

Supplementary files

Figure S1. The IPA results showed that 109 signaling pathways were regulated by Danu in Hep3B cell line.

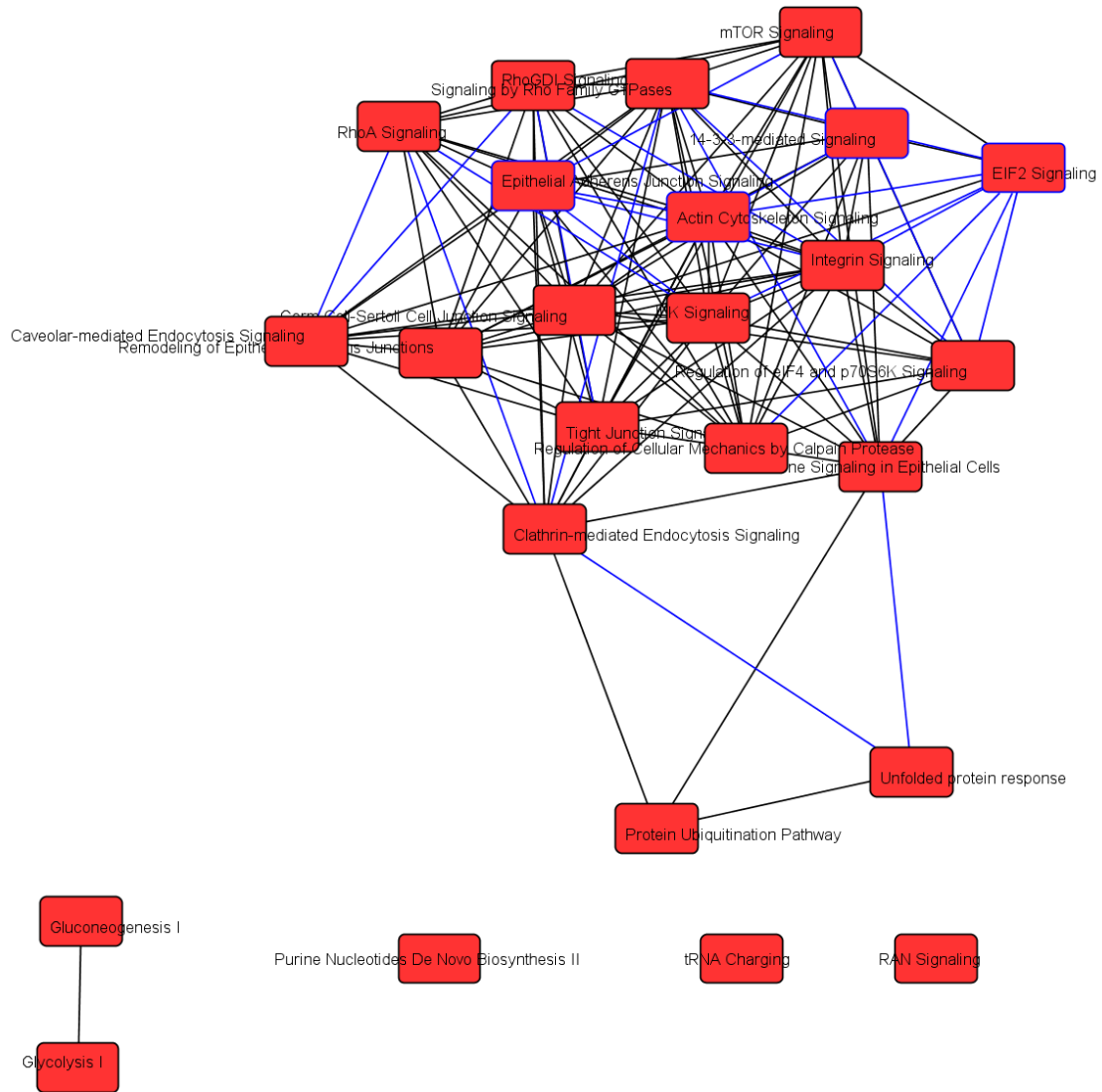


Table S1. The 542 protein molecules regulated by Danu in Hep3B cells.

	Protein IDs	Protein Names	Gene Names	H/L Ratio
1	P35613	Basigin	<i>BSG</i>	1.964
2	P21266	Glutathione S-transferase Mu 3	<i>GSTM3</i>	1.740
3	E9PHY5	Band 4.1-like protein 2	<i>EPB41L2</i>	1.723
4	P0DMN0	—	<i>SULT1A4</i>	1.608
5	C9JZR2	Catenin delta-1	<i>CTNND1</i>	1.557
6	P07942	Laminin subunit beta-1	<i>LAMB1</i>	1.517
7	P28482	Mitogen-activated protein kinase 1	<i>MAPK1</i>	1.517
8	P09960	Leukotriene A-4 hydrolase	<i>LTA4H</i>	1.517
9	P20618	Proteasome subunit beta type-1	<i>PSMB1</i>	1.454
10	Q9C005	Protein dpy-30 homolog	<i>DPY30</i>	1.446
11	Q99733	Nucleosome assembly protein 1-like 4	<i>NAP1L4</i>	1.421
12	O14980	Exportin-1	<i>XPO1</i>	1.408
13	K7EJR3	26S proteasome non-ATPase regulatory subunit 8	<i>PSMD8</i>	1.394
14	B0QYK0	RNA-binding protein EWS	<i>EWSR1</i>	1.381
15	O75643	U5 small nuclear ribonucleoprotein 200 kDa helicase	<i>SNRNP200</i>	1.358
16	F5H3U9	Protein mago nashi homolog	<i>MAGOHB</i>	1.345
17	Q15019	Septin-2	<i>SEPT2</i>	1.340
18	B4DGU4	Catenin beta-1	<i>CTNNB1</i>	1.326
19	P35579	Myosin-9	<i>MYH9</i>	1.306
20	Q9P0L0	Vesicle-associated membrane protein-associated protein A	<i>VAPA</i>	1.301
21	P00367	Glutamate dehydrogenase 1, mitochondrial	<i>GLUD1</i>	1.297
22	Q9Y2V2	Calcium-regulated heat stable protein 1	<i>CARHSP1</i>	1.296
23	P04843	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	<i>RPN1</i>	1.294
24	P52292	Importin subunit alpha-1	<i>KPNA2</i>	1.293
25	Q9P258	Protein RCC2	<i>RCC2</i>	1.288
26	O75369	Filamin-B	<i>FLNB</i>	1.285
27	P31930	Cytochrome b-c1 complex subunit 1, mitochondrial	<i>UQCRC1</i>	1.279
28	Q8N8S7	Protein enabled homolog	<i>ENAH</i>	1.275
29	P38919	Eukaryotic initiation factor 4A-III	<i>EIF4A3</i>	1.272
30	Q04917	14-3-3 protein eta	<i>YWHAH</i>	1.269
31	C9JRL4	—	<i>MDH1</i>	1.269
32	F8W1N5	Nascent polypeptide-associated complex subunit alpha	<i>NACA</i>	1.259
33	G8JLD5	Dynamin-1-like protein	<i>DNM1L</i>	1.252
34	P17655	Calpain-2 catalytic subunit	<i>CAPN2</i>	1.249
35	P00441	Superoxide dismutase [Cu-Zn]	<i>SOD1</i>	1.244
36	P22314	Ubiquitin-like modifier-activating enzyme 1	<i>UBA1</i>	1.243
37	H7C4B7	Delta(24)-sterol reductase	<i>DHCR24</i>	1.236
38	P35237	Serpin B6	<i>SERPINB6</i>	1.233
39	O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	<i>DDAH2</i>	1.233
40	Q8TAT6	Nuclear protein localization protein 4 homolog	<i>NPLOC4</i>	1.232
41	P49748	Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	<i>ACADVL</i>	1.231

42	P38117	Electron transfer flavoprotein subunit beta	<i>ETFB</i>	1.227
43	Q6XQN6	Nicotinate phosphoribosyltransferase	<i>NAPRT1</i>	1.227
44	P19105	Myosin regulatory light chain 12A	<i>MYL12A</i>	1.225
45	P49589	Cysteine--tRNA ligase, cytoplasmic	<i>CARS</i>	1.223
46	Q8IV08	Phospholipase D3	<i>PLD3</i>	1.222
47	P11413	Glucose-6-phosphate 1-dehydrogenase	<i>G6PD</i>	1.221
48	Q86V81	THO complex subunit 4	<i>ALYREF</i>	1.220
49	P25325	3-mercaptopyruvate sulfurtransferase	<i>MPST</i>	1.218
50	H3BQF1	Adenine phosphoribosyltransferase	<i>APRT</i>	1.215
51	H3BQZ7	Heterogeneous nuclear ribonucleoprotein U-like protein 2	<i>hCG_2044799</i>	1.213
52	P08107	Heat shock 70 kDa protein 1A/1B	<i>HSPA1A</i>	1.212
53	P02545	Prelamin-A/C	<i>LMNA</i>	1.210
54	P49321	Nuclear autoantigenic sperm protein	<i>NASP</i>	1.210
55	Q9Y310	tRNA-splicing ligase RtcB homolog	<i>C22orf28</i>	1.209
56	E9PF10	Nuclear pore complex protein Nup155	<i>NUP155</i>	1.206
57	A6NKB8	Aminopeptidase B	<i>RNPEP</i>	1.202
58	P35221	Catenin alpha-1	<i>CTNNA1</i>	1.201
59	P04080	Cystatin-B	<i>CSTB</i>	1.200
60	P34897	Serine hydroxymethyltransferase, mitochondrial	<i>SHMT2</i>	1.193
61	P63208	S-phase kinase-associated protein 1	<i>SKP1</i>	1.189
62	Q07065	Cytoskeleton-associated protein 4	<i>CKAP4</i>	1.186
63	P30086	Phosphatidylethanolamine-binding protein 1	<i>PEBP1</i>	1.186
64	O75874	Isocitrate dehydrogenase [NADP] cytoplasmic	<i>IDH1</i>	1.184
65	H7C469	Cathepsin D	<i>CTSD</i>	1.184
66	P00352	Retinal dehydrogenase 1	<i>ALDH1A1</i>	1.183
67	Q16555	Dihydropyrimidinase-related protein 2	<i>DPYSL2</i>	1.183
68	P62158	Calmodulin	<i>CALM1</i>	1.183
69	O75367	Core histone macro-H2A.1	<i>H2AFY</i>	1.183
70	H0YK49	Electron transfer flavoprotein subunit alpha, mitochondrial	<i>ETFa</i>	1.182
71	P35580	Myosin-10	<i>MYH10</i>	1.178
72	P68402	Platelet-activating factor acetylhydrolase IB subunit beta	<i>PAFAH1B2</i>	1.178
73	P07858	Cathepsin B	<i>CTSB</i>	1.177
74	A8MU58	Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	<i>AIMP2</i>	1.176
75	C9JH92	Quinone oxidoreductase	<i>CRYZ</i>	1.175
76	P09417	Dihydropteridine reductase	<i>QDPR</i>	1.174
77	E9PGT1	Translin	<i>TSN</i>	1.174
78	Q15274	Nicotinate-nucleotide pyrophosphorylase [carboxylating]	<i>QPRT</i>	1.170
79	Q9H307	Pinin	<i>PNN</i>	1.167
80	E7EMD0	NADPH--cytochrome P450 reductase	<i>POR</i>	1.166
81	C9J9W2	LIM and SH3 domain protein 1	<i>LASP1</i>	1.164
82	H0YJX6	Protein arginine N-methyltransferase 5	<i>PRMT5</i>	1.163
83	P51654	Glypican-3	<i>GPC3</i>	1.159
84	Q6DKJ4	Nucleoredoxin	<i>NXN</i>	1.153

85	P07384	Calpain-1 catalytic subunit	<i>CAPN1</i>	1.153
86	Q15417	Calponin-3	<i>CNN3</i>	1.152
87	P25786	Proteasome subunit alpha type-1	<i>PSMA1</i>	1.152
88	Q09666	Neuroblast differentiation-associated protein AHNAK	<i>AHNAK</i>	1.151
89	O43707	Alpha-actinin-4	<i>ACTN4</i>	1.151
90	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3	<i>FKBP3</i>	1.150
91	A6PVH9	Copine-1	<i>CPNE1</i>	1.149
92	Q9BWD1	Acetyl-CoA acetyltransferase, cytosolic	<i>ACAT2</i>	1.147
93	P61160	Actin-related protein 2	<i>ACTR2</i>	1.145
94	Q15293	Reticulocalbin-1	<i>RCN1</i>	1.143
95	P04632	Calpain small subunit 1	<i>CAPNS1</i>	1.143
96	P11766	Alcohol dehydrogenase class-3	<i>ADH5</i>	1.143
97	A6PVN8	Serine/threonine-protein phosphatase 2A activator	<i>PPP2R4</i>	1.142
98	H0Y3Y4	Septin-7	<i>42254</i>	1.140
99	P30084	Enoyl-CoA hydratase, mitochondrial	<i>ECHS1</i>	1.137
100	P37837	Transaldolase	<i>TALDO1</i>	1.137
101	P46783	40S ribosomal protein S10	<i>RPS10</i>	1.135
102	Q9BSJ8	Extended synaptotagmin-1	<i>ESYT1</i>	1.134
103	O00425	Insulin-like growth factor 2 mRNA-binding protein 3	<i>IGF2BP3</i>	1.132
104	P55735	Protein SEC13 homolog	<i>SEC13</i>	1.130
105	O43390	Heterogeneous nuclear ribonucleoprotein R	<i>HNRNPR</i>	1.130
106	P10768	S-formylglutathione hydrolase	<i>ESD</i>	1.125
107	P48735	Isocitrate dehydrogenase [NADP], mitochondrial	<i>IDH2</i>	1.125
108	P32119	Peroxisredoxin-2	<i>PRDX2</i>	1.125
109	Q15149	Plectin	<i>PLEC</i>	1.121
110	H7C2U6	Protein NipSnap homolog 1	<i>NIPSNAP1</i>	1.120
111	P30044	Peroxisredoxin-5, mitochondrial	<i>PRDX5</i>	1.117
112	Q9NY33	Dipeptidyl peptidase 3	<i>DPP3</i>	1.115
113	P21333	Filamin-A	<i>FLNA</i>	1.115
114	P62263	40S ribosomal protein S14	<i>RPS14</i>	1.115
115	O75533	Splicing factor 3B subunit 1	<i>SF3B1</i>	1.113
116	C9JUG7	F-actin-capping protein subunit alpha-2	<i>CAPZA2</i>	1.113
117	P45880	Voltage-dependent anion-selective channel protein 2	<i>VDAC2</i>	1.111
118	Q86VP6	Cullin-associated NEDD8-dissociated protein 1	<i>CAND1</i>	1.111
119	P68133	Actin, alpha skeletal muscle	<i>ACTA1</i>	1.110
120	B8ZZQ6	Prothymosin alpha	<i>PTMA</i>	1.110
121	P46379	Large proline-rich protein BAG6	<i>BAG6</i>	1.109
122	P12270	Nucleoprotein TPR	<i>TPR</i>	1.107
123	P26038	Moesin	<i>MSN</i>	1.107
124	P68036	Ubiquitin-conjugating enzyme E2 L3	<i>UBE2L3</i>	1.106
125	Q14315	Filamin-C	<i>FLNC</i>	1.102
126	H0YLC2	Proteasome subunit alpha type	<i>PSMA4</i>	1.099
127	P13797	Plastin-3	<i>PLS3</i>	1.097
128	P30040	Endoplasmic reticulum resident protein 29	<i>ERP29</i>	1.096

129	P35232	Prohibitin	<i>PHB</i>	1.094
130	Q96AE4	Far upstream element-binding protein 1	<i>FUBP1</i>	1.093
131	P31948	Stress-induced-phosphoprotein 1	<i>STIP1</i>	1.092
132	E7EQR4	Ezrin	<i>EZR</i>	1.091
133	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1	<i>HNRNPA2B1</i>	1.091
134	P50395	Rab GDP dissociation inhibitor beta	<i>GDI2</i>	1.091
135	F8VVM2	Phosphate carrier protein, mitochondrial	<i>SLC25A3</i>	1.091
136	P14324	Farnesyl pyrophosphate synthase	<i>FDPS</i>	1.090
137	F8VZ29	Ubiquitin-conjugating enzyme E2 N	<i>UBE2N</i>	1.089
138	P40925	Malate dehydrogenase, cytoplasmic	<i>MDH1</i>	1.089
139	P54727	UV excision repair protein RAD23 homolog B	<i>RAD23B</i>	1.089
140	P08727	Keratin, type I cytoskeletal 19	<i>KRT19</i>	1.088
141	Q9Y4L1	Hypoxia up-regulated protein 1	<i>HYOU1</i>	1.086
142	E9PMH2	Peptidyl-prolyl cis-trans isomerase	<i>AIP</i>	1.086
143	Q99460	26S proteasome non-ATPase regulatory subunit 1	<i>PSMD1</i>	1.085
144	P07108	Acyl-CoA-binding protein	<i>DBI</i>	1.083
145	P00387	NADH-cytochrome b5 reductase 3	<i>CYB5R3</i>	1.082
146	P04792	Heat shock protein beta-1	<i>HSPB1</i>	1.081
147	P16422	Epithelial cell adhesion molecule	<i>EPCAM</i>	1.080
148	O96019	Actin-like protein 6A	<i>ACTL6A</i>	1.079
149	P09972	Fructose-bisphosphate aldolase C	<i>ALDOC</i>	1.077
150	Q92945	Far upstream element-binding protein 2	<i>KHSRP</i>	1.076
151	Q15029	116 kDa U5 small nuclear ribonucleoprotein component	<i>EFTUD2</i>	1.075
152	Q9H444	Charged multivesicular body protein 4b	<i>CHMP4B</i>	1.074
153	P53396	ATP-citrate synthase	<i>ACLY</i>	1.074
154	P51991	Heterogeneous nuclear ribonucleoprotein A3	<i>HNRNPA3</i>	1.074
155	K7EJE8	Lon protease homolog, mitochondrial	<i>LONP1</i>	1.073
156	P18206	Vinculin	<i>VCL</i>	1.073
157	Q99832	T-complex protein 1 subunit eta	<i>CCT7</i>	1.072
158	P68371	Tubulin beta-4B chain	<i>TUBB4B</i>	1.071
159	P52209	6-phosphogluconate dehydrogenase, decarboxylating	<i>PGD</i>	1.068
160	Q12906	Interleukin enhancer-binding factor 3	<i>ILF3</i>	1.067
161	P23528	Cofilin-1	<i>CFL1</i>	1.066
162	P46940	Ras GTPase-activating-like protein IQGAP1	<i>IQGAP1</i>	1.065
163	Q92841	Probable ATP-dependent RNA helicase DDX17	<i>DDX17</i>	1.065
164	P19338	Nucleolin	<i>NCL</i>	1.061
165	P12004	Proliferating cell nuclear antigen	<i>PCNA</i>	1.061
166	O60701	UDP-glucose 6-dehydrogenase	<i>UGDH</i>	1.060
167	P23246	Splicing factor, proline- and glutamine-rich	<i>SFPQ</i>	1.059
168	F5H018	GTP-binding nuclear protein Ran	<i>RAN</i>	1.059
169	P61981	14-3-3 protein gamma	<i>YWHAQ</i>	1.059
170	P09874	Poly [ADP-ribose] polymerase 1	<i>PARP1</i>	1.059
171	H0YE29	Rho GTPase-activating protein 1	<i>ARHGAP1</i>	1.058
172	P35637	RNA-binding protein FUS	<i>FUS</i>	1.058

173	Q12905	Interleukin enhancer-binding factor 2	<i>ILF2</i>	1.058
174	Q13263	Transcription intermediary factor 1-beta	<i>TRIM28</i>	1.057
175	D6RG15	Twinfilin-2	<i>TWF2</i>	1.056
176	O15144	Actin-related protein 2/3 complex subunit 2	<i>ARPC2</i>	1.055
177	Q07666	KH domain-containing, RNA-binding, signal transduction-associated protein 1	<i>KHDRBS1</i>	1.055
178	P68363	Tubulin alpha-1B chain	<i>TUBA1B</i>	1.055
179	O60664	Perilipin-3	<i>PLIN3</i>	1.053
180	Q3ZCM7	Tubulin beta-8 chain	<i>TUBB8</i>	1.053
181	H7BZJ3	Thioredoxin	<i>PDIA3</i>	1.053
182	P62258	14-3-3 protein epsilon	<i>YWHAE</i>	1.052
183	Q9Y617	Phosphoserine aminotransferase	<i>PSAT1</i>	1.052
184	P08758	Annexin A5	<i>ANXA5</i>	1.052
185	P52272	Heterogeneous nuclear ribonucleoprotein M	<i>HNRNPM</i>	1.051
186	P00558	Phosphoglycerate kinase 1	<i>PGK1</i>	1.050
187	B4DS13	Eukaryotic translation initiation factor 4B	<i>EIF4B</i>	1.050
188	F8VPF3	Myosin light polypeptide 6	<i>MYL6</i>	1.050
189	P49411	Elongation factor Tu, mitochondrial	<i>TUFM</i>	1.049
190	P46109	Crk-like protein	<i>CRKL</i>	1.049
191	Q08211	ATP-dependent RNA helicase A	<i>DHX9</i>	1.049
192	F8VZX2	Poly(rC)-binding protein 2	<i>PCBP2</i>	1.048
193	P30101	Protein disulfide-isomerase A3	<i>PDIA3</i>	1.048
194	P37802	Transgelin-2	<i>TAGLN2</i>	1.047
195	D6R938	Calcium/calmodulin-dependent protein kinase type II subunit delta	<i>CAMK2D</i>	1.047
196	O60506	Heterogeneous nuclear ribonucleoprotein Q	<i>SYNCRIP</i>	1.046
197	P62424	60S ribosomal protein L7a	<i>RPL7A</i>	1.045
198	P04075	Fructose-bisphosphate aldolase A	<i>ALDOA</i>	1.045
199	Q9NYU2	UDP-glucose:glycoprotein glucosyltransferase 1	<i>UGGT1</i>	1.044
200	P25705	ATP synthase subunit alpha, mitochondrial	<i>ATP5A1</i>	1.043
201	K7EK07	Histone H3	<i>H3F3B</i>	1.043
202	P07814	Bifunctional glutamate/proline--tRNA ligase	<i>EPRS</i>	1.042
203	P30041	Peroxiredoxin-6	<i>PRDX6</i>	1.041
204	P04406	Glyceraldehyde-3-phosphate dehydrogenase	<i>GAPDH</i>	1.040
205	O14979	Heterogeneous nuclear ribonucleoprotein D-like	<i>HNRPDL</i>	1.040
206	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein	<i>SERBP1</i>	1.040
207	O60888	Protein CutA	<i>CUTA</i>	1.039
208	Q9UHD8	Septin-9	<i>42256</i>	1.038
209	Q14697	Neutral alpha-glucosidase AB	<i>GANAB</i>	1.038
210	Q9UL46	Proteasome activator complex subunit 2	<i>PSME2</i>	1.038
211	Q9NTK5	Obg-like ATPase 1	<i>OLA1</i>	1.038
212	Q9HC35	Echinoderm microtubule-associated protein-like 4	<i>EML4</i>	1.037
213	P35520	Cystathionine beta-synthase	<i>CBS</i>	1.037
214	P15924	Desmoplakin	<i>DSP</i>	1.037
215	P20700	Lamin-B1	<i>LMNB1</i>	1.036

216	P31946	14-3-3 protein beta/alpha	<i>YWHAB</i>	1.036
217	Q15459	Splicing factor 3A subunit 1	<i>SF3A1</i>	1.036
218	Q04760	Lactoylglutathione lyase	<i>GLO1</i>	1.036
219	Q01105	Protein SET	<i>SET</i>	1.035
220	Q13907	Isopentenyl-diphosphate Delta-isomerase 1	<i>IDII</i>	1.035
221	P27695	DNA-(apurinic or apyrimidinic site) lyase	<i>APEX1</i>	1.035
222	P78344	Eukaryotic translation initiation factor 4 gamma 2	<i>EIF4G2</i>	1.035
223	P39748	Flap endonuclease 1	<i>FEN1</i>	1.034
224	Q9UNZ2	NSFL1 cofactor p47	<i>NSFL1C</i>	1.034
225	P43243	Matrin-3	<i>MATR3</i>	1.034
226	P54136	Arginine--tRNA ligase, cytoplasmic	<i>RARS</i>	1.033
227	Q9P2E9	Ribosome-binding protein 1	<i>RRBP1</i>	1.033
228	P60174	Triosephosphate isomerase	<i>TPII</i>	1.032
229	P42167	Lamina-associated polypeptide 2, isoforms beta/gamma	<i>TMPO</i>	1.032
230	P12955	Xaa-Pro dipeptidase	<i>PEPD</i>	1.032
231	A2A2D0	Stathmin	<i>STMN1</i>	1.031
232	H0YA96	Heterogeneous nuclear ribonucleoprotein D0	<i>HNRNPD</i>	1.031
233	P12277	Creatine kinase B-type	<i>CKB</i>	1.031
234	Q00839	Heterogeneous nuclear ribonucleoprotein U	<i>HNRNPU</i>	1.030
235	P62937	Peptidyl-prolyl cis-trans isomerase A	<i>PPIA</i>	1.030
236	P07355	Annexin A2	<i>ANXA2</i>	1.028
237	P61158	Actin-related protein 3	<i>ACTR3</i>	1.027
238	Q5JP53	Tubulin beta chain	<i>TUBB</i>	1.026
239	P63104	14-3-3 protein zeta/delta	<i>YWHAZ</i>	1.025
240	F6SBX2	Isoleucine--tRNA ligase, mitochondrial	<i>LARS2</i>	1.025
241	E7ETK0	40S ribosomal protein S24	<i>RPS24</i>	1.024
242	P09327	Villin-1	<i>VIL1</i>	1.023
243	P22102	Trifunctional purine biosynthetic protein adenosine-3	<i>GART</i>	1.021
244	P49588	Alanine--tRNA ligase, cytoplasmic	<i>AARS</i>	1.021
245	P06576	ATP synthase subunit beta, mitochondrial	<i>ATP5B</i>	1.020
246	P48643	T-complex protein 1 subunit epsilon	<i>CCT5</i>	1.019
247	P14866	Heterogeneous nuclear ribonucleoprotein L	<i>HNRNPL</i>	1.019
248	Q00610	Clathrin heavy chain 1	<i>CLTC</i>	1.017
249	B4DJV2	Citrate synthase	<i>CS</i>	1.016
250	P28066	Proteasome subunit alpha type-5	<i>PSMA5</i>	1.016
251	P50502	Hsc70-interacting protein	<i>STI3</i>	1.016
252	P63261	Actin, cytoplasmic 2	<i>ACTG1</i>	1.015
253	P34932	Heat shock 70 kDa protein 4	<i>HSPA4</i>	1.015
254	Q07955	Serine/arginine-rich splicing factor 1	<i>SRSF1</i>	1.014
255	Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1	<i>AIMP1</i>	1.013
256	Q9Y5B9	FACT complex subunit SPT16	<i>SUPT16H</i>	1.013
257	Q9Y265	RuvB-like 1	<i>RUVBL1</i>	1.013
258	P63010	AP-2 complex subunit beta	<i>AP2B1</i>	1.012
259	P55060	Exportin-2	<i>CSE1L</i>	1.012

260	Q99613	Eukaryotic translation initiation factor 3 subunit C	<i>EIF3C</i>	1.012
261	P55072	Transitional endoplasmic reticulum ATPase	<i>VCP</i>	1.009
262	D6R9A6	High mobility group protein B2	<i>HMGB2</i>	1.009
263	K7EJ78	40S ribosomal protein S15	<i>RPS15</i>	1.009
264	Q12874	Splicing factor 3A subunit 3	<i>SF3A3</i>	1.009
265	P38646	Stress-70 protein, mitochondrial	<i>HSPA9</i>	1.007
266	Q9NYL9	Tropomodulin-3	<i>TMOD3</i>	1.006
267	C9JJ34	Ran-specific GTPase-activating protein	<i>RANBP1</i>	1.006
268	E9PLK3	Puromycin-sensitive aminopeptidase	<i>NPEPPS</i>	1.006
269	P14868	Aspartate--tRNA ligase, cytoplasmic	<i>DARS</i>	1.005
270	P27824	Calnexin	<i>CANX</i>	1.005
271	Q16643	Drebrin	<i>DBN1</i>	1.004
272	P05787	Keratin, type II cytoskeletal 8	<i>KRT8</i>	1.004
273	Q9H6S3	Epidermal growth factor receptor kinase substrate 8-like protein 2	<i>EPS8L2</i>	1.004
274	E9PCY7	Heterogeneous nuclear ribonucleoprotein H	<i>HNRNPH1</i>	1.002
275	P09382	Galectin-1	<i>LGALS1</i>	1.002
276	Q8WXF1	Paraspeckle component 1	<i>PSPC1</i>	1.002
277	P13489	Ribonuclease inhibitor	<i>RNH1</i>	1.001
278	P27348	14-3-3 protein theta	<i>YWHAQ</i>	1.001
279	P30740	Leukocyte elastase inhibitor	<i>SERPINB1</i>	1.001
280	B1AK85	F-actin-capping protein subunit beta	<i>CAPZB</i>	1.000
281	P30048	Thioredoxin-dependent peroxide reductase, mitochondrial	<i>PRDX3</i>	1.000
282	O75083	WD repeat-containing protein 1	<i>WDR1</i>	1.000
283	Q16777	Histone H2A type 2-C	<i>HIST2H2AC</i>	0.999
284	Q9Y490	Talin-1	<i>TLN1</i>	0.997
285	Q5T7C4	High mobility group protein B1	<i>HMGB1</i>	0.997
286	P13010	X-ray repair cross-complementing protein 5	<i>XRCC5</i>	0.997
287	P26368	Splicing factor U2AF 65 kDa subunit	<i>U2AF2</i>	0.997
288	P04844	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	<i>RPN2</i>	0.997
289	Q14204	Cytoplasmic dynein 1 heavy chain 1	<i>DYNC1H1</i>	0.996
290	Q5VU59	—	<i>TPM3</i>	0.996
291	P11047	Laminin subunit gamma-1	<i>LAMC1</i>	0.995
292	P35606	Coatomer subunit beta	<i>COPB2</i>	0.995
293	P17174	Aspartate aminotransferase, cytoplasmic	<i>GOT1</i>	0.995
294	K7ELL7	Glucosidase 2 subunit beta	<i>PRKCSH</i>	0.995
295	P07237	Protein disulfide-isomerase	<i>P4HB</i>	0.994
296	P61978	Heterogeneous nuclear ribonucleoprotein K	<i>HNRNPK</i>	0.994
297	Q9BTT0	Acidic leucine-rich nuclear phosphoprotein 32 family member E	<i>ANP32E</i>	0.994
298	Q9Y624	Junctional adhesion molecule A	<i>F11R</i>	0.993
299	F8WJN3	Cleavage and polyadenylation specificity factor subunit 6	<i>CPSF6</i>	0.992
300	P61026	Ras-related protein Rab-10	<i>RAB10</i>	0.992
301	Q01081	Splicing factor U2AF 35 kDa subunit	<i>U2AF1</i>	0.991
302	Q15084	Protein disulfide-isomerase A6	<i>PDIA6</i>	0.989
303	K7ERT7	Synaptic vesicle membrane protein VAT-1 homolog	<i>VAT1</i>	0.989

304	Q71DI3	Histone H3.2	<i>HIST2H3A</i>	0.988
305	O43809	Cleavage and polyadenylation specificity factor subunit 5	<i>NUDT21</i>	0.988
306	P26639	Threonine--tRNA ligase, cytoplasmic	<i>TARS</i>	0.988
307	P51858	Hepatoma-derived growth factor	<i>HDGF</i>	0.988
308	P56192	Methionine--tRNA ligase, cytoplasmic	<i>MARS</i>	0.987
309	F8W7C6	—	<i>RPL10</i>	0.987
310	P49327	Fatty acid synthase	<i>FASN</i>	0.987
311	Q15185	Prostaglandin E synthase 3	<i>PTGES3</i>	0.987
312	P62314	Small nuclear ribonucleoprotein Sm D1	<i>SNRPD1</i>	0.986
313	Q13813	Spectrin alpha chain, non-erythrocytic 1	<i>SPTAN1</i>	0.984
314	Q96P70	Importin-9	<i>IPO9</i>	0.983
315	P26196	Probable ATP-dependent RNA helicase DDX6	<i>DDX6</i>	0.983
316	F8W6I7	Heterogeneous nuclear ribonucleoprotein A1	<i>HNRNPA1</i>	0.982
317	Q14974	Importin subunit beta-1	<i>KPNB1</i>	0.980
318	P50990	T-complex protein 1 subunit theta	<i>CCT8</i>	0.980
319	P06733	Alpha-enolase	<i>ENO1</i>	0.979
320	Q15233	Non-POU domain-containing octamer-binding protein	<i>NONO</i>	0.979
321	P18669	Phosphoglycerate mutase 1	<i>PGAM1</i>	0.978
322	Q13492	Phosphatidylinositol-binding clathrin assembly protein	<i>PICALM</i>	0.978
323	Q01518	Adenylyl cyclase-associated protein 1	<i>CAP1</i>	0.977
324	E7EUY0	DNA-dependent protein kinase catalytic subunit	<i>PRKDC</i>	0.977
325	P12956	X-ray repair cross-complementing protein 6	<i>XRCC6</i>	0.977
326	Q13162	Peroxiredoxin-4	<i>PRDX4</i>	0.976
327	B7Z7P8	Eukaryotic peptide chain release factor subunit 1	<i>ETF1</i>	0.976
328	P13667	Protein disulfide-isomerase A4	<i>PDIA4</i>	0.975
329	P26599	Polypyrimidine tract-binding protein 1	<i>PTBP1</i>	0.975
330	F8VWS0	60S acidic ribosomal protein P0	<i>RPLP0</i>	0.975
331	P62979	Ubiquitin-40S ribosomal protein S27a	<i>RPS27A</i>	0.975
332	P35268	60S ribosomal protein L22	<i>RPL22</i>	0.974
333	Q9Y281	Cofilin-2	<i>CFL2</i>	0.973
334	O00299	Chloride intracellular channel protein 1	<i>CLIC1</i>	0.973
335	P62136	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	<i>PPP1CA</i>	0.972
336	Q96PK6	RNA-binding protein 14	<i>RBM14</i>	0.972
337	P08238	Heat shock protein HSP 90-beta	<i>HSP90AB1</i>	0.971
338	O43143	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	<i>DHX15</i>	0.970
339	P62805	Histone H4	<i>HIST1H4A</i>	0.970
340	P41250	Glycine--tRNA ligase	<i>GARS</i>	0.969
341	Q92598	Heat shock protein 105 kDa	<i>HSPH1</i>	0.969
342	B7Z972	Protein-L-isoaspartate O-methyltransferase	<i>PCMT1</i>	0.969
343	P10809	60 kDa heat shock protein, mitochondrial	<i>HSPD1</i>	0.967
344	Q86UY0	Thioredoxin domain-containing protein 5	<i>TXNDC5</i>	0.967
345	O60488	Long-chain-fatty-acid--CoA ligase 4	<i>ACSL4</i>	0.967
346	Q13838	Spliceosome RNA helicase DDX39B	<i>DDX39B</i>	0.966
347	P49773	Histidine triad nucleotide-binding protein 1	<i>HINT1</i>	0.966

348	O14579	Coatomer subunit epsilon	<i>COPE</i>	0.966
349	Q9UJZ1	Stomatin-like protein 2, mitochondrial	<i>STOML2</i>	0.965
350	P14625	Endoplasmic	<i>HSP90B1</i>	0.965
351	Q92499	ATP-dependent RNA helicase DDX1	<i>DDX1</i>	0.964
352	Q32Q12	Nucleoside diphosphate kinase	<i>NME1-NME2</i>	0.964
353	Q9NQC3	Reticulon-4	<i>RTN4</i>	0.964
354	F5GY37	Prohibitin-2	<i>PHB2</i>	0.963
355	P49915	GMP synthase [glutamine-hydrolyzing]	<i>GMPS</i>	0.961
356	P26640	Valine--tRNA ligase	<i>VARS</i>	0.960
357	Q08945	FACT complex subunit SSRP1	<i>SSRP1</i>	0.960
358	Q10567	AP-1 complex subunit beta-1	<i>AP1B1</i>	0.960
359	P49257	Protein ERGIC-53	<i>LMAN1</i>	0.959
360	P50454	Serpin H1	<i>SERPINH1</i>	0.958
361	Q9UKY7	Protein CDV3 homolog	<i>CDV3</i>	0.957
362	P14618	Pyruvate kinase PKM	<i>PKM</i>	0.957
363	Q14444	Caprin-1	<i>CAPRIN1</i>	0.955
364	P40926	Malate dehydrogenase, mitochondrial	<i>MDH2</i>	0.955
365	P05455	Lupus La protein	<i>SSB</i>	0.955
366	F8VY35	Nucleosome assembly protein 1-like 1	<i>NAP1L1</i>	0.955
367	P05198	Eukaryotic translation initiation factor 2 subunit 1	<i>EIF2S1</i>	0.955
368	P05783	Keratin, type I cytoskeletal 18	<i>KRT18</i>	0.955
369	P11021	78 kDa glucose-regulated protein	<i>HSPA5</i>	0.954
370	Q9NZI8	Insulin-like growth factor 2 mRNA-binding protein 1	<i>IGF2BP1</i>	0.954
371	P12814	Alpha-actinin-1	<i>ACTN1</i>	0.953
372	E9PPJ0	Splicing factor 3B subunit 2	<i>SF3B2</i>	0.953
373	P28838	Cytosol aminopeptidase	<i>LAP3</i>	0.953
374	P23526	Adenosylhomocysteinase	<i>AHCY</i>	0.952
375	Q5QPQ0	Acyl-protein thioesterase 2	<i>LYPLA2</i>	0.951
376	Q06830	Peroxiredoxin-1	<i>PRDX1</i>	0.951
377	Q9BR76	Coronin-1B	<i>CORO1B</i>	0.951
378	P42224	Signal transducer and activator of transcription 1-alpha/beta	<i>STAT1</i>	0.950
379	H0YEN5	40S ribosomal protein S2	<i>RPS2</i>	0.950
380	P43686	26S protease regulatory subunit 6B	<i>PSMC4</i>	0.949
381	P07900	Heat shock protein HSP 90-alpha	<i>HSP90AA1</i>	0.949
382	Q99714	3-hydroxyacyl-CoA dehydrogenase type-2	<i>HSD17B10</i>	0.947
383	H0YFA4	Cysteine-rich protein 2	<i>CRIP2</i>	0.947
384	J3KPE3	Guanine nucleotide-binding protein subunit beta-2-like 1	<i>GNB2L1</i>	0.946
385	Q14247	Src substrate cortactin	<i>CTTN</i>	0.945
386	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	<i>PPP2R1A</i>	0.945
387	P18124	60S ribosomal protein L7	<i>RPL7</i>	0.944
388	P04040	Catalase	<i>CAT</i>	0.944
389	P53618	Coatomer subunit beta	<i>COPB1</i>	0.943
390	P30050	60S ribosomal protein L12	<i>RPL12</i>	0.943
391	P07737	Profilin-1	<i>PFN1</i>	0.942

392	P68431	Histone H3.1	<i>HIST1H3A</i>	0.942
393	P27797	Calreticulin	<i>CALR</i>	0.941
394	P21796	Voltage-dependent anion-selective channel protein 1	<i>VDAC1</i>	0.940
395	Q00341	Vigilin	<i>HDLBP</i>	0.940
396	P01024	Complement C3	<i>C3</i>	0.939
397	P50991	T-complex protein 1 subunit delta	<i>CCT4</i>	0.939
398	A0A075B730	Epiplakin	<i>EPPK1</i>	0.937
399	Q13200	26S proteasome non-ATPase regulatory subunit 2	<i>PSMD2</i>	0.937
400	Q9HB71	Calcyclin-binding protein	<i>CACYBP</i>	0.936
401	P60228	Eukaryotic translation initiation factor 3 subunit E	<i>EIF3E</i>	0.934
402	P00390	Glutathione reductase, mitochondrial	<i>GSR</i>	0.933
403	P17844	Probable ATP-dependent RNA helicase DDX5	<i>DDX5</i>	0.932
404	Q92616	Translational activator GCN1	<i>GCN1L1</i>	0.932
405	Q99880	Histone H2B type 1-L	<i>HIST1H2BL</i>	0.931
406	O43776	Asparagine--tRNA ligase, cytoplasmic	<i>NARS</i>	0.931
407	Q15942	Zyxin	<i>ZYX</i>	0.931
408	P26641	Elongation factor 1-gamma	<i>EEF1G</i>	0.931
409	P53621	Coatomer subunit alpha	<i>COPA</i>	0.930
410	P25787	Proteasome subunit alpha type-2	<i>PSMA2</i>	0.927
411	E7ES10	Calpastatin	<i>CAST</i>	0.925
412	P46777	60S ribosomal protein L5	<i>RPL5</i>	0.923
413	O95373	Importin-7	<i>IPO7</i>	0.923
414	O00151	PDZ and LIM domain protein 1	<i>PDLIM1</i>	0.923
415	E9PLD0	Ras-related protein Rab-1B	<i>RAB1B</i>	0.920
416	C9J9K3	40S ribosomal protein SA	<i>RPSA</i>	0.919
417	Q96124	Far upstream element-binding protein 3	<i>FUBP3</i>	0.918
418	E7EQV3	Polyadenylate-binding protein 1	<i>PABPC1</i>	0.918
419	G3V119	DBIRD complex subunit KIAA1967	<i>KIAA1967</i>	0.918
420	P05387	60S acidic ribosomal protein P2	<i>RPLP2</i>	0.917
421	P00338	L-lactate dehydrogenase A chain	<i>LDHA</i>	0.917
422	O00303	Eukaryotic translation initiation factor 3 subunit F	<i>EIF3F</i>	0.916
423	Q01082	Spectrin beta chain, non-erythrocytic 1	<i>SPTBN1</i>	0.916
424	P61604	10 kDa heat shock protein, mitochondrial	<i>HSPE1</i>	0.915
425	Q9NS69	Mitochondrial import receptor subunit TOM22 homolog	<i>TOMM22</i>	0.915
426	P63241	Eukaryotic translation initiation factor 5A-1	<i>EIF5A</i>	0.914
427	E9PBS1	Multifunctional protein ADE2	<i>PAICS</i>	0.914
428	P29692	Elongation factor 1-delta	<i>EEF1D</i>	0.910
429	P24534	Elongation factor 1-beta	<i>EEF1B2</i>	0.910
430	H0Y4R1	Inosine-5-monophosphate dehydrogenase 2	<i>IMPDH2</i>	0.908
431	P36578	60S ribosomal protein L4	<i>RPL4</i>	0.907
432	P39023	60S ribosomal protein L3	<i>RPL3</i>	0.906
433	Q9BSE5	Agmatinase, mitochondrial	<i>AGMAT</i>	0.906
434	P06748	Nucleophosmin	<i>NPM1</i>	0.906
435	Q8NE71	ATP-binding cassette sub-family F member 1	<i>ABCF1</i>	0.906

436	P07954	Fumarate hydratase, mitochondrial	<i>FH</i>	0.905
437	Q15181	Inorganic pyrophosphatase	<i>PPA1</i>	0.905
438	O00410	Importin-5	<i>IPO5</i>	0.905
439	H3BT13	Small nuclear ribonucleoprotein Sm D3	<i>SNRPD3</i>	0.903
440	P31689	DnaJ homolog subfamily A member 1	<i>DNAJAI</i>	0.903
441	Q15056	Eukaryotic translation initiation factor 4H	<i>EIF4H</i>	0.902
442	Q96QK1	Vacuolar protein sorting-associated protein 35	<i>VPS35</i>	0.902
443	Q15365	Poly(rC)-binding protein 1	<i>PCBP1</i>	0.902
444	P23381	Tryptophan--tRNA ligase, cytoplasmic	<i>WARS</i>	0.902
445	P05386	60S acidic ribosomal protein P1	<i>RPLP1</i>	0.900
446	O75937	DnaJ homolog subfamily C member 8	<i>DNAJC8</i>	0.900
447	Q9Y333	U6 snRNA-associated Sm-like protein LSm2	<i>LSM2</i>	0.900
448	P58546	Myotrophin	<i>MTPN</i>	0.900
449	P62701	40S ribosomal protein S4, X isoform	<i>RPS4X</i>	0.899
450	Q9Y678	Coatomer subunit gamma-1	<i>COPG1</i>	0.898
451	E7EX73	Eukaryotic translation initiation factor 4 gamma 1	<i>EIF4G1</i>	0.897
452	Q7KZF4	Staphylococcal nuclease domain-containing protein 1	<i>SND1</i>	0.897
453	P62081	40S ribosomal protein S7	<i>RPS7</i>	0.894
454	P06744	Glucose-6-phosphate isomerase	<i>GPI</i>	0.893
455	P31942	Heterogeneous nuclear ribonucleoprotein H3	<i>HNRNPH3</i>	0.891
456	P40227	T-complex protein 1 subunit zeta	<i>CCT6A</i>	0.891
457	P78347	General transcription factor II-I	<i>GTF2I</i>	0.890
458	P11387	DNA topoisomerase 1	<i>TOP1</i>	0.889
459	Q13347	Eukaryotic translation initiation factor 3 subunit I	<i>EIF3I</i>	0.889
460	M0QZS6	SUMO-activating enzyme subunit 1	<i>SAE1</i>	0.888
461	E9PRQ7	UBX domain-containing protein 1	<i>UBXN1</i>	0.887
462	P42704	Leucine-rich PPR motif-containing protein	<i>LRPPRC</i>	0.887
463	P11142	Heat shock cognate 71 kDa protein	<i>HSPA8</i>	0.886
464	K7EJL1	AP-1 complex subunit mu-1	<i>AP1M1</i>	0.886
465	P61353	60S ribosomal protein L27	<i>RPL27</i>	0.885
466	Q99497	Protein DJ-1	<i>PARK7</i>	0.884
467	Q13126	S-methyl-5-thioadenosine phosphorylase	<i>MTAP</i>	0.884
468	Q14566	DNA replication licensing factor MCM6	<i>MCM6</i>	0.883
469	B4DUR8	T-complex protein 1 subunit gamma	<i>CCT3</i>	0.882
470	P55884	Eukaryotic translation initiation factor 3 subunit B	<i>EIF3B</i>	0.882
471	B4DQU5	Ras-related protein Rab-11A	<i>RAB11A</i>	0.881
472	O43852	Calumenin	<i>CALU</i>	0.879
473	P13639	Elongation factor 2	<i>EEF2</i>	0.878
474	P33991	DNA replication licensing factor MCM4	<i>MCM4</i>	0.877
475	P68104	Elongation factor 1-alpha 1	<i>EEF1A1</i>	0.875
476	G3V1A1	60S ribosomal protein L8	<i>RPL8</i>	0.875
477	P06493	Cyclin-dependent kinase 1	<i>CDK1</i>	0.873
478	P42166	Lamina-associated polypeptide 2, isoform alpha	<i>TMPO</i>	0.873
479	P60842	Eukaryotic initiation factor 4A-I	<i>EIF4A1</i>	0.871

480	P84077	ADP-ribosylation factor 1	<i>ARF1</i>	0.868
481	P62906	60S ribosomal protein L10a	<i>RPL10A</i>	0.868
482	P51149	Ras-related protein Rab-7a	<i>RAB7A</i>	0.867
483	P25398	40S ribosomal protein S12	<i>RPS12</i>	0.862
484	P08670	Vimentin	<i>VIM</i>	0.862
485	J3KTF8	Rho GDP-dissociation inhibitor 1	<i>ARHGDI1</i>	0.861
486	B4E022	Transketolase	<i>TKT</i>	0.860
487	Q92575	UBX domain-containing protein 4	<i>UBXN4</i>	0.859
488	P02768	Serum albumin	<i>ALB</i>	0.857
489	Q9UMS4	Pre-mRNA-processing factor 19	<i>PRPF19</i>	0.855
490	Q96AG4	Leucine-rich repeat-containing protein 59	<i>LRRC59</i>	0.854
491	P02787	Serotransferrin	<i>TF</i>	0.853
492	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4	<i>FKBP4</i>	0.852
493	Q06210	Glutamine--fructose-6-phosphate aminotransferase 1	<i>GFPT1</i>	0.852
494	P78371	T-complex protein 1 subunit beta	<i>CCT2</i>	0.849
495	P29966	Myristoylated alanine-rich C-kinase substrate	<i>MARCKS</i>	0.849
496	M0QXN5	Nuclear pore glycoprotein p62	<i>NUP62</i>	0.848
497	P62633	Cellular nucleic acid-binding protein	<i>CNBP</i>	0.848
498	P46060	Ran GTPase-activating protein 1	<i>RANGAP1</i>	0.847
499	P30085	UMP-CMP kinase	<i>CMPK1</i>	0.845
500	P31939	Bifunctional purine biosynthesis protein PURH	<i>ATIC</i>	0.844
501	K7EL02	Thimet oligopeptidase	<i>THOP1</i>	0.844
502	P40939	Trifunctional enzyme subunit alpha, mitochondrial	<i>HADHA</i>	0.839
503	P20290	Transcription factor BTF3	<i>BTF3</i>	0.839
504	D6RG13	40S ribosomal protein S3a	<i>RPS3A</i>	0.837
505	E5RI99	60S ribosomal protein L30	<i>RPL30</i>	0.832
506	Q9UQ80	Proliferation-associated protein 2G4	<i>PA2G4</i>	0.831
507	C9JNR4	Transforming protein RhoA	<i>RHOA</i>	0.830
508	F8VUA6	60S ribosomal protein L18	<i>RPL18</i>	0.827
509	Q96KP4	Cytosolic non-specific dipeptidase	<i>CNDP2</i>	0.822
510	Q6P2Q9	Pre-mRNA-processing-splicing factor 8	<i>PRPF8</i>	0.821
511	P13284	Gamma-interferon-inducible lysosomal thiol reductase	<i>IFI30</i>	0.819
512	Q15424	Scaffold attachment factor B1	<i>SAFB</i>	0.819
513	O95433	Activator of 90 kDa heat shock protein ATPase homolog 1	<i>AHSA1</i>	0.815
514	P21291	Cysteine and glycine-rich protein 1	<i>CSRPI</i>	0.815
515	O00571	ATP-dependent RNA helicase DDX3X	<i>DDX3X</i>	0.813
516	P67809	Nuclease-sensitive element-binding protein 1	<i>YBX1</i>	0.812
517	A6NHL2	Tubulin alpha chain-like 3	<i>TUBAL3</i>	0.810
518	Q9UHX1	Poly(U)-binding-splicing factor PUF60	<i>PUF60</i>	0.808
519	P41252	Isoleucine--tRNA ligase, cytoplasmic	<i>IARS</i>	0.802
520	Q8WUM4	Programmed cell death 6-interacting protein	<i>PDCD6IP</i>	0.800
521	Q14152	Eukaryotic translation initiation factor 3 subunit A	<i>EIF3A</i>	0.796
522	E7EMC7	Sequestosome-1	<i>SQSTM1</i>	0.794
523	O95573	Long-chain-fatty-acid--CoA ligase 3	<i>ACSL3</i>	0.793

524	F5GWX5	Chromodomain-helicase-DNA-binding protein 4	<i>CHD4</i>	0.785
525	K7EJ57	Mitochondrial import receptor subunit TOM40 homolog	<i>TOMM40</i>	0.782
526	P20042	Eukaryotic translation initiation factor 2 subunit 2	<i>EIF2S2</i>	0.778
527	Q9ULV4	Coronin-1C	<i>CORO1C</i>	0.772
528	P02786	Transferrin receptor protein 1	<i>TFRC</i>	0.771
529	P36542	ATP synthase subunit gamma, mitochondrial	<i>ATP5C1</i>	0.751
530	Q9BXP5	Serrate RNA effector molecule homolog	<i>SRRT</i>	0.750
531	Q13185	Chromobox protein homolog 3	<i>CBX3</i>	0.710
532	D3YTB1	60S ribosomal protein L32	<i>RPL32</i>	0.704
533	Q15393	Splicing factor 3B subunit 3	<i>SF3B3</i>	0.700
534	Q16836	Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	<i>HADH</i>	0.689
535	P00505	Aspartate aminotransferase, mitochondrial	<i>GOT2</i>	0.667
536	Q96FW1	Ubiquitin thioesterase OTUB1	<i>OTUB1</i>	0.637
537	H0Y8E6	DNA replication licensing factor MCM2	<i>MCM2</i>	0.623
538	B4DDF4	Calponin-2	<i>CNN2</i>	0.618
539	Q9UDY2	Tight junction protein ZO-2	<i>TJP2</i>	0.582
540	Q70CQ2	Ubiquitin carboxyl-terminal hydrolase 34	<i>USP34</i>	0.553
541	P04264	Keratin, type II cytoskeletal 1	<i>KRT1</i>	0.441
542	P35527	Keratin, type I cytoskeletal 9	<i>KRT9</i>	0.155

Table S2. The 94 Ingenuity Canonical Pathways regulated by Danu in Hep3B cells (sorted by log P value).

No.	Ingenuity canonical pathways
1	EIF2 Signaling
2	Regulation of eIF4 and p70S6K Signaling
3	Remodeling of Epithelial Adherens Junctions
4	mTOR Signaling
5	Protein Ubiquitination Pathway
6	tRNA Charging
7	Epithelial Adherens Junction Signaling
8	RAN Signaling
9	Glycolysis I
10	Gluconeogenesis I
11	Actin Cytoskeleton Signaling
12	RhoA Signaling
13	ILK Signaling
14	Unfolded protein response
15	Regulation of Cellular Mechanics by Calpain Protease
16	Tight Junction Signaling
17	Germ Cell-Sertoli Cell Junction Signaling
18	Integrin Signaling
19	Caveolar-mediated Endocytosis Signaling
20	14-3-3-mediated Signaling
21	Aldosterone Signaling in Epithelial Cells
22	Signaling by Rho Family GTPases
23	Clathrin-mediated Endocytosis Signaling

24	Purine Nucleotides De Novo Biosynthesis II
25	RhoGDI Signaling
26	HIPPO signaling
27	Aspartate Degradation II
28	Leukocyte Extravasation Signaling
29	PI3K/AKT Signaling
30	Cell Cycle: G2/M DNA Damage Checkpoint Regulation
31	Regulation of Actin-based Motility by Rho
32	Glutaryl-CoA Degradation
33	Pentose Phosphate Pathway
34	Fc γ Receptor-mediated Phagocytosis in Macrophages and Monocytes
35	BER pathway
36	p70S6K Signaling
37	Isoleucine Degradation I
38	ERK/MAPK Signaling
39	Lipid Antigen Presentation by CD1
40	Telomere Extension by Telomerase
41	Virus Entry via Endocytic Pathways
42	Mitochondrial Dysfunction
43	Ephrin B Signaling
44	Mechanisms of Viral Exit from Host Cells
45	VEGF Signaling
46	Spliceosomal Cycle
47	L-cysteine Degradation
48	Formaldehyde Oxidation II (Glutathione-dependent)
49	Superpathway of Cholesterol Biosynthesis

50	Superpathway of Geranylgeranyldiphosphate Biosynthesis I
51	Protein Kinase A Signaling
52	Sucrose Degradation V (Mammalian)
53	Superpathway of Methionine Degradation
54	Hypoxia Signaling in the Cardiovascular System
55	Breast Cancer Regulation by Stathmin 1
56	Tryptophan Degradation III (Eukaryotic)
57	Mitotic Roles of Polo-like Kinase
58	Endoplasmic Reticulum Stress Pathway
59	FAK signaling
60	Inosine-5'-phosphate Biosynthesis II
61	Glutamate Degradation II
62	Aspartate Biosynthesis
63	Apoptosis signaling
64	Semaphorin signaling in neurons
65	TCA cycle II (Eukaryotic)
66	Myc mediated Apoptosis signaling
67	L-cysteine Degradation I
68	Mevalonate Pathway I
69	Paxillin Signaling
70	DNA Double-Strand Break Repair by Non-Homologous End Joining
71	Rac Signaling
72	ERK5 Signaling
73	Pentose Phosphate Pathway (Oxidative Branch)
74	Trans-farnesyl Diphosphate Biosynthesis
75	Huntingtons Disease Signaling

76	Gap junction Signaling
77	Agrin Interactions at Neuromuscular Junction
78	γ -linolenate Biosynthesis II (Animals)
79	Pentose Phosphate Pathway (Non-oxidative Branch)
80	Ethanol Degradation II
81	Aryl Hydrocarbon Receptor Signaling
82	Xenobiotic Metabolism Signaling
83	Ethanol Degradation IV
84	Cysteine biosynthesis III (mammalia)
85	Stearate Biosynthesis I (Animals)
86	Superpathway of Serine and Glycine Biosynthesis I
87	Superoxide Radicals Degradation
88	IGF-1 Signaling
89	Granzyme A Signaling
90	CDK 5 Signaling
91	Telomerase Signaling
92	Axonal Guidance Signaling
93	Prostate Cancer Signaling
94	Ketolysis
95	Acetyl-CoA biosynthesis III (from Citrate)
96	Ketogenesis

Table S3. The top 18 enriched clusters (Enrichment score >5) by the DAVID database for the target list of Danu.

Category	Term	Gene Count	P-Value	Fold Enrichment	FDR
Annotation Cluster 1	Enrichment Score: 18.57				
GOTERM_CC_FAT	intracellular organelle lumen	134	8.00E-25	2.46	1.12E-21
GOTERM_CC_FAT	membrane-enclosed lumen	137	1.29E-24	2.41	1.80E-21
GOTERM_CC_FAT	organelle lumen	135	2.13E-24	2.42	2.97E-21
GOTERM_CC_FAT	nuclear lumen	98	2.89E-14	2.20	4.02E-11
GOTERM_CC_FAT	nucleoplasm	59	2.12E-08	2.18	2.95E-05
Annotation Cluster 2	Enrichment Score: 17.19				
GOTERM_CC_FAT	ribonucleoprotein complex	78	1.61E-32	4.94	2.24E-29
SP_PIR_KEYWORDS	RNA-binding	63	4.11E-26	5.07	5.82E-23
GOTERM_MF_FAT	RNA binding	82	1.05E-24	3.62	1.57E-21
SP_PIR_KEYWORDS	mRNA splicing	33	1.40E-17	6.86	1.98E-14
GOTERM_BP_FAT	mRNA metabolic process	48	2.27E-17	4.32	3.91E-14
GOTERM_BP_FAT	RNA splicing	42	2.96E-17	4.93	5.09E-14
Annotation Cluster 3	Enrichment Score: 16.37				
GOTERM_CC_FAT	Intracellular non-membrane-bounded organelle	161	1.82E-21	2.02	2.54E-18
GOTERM_CC_FAT	non-membrane-bounded organelle	161	1.82E-21	2.02	2.54E-18
GOTERM_CC_FAT	cytoskeleton	80	2.18E-08	1.89	3.04E-05
Annotation Cluster 4	Enrichment Score: 13.89				
SP_PIR_KEYWORDS	isopeptide bond	39	7.06E-17	5.31	1.55E-13
UP_SEQ_FEATURE	cross-link: Glycyl lysine isopeptide (Lys-Gly)	29	1.85E-14	6.29	3.08E-11
SP_PIR_KEYWORDS	ubl conjugation	46	1.57E-12	3.40	2.22E-09
Annotation Cluster 5	Enrichment Score: 13.72				
SP_PIR_KEYWORDS	Chaperone	28	2.94E-16	7.69	4.66E-13

GOTERM_MF_FAT	unfolded protein binding	27	1.35E-15	7.43	1.99E-12
GOTERM_BP_FAT	protein folding	27	1.73E-11	5.08	2.98E-08
Annotation Cluster 6	Enrichment Score: 13.12				
GOTERM_CC_FAT	pigment granule	30	1.71E-22	10.99	2.38E-19
GOTERM_CC_FAT	melanosome	30	1.71E-22	10.99	2.38E-19
GOTERM_CC_FAT	membrane-bounded vesicle	48	4.30E-10	2.76	5.99E-07
GOTERM_CC_FAT	cytoplasmic membrane-bounded vesicle	47	4.76E-10	2.79	6.64E-07
GOTERM_CC_FAT	vesicle	51	3.92E-09	2.48	5.46E-06
GOTERM_CC_FAT	cytoplasmic vesicle	49	7.84E-09	2.49	1.09E-05
Annotation Cluster 7	Enrichment Score: 12.00				
SP_PIR_KEYWORDS	RNA-binding	63	4.11E-26	5.07	5.82E-23
UP_SEQ_FEATURE	RRM 1	20	1.61E-12	8.54	2.67E-09
UP_SEQ_FEATURE	RRM 2	20	1.61E-12	8.54	2.67E-09
SMART	RRM	27	2.04E-12	5.51	2.38E-09
INTERPRO	RNA recognition motif, RNP-1	27	6.03E-11	4.86	9.40E-08
INTERPRO	Nucleotide-binding, alpha-beta plait	27	7.46E-11	4.81	1.16E-07
UP_SEQ_FEATURE	RRM 3	7	9.93E-04	6.04	1.635972
Annotation Cluster 8	Enrichment Score: 11.14				
SP_PIR_KEYWORDS	protein biosynthesis	51	5.11E-39	11.78	7.24E-36
GOTERM_BP_FAT	translation	56	6.37E-26	5.64	1.10E-22
GOTERM_BP_FAT	translational elongation	27	1.20E-17	8.91	2.07E-14
SP_PIR_KEYWORDS	ribonucleoprotein	37	3.65E-17	5.76	5.16E-14
SP_PIR_KEYWORDS	ribosome	19	3.90E-14	11.30	5.52E-11
GOTERM_CC_FAT	cytosolic part	27	7.44E-13	5.79	1.04E-09
Annotation Cluster 9	Enrichment Score: 7.55				
GOTERM_BP_FAT	response to unfolded protein	17	2.20E-10	7.98	3.79E-07

GOTERM_BP_FAT	response to protein stimulus	18	1.76E-08	5.61	3.02E-05
SP_PIR_KEYWORDS	stress response	13	2.99E-08	8.55	4.24E-05
GOTERM_BP_FAT	response to organic substance	45	5.31E-06	2.08	0.009138
Annotation Cluster 10	Enrichment Score: 7.45				
GOTERM_BP_FAT	cellular macromolecular complex assembly	34	4.66E-10	3.56	8.03E-07
GOTERM_BP_FAT	cellular macromolecular complex subunit organization	36	6.33E-10	3.36	1.09E-06
GOTERM_BP_FAT	macromolecular complex assembly	51	1.56E-09	2.56	2.68E-06
GOTERM_BP_FAT	macromolecular complex subunit organization	53	1.79E-09	2.49	3.07E-06
GOTERM_BP_FAT	protein complex assembly	36	3.41E-06	2.38	0.005866
GOTERM_BP_FAT	protein complex biogenesis	36	3.41E-06	2.38	0.005866
Annotation Cluster 11	Enrichment Score: 7.41				
GOTERM_MF_FAT	nucleotide binding	137	1.37E-15	1.93	1.99E-12
SP_PIR_KEYWORDS	nucleotide-binding	91	2.13E-14	2.34	3.02E-11
SP_PIR_KEYWORDS	ATP-binding	76	2.81E-13	2.49	3.98E-10
GOTERM_MF_FAT	ATP binding	81	6.82E-07	1.74	0.001018
GOTERM_MF_FAT	adenyl ribonucleotide binding	81	1.16E-06	1.71	0.001735
GOTERM_MF_FAT	ribonucleotide binding	94	1.37E-06	1.62	0.00204
Annotation Cluster 12	Enrichment Score: 6.54				
SP_PIR_KEYWORDS	actin binding	14	2.86E-12	15.20	4.05E-09
SP_PIR_KEYWORDS	actin-binding	29	3.65E-12	5.10	5.16E-09
GOTERM_MF_FAT	actin binding	34	3.11E-09	3.30	4.64E-06
GOTERM_MF_FAT	cytoskeletal protein binding	43	7.82E-09	2.70	1.17E-05
GOTERM_CC_FAT	cytoskeleton	80	2.18E-08	1.89	3.04E-05
SP_PIR_KEYWORDS	cytoskeleton	39	8.33E-08	2.66	1.18E-04
Annotation Cluster 13	Enrichment Score: 5.97				
UP_SEQ_FEATURE	KH 3	8	1.01E-08	24.65	1.67E-05

UP_SEQ_FEATURE	KH 4	6	1.31E-07	36.98	2.17E-04
UP_SEQ_FEATURE	KH 1	8	6.00E-07	15.01	9.96E-04
UP_SEQ_FEATURE	KH 2	8	6.00E-07	15.01	9.96E-04
INTERPRO	K Homology, type 1	9	1.67E-06	10.35	0.002605
INTERPRO	K Homology, type 1, subgroup	9	2.70E-06	9.76	0.004217
Annotation Cluster 14	Enrichment Score: 5.84				
GOTERM_BP_FAT	glucose catabolic process	15	1.14E-09	8.62	1.95E-06
GOTERM_BP_FAT	hexose catabolic process	15	1.28E-08	7.24	2.21E-05
GOTERM_BP_FAT	monosaccharide catabolic process	15	1.89E-08	7.04	3.25E-05
GOTERM_BP_FAT	glycolysis	12	9.98E-08	8.51	1.72E-04
GOTERM_BP_FAT	alcohol catabolic process	15	1.09E-07	6.17	1.88E-04
GOTERM_BP_FAT	cellular carbohydrate catabolic process	15	2.04E-07	5.88	3.51E-04
Annotation Cluster 15	Enrichment Score: 5.81				
SP_PIR_KEYWORDS	stress response	13	2.99E-08	8.55	4.24E-05
INTERPRO	Heat shock protein 70	7	2.58E-07	22.14	4.03E-04
INTERPRO	Heat shock protein Hsp70	7	2.58E-07	22.14	4.03E-04
INTERPRO	Heat shock protein 70, conserved site	7	1.31E-06	17.71	0.002039
PIR_SUPERFAMILY	chaperone HSP70	4	0.003395	12.01	4.440052
Annotation Cluster 16	Enrichment Score: 5.65				
GOTERM_BP_FAT	tRNA aminoacylation	14	5.32E-10	10.14	9.15E-07
GOTERM_BP_FAT	amino acid activation	14	5.32E-10	10.14	9.15E-07
GOTERM_BP_FAT	tRNA aminoacylation for protein translation	14	5.32E-10	10.14	9.15E-07
SP_PIR_KEYWORDS	Aminoacyl-tRNA synthetase	12	7.83E-10	13.36	1.11E-06
GOTERM_MF_FAT	ligase activity, forming aminoacyl-tRNA and related compounds	13	1.57E-08	8.76	2.34E-05
GOTERM_MF_FAT	ligase activity, forming carbon-oxygen bonds	13	1.57E-08	8.76	2.34E-05

Annotation Cluster 17		Enrichment Score: 5.49			
INTERPRO	Chaperone, tailless complex polypeptide 1	7	1.32E-07	24.15	2.06E-04
INTERPRO	Chaperonin Cpn60/TCP-1	7	1.31E-06	17.71	0.002039
INTERPRO	Chaperonin TCP-1, conserved site	6	2.78E-06	22.77	0.004332
PIR_SUPERFAMILY	molecular chaperone t-complex-type	6	2.53E-05	14.41	0.033807
GOTERM_CC_FAT	chaperonin-containing T-complex	5	2.81E-05	23.29	0.039078
Annotation Cluster 18		Enrichment Score: 5.18			
GOTERM_BP_FAT	negative regulation of apoptosis	29	2.84E-06	2.73	0.004896
GOTERM_BP_FAT	negative regulation of programmed cell death	29	3.73E-06	2.69	0.00642
GOTERM_BP_FAT	negative regulation of cell death	29	3.93E-06	2.68	0.006773
GOTERM_BP_FAT	regulation of apoptosis	48	7.92E-06	1.99	0.01364
GOTERM_BP_FAT	regulation of programmed cell death	48	1.03E-05	1.97	0.017716
GOTERM_BP_FAT	regulation of cell death	48	1.13E-05	1.96	0.019376
GOTERM_BP_FAT	anti-apoptosis	20	1.39E-05	3.23	0.023852