
094888	UBXN7	UBX domain protein 7			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
095486	SEC24A	SEC24 homolog A, COPII coat complex component			Cytoplasm	0	4	0	3	0	5	12	2.28E-03	
095671	ASMTL	N-acetylserotonin O-methyltransferase-like protein			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
095678	KRT75	keratin 75, type II			Cytoplasm	0	2	0	1	0	1	4	1.61E-02	
095861	BPNT1	3'(2'),5'-bisphosphate nucleotidase 1			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
096013	PAK4 KIAA1142	Serine/threonine-protein kinase PAK 4			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
P02538	KRT6A K6A KRT6D	Keratin, type II cytoskeletal 6A			Cytoplasm	0	1	0	2	0	2	5	7.49E-03	
P04259	KRT6B K6B KRTL1	Keratin, type II cytoskeletal 6B			Cytoplasm	0	3	0	3	0	3	9	0.00E+00	
P06753	TPM3	Tropomyosin alpha-3 chain			Cytoplasm	0	3	0	3	0	3	9	0.00E+00	
P08243	ASNS	asparagine synthetase			Cytoplasm	2	6	1	7	2	6	19	5.84E-04	
P12955	PEPD PRD	Xaa-Pro dipeptidase (X-Pro dipeptidase)			Cytoplasm	0	2	0	2	0	2	6	0.00E+00	
P13647	KRT5	Keratin, type II cytoskeletal 5			Cytoplasm	0	2	0	2	0	2	6	0.00E+00	11a
P19174	PLCG1 PLC1	1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase			Cytoplasm	0	1	0	2	0	2	5	7.49E-03	

gamma-1													
				Cytoplasm	0	2	0	1	0	2	5	7.49E-03	11a
P22061	PCMT1	protein-L-isoaspartate (D-aspartate) O-methyltransferase		Cytoplasm	0	2	0	1	0	2	5	7.49E-03	11a
P29218	IMPA1 IMPA	Inositol monophosphatase 1		Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
P30291	WEE1	Wee1-like protein kinase		Cytoplasm	0	2	0	1	0	1	4	1.61E-02	
P31153	MAT2A	methionine adenosyltransferase II, alpha		Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
P35080	PFN2	profilin 2		Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
P40616	ARL1	ADP-ribosylation factor-like protein 1		Cytoplasm	0	2	0	1	0	2	5	7.49E-03	
P41091	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa		Cytoplasm	0	2	0	2	0	1	5	7.49E-03	9, 11a, 12a, 13
P41240	CSK	Tyrosine-protein kinase CSK		Cytoplasm	0	2	0	3	0	1	6	2.57E-02	
P46013	MKI67	Antigen Ki-67		Cytoplasm	5	15	3	17	4	18	50	2.75E-04	10, 11a, 12a, 13
P48507	GCLM GLCLR	Glutamate--cysteine ligase regulatory subunit		Cytoplasm	0	1	0	2	0	1	4	1.61E-02	11a
P48668	KRT6C KRT6E	Keratin, type II cytoskeletal 6C		Cytoplasm	0	1	0	1	0	2	4	1.61E-02	
P49356	FNTB	Protein farnesyltransferase subunit beta (FTase-beta)		Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
P49585	PCYT1A CTPCT			Cytoplasm	0	2	0	1	0	2	5	7.49E-03	11a
	PCYT1	Choline-phosphate cytidylyltransferase A											
P51812	RPS6KA3 ISPK1			Cytoplasm	0	2	0	1	0	1	4	1.61E-02	11a
	MAPKAPK1B												
P54646	RSK2	Ribosomal protein S6 kinase alpha-3 (S6K-alpha-3)		Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
	PRKAA2 AMPK	5'-AMP-activated protein kinase catalytic subunit alpha-2 (AMPK subunit alpha-2)											
P61006	RAB8A MEL			Cytoplasm	0	2	0	2	0	2	6	0.00E+00	
	RAB8	Ras-related protein Rab-8A (Oncogene c-mel)											
P61221	ABCE1 RLI			Cytoplasm	0	3	0	3	0	2	8	1.32E-03	
	RNASEL1												
P61221	RNASEL1 RNS4I			Cytoplasm	0	3	0	3	0	2	8	1.32E-03	
	OK/SW-cl.40	ATP-binding cassette sub-family E member 1											

P61289	PSME3	proteasome activator subunit 3	Cytoplasm	0	3	0	2	0	3	8	1.32E-03	11a
P62314	SNRPD1	Small nuclear ribonucleoprotein Sm D1	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
P62829	RPL23	60S ribosomal protein L23	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
P62851	RPS25	40S ribosomal protein S25	Cytoplasm	0	1	0	2	0	3	6	2.57E-02	
P62854	RPS26	ribosomal protein S26	Cytoplasm	0	1	0	2	0	1	4	1.61E-02	
Q07866	KLC1 KLC KNS2	Kinesin light chain 1 (KLC 1)	Cytoplasm	0	2	0	1	0	2	5	7.49E-03	
Q12894	IFRD2	Interferon-related developmental regulator 2 (Protein SKMC15)	Cytoplasm	0	2	0	2	0	2	6	0.00E+00	
Q12955	ANK3	Ankyrin-3 (ANK-3) (Ankyrin-G)	Cytoplasm	0	1	0	3	0	1	5	6.68E-02	12a, 13
Q13011	ECH1	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	Cytoplasm	0	1	0	3	0	2	6	2.57E-02	
Q13232	NME3	NME/NM23 nucleoside diphosphate kinase 3	Cytoplasm	0	1	0	3	0	3	7	2.49E-02	
Q14012	CAMK1	Calcium/calmodulin-dependent protein kinase type 1	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
Q14139	UBE4A KIAA0126	Ubiquitin conjugation factor E4 A	Cytoplasm	0	1	0	2	0	1	4	1.61E-02	11a
Q14247	CTTN EMS1	Src substrate cortactin	Cytoplasm	1	3	1	4	1	4	11	1.32E-03	11a
Q14684	RRP1B KIAA0179	Ribosomal RNA processing protein 1 homolog B	Cytoplasm	0	1	0	3	0	2	6	2.57E-02	10, 12a, 13
	PDCD11											
Q14690	KIAA0185	Protein RRP5 homolog	Cytoplasm	0	2	0	1	0	1	4	1.61E-02	
Q14694	USP10 KIAA0190	Ubiquitin carboxyl-terminal hydrolase 10	Cytoplasm	0	4	0	2	0	4	10	7.49E-03	11a
Q14807	KIF22 KID KNSL4	Kinesin-like protein KIF22	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
	NOLC1 KIAA0035											
Q14978	NS5ATP13	Nucleolar and coiled-body phosphoprotein 1	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	10, 12a, 13
	TNIP1 KIAA0113											
Q15025	NAF1	TNFAIP3-interacting protein 1	Cytoplasm	0	1	0	2	0	1	4	1.61E-02	11a
Q15067	ACOX1 ACOX	Peroxisomal acyl-coenzyme A oxidase 1 (AOX)	Cytoplasm	0	1	0	2	0	1	4	1.61E-02	
Q15154	PCM1	Pericentriolar material 1 protein	Cytoplasm	0	2	0	1	0	2	5	7.49E-03	
	LLGL1 DLG4											
Q15334	HUGL HUGL1	Lethal(2) giant larvae protein homolog 1	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a

	RPS6KA1										
Q15418	MAPKAPK1A										
	RSK1	Ribosomal protein S6 kinase alpha-1 (S6K-alpha-1)		Cytoplasm	0	1	0	1	0	1	3
	SKIV2L DDX13										0.00E+00
Q15477	SKI2W SKIV2 W	Helicase SKI2W (Ski2)		Cytoplasm	0	1	0	4	0	1	6
	ELAVL1	ELAV like RNA binding protein 1		Cytoplasm	0	2	0	1	0	2	5
Q15717											7.49E-03
Q16204	CCDC6	coiled-coil domain containing 6		Cytoplasm	0	1	0	2	0	1	4
	PKN1 PAK1 PKN										1.61E-02
Q16512	PRK1 PRKCL1	Serine/threonine-protein kinase N1		Cytoplasm	0	1	0	2	0	3	6
	PKN2 PRK2										2.57E-02
Q16513	PRKCL2	Serine/threonine-protein kinase N2		Cytoplasm	0	1	0	1	0	1	3
	SMN1	Survival motor neuron protein		Cytoplasm	0	1	0	1	0	3	5
	INF2 C14orf151										6.68E-02
Q27J81	C14orf173	Inverted formin-2 (HBEBP2-binding protein C)		Cytoplasm	0	1	0	1	0	1	3
	Q2KHR3	Glutamine and serine-rich protein 1		Cytoplasm	0	1	0	2	0	2	5
Q2NL82	TSR1 KIAA1401	Pre-rRNA-processing protein TSR1 homolog		Cytoplasm	0	2	0	1	0	1	4
	LRRFIP1 GCF2										1.61E-02
Q32MZ4	TRIP	Leucine-rich repeat flightless-interacting protein 1		Cytoplasm	0	1	0	2	0	2	5
	Q5JTH9	RRP12 KIAA0690	RRP12-like protein								7.49E-03
	Q5T6F2	ubiquitin associated protein 2		Cytoplasm	0	2	0	3	0	2	7
	ATAD3B										2.19E-03
Q5T9A4	KIAA1273 TOB3	ATPase family AAA domain-containing protein 3B (AAA-TOB3)		Cytoplasm	1	5	1	6	1	4	15
	FAM91A1	Protein FAM91A1		Cytoplasm	0	1	0	3	0	1	5
	Q658Y4										6.68E-02
Q659C4	LARP1B	La ribonucleoprotein domain family, member 1B		Cytoplasm	0	2	0	3	0	2	7
	Q66K74	MAP1S	microtubule-associated protein 1S								2.19E-03
Q69YN4	KIAA1429	Protein virilizer homolog		Cytoplasm	0	1	0	3	0	1	5
											5.72E-02
											11a
											11a, 12a, 13

MSTP054										
	DHRS7B									
	SDR32C1 CGI-93									
	UNQ212/PRO23									
Q6IAN0	8	Dehydrogenase/reductase SDR family member 7B		Cytoplasm	0	1	0	1	0	1
Q6NZY4	ZCCHC8	Zinc finger CCHC domain-containing protein 8		Cytoplasm	0	1	0	2	0	1
Q6P1N0	CC2D1A AKI1	Coiled-coil and C2 domain-containing protein 1A		Cytoplasm	0	2	0	3	0	2
Q6P2E9	EDC4	enhancer of mRNA decapping 4		Cytoplasm	0	9	0	5	0	3
Q6PJG6	BRAT1 BAAT1			Cytoplasm	0	3	0	2	0	2
	C7orf27	BRCA1-associated ATM activator 1		Cytoplasm	0	3	0	2	0	2
Q6PL18	ATAD2 L16			Cytoplasm	0	3	0	2	0	3
	PRO2000	ATPase family AAA domain-containing protein 2		Cytoplasm	0	3	0	2	0	3
Q6WCQ1	MPRIP KIAA0864			Cytoplasm	0	1	0	1	0	1
	MRIP RHOIP3	Myosin phosphatase Rho-interacting protein		Cytoplasm	0	1	0	1	0	1
Q7L2J0	MEPCE BCDIN3	7SK snRNA methylphosphate capping enzyme (MePCE)		Cytoplasm	0	1	0	1	0	3
Q7Z3K3	POGZ	pogo transposable element with ZNF domain		Cytoplasm	0	3	0	2	0	3
	HAUS6 DGT6			Cytoplasm	0	3	0	2	0	3
Q7Z4H7	FAM29A			Cytoplasm	0	4	0	1	0	2
	KIAA1574	HAUS augmin-like complex subunit 6		Cytoplasm	0	4	0	1	0	2
Q7Z4Q2	HEATR3	HEAT repeat containing 3		Cytoplasm	1	4	1	5	1	5
				Cytoplasm	1	4	1	5	1	5
Q7Z6Z7	HUWE1	HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase		Cytoplasm	0	1	0	1	0	1
				Cytoplasm	0	1	0	1	0	1
Q86Y91	KIF18B	Kinesin-like protein KIF18B		Cytoplasm	0	3	0	2	0	2
Q86YS7	C2CD5 CDP138			Cytoplasm	0	3	0	2	0	2
	KIAA0528	C2 domain-containing protein 5		Cytoplasm	0	1	0	2	0	2
Q8IWZ3	ANKHD1/ANKHD1-EIF4EBP3	ankyrin repeat and KH domain containing 1		Cytoplasm	0	1	0	1	0	2
				Cytoplasm	0	1	0	1	0	2
Q8IXT5	RBM12B	RNA-binding protein 12B		Cytoplasm	0	2	0	1	0	1
				Cytoplasm	0	2	0	1	0	1

Q8IXW5	RPAP2 C1orf82	Putative RNA polymerase II subunit B1 CTD phosphatase RPAP2	Cytoplasm	0	2	0	2	0	1	5	7.49E-03	11a
	DHX37 DDX37											
Q8IY37	KIAA1517	Probable ATP-dependent RNA helicase DHX37	Cytoplasm	0	2	0	1	0	1.5	4.5	6.53E-03	
Q8IY67	RAVER1	ribonucleoprotein, PTB-binding 1	Cytoplasm	0	1	0	2	0	1	4	1.61E-02	11a
Q8IY81	FTSJ3 SB92	pre-rRNA processing protein FTSJ3	Cytoplasm	0	4	0	4	0	3	11	3.88E-04	
	PELP1 HMX3											
Q8IZL8	MNAR	Proline-, glutamic acid- and leucine-rich protein 1	Cytoplasm	0	2	0	3	0	2	7	2.19E-03	
Q8NOV3	RBFA C18orf22	Putative ribosome-binding factor A, mitochondrial	Cytoplasm	0	1	0	2	0	2	5	7.49E-03	
Q8N3C0	ASCC3 HELIC1	Activating signal cointegrator 1 complex subunit 3	Cytoplasm	0	2	0	1	0	2	5	7.49E-03	
Q8ND83	SLAIN1 C13orf32	SLAIN motif-containing protein 1	Cytoplasm	0	1	0	2	0	1	4	1.61E-02	11a
Q8NFF5	FLAD1 PP591	FAD synthase	Cytoplasm	0	2	0	1	0	2	5	7.49E-03	
	NOC3L AD24											
	C10orf117											
Q8WTT2	FAD24	Nucleolar complex protein 3 homolog	Cytoplasm	0	2	0	1	0	2	5	7.49E-03	
	NELFB COBRA1											
Q8WX92	KIAA1182	Negative elongation factor B	Cytoplasm	1	3	1	4	1	3	10	2.19E-03	
Q92552	MRPS27	mitochondrial ribosomal protein S27	cytoplasm	0	2	0	4	0	4	10	7.49E-03	
Q92576	PHF3 KIAA0244	PHD finger protein 3	Cytoplasm	0	1	0	2	0	2	5	7.49E-03	11a
Q92615	LARP4B	La ribonucleoprotein domain family, member 4B	Cytoplasm	0	1	0	1	0	2	4	1.61E-02	11a
	ANKS1A ANKS1											
Q92625	KIAA0229 ODIN	Ankyrin repeat and SAM domain-containing protein 1A (Odin)	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
	LRRC59											
Q96AG4	PRO1855	Leucine-rich repeat-containing protein 59	Cytoplasm	0	2	0	2	0	2	6	0.00E+00	
Q96BH1	RNF25	E3 ubiquitin-protein ligase RNF25	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
	PTCD3 MRPS39											
Q96EY7	TRG15	Pentatricopeptide repeat domain-containing protein 3, mitochondrial	Cytoplasm	0	2	0	1	0	2	5	7.49E-03	
Q96F45	ZNF503	zinc finger protein 503	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
Q96H55	MYO19	Unconventional myosin-XIX (Myosin head domain-containing	Cytoplasm	0	2	0	2	0	1	5	7.49E-03	

	MYOHD1	protein 1)									
	CDK5RAP3	IC53									
	LZAP	MSTP016									
	OK/SW-cl.114										
Q96JB5	PP1553	CDK5 regulatory subunit-associated protein 3	Cytoplasm	0	2	0	2	0	1	5	
Q96KB5	PBK	PDZ binding kinase	Cytoplasm	0	1	0	2	0	2	5	
	EXOC2	SEC5									
Q96KP1	SEC5L1	Exocyst complex component 2	Cytoplasm	0	1	0	2	0	2	5	
	CEP170P1										
	CEP170L										
Q96L14	KIAA0470L	Cep170-like protein	Cytoplasm	0	1	0	2	0	1	4	
Q9BRF8	CPPED1	CSTP1	Serine/threonine-protein phosphatase CPPED1	Cytoplasm	0	2	0	1	0	2	
Q9BRP1	PDCD2L	Programmed cell death protein 2-like	Cytoplasm	0	2	0	1	0	1	4	
Q9BTE7	DCUN1D5	DCN1-like protein 5	Cytoplasm	0	1	0	1	0	1	3	
	MMTAG2										
Q9BU76	C1orf35	Multiple myeloma tumor-associated protein 2	Cytoplasm	0	1	0	1	0	1	3	
Q9BXW7	CECR5	cat eye syndrome chromosome region, candidate 5	Cytoplasm	0	2	0	2	0	1	5	
	UBE2O										
Q9C0C9	KIAA1734	(E3-independent) E2 ubiquitin-conjugating enzyme	Cytoplasm	0	4	0	2	0	3	9	
Q9H0Q0	FAM49A	Protein FAM49A	Cytoplasm	0	1	0	2	0	1	4	
Q9H0S4	DDX47	Probable ATP-dependent RNA helicase DDX47	Cytoplasm	0	2	0	1	0	1	4	
Q9H4A3	WNK1	WNK lysine deficient protein kinase 1	Cytoplasm	0	1	0	2	0	2	5	
Q9H6Z4	RANBP3	RAN binding protein 3	Cytoplasm	0	1	0	1	0	1	3	
Q9H857	NT5DC2	5'-nucleotidase domain containing 2	Cytoplasm	0	4	0	1	0	3	8	
Q9NQW6	ANLN	Actin-binding protein anillin	Cytoplasm	0	1	0	2	0	1	4	
Q9NR3	STRN4	ZIN	Striatin-4 (Zinedin)	Cytoplasm	0	1	0	2	0	1	4
Q9NRR5	UBQLN4	ubiquilin 4	Cytoplasm	0	1	0	1	0	1	3	
Q9NUQ3	TXLNG	taxilin gamma	Cytoplasm	0	5	0	6	0	6	17	

Q9UBB6	NCDN KIAA0607	Neurochondrin	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a, 12a
	RNF14 ARA54											
Q9UBS8	HRIHFB2038	E3 ubiquitin-protein ligase RNF14	Cytoplasm	0	1	0	2	0	1	4	1.61E-02	
	LIMA1 EPLIN											
Q9UHB6	SREBP3 PP624	LIM domain and actin-binding protein 1	Cytoplasm	0	2	0	2	0	1	5	7.49E-03	11a
	SRP68											
Q9UHB9	LCMT1 LCMT	Signal recognition particle subunit SRP68	Cytoplasm	1	3	1	4	1	3	10	2.19E-03	
	CGI-68											
	FAM208A											
	C3orf63											
Q9UK61	KIAA1105 TASOR	Protein TASOR	Cytoplasm	0	1	0	3	0	2	6	2.57E-02	11a
	BAG5											
Q9UL15	UBQLN1	BCL2-associated athanogene 5	Cytoplasm	0	1	0	2	0	1	4	1.61E-02	11a
	POLDIP2 PDIP38											
Q9Y2S7	POLD4 HSPC017	Polymerase delta-interacting protein 2	Cytoplasm	0	2	0	1	0	1	4	1.61E-02	
	ATG4B APG4B											
Q9Y4P1	AUTL1 KIAA0943	Cysteine protease ATG4B	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
	TELO2											
Q9Y4R8	telomere maintenance 2		Cytoplasm	1	5	1	4	1	3	12	6.53E-03	
	PRRC2C	proline-rich coiled-coil 2C	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	10, 11a, 12a, 13
	DYNC1LI1	dynein, cytoplasmic 1, light intermediate chain 1	Cytoplasm	0	2	0	1	0	2	5	7.49E-03	11a
A2RRP1	NBAS NAG	Neuroblastoma-amplified sequence	Cytoplasm-ER	0	1	0	1	0	1	3	0.00E+00	
O15226	NKRF ITBA4 NRF	NF-kappa-B-repressing factor	Cytoplasm-ER	0	1	0	1	0	1	3	0.00E+00	
	GNPAT DAPAT											
O15228	DHAPAT	Dihydroxyacetone phosphate acyltransferase	Cytoplasm-ER	0	1	0	1	0	2	4	1.61E-02	
	SPTLC2											
O15270	Serine palmitoyltransferase 2		Cytoplasm-	0	1	0	1	0	1	3	0.00E+00	

	KIAA0526 LCB2		ER						
	ERLIN1 C10orf69								
	KE04 KEO4								
075477	SPFH1	Erlin-1	Cytoplasm-ER	0	2	0	2	0	2
	ERLIN2 C8orf2								
	SPFH2								
	UNQ2441/PRO5								
094905	003/PRO9924	Erlin-2	Cytoplasm-ER	0	1	0	1	0	1
	SEC31A	SEC31 homolog A, COPII coat complex component	Cytoplasm-ER	0	4	0	4	0	4
									10,11a, 12a, 13
P08240	SRPRA SRPR	Signal recognition particle receptor subunit alpha	Cytoplasm-ER	0	1	0	3	0	1
									6.68E-02
P16333	NCK1 NCK	Cytoplasmic protein NCK1	Cytoplasm-ER	0	1	0	1	0	1
									0.00E+00
P18031	PTPN1 PTP1B	Tyrosine-protein phosphatase non-receptor type 1	Cytoplasm-ER	1	3	2	4	1	3
									1.32E-02
P27797	CALR CRTC	Calreticulin	Cytoplasm-ER	0	1	0	2	0	1
	MTOR FRAP								
	FRAP1 FRAP2								
P42345	RAFT1 RAPT1	Serine/threonine-protein kinase mTOR	Cytoplasm-ER	0	1	0	1	0	1
	LMAN1 ERGIC53								
P49257	F5F8D	Protein ERGIC-53	Cytoplasm-ER	0	1	0	1	0	1
									0.00E+00
P51571	SSR4 TRAPD	Translocon-associated protein subunit delta	Cytoplasm-ER	0	1	0	1	0	1
									0.00E+00
P61019	RAB2A RAB2	Ras-related protein Rab-2A	Cytoplasm-ER	0	1	0	2	0	1
									1.61E-02
P61803	DAD1	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit DAD1	Cytoplasm-ER	0	1	0	1	0	1
	SEC11A SEC11L1								
P67812	SPC18 SPCS4A	Signal peptidase complex catalytic subunit SEC11A	Cytoplasm-ER	0	1	0	1	0	2
									1.61E-02

			Cytoplasm-						
Q13724	MOGS	mannosyl-oligosaccharide glucosidase	ER	0	1	0	2	0	1.61E-02
Q15392	DHCR24 KIAA0018	Delta(24)-sterol reductase	Cytoplasm- ER	0	2	0	1	0	1.61E-02
	TMX1 TMX TXNDC TXNDC1 PSEC0085 UNQ235/PRO26								
Q9H3N1	8	Thioredoxin-related transmembrane protein 1	Cytoplasm- ER	0	1	0	1	0	0.00E+00
Q9NTJ5	SACM1L KIAA0851	Phosphatidylinositide phosphatase SAC1	Cytoplasm- ER	0	1	0	1	0	0.00E+00
Q9Y6Y8	SEC23IP	SEC23 interacting protein	Cytoplasm- ER	0	2	0	1	0	7.49E-03
O94766	B3GAT3	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 3	Cytoplasm- Golgi	0	1	0	1	0	0.00E+00
P22059	OSBP OSBP1	Oxysterol-binding protein 1	Cytoplasm- Golgi	0	1	0	1	0	0.00E+00
Q08379	GOLGA2	Golgin subfamily A member 2	Cytoplasm- Golgi	0	1	0	3	0	2.57E-02
Q13492	PICALM	phosphatidylinositol binding clathrin assembly protein	Cytoplasm- Golgi	0	1	0	2	0	1.61E-02
Q15771	RAB30	Ras-related protein Rab-30	Cytoplasm- Golgi	0	1	0	1	0	0.00E+00
P11279	LAMP1	Lysosome-associated membrane glycoprotein 1	Cytoplasm- Lysosome	0	2	0	2	0	0.00E+00
P13473	LAMP2	Lysosome-associated membrane glycoprotein 2	Cytoplasm- Lysosome	0	2	0	2	0	0.00E+00
Q9P253	VPS18 KIAA1475	Vacuolar protein sorting-associated protein 18 homolog (hVPS18)	Cytoplasm- Lysosome	0	1	0	2	0	7.49E-03
O60641	SNAP91	synaptosomal-associated protein, 91kDa	Cytoplasm- Membrane	0	1	0	1	0	0.00E+00
									11a, 12a, 13

	CAND2 KIAA0667											
075155	TIP120B	Cullin-associated NEDD8-dissociated protein 2	Cytoplasm-Membrane	0	2	0	2	0	2	6	0.00E+00	
	ATP6V1G1 ATP6G ATP6G1 ATP6J	V-type proton ATPase subunit G 1	Cytoplasm-Membrane	0	1	0	2	0	1	4	1.61E-02	
	TOMM40 C19orf1 PEREC1 TOM40	Mitochondrial import receptor subunit TOM40 homolog	Cytoplasm-Membrane	0	2	0	3	0	3	8	1.32E-03	11a
P03915	MT-ND5 MTND5 NADH5 ND5	NADH-ubiquinone oxidoreductase chain 5	Cytoplasm-membrane	0	1	0	1	0	1	3	0.00E+00	
P07099	EPHX1 EPHX EPOX	Epoxide hydrolase 1	Cytoplasm-membrane	0	1	0	1	0	1	3	0.00E+00	
P28288	ABCD3 PMP70 PXMP1	ATP-binding cassette sub-family D member 3	Cytoplasm-Membrane	0	2	0	2	0	2	6	0.00E+00	
Q13162	PRDX4	Peroxiredoxin-4	Cytoplasm-Membrane	0	1	0	2	0	2	5	7.49E-03	9,11a, 12a, 13
Q14061	COX17	Cytochrome c oxidase copper chaperone	Cytoplasm-membrane	0	1	0	1	0	1	3	0.00E+00	
Q14692	BMS1 BMS1L KIAA0187	Ribosome biogenesis protein BMS1 homolog	Cytoplasm-Membrane	0	2	0	1	0	2	5	7.49E-03	
Q15061	WDR43 KIAA0007 UTP5	WD repeat-containing protein 43	Cytoplasm-Membrane	0	4	0	2	0	1	7	5.72E-02	11a
Q5VTL8	PRPF38B	Pre-mRNA-splicing factor 38B	Cytoplasm-Membrane	0	2	0	3	0	2	7	2.19E-03	11a
Q8IV08	PLD3	phospholipase D family, member 3	Cytoplasm-Membrane	0	1	0	1	0	1	3	0.00E+00	
Q93034	CUL5 VACM1	Cullin-5	Cytoplasm-Membrane	0	1	0	2	0	1	4	1.61E-02	
Q9BPX6	MICU1 CALC CBARA1	Calcium uptake protein 1, mitochondrial	Cytoplasm-Membrane	0	2	0	1	0	2	5	7.49E-03	

Q9P2E9	RRBP1 KIAA1398	Ribosome-binding protein 1	Cytoplasm-Membrane	0	4	0	5	0	4	13	2.02E-04
Q9UI26	IPO11 RANBP11	Importin-11 (Imp11) (Ran-binding protein 11) (RanBP11)	Cytoplasm-Membrane	0	2	0	1	0	2	5	7.49E-03
O14874	BCKDK	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase	Cytoplasm-mitochondria	0	1	0	2	0	1	4	1.61E-02
O75153	CLUH KIAA0664	Clustered mitochondria protein homolog	Cytoplasm-mitochondria	0	2	0	1	0	1	4	1.61E-02
P06576	ATP5B ATPMB ATPSB	ATP synthase subunit beta, mitochondrial	Cytoplasm-mitochondria	0	2	0	3	0	2	7	2.19E-03
P82675	MRPS5	28S ribosomal protein S5, mitochondrial	Cytoplasm-mitochondria	0	1	0	2	0	1	4	1.61E-02
Q02241	KIF23 KNSL5 MKLP1	Kinesin-like protein KIF23	Cytoplasm-mitochondria	0	1	0	2	0	1	4	1.61E-02
Q12840	KIF5A NKHC1	Kinesin heavy chain isoform 5A	Cytoplasm-mitochondria	0	3	0	2	0	1	6	2.57E-02
Q16891	IMMT	inner membrane protein, mitochondrial	Cytoplasm-mitochondria	0	4	0	5	0	7	16	3.77E-03
Q5JTZ9	AARS2 AARSL KIAA1270	Alanine--tRNA ligase, mitochondrial	Cytoplasm-mitochondria	2	6	1	8	2	4	18	2.26E-02
Q5ST30	VARS2 KIAA1885 VARS2L VARSL	Valine--tRNA ligase, mitochondrial	Cytoplasm-mitochondria	0	1	0	3	0	2	6	2.57E-02
Q6L8Q7	PDE12	2',5'-phosphodiesterase 12 (2'-PDE) (2-PDE)	Cytoplasm-mitochondria	1	3	1	5	1	4	12	6.53E-03

		MTCH1 PSAP CGI-64 UNQ1871/PRO4		Cytoplasm-mitochondria	0	5	0	2	0	4	11	1.42E-02
Q9NZJ7	314	Mitochondrial carrier homolog 1		Cytoplasm-mitochondria	0	3	0	3	0	2	8	1.32E-03
Q9Y305	ACOT9	acyl-CoA thioesterase 9		Cytoplasm-mitochondria	0	2	0	1	0	1	4	1.61E-02
P83111	81	LACTB MRPL56 UNQ843/PRO17	Serine beta-lactamase-like protein LACTB, mitochondrial	Cytoplasm-mitochondria	0	1	0	1	0	2	4	1.61E-02
Q00059	TFAM	transcription factor A, mitochondrial		Cytoplasm-mitochondria	0	1	0	1	0	2	4	1.61E-02
Q15031	LARS2 KIAA0028	Probable leucine--tRNA ligase, mitochondrial		Cytoplasm-mitochondria	0	1	0	1	0	2	4	1.61E-02
Q16795	NDUFA9 NDUFS2L	NADH dehydrogenase		Cytoplasm-mitochondria	0	1	0	2	0	2	5	7.49E-03
Q5TC12	ATPAF1	ATP synthase mitochondrial F1 complex assembly factor 1		Cytoplasm-mitochondria	0	1	0	1	0	1	3	0.00E+00
Q969S9	GFM2 EFG2 MSTP027	Ribosome-releasing factor 2, mitochondrial		Cytoplasm-mitochondria	0	1	0	2	0	2	5	7.49E-03
Q96GW9	MARS2	Methionine--tRNA ligase, mitochondrial		Cytoplasm-mitochondria	0	1	0	1	0	1	3	0.00E+00
Q00411	POLRMT	polymerase (RNA) mitochondrial (DNA directed)		Cytoplasm-mitochondron	2	6	1	5	1	6	17	7.78E-04
A6NCN2	KRT87P KRT121P KRTBHP4	Putative keratin-87 protein		Extracellular	0	1	0	1	0	1	3	0.00E+00
Q69YN2	CWF19L1	CWF19-like protein 1 (C19L1)		Extracellular	0	2	0	1	0	1	4	1.61E-02

A6NHR9	SMCHD1	structural maintenance of chromosomes flexible hinge domain containing 1	Nucleus	2	8	1	7	1	6	21	1.05E-03	11a
A6NKT7	RGPD4 (includes others)*	RANBP2-like and GRIP domain containing 5	Nucleus	0	2	0	1	0	1	4	1.61E-02	
A7E2V4	ZSWIM8 KIAA0913	Zinc finger SWIM domain-containing protein 8	Nucleus	0	1	0	1	0	1	3	0.00E+00	
O14646	CHD1	Chromodomain-helicase-DNA-binding protein 1	Nucleus	0	2	0	2	0	2	6	0.00E+00	
O14647	CHD2	Chromodomain-helicase-DNA-binding protein 2	Nucleus	0	1	0	1	0	1	3	0.00E+00	
O14776	TCERG1	transcription elongation regulator 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	10, 11a, 12a, 13
O15047	SETD1A	SET domain containing 1A	Nucleus	0	1	0	1	0	1	3	0.00E+00	10, 11a, 12a, 13
O15355	PPM1G PPM1C	Protein phosphatase 1G	Nucleus	1	3	1	4	1	3	10	2.19E-03	
O15381	NVL	Nuclear valosin-containing protein-like	Nucleus	0	2	0	1	0	1	4	1.61E-02	
O43148	RNMT KIAA0398	mRNA cap guanine-N7 methyltransferase	Nucleus	0	2	0	2	0	2	6	0.00E+00	10, 11a, 13
O43663	PRC1	Protein regulator of cytokinesis 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	
O43670	ZNF207	zinc finger protein 207	Nucleus	0	2	0	2	0	2	6	0.00E+00	10, 12a, 13
SPAG9 HSS KIAA0516 MAPK8IP4 SYD1												
060271	HLC6	C-Jun-amino-terminal kinase-interacting protein 4	Nucleus	0	2	0	2	0	2	6	0.00E+00	
060664	PLIN3	perilipin 3	Nucleus	0	2	0	2	0	2	6	0.00E+00	11a
NBN NBS NBS1												
060934	P95	Nibrin	Nucleus	0	1	0	1	0	1	3	0.00E+00	
O75179	ANKRD17	ankyrin repeat domain 17	Nucleus	0	1	0	2	0	1	4	1.61E-02	11a, 12a, 13
075691	UTP20 DRIM	Small subunit processome component 20 homolog	Nucleus	0	1	0	1	0	1	3	0.00E+00	
LTN1 C21orf10 C21orf98 KIAA0714												
094822	E3 ubiquitin-protein ligase listerin	Nucleus	0	2	0	2	0	2	6	0.00E+00		

	RNF160 ZNF294								
	HSPC087								
095059	RPP14	Ribonuclease P protein subunit p14	Nucleus	0	1	0	1	0	1.00E+00
095239	KIF4A KIF4	Chromosome-associated kinesin KIF4A	Nucleus	0	3	0	4	0	5.12.28E-03 11a
	SMC2 CAPE								
	SMC2L1								
095347	PRO0324	Structural maintenance of chromosomes protein 2	Nucleus	0	5	0	7	0	6.18.4.84E-04
095696	BRD1 BRL BRPF2	Bromodomain-containing protein 1	Nucleus	0	2	0	2	0	3.7.2.19E-03
P02545	LMNA	lamin A/C	Nucleus	2	6	1	7	1	6.19.4.47E-04 11a, 12b, 12a, 13
P04083	ANXA1 ANX1								
	LPC1	Annexin A1	Nucleus	0	3	0	4	0	3.10.5.62E-04 10, 12a, 13
P04818	TYMS TS OK/SW-cl.29	Thymidylate synthase (TS) (TSase) (EC 2.1.1.45)	Nucleus	0	3	0	2	0	2.7.2.19E-03
	ANXA5 ANX5								
P08758	ENX2 PP4	Annexin A5	Nucleus	1	6	1	6	1	6.18.0.00E+00
P09086	POU2F2	POU class 2 homeobox 2	Nucleus	0	1	0	1	0	1.3.0.00E+00
P11387	TOP1	DNA topoisomerase 1	Nucleus	1	6	2	5	1	7.18.2.19E-03
P14859	POU2F1	POU class 2 homeobox 1	Nucleus	0	1	0	1	0	1.3.0.00E+00 10, 11a, 13
P17480	UBTF UBF UBF1	Nucleolar transcription factor 1	Nucleus	0	2	0	2	0	2.6.0.00E+00
P18858	LIG1	DNA ligase 1	Nucleus	0	1	0	1	0	1.3.0.00E+00
P23588	EIF4B	Eukaryotic translation initiation factor 4B (eIF-4B)	Nucleus	0	1	0	1	0	1.3.0.00E+00
P27816	MAP4	microtubule-associated protein 4	Nucleus	0	9	0	9	0	9.27.0.00E+00 10, 11a, 12a, 13
P28702	RXRβ NR2B2	Retinoic acid receptor RXR-beta	Nucleus	0	1	0	1	0	1.3.0.00E+00
	CDC27 ANAPC3								
	DOS1430E								
P30260	D17S978E	Cell division cycle protein 27 homolog	Nucleus	0	1	0	2	0	1.4.1.61E-02

P31271	HOXA13 HOX1J	Homeobox protein Hox-A13	Nucleus	0	1	0	1	0	1	3	0.00E+00
P31276	HOXC13 HOX3G	Homeobox protein Hox-C13	Nucleus	0	1	0	1	0	1	3	0.00E+00
P31689	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	Nucleus	0	3	0	2	0	3	8	1.32E-03 10, 13
P35637	FUS	FUS RNA binding protein	Nucleus	0	2	0	3	0	1	6	2.57E-02
P35658	NUP214	nucleoporin 214kDa	Nucleus	0	5	0	7	0	6	18	4.84E-04 10, 11a, 11b, 13
P35659	DEK	DEK proto-oncogene	Nucleus	0	4	0	3	0	4	11	3.88E-04 11a
P35813	PPM1A PPPM1A	Protein phosphatase 1A	Nucleus	0	1	0	1	0	1	3	0.00E+00
P42694	HELZ DRHC KIAA0054	Probable helicase with zinc finger domain	Nucleus	0	1	0	1	0	1	3	0.00E+00
P49790	NUP153	nucleoporin 153kDa	Nucleus	0	7	0	9	0	5	21	3.74E-03 10, 11a, 11b, 13
P49792	RANBP2	RAN binding protein 2	Nucleus	0	4	0	3	0	4	11	3.88E-04 11a, 11b, 13
P51610	HCFC1	host cell factor C1	Nucleus	3	14	4	12	2	13	39	2.55E-04 13, 12a, 13
P52948	NUP98	nucleoporin 98kDa	Nucleus	0	4	0	6	0	4	14	2.19E-03 10,11a, 13
P53804	TTC3 DCRR1 RNF105 TPRD	E3 ubiquitin-protein ligase TTC3	Nucleus	0	1	0	1	0	2	4	1.61E-02
P54727	RAD23B	RAD23 homolog B, nucleotide excision repair protein	Nucleus	0	1	0	2	0	1	4	1.61E-02 12a
P68431	HIST1H3A	Histone H3.1	Nucleus	0	1	0	1	0	2	4	1.61E-02 12a, 13
P84243	H3F3A	Histone H3.3	Nucleus	0	1	0	2	0	1	4	1.61E-02
Q00577	PURA PUR1	Transcriptional activator protein Pur-alpha	Nucleus	0	1	0	1	0	2	4	1.61E-02
Q02040	AKAP17A CXorf3 DXYS155E SFRS17A XE7	A-kinase anchor protein 17A	Nucleus	0	1	0	2	0	1	4	1.61E-02
Q03252	LMNB2	lamin B2	Nucleus	0	1	0	1	0	1	3	0.00E+00 11a
Q03701	CEBPZ CBF2	CCAAT/enhancer-binding protein zeta	Nucleus	0	4	0	3	0	4	11	3.88E-04

Q06323	PSME1	proteasome activator subunit 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q12874	SF3A3	splicing factor 3a, subunit 3, 60kDa	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a
Q13131	PRKAA1 AMPK1	5'-AMP-activated protein kinase catalytic subunit alpha-1	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q13185	CBX3	chromobox homolog 3	Nucleus	1	5	1	4	1	5	14	3.88E-04	
	TARBP1 TRM3											
Q13395	TRP185	Probable methyltransferase TARBP1	Nucleus	0	1	0	2	0	1	4	1.61E-02	
Q13428	TCOF1	Treacher Collins-Franceschetti syndrome 1	Nucleus	0	3	0	4	0	4	11	3.88E-04	11a
	PRPF4B KIAA0536 PRP4											
Q13523	PRP4H PRP4K	Serine/threonine-protein kinase PRP4 homolog	Nucleus	0	2	0	2	0	2	6	0.00E+00	
Q13618	CUL3	cullin 3	Nucleus	0	1	0	2	0	2	5	7.49E-03	
Q14157	UBAP2L	ubiquitin associated protein 2-like	Nucleus	0	5	0	3	0	5	13	2.89E-03	10, 12a, 13
Q14562	DHX8 DDX8	ATP-dependent RNA helicase DHX8	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q14676	MDC1 KIAA0170 NFBD1	Mediator of DNA damage checkpoint protein 1	Nucleus	2	5	1	8	2	7	20	6.07E-03	11a, 12a, 13
	ARL6IP1 ARL6IP ARMER											
Q15041	KIAA0069	ADP-ribosylation factor-like protein 6-interacting protein 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q15058	KIF14 KIAA0042	Kinesin-like protein KIF14	Nucleus	0	1	0	2	0	1	4	1.61E-02	
Q15417	CNN3	calponin 3, acidic	Nucleus	0	1	0	2	0	1	4	1.61E-02	11a
Q15459	SF3A1	splicing factor 3a, subunit 1, 120kDa	Nucleus	0	2	0	3	0	3	8	1.32E-03	11a
Q15942	ZYX	zyxin	Nucleus	0	3	0	3	0	2	8	1.32E-03	
Q16695	HIST3H3	histone cluster 3, H3	Nucleus	0	1	0	2	0	1	4	1.61E-02	
	PDS5A KIAA0648											
Q29RF7	PDS5 PIG54	Sister chromatid cohesion protein PDS5 homolog A	Nucleus	0	4	0	2	0	1	7	5.72E-02	
Q2NKX8	ERCC6L PICH	DNA excision repair protein ERCC-6-like	Nucleus	0	1	0	2	0	3	6	2.57E-02	11a
Q5QE6	DNTTIP2	deoxynucleotidyltransferase, terminal, interacting protein 2	Nucleus	0	1	0	2	0	1	4	1.61E-02	

	CEP170 FAM68A											
Q5SW79	KAB KIAA0470	Centrosomal protein of 170 kDa	Nucleus	0	4	0	1	0	4	9	3.99E-02	11a
Q5TFE4	NT5DC1	5'-nucleotidase domain containing 1	Nucleus	1	4	1	3	1	4	11	1.32E-03	11a
Q6NXT2	H3F3C	H3 histone, family 3C	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q6ZRS2	SRCAP	Snf2-related CREBBP activator protein	Nucleus	0	2	0	1	0	2	5	7.49E-03	11a, 12a, 13
Q71DI3	HIST2H3A	Histone H3.2	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q7Z3B4	NUP54	nucleoporin 54kDa	Nucleus	0	2	0	3	0	2	7	2.19E-03	11a
Q7Z3J3	RGPD4 (includes others)*	RANBP2-like and GRIP domain containing 5	Nucleus	0	1	0	1	0	1	3	0.00E+00	12a, 13
Q7Z5L9	IRF2BP2	interferon regulatory factor 2 binding protein 2	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q86UK7	ZNF598	zinc finger protein 598	Nucleus	0	5	0	6	0	5	16	8.92E-05	11a
Q86WB0	ZC3HC1	zinc finger, C3HC-type containing 1	Nucleus	0	2	0	1	0	2	5	7.49E-03	11a
Q8IV63	VRK3	Inactive serine/threonine-protein kinase VRK3	Nucleus	0	2	0	2	0	2	6	0.00E+00	
Q8NOX7	SPG20	spastic paraplegia 20 (Troyer syndrome)	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q8N684	CPSF7	cleavage and polyadenylation specific factor 7, 59kDa	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q8NI36	WDR36	WD repeat domain 36	Nucleus	0	1	0	1	0	2	4	1.61E-02	
Q8TEQ6	GEMIN5	gem (nuclear organelle) associated protein 5	Nucleus	1	3	1	5	1	4	12	6.53E-03	
Q8WWK9	CKAP2	cytoskeleton associated protein 2	Nucleus	0	3	0	2	0	3	8	1.32E-03	
Q92804	TAF15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	Nucleus	0	1	0	2	0	1	4	1.61E-02	11a
Q96HS1	PGAM5	PGAM family member 5, serine/threonine protein phosphatase	Nucleus	0	2	0	1	0	1	4	1.61E-02	11a
Q96JM3	CHAMP1	chromosome alignment maintaining phosphoprotein 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q96M27	PRRC1	proline-rich coiled-coil 1	Nucleus	0	2	0	2	0	2	6	0.00E+00	12a, 13
Q96ST3	SIN3A	SIN3 transcription regulator family member A	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q96T88	UHFR1 ICBP90	E3 ubiquitin-protein ligase UHFR1	Nucleus	1	3	1	4	1	3	10	2.19E-03	11a

		NP95 RNF106									
		RMDN3									
		FAM82A2									
		FAM82C PTPIP51									
		hucep-10									
		UNQ3122/PRO1									
Q96TC7	0274	Regulator of microtubule dynamics protein 3	Nucleus	0	1	0	1	0	1	3	0.00E+00
Q99504	EYA3	EYA transcriptional coactivator and phosphatase 3	Nucleus	0	1	0	1	0	1	3	0.00E+00
Q9BTC0	DIDO1	death inducer-obliterator 1	Nucleus	0	1	0	1	0	1	3	0.00E+00
Q9BTE3	MCMBP	minichromosome maintenance complex binding protein	Nucleus	0	2	0	3	0	1	6	2.57E-02
Q9BVL2	NUP58	nucleoporin 58kDa	Nucleus	0	1	0	2	0	1	4	1.61E-02
Q9BVP2	GNL3	guanine nucleotide binding protein-like 3	Nucleus	0	2	0	3	0	2	7	2.19E-03
Q9BYG3	NIFK	nucleolar protein interacting with the FHA domain of MKI67	Nucleus	0	3	0	3	0	2	8	1.32E-03
Q9BZA5	TXLNGY	taxilin gamma pseudogene, Y-linked	Nucleus	0	1	0	1	0	1	3	0.00E+00
	CRNL1 CRN CGI-201										
Q9BZJ0	MSTP021	Crooked neck-like protein 1	Nucleus	0	1	0	2	0	2	5	7.49E-03
Q9GZR7	DDX24	ATP-dependent RNA helicase DDX24	Nucleus	0	2	0	2	0	1	5	7.49E-03
Q9H6S0	YTHDC2	Probable ATP-dependent RNA helicase YTHDC2	Nucleus	2	5	1	6	2	6	17	1.06E-03
Q9H814	PHAX RNUXA	Phosphorylated adapter RNA export protein	Nucleus	0	1	0	2	0	2	5	7.49E-03
Q9HC38	GLOD4	glyoxalase domain containing 4	Nucleus	0	1	0	1	0	1	3	0.00E+00
	CWC22										
Q9HCG8	KIAA1604 NCM	Pre-mRNA-splicing factor CWC22 homolog	Nucleus	0	1	0	1	0	1	3	0.00E+00
Q9NQT5	EXOSC3 RRP40 CGI-102	Exosome complex component RRP40	Nucleus	0	2	0	1	0	1	4	1.61E-02
Q9NTZ6	RBM12	RNA binding motif protein 12	Nucleus	0	1	0	2	0	2	5	7.49E-03
Q9NW13	RBM28	RNA-binding protein 28	Nucleus	0	1	0	1	0	2	4	1.61E-02

Q9NXV6	CDKN2AIP	CDKN2A interacting protein	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a, 12a, 13
Q9P2N5	RBM27	RNA binding motif protein 27	Nucleus	0	2	0	1	0	2	5	7.49E-03	10,11a, 12a, 13
Q9UBV8	PEF1	penta-EF-hand domain containing 1	Nucleus	0	2	0	1	0	1	4	1.61E-02	11a
Q9UHD9	UBQLN2	ubiquilin 2	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q9UIV1	CNOT7 CAF1	CCR4-NOT transcription complex subunit 7	Nucleus	0	2	0	2	0	1	5	7.49E-03	
Q9UJX3	ANAPC7 APC7	Anaphase-promoting complex subunit 7	Nucleus	0	4	0	3	0	4	11	3.88E-04	
Q9UJZ1	STOML2	stomatin (EPB72)-like 2	Nucleus	0	4	0	5	0	3	12	2.28E-03	11a
Q9UKI9	POU2F3	POU class 2 homeobox 3	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q9UKV3	ACIN1 ACINUS KIAA0670	Apoptotic chromatin condensation inducer in the nucleus (Acinus)	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
	DICER1 DICER HERNA KIAA0928	Endoribonuclease Dicer	Nucleus	0	4	0	5	0	5	14	1.51E-04	11a
Q9Y2R4	DDX52 ROK1 HUSSY-19	Probable ATP-dependent RNA helicase DDX52	Nucleus	0	1	0	1	0	1	3	0.00E+00	
	SUGT1	SGT1 homolog, MIS12 kinetochore complex assembly cochaperone	Nucleus	0	2	0	1	0	1	4	1.61E-02	11a
Q9Y3B4	SF3B6	splicing factor 3b, subunit 6, 14kDa	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q9Y3C1	NOP16 CGI-117 HSPC111	Nucleolar protein 16	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
	SAMHD1 MOP5	Deoxynucleoside triphosphate triphosphohydrolase SAMHD1	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q9Y4W2	LAS1L	LAS1-like, ribosome biogenesis factor	Nucleus	1	4	1	5	1	6	15	2.28E-03	11a
P02786	TFRC	Transferrin receptor protein 1	Plasma Membrane	0	2	0	3	0	2	7	2.19E-03	
P08195	SLC3A2 MDU1	4F2 cell-surface antigen heavy chain	Plasma Membrane	0	2	0	2	0	3	7	2.19E-03	

P35613	BSG	basigin (Ok blood group)	Plasma Membrane	0	1	0	2	0	1	4	1.61E-02	11a, 12a, 13
P46379	BAG6 BAT3 G3	Large proline-rich protein BAG6	Plasma Membrane	0	3	0	2	0	3	8	1.32E-03	12a, 13
P61758	VBP1	von Hippel-Lindau binding protein 1	Plasma Membrane	1	5	1	3	1	4	12	6.53E-03	
Q00341	HDLBP HBP VGL	Vigilin	Plasma Membrane	0	2	0	3	0	2	7	2.19E-03	11a,13
	SNTB2 D16S2531E											
Q13425	SNT2B2 SNTL	Beta-2-syntrophin	Plasma Membrane	0	1	0	1	0	1	3	0.00E+00	
Q15836	VAMP3 SYB3	Vesicle-associated membrane protein 3	Plasma Membrane	0	1	0	1	0	1	3	0.00E+00	
Q9Y2A7	NCKAP1 HEM2 KIAA0587 NAP1	Nck-associated protein 1	Plasma Membrane	0	1	0	1	0	1	3	0.00E+00	12a
	UBA6 MOP4 AOAVT1											
A00170	AIP	aryl hydrocarbon receptor interacting protein	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
000203	AP3B1 ADTB3A	AP-3 complex subunit beta-1	Cytoplasm	0	2	0	2	0	2	6	0.00E+00	
O14920	IKBKB IKKB	Inhibitor of nuclear factor kappa-B kinase subunit beta	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	12a, 13
O14974	PPP1R12A	protein phosphatase 1, regulatory subunit 12A	Cytoplasm	0	2	0	3	0	3	8	1.32E-03	10, 12a, 13
	ARHGEF10 O15013											
O15013	KIAA0294	Rho guanine nucleotide exchange factor 10	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
O15042	U2SURP KIAA0332 SR140	U2 snRNP-associated SURP motif-containing protein	Cytoplasm	1	4	1	3	1	3	10	2.19E-03	11a
			Plasma Membrane	0	3	0	3	0	3	9	0.000E+00	
Q9BVK6	TMED9	transmembrane p24 trafficking protein 9										

**Table S5.** Proteins identified from HEK293 cells treated with **2** (Ac<sub>4</sub>GalNAz) (indicated the proteins identified in previous reports)

ID	Gene	Description	Location	2 (Ac <sub>4</sub> GalNAz)								t-test	Reference
				Spectral counts									
				Exp. 1	Exp. 2	Exp. 3	Sum	-	+	-	+		
A6NEC2	LOC440434	aminopeptidase puromycin sensitive pseudogene	Cytoplasm	0	4	0	4	0	5	13	2.93E-03	13	
A6NHL2	TUBAL3	tubulin, alpha-like 3	Cytoplasm	0	2	0	2	0	2	6	0.00E+00		
O00154	ACOT7	acyl-CoA thioesterase 7	Cytoplasm	0	2	0	3	0	4	9	1.76E-02	11a	
O00232	PSMD12	proteasome 26S subunit, non-ATPase 12	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a	
O14964	HGS	hepatocyte growth factor-regulated tyrosine kinase substrate	Cytoplasm	0	11	0	11	0	11	33	0.00E+00		
O14974	PPP1R12A	protein phosphatase 1, regulatory subunit 12A	Cytoplasm	0	8	0	8	0	8	24	0.00E+00	10, 12a, 13	
O15164	TRIM24	tripartite motif containing 24	Cytoplasm	0	2	0	4	0	6	12	3.71E-02		
O15294	OGT	O-linked N-acetylglucosamine (GlcNAc) transferase	Cytoplasm	0	3	0	3	0	4	10	4.93E-03	10,13, 11a	
O15405	TOX3	TOX high mobility group box family member 3	Cytoplasm	0	3	0	3	0	3	9	0.00E+00		
O43432	EIF4G3	eukaryotic translation initiation factor 4 gamma, 3	Cytoplasm	0	2	0	2	0	2	6	0.00E+00		
O43617	TRAPP C3	trafficking protein particle complex 3	Cytoplasm	0	1	0	1	0	1	3	0.00E+00		
O43765	SGTA	small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha	Cytoplasm	0	1	0	1	0	1	3	0.00E+00		
O43776	NARS	asparaginyl-tRNA synthetase	Cytoplasm	0	4	0	5	0	6	15	6.54E-03	9,13, 11a	
O60518	RANBP6	RAN binding protein 6	Cytoplasm	0	3	0	3	0	3	9	0.00E+00		
O75390	CS	citrate synthase	Cytoplasm	0	3	0	3	0	3	9	0.00E+00		
O95373	IPO7	importin 7	Cytoplasm	0	3	0	3	0	4	10	4.93E-03	13, 11a	
O95486	SEC24A	SEC24 homolog A, COPII coat complex component	Cytoplasm	0	8	0	8	0	9	25	7.98E-04		

O95487	SEC24B	SEC24 homolog B, COPII coat complex component	Cytoplasm	0	11	0	12	0	14	37	2.54E-03	11a
O95628	CNOT4	CCR4-NOT transcription complex, subunit 4	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
O95677	EYA4	EYA transcriptional coactivator and phosphatase 4	Cytoplasm	0	3	0	3	0	3	9	0.00E+00	
O95678	KRT75	keratin 75, type II	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
P00492	HPRT1	hypoxanthine phosphoribosyltransferase 1	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	10,13
P05412	JUN	jun proto-oncogene	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	13
P05783	KRT18	keratin 18, type I	Cytoplasm	0	7	0	6	0	6	19	1.38E-03	13
P05787	KRT8	keratin 8, type II	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	13
P09960	LTA4H	leukotriene A4 hydrolase	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	9, 13
P13489	RNH1	ribonuclease/angiogenin inhibitor 1	Cytoplasm	0	4	0	4	0	4	12	0.00E+00	11a
P19367	HK1	hexokinase 1	Cytoplasm	0	5	0	5	0	5	15	0.00E+00	
P20042	EIF2S2	eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
P21266	GSTM3	glutathione S-transferase mu 3 (brain)	Cytoplasm	0	6	0	4	0	2	12	3.71E-02	13
P23921	RRM1	ribonucleotide reductase M1	Cytoplasm	0	4	0	3	0	2	9	1.76E-02	9, 13, 11a
P24752	ACAT1	acetyl-CoA acetyltransferase 1	Cytoplasm	0	3	0	3	0	3	9	0.00E+00	11a
P25325	MPST	mercaptopyruvate sulfurtransferase	Cytoplasm	0	3	0	3	0	3	9	0.00E+00	11a
P26641	EEF1G	eukaryotic translation elongation factor 1 gamma	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	9, 13, 11a
P30041	PRDX6	peroxiredoxin 6	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
P30154	PPP2R1B	protein phosphatase 2, regulatory subunit A, beta	Cytoplasm	0	4	0	3	0	3	10	4.93E-03	
P41091	EIF2S3	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	9, 13, 11a
P41250	GARS	glycyl-tRNA synthetase	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	13, 11a
P46109	CRKL	v-crk avian sarcoma virus CT10 oncogene homolog-like	Cytoplasm	0	2	0	2	0	2	6	0.00E+00	11a

P46781	RPS9	ribosomal protein S9	Cytoplasm	0	3	0	3	0	4	10	4.93E-03	13
P46977	STT3A	STT3A, subunit of the oligosaccharyltransferase complex (catalytic)	Cytoplasm	0	4	0	3	0	3	10	4.93E-03	
P47756	CAPZB	capping protein (actin filament) muscle Z-line, beta	Cytoplasm	0	3	0	3	0	3	9	0.00E+00	12a, 13
P48147	PREP	prolyl endopeptidase	Cytoplasm	0	10	0	9	0	8	27	2.05E-03	
P49589	CARS	cysteinyl-tRNA synthetase	Cytoplasm	0	3	0	4	0	5	12	1.01E-02	11a
P53396	ACLY	ATP citrate lyase	Cytoplasm	0	14	0	14	0	14	42	0.00E+00	13, 11a
P60981	DSTN	destrin (actin depolymerizing factor)	Cytoplasm	0	3	0	3	0	3	9	0.00E+00	11a
P61026	RAB10	RAB10, member RAS oncogene family	Cytoplasm	0	3	0	3	0	3	9	0.00E+00	
P61081	UBE2M	ubiquitin-conjugating enzyme E2M	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
P62136	PPP1CA	protein phosphatase 1, catalytic subunit, alpha isozyme	Cytoplasm	0	4	0	4	0	4	12	0.00E+00	
P62854	RPS26	ribosomal protein S26	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
P68036	UBE2L3	ubiquitin-conjugating enzyme E2L 3	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
Q02543	RPL18A	ribosomal protein L18a	Cytoplasm	0	3	0	3	0	4	10	4.93E-03	10, 13
Q06210	GFPT1	glutamine-fructose-6-phosphate transaminase 1	Cytoplasm	0	4	0	3	0	2	9	1.76E-02	11a
Q06413	MEF2C	myocyte enhancer factor 2C	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
Q13085	ACACA	acetyl-CoA carboxylase alpha	Cytoplasm	0	4	0	3	0	2	9	1.76E-02	11a
Q13232	NME3	NME/NM23 nucleoside diphosphate kinase 3	Cytoplasm	0	4	0	3	0	2	9	1.76E-02	
Q14671	PUM1	pumilio RNA-binding family member 1	Cytoplasm	1	4	1	4	2	4	12	7.63E-03	
Q15436	SEC23A	Sec23 homolog A, COPII coat complex component	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	10
Q15717	ELAVL1	ELAV like RNA binding protein 1	Cytoplasm	0	4	0	3	0	3	10	4.93E-03	10, 13, 11a
Q16204	CCDC6	coiled-coil domain containing 6	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
Q16543	CDC37	cell division cycle 37	Cytoplasm	0	2	0	2	0	2	6	0.00E+00	11a
Q58FF3	HSP90B2P	heat shock protein 90kDa beta (Grp94), member 2, pseudogene	Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
Q58FG0	HSP90AA5P	heat shock protein 90kDa alpha (cytosolic), class A member 5,	Cytoplasm	0	4	0	3	0	3	10	4.93E-03	

pseudogene														
					Cytoplasm	0	7	0	7	0	7	21	0.00E+00	11a
Q5JSZ5	PRRC2B	proline-rich coiled-coil 2B			Cytoplasm	0	7	0	7	0	7	21	0.00E+00	11a
Q5T6F2	UBAP2	ubiquitin associated protein 2			Cytoplasm	0	8	0	8	0	8	24	0.00E+00	13, 11a
Q7Z3K3	POGZ	pogo transposable element with ZNF domain			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	13, 11a
Q7Z4Q2	HEATR3	HEAT repeat containing 3			cytoplasm	0	4	0	3	0	2	9	1.76E-02	11a
Q7Z6Z7	HUWE1	HECT, UBA and WWE domain containing 1, E3 ubiquitin protein ligase			Cytoplasm	0	6	0	6	0	6	18	0.00E+00	11a
Q86YP4	GATAD2A	GATA zinc finger domain containing 2A			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
Q8IWZ3	ANKHD1/A				Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
	NKHD1- EIF4EBP3	ankyrin repeat and KH domain containing 1			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
Q8NHV4	NEDD1	neural precursor cell expressed, developmentally down-regulated 1			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
Q8WXI9	GATAD2B	GATA zinc finger domain containing 2B			Cytoplasm	0	5	0	5	0	5	15	0.00E+00	13, 11a
Q92879	CELF1	CUGBP, Elav-like family member 1			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
Q96D71	REPS1	RALBP1 associated Eps domain containing 1			cytoplasm	0	3	0	3	0	3	9	0.00E+00	
Q96F45	ZNF503	zinc finger protein 503			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	11a
Q96KB5	PBK	PDZ binding kinase			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
Q96RN5	MED15	mediator complex subunit 15			Cytoplasm	0	4	0	4	0	5	13	2.93E-03	11a
Q9C0B0	UNK	unkempt family zinc finger			Cytoplasm	0	3	0	3	0	3	9	0.00E+00	11a
Q9H3U1	UNC45A	unc-45 myosin chaperone A			cytoplasm	0	5	0	5	0	5	15	0.00E+00	11a
Q9H4A3	WNK1	WNK lysine deficient protein kinase 1			Cytoplasm	0	4	0	4	0	4	12	0.00E+00	10, 13
Q9H4A4	RNPEP	arginyl aminopeptidase (aminopeptidase B)			Cytoplasm	0	3	0	3	0	3	9	0.00E+00	
Q9H6Z4	RANBP3	RAN binding protein 3			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	
Q9H857	NT5DC2	5'-nucleotidase domain containing 2			Cytoplasm	0	4	0	4	0	5	13	2.93E-03	
Q9NRR5	UBQLN4	ubiquilin 4			Cytoplasm	0	2	0	2	0	2	6	0.00E+00	
Q9NYJ8	TAB2	TGF-beta activated kinase 1/MAP3K7 binding protein 2			Cytoplasm	0	1	0	1	0	1	3	0.00E+00	

Q9UBT2	UBA2	ubiquitin-like modifier activating enzyme 2	Cytoplasm	0	5	0	4	0	4	13	2.93E-03	
Q9UGR2	ZC3H7B	zinc finger CCCH-type containing 7B	Cytoplasm	0	4	0	3	0	3	10	4.93E-03	
Q9UIU6	SIX4	SIX homeobox 4	cytoplasm	0	1	0	1	0	1	3	0.00E+00	
Q9UL15	BAG5	BCL2-associated athanogene 5	Cytoplasm	0	4	0	3	0	2	9	1.76E-02	11a
Q9UL46	PSME2	proteasome activator subunit 2	Cytoplasm	0	3	0	3	0	4	10	4.93E-03	13
Q9UMX0	UBQLN1	ubiquilin 1	Cytoplasm	0	10	0	10	0	10	30	0.00E+00	
Q9Y4R8	TELO2	telomere maintenance 2	Cytoplasm	0	4	0	4	0	4	12	0.00E+00	
Q9Y520	PRRC2C	proline-rich coiled-coil 2C	Cytoplasm	0	10	0	10	0	10	30	0.00E+00	10, 13, 11a
Q9Y5A9	YTHDF2	YTH N(6)-methyladenosine RNA binding protein 2	Cytoplasm	0	6	0	6	0	6	18	0.00E+00	11a
P04062	GBA	glucosidase, beta, acid	Cytoplasm-Endosome	0	1	0	1	0	1	3	0.00E+00	
P06280	GLA	galactosidase, alpha	Cytoplasm-Endosome	0	1	0	1	0	2	4	2.86E-02	
P15586	GNS	glucosamine (N-acetyl)-6-sulfatase	Cytoplasm-Endosome	0	4	0	4	0	4	12	0.00E+00	
P51148	RAB5C	RAB5C, member RAS oncogene family	Cytoplasm-Endosome	0	3	0	3	0	4	10	4.93E-03	11a
Q12788	TBL3	transducin (beta)-like 3	Cytoplasm-Endosome	0	1	0	1	0	1	3	0.00E+00	11a
O00429	DNM1L	dynamin 1-like	Cytoplasm-ER	0	7	0	6	0	6	19	1.38E-03	
O00469	PLOD2	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	Cytoplasm-ER	0	9	0	8	0	7	24	2.58E-03	
O15027	SEC16A	SEC16 homolog A, endoplasmic reticulum export factor	Cytoplasm-ER	0	2	0	2	0	2	6	0.00E+00	11a
O43852	CALU	calumenin	Cytoplasm-ER	0	1	0	1	0	1	3	0.00E+00	11a
O94979	SEC31A	SEC31 homolog A, COPII coat complex component	Cytoplasm-ER	0	1	0	1	0	1	3	0.00E+00	10, 13, 11a
P00387	CYB5R3	cytochrome b5 reductase 3	Cytoplasm-ER	0	2	0	3	0	4	9	1.76E-02	

P08133	ANXA6	annexin A6	Cytoplasm-ER	0	3	0	3	0	3	9	0.00E+00
Q13724	MOGS	mannosyl-oligosaccharide glucosidase	Cytoplasm-ER	0	1	0	2	0	1	4	2.86E-02
Q15084	PDIA6	protein disulfide isomerase family A, member 6	Cytoplasm-ER	0	5	0	5	0	5	15	0.00E+00
Q96HE7	ERO1A	endoplasmic reticulum oxidoreductase alpha	Cytoplasm-ER	0	4	0	5	0	6	15	6.54E-03
Q9BS26	ERP44	endoplasmic reticulum protein 44	Cytoplasm-ER	0	2	0	3	0	4	9	1.76E-02
Q9NZM3	ITSN2	intersectin 2	Cytoplasm-ER	0	2	0	2	0	2	6	0.00E+00
Q9Y4L1	HYOU1	hypoxia up-regulated 1	Cytoplasm-ER	0	7	0	8	0	10	25	5.51E-03
Q9Y6Y8	SEC23IP	SEC23 interacting protein	Cytoplasm-ER	0	11	0	10	0	10	31	5.20E-04
P04899	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	Cytoplasm-Golgi	0	5	0	5	0	5	15	0.00E+00
			Cytoplasm-Golgi	0	2	0	3	0	5	10	3.17E-02
P53621	COPA	coatomer protein complex, subunit alpha	Cytoplasm-Golgi	0	7	0	9	0	12	28	1.17E-02
P55786	NPEPPS	aminopeptidase puromycin sensitive	Cytoplasm-Golgi	0	2	0	4	0	6	12	3.71E-02
Q10567	AP1B1	adaptor-related protein complex 1, beta 1 subunit	Cytoplasm-Golgi	0	5	0	5	0	5	15	0.00E+00
Q13492	PICALM	phosphatidylinositol binding clathrin assembly protein	Cytoplasm-Golgi	0	1	0	1	0	1	3	0.00E+00
Q14677	CLINT1	clathrin interactor 1	Cytoplasm-Golgi	0	3	0	3	0	3	9	0.00E+00
Q9H8Y8	GORASP2	golgi reassembly stacking protein 2, 55kDa	Cytoplasm-Membrane	0	1	0	1	0	1	3	0.00E+00
O60641	SNAP91	synaptosomal-associated protein, 91kDa	Cytoplasm-Membrane	0	3	0	3	0	3	9	0.00E+00
P07384	CAPN1	calpain 1, (mu/l) large subunit	Cytoplasm-Membrane	0	1	0	1	0	1	3	0.00E+00
P20839	IMPDH1	IMP (inosine 5'-monophosphate) dehydrogenase 1	Cytoplasm-Membrane	0	1	0	1	0	1	3	0.00E+00

P45880	VDAC2	voltage-dependent anion channel 2	Cytoplasm-Membrane	2	8	2	8	4	8	24	7.63E-03	11a
P84085	ARF5	ADP-ribosylation factor 5	Cytoplasm-Membrane	0	1	0	1	0	1	3	0.00E+00	
Q07812	BAX	BCL2-associated X protein	Cytoplasm-Membrane	0	3	0	4	0	5	12	1.01E-02	
Q8IUD2	ERC1	ELKS/RAB6-interacting/CAST family member 1	Cytoplasm-Membrane	0	1	0	1	0	1	3	0.00E+00	12a, 11a
Q8IV08	PLD3	phospholipase D family, member 3	Cytoplasm-Membrane	0	5	0	3	0	2	10	3.17E-02	
Q9NZB2	FAM120A	family with sequence similarity 120A	Cytoplasm-Membrane	0	1	0	1	0	1	3	0.00E+00	
P04181	OAT	ornithine aminotransferase	Cytoplasm-mitochondria	0	3	0	4	0	6	13	1.95E-02	11a
P11498	PC	pyruvate carboxylase	Cytoplasm-mitochondria	0	1	0	1	0	1	3	0.00E+00	
Q9Y277	VDAC3	voltage-dependent anion channel 3	Cytoplasm-mitochondria	0	2	0	2	0	2	6	0.00E+00	11a
O00411	POLRMT	polymerase (RNA) mitochondrial (DNA directed)	Cytoplasm-Mitochondrion	0	4	0	4	0	4	12	0.00E+00	
P00390	GSR	glutathione reductase	Cytoplasm-Mitochondrion	0	2	0	2	0	2	6	0.00E+00	11a
P11216	PYGB	phosphorylase, glycogen; brain	Cytoplasm-Mitochondrion	0	5	0	4	0	4	13	2.93E-03	
Q10713	PMPCA	peptidase (mitochondrial processing) alpha	Cytoplasm-Mitochondrion	0	3	0	3	0	3	9	0.00E+00	
Q16891	IMMT	inner membrane protein, mitochondrial	Cytoplasm-Mitochondrion	0	5	0	5	0	5	15	0.00E+00	

				n							
Q9H845	ACAD9	acyl-CoA dehydrogenase family, member 9	Cytoplasm-Mitochondrion	0	1	0	1	0	1	3	0.00E+00
P14174	MIF	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	Extracellular Space	0	2	0	2	0	2	6	0.00E+00
Q02809	PLOD1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	Extracellular Space	0	3	0	3	0	4	10	4.93E-03
Q8NB5	COLGALT1	collagen beta(1-O)galactosyltransferase 1	Extracellular Space	0	5	0	5	0	5	15	0.00E+00
Q92820	GGH	gamma-glutamyl hydrolase (conjugase, folylpolygammaglutamyl hydrolase)	Extracellular Space	0	6	0	6	0	7	19	1.38E-03
Q9H3G5	CPVL	carboxypeptidase, vitellogenin-like	Extracellular Space	0	3	0	4	0	5	12	1.01E-02
A6NKT7	RGPD4 (includes others)*	RANBP2-like and GRIP domain containing 5	Nucleus	0	1	0	1	0	1	3	0.00E+00
A6NMY6	ANXA2P2	annexin A2 pseudogene 2	Nucleus	0	1	0	1	0	1	3	0.00E+00
A8CG34	POM121/P OM121C*	POM121 transmembrane nucleoporin	Nucleus	0	2	0	2	0	2	6	0.00E+00
O00268	TAF4	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	Nucleus	0	1	0	1	0	1	3	0.00E+00
O00273	DFFA	DNA fragmentation factor, 45kDa, alpha polypeptide	Nucleus	0	2	0	2	0	2	6	0.00E+00
O00442	RTCA	RNA 3'-terminal phosphate cyclase	Nucleus	0	2	0	2	0	2	6	0.00E+00
O00567	NOP56	NOP56 ribonucleoprotein	Nucleus	0	7	0	6	0	6	19	1.38E-03
O14497	ARID1A	AT rich interactive domain 1A (SWI-like)	Nucleus	0	4	0	4	0	4	12	0.00E+00
O14776	TCERG1	transcription elongation regulator 1	Nucleus	0	6	0	6	0	6	18	0.00E+00

O14980	XPO1	exportin 1	Nucleus	0	9	0	7	0	6	22	7.08E-03	11a, 11b
O15047	SETD1A	SET domain containing 1A	Nucleus	0	1	0	1	0	1	3	0.00E+00	10, 13, 11a
O43143	DHX15	DEAH (Asp-Glu-Ala-His) box helicase 15	Nucleus	0	11	0	11	0	12	34	4.32E-04	11a, 13
O43524	FOXO3	forkhead box O3	Nucleus	0	1	0	1	0	1	3	0.00E+00	
O43670	ZNF207	zinc finger protein 207	Nucleus	0	3	0	3	0	3	9	0.00E+00	10, 13
O43684	BUB3	BUB3 mitotic checkpoint protein	Nucleus	0	2	0	2	0	2	6	0.00E+00	
O43823	AKAP8	A kinase (PRKA) anchor protein 8	Nucleus	0	2	0	3	0	4	9	1.76E-02	
O75152	ZC3H11A	zinc finger CCCH-type containing 11A	Nucleus	0	1	0	1	0	1	3	0.00E+00	
O75179	ANKRD17	ankyrin repeat domain 17	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a, 13
O75376	NCOR1	nuclear receptor corepressor 1	Nucleus	0	2	0	2	0	2	6	0.00E+00	11a, 13
O75400	PRPF40A	PRP40 pre-mRNA processing factor 40 homolog A	Nucleus	1	5	2	5	1	5	15	4.08E-03	11a,
O75909	CCNK	cyclin K	Nucleus	0	1	0	1	0	1	3	0.00E+00	13
O75925	PIAS1	protein inhibitor of activated STAT, 1	Nucleus	0	3	0	3	0	4	10	4.93E-03	
O94842	TOX4	TOX high mobility group box family member 4	Nucleus	0	4	0	4	0	4	12	0.00E+00	
O94900	TOX	thymocyte selection-associated high mobility group box	Nucleus	0	3	0	3	0	3	9	0.00E+00	
P00491	PNP	purine nucleoside phosphorylase	Nucleus	0	6	0	6	0	6	18	0.00E+00	11a
P04632	CAPNS1	calpain, small subunit 1	Nucleus	0	1	0	2	0	1	4	2.86E-02	11a
P04637	TP53	tumor protein p53	Nucleus	0	1	0	1	0	1	3	0.00E+00	13
P05455	SSB	Sjogren syndrome antigen B (autoantigen La)	Nucleus	0	2	0	2	0	2	6	0.00E+00	
P07355	ANXA2	annexin A2	Nucleus	0	1	0	1	0	1	3	0.00E+00	9,11a, 13
P08047	SP1	Sp1 transcription factor	Nucleus	0	8	0	8	0	8	24	0.00E+00	10, 13
P09086	POU2F2	POU class 2 homeobox 2	Nucleus	0	2	0	2	0	2	6	0.00E+00	
P11388	TOP2A	topoisomerase (DNA) II alpha	Nucleus	0	6	0	7	0	9	22	7.08E-03	
P13010	XRCC5	X-ray repair complementing defective repair in Chinese hamster cells	Nucleus	0	13	0	13	0	13	39	0.00E+00	11a, 13

		5 (double-strand-break rejoining)										
P14859	POU2F1	POU class 2 homeobox 1	Nucleus	0	3	0	3	0	3	9	0.00E+00	10, 13, 11a
P17812	CTPS1	CTP synthase 1	Nucleus	0	5	0	8	0	12	25	2.72E-02	
P22234	PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	Nucleus	0	7	0	7	0	8	22	1.03E-03	10, 13, 11a
P22681	CBL	Cbl proto-oncogene, E3 ubiquitin protein ligase	Nucleus	0	3	0	5	0	8	16	3.34E-02	11a
P26358	DNMT1	DNA (cytosine-5-)methyltransferase 1	Nucleus	0	3	0	3	0	4	10	4.93E-03	11a
P26368	U2AF2	U2 small nuclear RNA auxiliary factor 2	Nucleus	0	3	0	3	0	3	9	0.00E+00	
P27816	MAP4	microtubule-associated protein 4	Nucleus	0	4	0	4	0	4	12	0.00E+00	10, 13, 11a
P31689	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	10, 13
P33992	MCM5	minichromosome maintenance complex component 5	Nucleus	0	4	0	4	0	4	12	0.00E+00	
P35658	NUP214	nucleoporin 214kDa	Nucleus	0	11	0	11	0	11	33	0.00E+00	10, 11a, 11b, 13
P35659	DEK	DEK proto-oncogene	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a
P36873	PPP1CC	protein phosphatase 1, catalytic subunit, gamma isozyme	Nucleus	0	4	0	4	0	4	12	0.00E+00	
P37198	NUP62	nucleoporin 62kDa	Nucleus	1	4	1	4	2	4	12	7.63E-03	10, 11a, 13
P38432	COIL	coilin	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a
P38919	EIF4A3	eukaryotic translation initiation factor 4A3	Nucleus	0	4	0	4	0	4	12	0.00E+00	
P40938	RFC3	replication factor C (activator 1) 3, 38kDa	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
P41219	PRPH	peripherin	Nucleus	0	1	0	1	0	1	3	0.00E+00	
P42166	TMPO*	thymopoietin	Nucleus	0	8	0	8	0	9	25	7.98E-04	
P42167	TMPO*	thymopoietin	Nucleus	0	5	0	5	0	5	15	0.00E+00	
P46063	RECQL	RecQ helicase-like	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a

P49736	MCM2	minichromosome maintenance complex component 2	Nucleus	0	2	0	2	0	2	6	0.00E+00	
P49756	RBM25	RNA binding motif protein 25	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
P49790	NUP153	nucleoporin 153kDa	Nucleus	0	16	0	16	0	16	48	0.00E+00	10, 11a, 11b, 13
P49792	RANBP2	RAN binding protein 2	Nucleus	0	12	0	12	0	12	36	0.00E+00	11a, 11b, 13
P49848	TAF6	TAF6 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 80kDa	Nucleus	0	1	0	1	0	1	3	0.00E+00	
P51114	FXR1	fragile X mental retardation, autosomal homolog 1	Nucleus	0	3	0	3	0	3	9	0.00E+00	
P51610	HCFC1	host cell factor C1	Nucleus	0	20	0	20	0	20	60	0.00E+00	13
P52594	AGFG1	ArfGAP with FG repeats 1	Nucleus	0	2	0	2	0	2	6	0.00E+00	10, 11a, 13
P52701	MSH6	mutS homolog 6	Nucleus	0	9	0	9	0	9	27	0.00E+00	13
P52732	KIF11	kinesin family member 11	Nucleus	0	2	0	3	0	4	9	1.76E-02	11a
P52948	NUP98	nucleoporin 98kDa	Nucleus	0	6	0	6	0	6	18	0.00E+00	10, 11a, 13
P53007	SLC25A1	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	Nucleus	0	4	0	4	0	4	12	0.00E+00	
P53675	CLTCL1	clathrin, heavy chain-like 1	Nucleus	0	2	0	4	0	6	12	3.71E-02	9, 13
P54105	CLNS1A	chloride channel, nucleotide-sensitive, 1A	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a
P54727	RAD23B	RAD23 homolog B, nucleotide excision repair protein	Nucleus	0	13	0	13	0	13	39	0.00E+00	12a
P55060	CSE1L	CSE1 chromosome segregation 1-like (yeast)	Nucleus	0	2	0	2	0	2	6	0.00E+00	11a, 13
P55265	ADAR	adenosine deaminase, RNA-specific	Nucleus	0	6	0	5	0	4	15	6.54E-03	
P60953	CDC42	cell division cycle 42	Nucleus	0	1	0	1	0	1	3	0.00E+00	
P68400	CSNK2A1*	casein kinase 2, alpha 1 polypeptide	Nucleus	0	12	0	12	0	13	37	3.65E-04	
P78364	PHC1	polyhomeotic homolog 1 (Drosophila)	Nucleus	0	4	0	4	0	4	12	0.00E+00	
P85037	FOXK1	forkhead box K1	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a

Q01780	EXOSC10	exosome component 10	Nucleus	0	2	0	3	0	4	9	1.76E-02	11a
Q01844	EWSR1	EWS RNA-binding protein 1	Nucleus	6	16	1	16	1	16	48	7.63E-03	13
Q02078	MEF2A	myocyte enhancer factor 2A	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q02880	TOP2B	topoisomerase (DNA) II beta	Nucleus	0	3	0	3	0	3	9	0.00E+00	
Q03252	LMNB2	lamin B2	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q04726	TLE3	transducin-like enhancer of split 3	Nucleus	0	3	0	3	0	3	9	0.00E+00	
Q06546	GABPA	GA binding protein transcription factor, alpha subunit 60kDa	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q08J23	NSUN2	NOP2/Sun RNA methyltransferase family, member 2	Nucleus	0	5	0	3	0	2	10	3.17E-02	11a
Q12778	FOXO1	forkhead box O1	Nucleus	0	2	0	3	0	4	9	1.76E-02	11a, 13
Q12830	BPTF	bromodomain PHD finger transcription factor	Nucleus	0	5	0	5	0	5	15	0.00E+00	10, 11a, 13
Q12948	FOXC1	forkhead box C1	Nucleus	0	10	0	10	0	10	30	0.00E+00	
Q13185	CBX3	chromobox homolog 3	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q13428	TCOF1	Treacher Collins-Franceschetti syndrome 1	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a
Q13547	HDAC1	histone deacetylase 1	Nucleus	0	3	0	3	0	4	10	4.93E-03	10, 13
Q13620	CUL4B	cullin 4B	Nucleus	0	2	0	2	0	2	6	0.00E+00	
Q14008	CKAP5	cytoskeleton associated protein 5	Nucleus	0	4	0	3	0	3	10	4.93E-03	11a
Q14137	BOP1	block of proliferation 1	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a
Q14157	UBAP2L	ubiquitin associated protein 2-like	Nucleus	0	43	0	43	0	43	12 9	0.00E+00	10, 12a, 13
Q14657	LAGE3	L antigen family, member 3	Nucleus	0	3	0	3	0	3	9	0.00E+00	
Q14814	MEF2D	myocyte enhancer factor 2D	Nucleus	0	1	0	1	0	1	3	0.00E+00	13
Q15003	NCAPH	non-SMC condensin I complex, subunit H	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q15059	BRD3	bromodomain containing 3	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q15365	PCBP1	poly(rC) binding protein 1	Nucleus	12	21	5	21	2	21	63	1.92E-02	

Q15417	CNN3	calponin 3, acidic	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a
Q15428	SF3A2	splicing factor 3a, subunit 2, 66kDa	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q15459	SF3A1	splicing factor 3a, subunit 1, 120kDa	Nucleus	0	26	0	26	0	26	78	0.00E+00	11a
Q15532	SS18	synovial sarcoma translocation, chromosome 18	Nucleus	0	7	0	7	0	7	21	0.00E+00	
Q15596	NCOA2	nuclear receptor coactivator 2	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q15637	SF1	splicing factor 1	Nucleus	2	14	1	14	1	14	42	3.46E-04	10, 11a, 13
Q15648	MED1	mediator complex subunit 1	Nucleus	0	3	0	3	0	3	9	0.00E+00	
Q15652	JMJD1C	jumonji domain containing 1C	Nucleus	0	2	0	2	0	2	6	0.00E+00	
Q15750	TAB1	TGF-beta activated kinase 1/MAP3K7 binding protein 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q15942	ZYX	zyxin	Nucleus	0	7	0	7	0	7	21	0.00E+00	
Q16576	RBBP7	retinoblastoma binding protein 7	Nucleus	0	8	0	7	0	7	22	1.03E-03	
Q16656	NRF1	nuclear respiratory factor 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q2VIR3	EIF2S3L	Putative eukaryotic translation initiation factor 2 subunit 3-like protein	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q3YEC7	RABL6	RAB, member RAS oncogene family-like 6	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q53EL6	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q5QJE6	DNTTIP2	deoxynucleotidyltransferase, terminal, interacting protein 2	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q5T8P6	RBM26	RNA binding motif protein 26	Nucleus	0	5	0	5	0	5	15	0.00E+00	10, 11a, 13
Q5TFE4	NT5DC1	5'-nucleotidase domain containing 1	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a
Q5VZL5	ZMYM4	zinc finger, MYM-type 4	Nucleus	0	4	0	3	0	3	10	4.93E-03	
Q68CP9	ARID2	AT rich interactive domain 2 (ARID, RFX-like)	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q6MZP7	LIN54	lin-54 DREAM MuvB core complex component	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a, 13
Q6P3W7	SCYL2	SCY1-like, kinase-like 2	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a

Q6PJT7	ZC3H14	zinc finger CCCH-type containing 14	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a, 13
Q6SZW1	SARM1	sterile alpha and TIR motif containing 1	Nucleus	0	2	0	2	0	2	6	0.00E+00	
Q6UN15	FIP1L1	factor interacting with PAPOLA and CPSF1	Nucleus	0	9	0	9	0	9	27	0.00E+00	11a
Q6UU9	CRTC1	CREB regulated transcription coactivator 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q6VMQ6	ATF7IP	activating transcription factor 7 interacting protein	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a
Q7L2E3	DHX30	DEAH (Asp-Glu-Ala-His) box helicase 30	Nucleus	0	6	0	5	0	4	15	6.54E-03	
Q7LBC6	KDM3B	lysine (K)-specific demethylase 3B	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q7Z2W4	ZC3HAV1	zinc finger CCCH-type, antiviral 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q7Z3B4	NUP54	nucleoporin 54kDa	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a
Q7Z3J3	RGPD4 (includes others)*	RANBP2-like and GRIP domain containing 5	Nucleus	0	1	0	1	0	1	3	0.00E+00	13
Q7Z4I7	NUFIP2	nuclear fragile X mental retardation protein interacting protein 2	Nucleus	0	5	0	5	0	5	15	0.00E+00	10, 13
Q7Z589	C11orf30	chromosome 11 open reading frame 30	Nucleus	0	1	0	1	0	1	3	0.00E+00	13
Q7Z5J4	RAI1	retinoic acid induced 1	Nucleus	1	6	1	6	1	6	18	0.00E+00	11a
Q7Z739	YTHDF3	YTH N(6)-methyladenosine RNA binding protein 3	Nucleus	0	5	0	5	0	5	15	0.00E+00	10, 13
Q7Z7K6	CENPV	centromere protein V	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q86UK7	ZNF598	zinc finger protein 598	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a
Q86WB0	ZC3HC1	zinc finger, C3HC-type containing 1	Nucleus	0	3	0	3	0	3	9	0.00E+00	11a
Q86X55	CARM1	coactivator-associated arginine methyltransferase 1	Nucleus	3	8	1	8	1	8	24	5.45E-03	10, 11a, 12a, 13
Q8IVH2	FOXP4	forkhead box P4	Nucleus	0	4	0	4	0	4	12	0.00E+00	
Q8IVW6	ARID3B	AT rich interactive domain 3B (BRIGHT-like)	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q8IX12	CCAR1	cell division cycle and apoptosis regulator 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	10, 11a, 13
Q8N0X7	SPG20	spastic paraparesis 20 (Troyer syndrome)	Nucleus	0	1	0	1	0	1	3	0.00E+00	

Q8N3X1	FNBP4	formin binding protein 4	Nucleus	0	4	0	4	0	4	12	0.00E+00
Q8N684	CPSF7	cleavage and polyadenylation specific factor 7, 59kDa	Nucleus	0	1	0	1	0	1	3	0.00E+00
Q8NEV1	CSNK2A1*	casein kinase 2, alpha 1 polypeptide	Nucleus	0	11	0	10	0	10	31	5.20E-04
Q8NEZ2	VPS37A	vacuolar protein sorting 37 homolog A ( <i>S. cerevisiae</i> )	Nucleus	0	1	0	1	0	1	3	0.00E+00
Q8TAQ2	SMARCC2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	Nucleus	0	1	0	1	0	1	3	0.00E+00
Q8TEX9	IPO4	importin 4	Nucleus	0	1	0	1	0	1	3	0.00E+00
Q8WWM7	ATXN2L	ataxin 2-like	Nucleus	0	5	0	5	0	5	15	0.00E+00
Q8WXF0	SRSF12	serine/arginine-rich splicing factor 12	Nucleus	0	1	0	1	0	1	3	0.00E+00
Q92734	TFG	TRK-fused gene	Nucleus	0	4	0	4	0	4	12	0.00E+00
Q92769	HDAC2	histone deacetylase 2	Nucleus	0	5	0	4	0	4	13	2.93E-03
Q92793	CREBBP	CREB binding protein	Nucleus	0	2	0	2	0	2	6	0.00E+00
Q92922	SMARCC1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1	Nucleus	0	2	0	2	0	2	6	0.00E+00
Q93009	USP7	ubiquitin specific peptidase 7 (herpes virus-associated)	Nucleus	0	7	0	6	0	5	18	4.57E-03
Q93052	LPP	LIM domain containing preferred translocation partner in lipoma	Nucleus	0	4	0	4	0	4	12	0.00E+00
Q96FV9	THOC1	THO complex 1	Nucleus	0	1	0	1	0	1	3	0.00E+00
Q96HA1	POM121/POM121C*	POM121 transmembrane nucleoporin	Nucleus	0	2	0	2	0	2	6	0.00E+00
Q96HC4	PDLIM5	PDZ and LIM domain 5	Nucleus	0	1	0	1	0	1	3	0.00E+00
Q96HS1	PGAM5	PGAM family member 5, serine/threonine protein phosphatase, mitochondrial	Nucleus	0	1	0	1	0	1	3	0.00E+00
Q96I24	FUBP3	far upstream element (FUSE) binding protein 3	Nucleus	0	6	0	6	0	6	18	0.00E+00
Q96KR1	ZFR	zinc finger RNA binding protein	Nucleus	4	23	3	23	1	23	69	9.38E-04
Q96M27	PRRC1	proline-rich coiled-coil 1	Nucleus	0	4	0	4	0	4	12	0.00E+00
Q96ME7	ZNF512	zinc finger protein 512	Nucleus	0	1	0	1	0	1	3	0.00E+00

Q96P70	IPO9	importin 9	Nucleus	0	4	0	3	0	2	9	1.76E-02	11a
Q96S59	RANBP9	RAN binding protein 9	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q96T58	SPEN	spen family transcriptional repressor	Nucleus	0	2	0	2	0	2	6	0.00E+00	11a, 13
Q99426	TBCB	tubulin folding cofactor B	Nucleus	0	4	0	4	0	4	12	0.00E+00	11a
Q99504	EYA3	EYA transcriptional coactivator and phosphatase 3	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q99613	EIF3C	eukaryotic translation initiation factor 3, subunit C	Nucleus	0	3	0	3	0	3	9	0.00E+00	
Q99700	ATXN2	ataxin 2	Nucleus	0	5	0	5	0	5	15	0.00E+00	10, 13
Q99829	CPNE1	copine I	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q99856	ARID3A	AT rich interactive domain 3A (BRIGHT-like)	Nucleus	0	3	0	3	0	3	9	0.00E+00	
Q99958	FOXC2	forkhead box C2	Nucleus	0	4	0	3	0	3	10	4.93E-03	
Q9BQ04	RBM4B	RNA binding motif protein 4B	Nucleus	0	2	0	3	0	5	10	3.17E-02	
Q9BQ52	ELAC2	elaC ribonuclease Z 2	Nucleus	0	2	0	3	0	4	9	1.76E-02	
Q9BQA1	WDR77	WD repeat domain 77	Nucleus	0	4	0	2	0	3	9	1.76E-02	11a
Q9BTE3	MCMBP	minichromosome maintenance complex binding protein	Nucleus	0	7	0	4	0	2	13	4.82E-02	11a
Q9BUJ2	HNRNPUL1	heterogeneous nuclear ribonucleoprotein U-like 1	Nucleus	0	9	0	9	0	9	27	0.00E+00	
Q9BVL2	NUP58	nucleoporin 58kDa	Nucleus	0	9	0	9	0	9	27	0.00E+00	
Q9BW19	KIFC1	kinesin family member C1	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q9BWF3	RBM4	RNA binding motif protein 4	Nucleus	0	4	0	5	0	6	15	6.54E-03	11a
Q9BYJ9	YTHDF1	YTH N(6)-methyladenosine RNA binding protein 1	Nucleus	0	3	0	3	0	3	9	0.00E+00	10, 13
Q9C0B1	FTO	fat mass and obesity associated	Nucleus	0	8	0	6	0	5	19	9.42E-03	
Q9H1B7	IRF2BPL	interferon regulatory factor 2 binding protein-like	Nucleus	0	8	0	8	0	8	24	0.00E+00	11a
Q9H3S7	PTPN23	protein tyrosine phosphatase, non-receptor type 23	Nucleus	0	2	0	4	0	7	13	4.82E-02	
Q9H4W6	EBF3	early B-cell factor 3	Nucleus	0	2	0	2	0	2	6	0.00E+00	
Q9H7N4	SCAF1	SR-related CTD-associated factor 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a

Q9HAK2	EBF2	early B-cell factor 2	Nucleus	0	2	0	2	0	2	6	0.00E+00	
Q9HC38	GLOD4	glyoxalase domain containing 4	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q9NTZ6	RBM12	RNA binding motif protein 12	Nucleus	0	9	0	9	0	9	27	0.00E+00	11a
Q9NVP1	DDX18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	Nucleus	0	4	0	3	0	3	10	4.93E-03	
Q9NXV6	CDKN2AIP	CDKN2A interacting protein	Nucleus	0	5	0	5	0	5	15	0.00E+00	11a, 13
Q9NZN8	CNOT2	CCR4-NOT transcription complex, subunit 2	Nucleus	0	1	0	1	0	1	3	0.00E+00	
Q9P2N5	RBM27	RNA binding motif protein 27	Nucleus	0	3	0	3	0	3	9	0.00E+00	10, 11a, 13
Q9UH73	EBF1	early B-cell factor 1	Nucleus	0	2	0	2	0	2	6	0.00E+00	
Q9UHD9	UBQLN2	ubiquilin 2	Nucleus	0	11	0	11	0	11	33	0.00E+00	
Q9UHR5	SAP30BP	SAP30 binding protein	Nucleus	0	2	0	2	0	2	6	0.00E+00	11a, 13
Q9UHX1	PUF60	poly-U binding splicing factor 60KDa	Nucleus	0	6	0	6	0	6	18	0.00E+00	11a
Q9UJZ1	STOML2	stomatin (EPB72)-like 2	Nucleus	0	2	0	2	0	2	6	0.00E+00	11a
Q9UKI9	POU2F3	POU class 2 homeobox 3	Nucleus	0	2	0	2	0	2	6	0.00E+00	
Q9UKY1	ZHX1	zinc fingers and homeoboxes 1	Nucleus	0	1	0	1	0	1	3	0.00E+00	13
Q9ULM3	YEATS2	YEATS domain containing 2	Nucleus	0	2	0	2	0	2	6	0.00E+00	10,11a, 13
Q9ULT8	HECTD1	HECT domain containing E3 ubiquitin protein ligase 1	Nucleus	0	3	0	3	0	4	10	4.93E-03	11a
Q9ULU4	ZMYND8	zinc finger, MYND-type containing 8	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a
Q9UPN6	SCAF8	SR-related CTD-associated factor 8	Nucleus	0	10	0	10	0	10	30	0.00E+00	
Q9UPN9	TRIM33	tripartite motif containing 33	Nucleus	0	2	0	2	0	2	6	0.00E+00	11a
Q9Y2X3	NOP58	NOP58 ribonucleoprotein	Nucleus	0	8	0	9	0	11	28	4.41E-03	11a
Q9Y2X9	ZNF281	zinc finger protein 281	Nucleus	0	4	0	4	0	4	12	0.00E+00	11a, 13
Q9Y2Z0	SUGT1	SGT1 homolog, MIS12 kinetochore complex assembly cochaperone	Nucleus	0	3	0	3	0	4	10	4.93E-03	11a
Q9Y383	LUC7L2	LUC7-like 2 pre-mRNA splicing factor	Nucleus	0	1	0	1	0	1	3	0.00E+00	11a

Q9Y467	SALL2	spalt-like transcription factor 2	Nucleus	0	2	0	2	0	2	6	0.00E+00	
Q9Y4B4	RAD54L2	RAD54-like 2 ( <i>S. cerevisiae</i> )	Nucleus	0	3	0	3	0	4	10	4.93E-03	11a, 13
Q9Y4W2	LAS1L	LAS1-like, ribosome biogenesis factor	Nucleus	0	4	0	3	0	2	9	1.76E-02	11a
A5D8V6	VPS37C	vacuolar protein sorting 37 homolog C ( <i>S. cerevisiae</i> )	Plasma Membrane	0	1	0	1	0	1	3	0.00E+00	
O43491	EPB41L2	erythrocyte membrane protein band 4.1-like 2	Plasma Membrane	0	1	0	1	0	1	3	0.00E+00	11a
P04844	RPN2	ribophorin II	Plasma Membrane	0	1	0	1	0	1	3	0.00E+00	
P07947	YES1	YES proto-oncogene 1, Src family tyrosine kinase	Plasma Membrane	0	6	0	5	0	4	15	6.54E-03	
P08962	CD63	CD63 molecule	Plasma Membrane	0	3	0	3	0	3	9	0.00E+00	
P16615	ATP2A2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	Plasma Membrane	0	3	0	3	0	3	9	0.00E+00	13
P17655	CAPN2	calpain 2, (m/II) large subunit	Plasma Membrane	0	5	0	4	0	4	13	2.93E-03	
P35613	BSG	basigin (Ok blood group)	Plasma Membrane	0	1	0	1	0	1	3	0.00E+00	11a, 13
P50454	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	Plasma Membrane	0	7	0	7	0	8	22	1.03E-03	
P53618	COPB1	coatomer protein complex, subunit beta 1	Plasma Membrane	0	1	0	1	0	1	3	0.00E+00	9, 11a, 13
P60468	SEC61B	Sec61 translocon beta subunit	Plasma Membrane	0	1	0	1	0	1	3	0.00E+00	
P61758	VBP1	von Hippel-Lindau binding protein 1	Plasma Membrane	0	3	0	3	0	3	9	0.00E+00	
P63010	AP2B1	adaptor-related protein complex 2, beta 1 subunit	Plasma Membrane	0	17	0	16	0	15	48	6.50E-04	12a
Q08380	LGALS3BP	lectin, galactoside-binding, soluble, 3 binding protein	Plasma	0	2	0	3	0	5	10	3.17E-02	

Membrane								
			Plasma Membrane	0	4	0	3	0
Q12907	LMAN2	lectin, mannose-binding 2	Plasma Membrane	0	4	0	3	0
Q16186	ADRM1	adhesion regulating molecule 1	Plasma Membrane	0	1	0	1	0
Q8N8S7	ENAH	enabled homolog (Drosophila)	Plasma Membrane	0	1	0	1	0
Q8NF37	LPCAT1	lysophosphatidylcholine acyltransferase 1	Plasma Membrane	0	1	0	1	0
Q96AY3	FKBP10	FK506 binding protein 10, 65 kDa	Plasma Membrane	0	4	0	3	0
Q9BSJ8	ESYT1	extended synaptotagmin-like protein 1	Plasma Membrane	0	3	0	3	0
Q9BVK6	TMED9	transmembrane p24 trafficking protein 9	Plasma Membrane	0	3	0	3	0
								11a
								0.00E+00
								4.93E-03
								0.00E+00
								0.00E+00
								1.76E-02
								4.93E-03
								0.00E+00

Table S6. NUPs identified by Ac<sub>4</sub>GlcNAz (**1**), Ac<sub>3</sub>6AzGlcNAc (**4**), Ac<sub>4</sub>GalNAz(**2**) Ac<sub>3</sub>4dGlcNAz (**5**)

	NUPL1	NUP42	NUP50	NUP54	NUP58	NUP62	NUP98	NUP153	NUP155	NUP121	NUP214	NUP358
Ac <sub>4</sub> GlcNAz ( <b>1</b> )				+	+		+	+			+	
Ac <sub>3</sub> 6AzGlcNAc ( <b>4</b> ) <sup>5</sup>				+								
Ac <sub>4</sub> GalNAz ( <b>2</b> )				+		+	+	+			+	
Ac <sub>3</sub> 4dGlcNAz ( <b>5</b> )	+	+		+	+	+	+	+	+	+	+	+