SUPPORTING INFORMATION

Characterizations of PMCA2-interacting complex and its role as a calcium oxalate crystal-binding protein

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Supplementary Table S1. Mass spectrometric parameters of PMCA2-interacting proteins identified by IP-MS.

Protein no.	Protein name	UniProt accession number	MudPIT identification score	%Cov	No. of distinct/total matched peptides	p*I*	MW (kDa)
1	14-3-3 protein theta	Q3SZI4	73	18.40	6/15	4.68	28.03
2	26S protease regulatory subunit 6B	Q3T030	210	7.20	3/6	5.09	47.45
3	26S protease regulatory subunit 7	Q4R4R0	63	25.40	11/12	5.71	49.00
4	26S proteasome non-ATPase regulatory subunit 13	Q9UNM6	54	15.70	6/7	5.53	43.20
5	26S proteasome non-ATPase regulatory subunit 14	O00487	130	11.60	3/4	6.06	34.73
6	26S proteasome non-ATPase regulatory subunit 3	O43242	69	16.90	8/10	8.47	61.05
7	26S proteasome non-ATPase regulatory subunit 7	Q3ZBD0	71	9.60	3/4	6.29	36.79
8	2-oxoglutarate dehydrogenase, mitochondrial	Q148N0	44	7.40	7/11	6.28	116.88
9	2-oxoglutarate dehydrogenase-like, mitochondrial	Q9ULD0	44	5.30	5/9	6.18	115.26
10	2-oxoisovalerate dehydrogenase subunit beta, mitochondrial	P35738	117	10.50	4/9	6.41	43.54
11	40S ribosomal protein SA	Q2L9X0	153	18.60	6/14	4.80	32.96
12	5'-AMP-activated protein kinase catalytic subunit alpha-1	Q5EG47	48	9.50	6/7	8.33	64.52
13	60 kDa heat shock protein, mitochondrial	P10809	260	26.90	14/30	5.70	61.19
14	60S acidic ribosomal protein P0	P05388	473	22.40	6/16	5.71	34.42
15	60S ribosomal protein L10	Q4R7Y2	38	13.10	3/7	10.22	25.04
16	60S ribosomal protein L3	P39872	40	6.50	2/3	10.24	46.28
17	60S ribosomal protein L5	Q58DW5	98	24.90	8/17	9.73	34.55
18	60S ribosomal protein L6	P21533	68	18.80	5/6	10.74	33.60
19	Abl interactor 1	Q8IZP0	78	5.30	2/3	6.57	55.16
20	Actin-binding LIM protein 3	O94929	431	16.40	11/21	8.86	79.46
21	Activating signal cointegrator 1	Q15650	40	6.50	4/9	8.05	66.96
22	Acyl-CoA dehydrogenase family member 11	Q709F0	138	11.00	6/11	8.35	88.03
23	Adenylyltransferase and sulfurtransferase MOCS3	A2BDX3	116	7.40	4/12	7.46	50.31
24	ADP/ATP translocase 1	P12235	445	29.90	10/27	9.78	33.27
25	ADP/ATP translocase 4	Q4R8M0	50	21.30	7/16	9.91	35.34
26	A-kinase anchor protein 8	Q5VK71	117	5.60	4/4	5.07	77.36
27	Alpha-aminoadipic semialdehyde dehydrogenase	P49419	44	13.40	6/17	8.21	59.02
28	Alpha-S2-casein-like A	Q02862	39	3.80	2/10	6.21	21.26
29	Aly/REF export factor 2	Q9JJW6	73	24.30	5/7	10.04	23.77

30	Angiotensin-converting enzyme 2	Q58DD0	44	7.20	5/9	5.19	93.46
31	Ankyrin repeat and EF-hand domain-containing protein 1	Q9D2J7	39	12.90	11/29	8.51	87.59
32	Ankyrin repeat and SOCS box protein 7	Q5RCK5	47	9.10	4/5	8.58	36.36
33	Annexin A1	P10107	152	6.90	3/14	6.97	39.00
34	AP-1 complex subunit beta-1	Q10567	75	10.00	10/11	4.94	105.48
35	AP-1 complex subunit mu-1	Q2KJ81	63	10.60	5/7	6.82	48.73
36	AP-1 complex subunit mu-2	Q9WVP1	72	14.70	6/6	7.07	48.22
37	AP-2 complex subunit beta	Q9DBG3	112	15.70	16/23	5.22	105.43
38	AP-2 complex subunit mu	Q5NVF7	49	10.60	4/8	9.53	49.98
39	APOBEC1 complementation factor	Q9NQ94	44	19.90	10/40	8.60	65.45
40	Aspartate aminotransferase, mitochondrial	P00507	40	14.20	6/12	9.13	47.68
41	Aspartate--tRNA ligase, cytoplasmic	Q5R9I5	109	29.90	15/22	6.02	57.65
42	ATPase family AAA domain-containing protein 3A	Q9NVI7	285	19.70	10/23	9.08	71.61
43	ATPase family AAA domain-containing protein 3B	Q5T9A4	298	17.40	11/88	9.30	73.10
44	ATP-binding cassette sub-family E member 1	P61221	123	12.20	7/16	8.63	68.24
45	ATP-binding cassette sub-family F member 3	Q66H39	60	9.20	6/14	6.06	80.21
46	ATP-citrate synthase	P53396	80	9.90	11/47	6.95	121.67
47	ATP-dependent 6-phosphofructokinase, platelet type	Q5R636	329	23.00	15/27	7.49	86.44
48	ATP-dependent RNA helicase DDX1	Q0IIK5	390	22.70	14/23	6.81	83.33
49	ATP-dependent RNA helicase DDX39A	O00148	49	15.90	9/14	5.46	49.61
50	ATP-dependent RNA helicase DHX8	Q14562	41	9.80	13/25	8.54	140.08
51	ATP-dependent zinc metalloprotease YME1L1	Q96TA2	45	15.90	10/16	8.86	86.69
52	Band 4.1-like protein 5	Q9HCM4	85	13.80	8/14	6.15	82.38
53	Basic leucine zipper and W2 domain-containing protein 2	Q9WTT7	47	12.90	4/5	6.26	48.25
54	Beta-enolase	Q1KYT0	154	14.10	5/12	8.05	47.44
55	Bifunctional glutamate/proline--tRNA ligase	P07814	87	10.00	13/32	7.02	172.08
56	Bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial	P13995	65	16.30	4/12	8.86	38.04
57	Breast cancer type 2 susceptibility protein homolog	O35923	46	7.80	27/101	6.13	376.26
58	BTB/POZ domain-containing protein 9	A4IFG2	38	2.80	2/2	5.47	69.83
59	Bystin	Q80WL2	41	16.30	7/23	8.15	50.27
60	CAD protein	P08955	58	5.30	12/28	6.02	245.54
61	Calcium uniporter protein, mitochondrial	Q8NE86	121	24.80	8/16	8.83	40.13
62	Calumenin	Q5RDD8	53	14.30	5/12	4.45	37.26
63	Cathepsin Z	Q9UBR2	218	11.60	4/23	6.70	34.53
64	Cell cycle and apoptosis regulator protein 2	Q8N163	42	7.60	7/26	5.14	103.47
65	Cell division control protein 45 homolog	Q9Z1X9	47	10.20	6/10	5.24	65.97
66	Cell division cycle 5-like protein	Q99459	140	14.20	12/16	8.22	92.42
67	Cell division cycle protein 123 homolog	Q62834	39	6.80	2/10	4.52	39.36
68	Centromere protein V	Q9CXS4	37	13.50	3/3	9.85	27.98
69	Centrosomal protein of 104 kDa	Q80V31	53	10.60	9/18	8.40	104.96
70	Centrosomal protein of 164 kDa	Q9UPV0	38	10.50	12/32	5.27	164.73

71	Chloride intracellular channel protein 1	Q5E9B7	75	21.20	5/8	5.16	27.32
72	Chromatin assembly factor 1 subunit B	Q9D0N7	80	5.80	4/12	6.12	63.61
73	Clathrin coat assembly protein AP180	Q05140	37	10.60	9/16	4.76	93.75
74	Cleavage and polyadenylation specificity factor subunit 3	Q9QXK7	68	9.90	6/8	5.37	78.08
75	Cleft lip and palate transmembrane protein 1 homolog	Q8VBZ3	48	5.90	4/7	5.88	75.59
76	Coatomer subunit delta	P53619	69	22.90	11/17	5.89	57.69
77	Coiled-coil domain-containing protein 28A	Q8IWP9	34	7.30	2/4	9.32	30.52
78	Coiled-coil domain-containing protein 61	Q9Y6R9	39	21.90	11/21	10.27	57.56
79	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial	Q5E9D3	149	27.30	6/9	8.52	26.31
80	Collagen alpha-2(IV) chain	P08122	67	9.30	13/36	8.75	168.42
81	Constitutive coactivator of PPAR-gamma-like protein 1	A6H7H1	39	6.80	7/11	9.10	122.67
82	Constitutive coactivator of PPAR-gamma-like protein 2	Q9NX05	56	7.20	7/19	9.19	121.65
83	Core histone macro-H2A.1	O75367	112	31.20	8/16	9.80	39.76
84	Core histone macro-H2A.2	Q8CCK0	75	13.40	3/14	9.71	40.30
85	Coronin-6	Q6QEF8	75	13.10	7/17	5.63	53.19
86	Cullin-1	Q5R4G6	81	13.80	12/19	8.19	90.31
87	Cyclin-dependent kinase 17	Q00537	146	10.90	7/21	9.10	59.83
88	Cyclin-dependent kinase 20	Q5EDC3	146	11.50	4/19	9.69	27.58
89	Cytokine-dependent hematopoietic cell linker	Q7Z7G1	54	9.10	4/8	9.11	49.81
90	Cytoskeleton-associated protein 2	A5D7U0	47	21.00	10/22	9.33	70.56
91	Cytosolic carboxypeptidase 4	Q09M05	57	7.00	7/19	6.91	110.78
92	Death-associated protein kinase 1	Q80YE7	82	13.90	19/41	6.43	163.22
93	Death-associated protein kinase 3	O43293	56	22.20	10/16	6.44	52.67
94	Delta-1-pyrroline-5-carboxylate synthase	Q9Z110	49	15.20	12/18	7.18	87.78
95	Deoxyribonuclease-1-like 1	Q2QDE9	66	6.60	2/4	5.52	35.49
96	Diacylglycerol kinase beta	Q9Y6T7	52	10.10	8/23	8.11	92.13
97	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial	P11179	566	23.30	11/30	9.11	49.28
98	Dihydropyrimidinase	Q14117	39	8.10	4/6	6.81	57.11
99	Dihydropyrimidinase-related protein 1	Q14194	39	12.10	5/9	6.55	62.49
100	Dihydropyrimidinase-related protein 2	Q5R9Y6	39	5.10	2/3	5.95	62.71
101	DNA mismatch repair protein Mlh1	Q5E954	208	20.90	7/13	6.65	45.60
102	DNA mismatch repair protein Msh2	Q2HJ94	81	19.20	7/11	6.06	46.36
103	DNA polymerase beta	Q9NXW2	99	14.70	5/9	8.67	42.02
104	DNA replication licensing factor MCM5	Q9DC23	132	12.50	12/21	6.53	91.89
105	DNA topoisomerase 2-beta	Q5RC70	59	10.40	6/24	8.54	63.54
106	DNA topoisomerase I, mitochondrial	P97679	87	19.00	10/30	5.63	85.17
107	DnaJ homolog subfamily A member 1	Q3MHE4	49	11.60	11/22	5.59	105.65
108	DnaJ homolog subfamily A member 2	P06746	46	19.40	5/10	9.01	38.33
109	DnaJ homolog subfamily B member 12	Q0V8B7	81	19.20	14/15	8.47	82.89
110	DnaJ homolog subfamily C member 10	Q64399	41	10.90	19/23	8.30	182.87
111	DnaJ homolog subfamily C member 11	Q969P6	53	11.60	7/10	9.46	70.40

112	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	Q05052	215	14.60	7/16	5.91	49.72
113	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	Q9GMB0	251	11.50	7/16	6.10	68.82
114	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2	Q3SZI6	77	2.20	1/1	5.48	69.29
115	Double-stranded RNA-binding protein Staufen homolog 1	D2GVP7	60	12.60	6/10	9.52	63.70
116	Drebrin-like protein	Q9UJU6	36	3.50	1/3	5.02	48.46
117	Dual serine/threonine and tyrosine protein kinase	Q4TVR5	49	12.40	10/150	6.40	106.16
118	Dual specificity tyrosine-phosphorylation-regulated kinase 1A	Q13627	94	11.50	10/19	8.90	86.04
119	Dual specificity tyrosine-phosphorylation-regulated kinase 1B	Q9Y463	62	10.30	8/14	9.25	69.73
120	Dynamin-3	Q8BZ98	66	11.60	9/19	8.52	97.53
121	Dystonin	Q03001	41	7.90	59/194	5.14	865.26
122	Dystrobrevin alpha	Q9Y4J8	45	13.50	11/19	6.43	84.65
123	Dystrobrevin beta	O70585	55	9.60	8/15	8.90	75.21
124	E3 SUMO-protein ligase RanBP2	Q9ERU9	45	6.50	21/44	5.82	344.73
125	E3 ubiquitin-protein ligase TRIM39	Q1XHU0	120	10.80	6/14	8.02	60.73
126	E3 ubiquitin-protein ligase TRIM56	E1BD59	43	15.00	10/15	8.33	80.81
127	E3 ubiquitin-protein ligase UHRF1	Q7TPK1	55	6.70	6/9	8.56	88.88
128	Echinoderm microtubule-associated protein-like 4	Q9HC35	58	11.30	9/13	5.96	109.93
129	EH domain-containing protein 1	Q9WVK4	85	19.50	10/13	6.35	60.62
130	EH domain-containing protein 2	Q8BH64	49	5.30	3/7	6.08	61.31
131	EH domain-containing protein 3	Q9NZN3	62	22.60	9/14	6.12	60.91
132	EH domain-containing protein 4	Q9H223	472	24.20	13/20	6.33	61.37
133	ELAV-like protein 4	O09032	54	8.60	3/6	9.45	41.22
134	Electron transfer flavoprotein subunit alpha, mitochondrial	Q5RC31	47	12.90	3/4	8.62	35.49
135	Elongation factor 1-alpha 2	Q32PH8	1153	18.60	11/65	9.11	50.78
136	Elongation factor 1-delta	A5D989	125	18.90	5/10	4.94	31.24
137	Elongation factor 1-gamma	Q9D8N0	291	21.50	11/19	6.31	50.37
138	Endonuclease domain-containing 1 protein	Q8C522	119	8.40	4/25	5.80	55.91
139	Ephrin type-A receptor 2	Q1KL86	77	12.10	11/56	5.89	109.98
140	Epidermal growth factor receptor kinase substrate 8	Q5R4H4	75	17.00	12/52	6.91	92.26
141	Epidermal growth factor receptor kinase substrate 8-like protein 2	Q99K30	651	19.10	16/67	6.73	82.69
142	Erlin-1	Q91X78	76	24.00	8/12	6.73	39.08
143	Erlin-2	Q1RMU4	76	18.90	6/8	5.36	37.93
144	Eukaryotic initiation factor 4A-III	Q91VC3	493	40.10	15/24	6.30	47.10
145	Eukaryotic peptide chain release factor GTP-binding subunit ERF3B	Q149F3	55	12.30	8/10	5.11	69.79
146	Eukaryotic translation initiation factor 2 subunit 3	P81795	62	17.80	8/17	8.66	51.62
147	Eukaryotic translation initiation factor 2 subunit 3, Y-linked	Q9Z0N2	65	14.40	6/15	8.76	51.67
148	Eukaryotic translation initiation factor 3 subunit B	Q4G061	58	9.30	6/7	4.97	91.25
149	Eukaryotic translation initiation factor 3 subunit C	B5DFC8	45	15.90	14/37	5.55	106.05
150	Eukaryotic translation initiation factor 3 subunit D	Q4R8R4	87	15.10	10/15	5.78	64.52
151	Eukaryotic translation initiation factor 3 subunit E	Q3T102	49	15.70	7/38	5.71	52.56
152	Exosome complex exonuclease RRP44	Q9Y2L1	42	8.70	7/27	6.69	110.02

153	Exportin-1	Q6P5F9	54	9.70	10/15	5.72	124.15
154	Exportin-4	Q9ESJ0	61	6.50	5/9	5.02	131.15
155	Exportin-7	Q9EPK7	55	10.00	10/53	5.96	125.16
156	Exportin-T	Q5RA02	113	6.70	7/9	5.27	111.14
157	F-actin-capping protein subunit alpha-2	Q108U5	1041	42.00	10/39	5.57	33.12
158	Far upstream element-binding protein 2	Q92945	153	22.10	11/16	6.85	73.36
159	FAS-associated factor 2	Q96CS3	58	13.90	5/5	5.46	52.93
160	Fatty acyl-CoA reductase 1	Q5R834	57	15.30	7/7	9.25	59.66
161	Folate receptor beta	P14207	96	11.40	2/4	7.49	30.29
162	Four and a half LIM domains protein 2	Q2KI95	47	5.40	2/4	7.59	34.07
163	Fragile X mental retardation protein 1	Q06787	59	6.80	5/21	6.99	71.47
164	Fragile X mental retardation syndrome-related protein 2	P51116	118	4.60	4/13	5.95	74.52
165	Fructose-bisphosphate aldolase A	P05064	79	7.40	3/3	8.31	39.79
166	Galectin-8	O00214	94	6.00	2/4	8.33	35.96
167	GDP-mannose 4,6 dehydratase	O60547	54	15.10	7/38	6.87	42.27
168	GEM-interacting protein	Q6PGG2	36	9.70	10/12	5.54	108.68
169	Glutamate dehydrogenase 1, mitochondrial	P00367	106	12.40	8/9	7.66	61.70
170	Glutamate dehydrogenase 2, mitochondrial	Q64HZ8	87	12.40	7/9	8.49	61.74
171	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 1	Q06210	61	9.40	7/13	6.66	79.56
172	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] 2	Q4KMC4	42	12.80	8/21	6.86	77.76
173	Glutamine--tRNA ligase	Q3MHH4	64	8.30	6/13	6.43	88.44
174	Glycogen debranching enzyme	A8BQB4	50	7.10	11/25	6.24	176.49
175	Glycosyltransferase-like domain-containing protein 1	Q8BW56	38	7.90	4/15	7.25	51.61
176	Golgin subfamily B member 1	Q14789	43	16.00	53/77	4.96	377.22
177	Golgi-specific brefeldin A-resistance guanine nucleotide exchange factor 1	Q9R1D7	49	5.40	10/19	5.48	208.17
178	Granulins	P28799	35	8.90	5/12	6.43	68.52
179	GTP-binding nuclear protein Ran	Q3T054	137	15.30	3/7	7.01	24.58
180	Guanine nucleotide-binding protein G(i) subunit alpha-1	Q5R5W8	396	18.50	6/15	5.47	38.15
181	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	B2RSH2	598	26.30	9/22	5.69	40.91
182	Guanine nucleotide-binding protein G(o) subunit alpha	P18872	502	9.90	3/15	5.34	40.63
183	Guanine nucleotide-binding protein G(olf) subunit alpha	Q8CGK7	501	9.20	3/14	6.23	44.79
184	Guanine nucleotide-binding protein G(q) subunit alpha	Q2PKF4	89	15.60	5/7	5.48	42.40
185	Guanine nucleotide-binding protein G(t) subunit alpha-1	P04695	501	11.40	4/15	5.48	40.40
186	Guanine nucleotide-binding protein subunit alpha-11	Q2XSV9	172	21.20	6/10	5.90	42.32
187	Guanine nucleotide-binding protein subunit alpha-14	P38408	89	14.10	4/5	5.81	41.93
188	Guanine nucleotide-binding protein subunit alpha-15	Q9TU29	89	8.60	3/6	8.68	43.36
189	H(+)/Cl(-) exchange transporter 3	Q5RDJ7	52	6.40	5/15	5.88	90.29
190	H(+)/Cl(-) exchange transporter 5	Q9GKE7	52	4.30	4/18	6.79	84.04
191	H/ACA ribonucleoprotein complex subunit 4	O60832	59	14.60	9/14	9.46	58.09
192	Hedgehog-interacting protein	Q7TN16	50	4.60	4/15	8.25	80.34
193	Hepatocyte nuclear factor 1-beta	P23899	118	15.40	7/8	7.38	61.56

194	Heterogeneous nuclear ribonucleoprotein A1-like 2	Q32P51	633	25.90	8/33	9.08	34.38
195	Heterogeneous nuclear ribonucleoprotein D0	Q14103	384	9.00	3/20	7.62	38.58
196	Heterogeneous nuclear ribonucleoprotein H2	Q6AY09	1091	35.90	13/54	5.89	49.55
197	Heterogeneous nuclear ribonucleoprotein K	O19049	645	28.50	12/35	5.39	51.21
198	Heterogeneous nuclear ribonucleoprotein L	P14866	387	19.90	9/16	8.46	64.72
199	Hexokinase-1	P17710	53	14.50	13/16	6.37	109.55
200	Hexokinase-2	P52789	97	12.30	9/22	5.71	103.74
201	Hexokinase-3	P52790	53	10.00	8/12	5.23	100.62
202	Histone acetyltransferase KAT2B	Q92831	54	10.00	8/12	9.16	94.04
203	Histone deacetylase 1	Q3MHL3	128	13.90	4/6	4.74	47.91
204	Histone deacetylase 2	Q4R304	125	14.80	4/6	4.89	48.13
205	Histone H1.1	Q4QQW4	46	11.20	6/15	5.31	55.63
206	Histone H1.2	P70288	46	7.20	5/7	5.59	55.84
207	Histone H1.3	G3N131	116	11.90	4/9	10.93	22.09
208	Histone H1t	P16403	116	18.30	5/10	10.94	21.35
209	Histone H2AX	P43277	116	20.40	6/11	11.03	22.09
210	Histone H2B type F-S	P06348	116	11.80	4/10	11.58	22.05
211	Histone H3.3C	P27661	564	12.60	2/39	10.74	15.13
212	Histone-binding protein RBBP4	P57053	412	35.70	5/44	10.37	13.94
213	Histone-binding protein RBBP7	A5PK61	156	31.60	4/19	11.48	15.42
214	Histone-lysine N-methyltransferase 2A	Q03164	41	6.80	28/119	9.22	436.06
215	Homeobox-containing protein 1	Q6NT76	49	8.10	3/4	5.72	47.42
216	Importin subunit beta-1	P52296	400	16.20	13/27	4.66	98.37
217	Insulin-like growth factor 2 mRNA-binding protein 1	Q9NZI8	825	35.90	21/49	9.26	63.78
218	Insulin-like growth factor 2 mRNA-binding protein 2	Q5SF07	378	11.00	6/21	7.81	65.66
219	Insulin-like growth factor 2 mRNA-binding protein 3	O00425	326	10.50	6/16	8.99	64.01
220	Integrin alpha-2 (Fragment)	P53710	37	6.90	7/22	5.47	130.16
221	Integrin beta-4	P16144	58	8.70	13/24	5.74	205.75
222	Interferon-induced protein with tetratricopeptide repeats 2	Q60462	65	14.70	6/88	8.73	55.58
223	Isocitrate dehydrogenase [NAD] subunit beta, mitochondrial	Q28479	122	27.50	7/13	8.45	42.51
224	Kelch domain-containing protein 7A	A2APT9	48	5.00	4/6	5.92	84.91
225	Kelch-like ECH-associated protein 1	Q9Z2X8	86	12.50	8/22	6.00	70.93
226	Kelch-like protein 7	Q5XHZ6	124	17.40	10/13	6.19	67.07
227	Kelch-like protein 9	Q2T9Z7	48	12.00	7/13	5.92	70.21
228	KH domain-containing, RNA-binding, signal transduction-associated protein 1	Q07666	101	12.00	7/16	8.73	48.31
229	Kinesin-like protein KIF12	Q9D2Z8	114	10.90	9/17	8.94	71.69
230	Kinesin-like protein KIF13B	Q9NQT8	64	11.80	18/164	5.64	203.97
231	Kinesin-like protein KIF1A	Q12756	64	13.00	22/41	5.86	192.54
232	Kinesin-like protein KIF1B	Q60575	64	15.20	28/41	5.43	205.32
233	Kinesin-like protein KIF1C	O43896	64	17.60	19/30	6.47	123.73
234	Kinesin-like protein KIF20A	Q29RT6	52	8.30	8/8	6.55	101.01

235	Kinesin-like protein KIF2B	Q95LT1	56	15.80	10/11	9.14	76.44
236	Kinesin-like protein KIF2C	P70096	56	10.70	8/9	8.05	81.72
237	Kinesin-like protein KIFC1	Q9BW19	68	15.80	11/25	9.15	74.27
238	Lamin-B2	P21619	55	22.00	16/58	5.40	67.39
239	Lebercilin-like protein	O95447	49	10.00	8/11	9.51	76.86
240	Leucine zipper putative tumor suppressor 1	P62046	181	9.20	9/22	5.74	79.94
241	Leucine zipper putative tumor suppressor 3	Q3UMG5	34	2.20	2/4	6.14	85.73
242	Leucine-rich repeat and calponin homology domain-containing protein 1	Q9D5S7	49	3.00	3/6	5.89	93.76
243	Leucine-rich repeat and calponin homology domain-containing protein 2	Q5RJR8	40	11.40	4/5	9.57	35.30
244	Leucine-rich repeat and guanylate kinase domain-containing protein	Q9Y250	55	14.90	10/13	6.64	66.97
245	Leucine-rich repeat-containing protein 59	O60299	119	20.40	13/59	7.56	72.26
246	Lipid phosphate phosphatase-related protein type 1	Q6WAY2	47	5.20	2/10	6.24	36.60
247	Long-chain-fatty-acid--CoA ligase 3	Q5R668	154	17.40	12/23	8.71	81.36
248	Long-chain-fatty-acid--CoA ligase 4	Q9QUJ7	85	13.50	10/14	8.57	80.22
249	Lymphoid-specific helicase	Q9NRZ9	43	12.20	10/19	8.07	97.64
250	Lysine-specific demethylase 7A	Q3UWM4	44	4.40	5/15	8.05	107.32
251	Lysozyme g-like protein 2	Q3V1I0	44	12.20	2/2	8.64	23.97
252	Major vault protein	Q5R9N2	37	10.60	9/13	5.36	99.46
253	MAP/microtubule affinity-regulating kinase 3	P27448	45	10.00	7/10	9.59	84.95
254	Maternal embryonic leucine zipper kinase	Q14680	52	8.60	8/66	8.92	75.51
255	Membrane progestin receptor beta	Q8TEZ7	39	4.20	2/3	8.69	41.24
256	Metastasis-associated protein MTA1	Q8K4B0	38	7.40	5/13	9.37	81.43
257	Metastasis-associated protein MTA2	Q9R190	38	21.90	12/33	9.71	75.72
258	Metastasis-associated protein MTA3	Q9BTC8	38	9.60	6/18	8.80	68.20
259	Methionine--tRNA ligase, cytoplasmic	Q68FL6	117	13.00	12/18	6.78	102.74
260	Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	Q5XIT9	68	8.30	4/8	8.56	61.99
261	Misshapen-like kinase 1	Q9JM52	43	8.10	10/22	7.07	147.89
262	Mitochondrial glutamate carrier 1	Q08DK4	85	16.80	5/17	9.42	34.97
263	Mitochondrial glutamate carrier 2	Q9H1K4	85	9.80	4/5	9.39	34.34
264	Mitochondrial Rho GTPase 1	Q2HJF8	47	5.20	4/9	6.02	73.06
265	Mitogen-activated protein kinase kinase kinase kinase 4	O95819	43	8.10	12/48	7.09	142.75
266	Mitotic checkpoint protein BUB3	Q1JQB2	69	16.60	5/8	6.36	37.33
267	Mitotic interactor and substrate of PLK1	Q8IVT2	62	12.10	9/16	6.36	75.48
268	MKI67 FHA domain-interacting nucleolar phosphoprotein	Q3SZM1	45	22.60	6/7	10.05	34.25
269	Mothers against decapentaplegic homolog 2	Q1W668	60	9.90	3/3	6.24	53.11
270	Mothers against decapentaplegic homolog 3	Q8BUN5	60	8.70	3/4	6.73	48.91
271	Mothers against decapentaplegic homolog 9	Q9JIW5	60	9.50	4/5	8.49	49.57
272	Myeloid differentiation primary response protein MyD88	Q99836	48	8.80	3/4	5.89	33.73
273	Myosin light chain 1/3, skeletal muscle isoform	P02600	88	33.30	4/9	4.99	20.78
274	N-acetyltransferase 10	Q9H0A0	65	11.00	13/39	8.50	116.57
275	NCK-interacting protein with SH3 domain	Q9NZQ3	67	8.70	6/6	5.94	79.65

276	Neurobeachin-like protein 2	Q6ZNJ1	43	4.70	13/31	5.95	305.41
277	Neurofilament light polypeptide	P02547	615	11.80	6/70	4.64	62.09
278	Neuron navigator 3	Q8IVL0	41	9.50	20/50	8.92	256.97
279	Neuropeptide Y receptor type 5	O97969	39	1.60	1/2	9.21	51.30
280	NF-kappa-B-repressing factor	O15226	61	15.20	10/15	8.94	78.31
281	Niban-like protein 1	Q8R1F1	103	10.50	8/19	5.65	85.39
282	Nuclear cap-binding protein subunit 1	Q09161	65	11.10	8/11	5.99	92.86
283	Nuclear fragile X mental retardation-interacting protein 2	Q7Z417	51	16.30	9/13	8.70	76.13
284	Nuclear pore complex protein Nup93	Q8BJ71	452	28.30	23/41	5.50	93.74
285	Nuclear receptor coactivator 5	Q9HCD5	71	11.90	7/12	9.62	65.73
286	Nuclease-sensitive element-binding protein 1	Q28618	139	19.80	3/4	9.82	35.80
287	Nucleolar protein 6	Q9H6R4	47	4.00	5/7	7.42	128.37
288	Nucleolar transcription factor 1	P17480	88	17.80	12/14	5.63	89.69
289	Nucleolysin TIAR	P70318	40	19.10	6/12	8.11	43.70
290	Nucleophosmin	Q3T160	137	21.40	7/18	4.62	32.85
291	Olfactory receptor 6N2	Q8NGY6	46	4.70	2/11	9.08	36.35
292	Ornithine aminotransferase, mitochondrial	P29758	53	9.60	5/9	6.19	48.72
293	Pachytene checkpoint protein 2 homolog	E2R222	87	7.90	3/3	5.83	48.92
294	Parafibromin	Q4V8C8	55	24.30	12/13	9.63	60.68
295	PCI domain-containing protein 2	Q2TBN6	120	24.30	7/13	8.94	47.41
296	PDZ and LIM domain protein 7	Q9Z1Z9	190	17.10	9/16	8.82	50.96
297	PDZ domain-containing protein GIPC1	O14908	469	31.20	14/33	5.90	36.14
298	Pericentriolar material 1 protein	Q9R0L6	46	8.20	17/37	4.94	230.13
299	Phosphatidylinositol-binding clathrin assembly protein	Q7M6Y3	49	10.60	5/7	7.71	71.67
300	Phosphoacetylglucosamine mutase	Q9CYR6	48	15.90	10/29	5.80	60.04
301	**Plasma membrane calcium-transporting ATPase 2**	**Q01814**	**86**	**10.00**	**28/12**	**5.66**	**137.98**
302	Poly(A) polymerase alpha	P51003	48	13.00	9/21	6.96	83.25
303	Poly(A) polymerase beta	Q9WVP6	48	8.60	7/18	6.28	72.50
304	Poly(rC)-binding protein 3	P57721	148	17.50	5/7	8.22	39.73
305	Polyadenylate-binding protein 1-like	Q4VXU2	311	21.70	13/24	9.06	68.98
306	Polyadenylate-binding protein 4-like	P0CB38	44	8.10	3/5	9.53	42.06
307	Polymerase delta-interacting protein 3	Q9BY77	79	16.60	5/5	10.00	46.29
308	Polypyrimidine tract-binding protein 2	Q9UKA9	134	6.20	3/12	8.72	57.57
309	Polypyrimidine tract-binding protein 3	O95758	134	6.90	4/18	9.13	59.94
310	Polyubiquitin-B	P0CG47	1041	27.50	8/55	6.86	25.80
311	Potassium-transporting ATPase alpha chain 2	P54708	46	7.80	8/25	6.16	115.64
312	POTE ankyrin domain family member F	A5A3E0	12372	21.50	21/389	5.83	123.02
313	POTE ankyrin domain family member J	P0CG39	4948	20.40	20/236	5.66	118.74
314	Pre-mRNA-processing factor 19	Q08E38	99	15.70	6/7	6.14	55.62
315	Probable ATP-dependent RNA helicase DDX20	Q9JJY4	52	5.90	4/30	6.30	92.57
316	Probable ATP-dependent RNA helicase DDX4	Q4R5S7	86	9.90	6/8	5.56	80.03

317	Probable ATP-dependent RNA helicase DDX47	Q29S22	64	14.70	7/9	9.21	51.22
318	Probable helicase senataxin	A2AKX3	47	7.50	20/41	6.41	301.62
319	Probable RNA-binding protein 46	Q4R2Z0	44	13.60	6/10	7.94	55.77
320	Programmed cell death 6-interacting protein (Alix)	Q8WUM4	146	17.70	15/40	6.13	96.59
321	Proliferating cell nuclear antigen	Q3ZBW4	118	16.10	4/5	4.57	29.07
322	Protein argonaute-2	Q8CJG0	56	15.10	14/24	9.32	98.50
323	Protein CYR61	A5A6L1	52	13.40	5/11	8.64	44.15
324	Protein FAM83B	Q0VBM2	146	11.30	10/17	9.19	115.12
325	Protein kinase C delta type	Q05655	159	19.20	7/11	5.46	27.84
326	Protein PRRC2A	Q6MG48	36	11.40	17/43	9.47	229.42
327	Protein RCC2	Q9P258	38	9.00	5/10	9.02	56.79
328	Protein TBRG4	Q7YS91	53	11.70	8/8	9.26	71.63
329	Protein TFG	Q92734	140	23.30	5/9	4.94	43.48
330	Protein transport protein Sec23B	Q9D662	52	10.40	8/13	6.51	87.29
331	Protein zyg-11 homolog B	Q9C0D3	104	11.20	8/17	6.38	84.95
332	Protein-lysine 6-oxidase	P28300	170	16.30	5/13	8.36	47.60
333	Puromycin-sensitive aminopeptidase-like protein	A6NEC2	159	18.60	11/18	5.17	54.23
334	Putative endoplasmin-like protein	Q58FF3	55	4.80	2/4	5.14	46.34
335	Putative eukaryotic translation initiation factor 2 subunit 3-like protein	Q2VIR3	62	14.60	6/15	8.67	51.77
336	Putative heat shock 70 kDa protein 7	P48741	952	17.70	5/28	7.72	40.45
337	Putative heat shock protein HSP 90-alpha A2	Q14568	337	16.90	6/15	4.57	39.45
338	Putative heat shock protein HSP 90-alpha A5	Q58FG0	50	17.70	6/18	6.15	38.94
339	Putative heat shock protein HSP 90-beta 4	Q58FF6	56	16.80	7/9	4.65	58.86
340	Putative pre-mRNA-splicing factor ATP-dependent RNA helicase DHX16	Q767K6	41	12.00	12/19	6.03	120.26
341	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial	P11966	108	22.30	7/11	6.21	39.44
342	Rab GDP dissociation inhibitor beta	Q5RCE1	40	17.80	10/12	6.11	51.09
343	Rab11 family-interacting protein 1	Q9D620	117	14.10	8/15	9.47	70.70
344	Rac GTPase-activating protein 1	Q9H0H5	54	15.80	9/12	9.08	71.67
345	RAF proto-oncogene serine/threonine-protein kinase	A7E3S4	86	20.10	10/19	9.33	73.63
346	RalA-binding protein 1	Q62796	44	14.20	12/35	5.65	75.66
347	Ran GTPase-activating protein 1	P46060	51	19.10	9/12	4.63	63.96
348	Ras GTPase-activating protein-binding protein 1	Q5RB87	141	13.90	5/15	5.36	52.22
349	Ras GTPase-activating protein-binding protein 2	P97379	86	16.60	7/10	5.44	54.11
350	Ras GTPase-activating-like protein IQGAP1	P46940	66	11.50	18/70	6.08	189.76
351	Ras-related C3 botulinum toxin substrate 1	Q6RUV5	90	12.50	2/6	8.77	21.84
352	Ras-related C3 botulinum toxin substrate 3	P60763	90	11.50	2/6	8.43	21.76
353	Ras-related protein Rab-1A	Q6NYB7	124	33.70	5/7	5.93	22.89
354	Ras-related protein Rab-26	Q29RR0	56	9.00	3/3	9.36	27.96
355	Ras-related protein Rab-37	Q96AX2	56	26.50	5/5	5.97	25.03
356	Ras-related protein Rab-39B	Q17QU4	56	19.20	4/5	7.70	24.82
357	Ras-related protein Rab-5A	Q0IIG7	103	10.70	2/3	8.32	23.90

358	Regulator of chromosome condensation	Q8VE37	42	13.10	5/5	8.34	45.36
359	Replication factor C subunit 2	Q9WUK4	97	14.90	5/7	6.04	39.16
360	Replication factor C subunit 4	Q99J62	71	17.00	6/8	6.29	40.36
361	Replication factor C subunit 5	Q9D0F6	154	19.80	8/21	7.67	38.36
362	Replication protein A 70 kDa DNA-binding subunit	Q5R7Q4	108	14.40	8/16	6.86	68.71
363	Rhotekin	Q6V7V2	55	17.90	7/14	6.13	61.86
364	Ribonucleoside-diphosphate reductase large subunit	Q5R919	64	13.60	10/17	6.76	90.88
365	Ribosome biogenesis protein BOP1	Q14137	59	9.70	7/9	5.80	84.26
366	RNA 3’-terminal phosphate cyclase-like protein	Q2KHX8	51	9.90	3/6	9.37	41.44
367	RNA-binding protein 47	Q9XSR3	74	12.50	6/11	8.21	63.94
368	RNA-binding protein Raly	Q64012	404	27.20	9/20	8.94	33.34
369	Rootletin	Q5TZA2	90	23.40	49/227	5.45	228.79
370	RuvB-like 1	Q9Y265	64	22.60	10/11	6.02	50.54
371	RuvB-like 2	Q2TBU9	205	18.40	8/14	5.57	51.31
372	S-adenosylmethionine synthase isoform type-1	P13444	92	12.80	4/12	5.61	44.24
373	S-adenosylmethionine synthase isoform type-2	Q3THS6	315	31.90	12/30	6.02	44.00
374	Septin-10	Q8C650	72	9.70	5/6	6.17	53.19
375	Septin-11	B3GNI6	72	15.10	8/13	6.24	50.01
376	Septin-14	Q9DA97	72	8.60	3/5	6.85	50.24
377	Septin-6	Q3SZN0	72	11.20	6/9	6.35	49.09
378	Septin-7	Q9WVC0	72	16.30	8/14	8.82	50.82
379	Septin-8	B1MTN8	72	4.70	2/3	5.84	50.05
380	Septin-9	Q9QZR6	33	7.80	5/6	8.65	64.09
381	Sequestosome-1	Q5RBA5	106	7.50	3/10	5.15	48.38
382	Serine hydroxymethyltransferase, mitochondrial	P14519	201	17.10	8/15	8.78	56.32
383	Serine/arginine-rich splicing factor 2	Q3MHR5	53	7.20	2/6	11.86	25.46
384	Serine/arginine-rich splicing factor 8	Q9BRL6	53	18.10	5/5	11.72	32.38
385	Serine/threonine-protein kinase A-Raf	P10398	76	11.10	6/12	9.20	68.34
386	Serine/threonine-protein kinase B-raf	P15056	86	11.00	8/21	7.29	85.13
387	Serine/threonine-protein kinase MARK1	Q9P0L2	45	16.10	11/18	9.42	89.46
388	Serine/threonine-protein kinase MARK2	Q7KZI7	270	26.80	19/34	9.73	88.26
389	Serine/threonine-protein kinase MRCK beta	Q9Y5S2	57	10.00	18/44	5.97	196.19
390	Serine/threonine-protein kinase Nek5	Q6P3R8	44	7.80	6/14	9.05	82.36
391	Serine/threonine-protein kinase PAK 2	Q8CIN4	64	17.70	7/14	5.57	58.18
392	Serine/threonine-protein kinase PLK1	P53350	49	12.40	7/8	9.08	68.95
393	Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform	Q4R7Z4	71	12.50	4/4	5.82	52.17
394	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	Q76MZ3	116	11.70	6/8	5.00	66.08
395	Serine/threonine-protein phosphatase 6 catalytic subunit	Q9CQR6	53	11.80	3/3	5.43	35.82
396	Serine/threonine-protein phosphatase PP1-alpha catalytic subunit	Q3T0E7	644	40.60	14/35	5.94	38.23
397	Serine/threonine-protein phosphatase PP1-beta catalytic subunit	Q3SWW9	599	28.40	10/27	5.84	37.96
398	Serine/threonine-protein phosphatase PP1-gamma catalytic subunit	Q8MJ46	546	31.60	11/26	6.13	37.73

399	SH3 domain-binding protein 4	Q9P0V3	70	11.90	11/22	7.78	108.40
400	Small nuclear ribonucleoprotein-associated protein N	Q17QN3	57	19.20	6/10	11.20	24.78
401	Smoothelin	P53814	52	18.00	15/30	9.20	99.51
402	SNW domain-containing protein 1	Q5R7R9	93	28.40	13/18	9.53	61.48
403	Sodium/potassium-transporting ATPase subunit alpha-2	A2VDL6	52	11.40	10/38	5.47	113.42
404	Sodium/potassium-transporting ATPase subunit alpha-3	Q6PIC6	48	13.80	13/23	5.26	113.05
405	Sodium/potassium-transporting ATPase subunit alpha-4	Q13733	46	7.90	7/11	6.23	115.12
406	Solute carrier family 2, facilitated glucose transporter member 1	P11166	44	2.80	2/3	8.93	54.39
407	Solute carrier family 22 member 4	A9CB25	42	6.40	3/33	6.85	62.77
408	Sorting nexin-2	Q9CWK8	71	22.40	10/22	5.04	58.55
409	Spermatid perinuclear RNA-binding protein	Q9JKU6	72	23.40	14/18	8.86	74.76
410	Spliceosome RNA helicase DDX39B	Q3T147	49	16.40	9/14	5.44	49.39
411	Splicing factor 3B subunit 2	Q13435	46	15.10	11/29	5.52	100.28
412	Splicing factor, proline- and glutamine-rich	P23246	329	14.90	10/14	9.45	76.22
413	Src substrate cortactin	Q60598	494	21.20	15/55	5.24	61.38
414	SRSF protein kinase 1	O70551	46	9.60	5/8	5.82	73.67
415	Stomatin-like protein 3	Q6PE84	37	16.70	5/20	9.00	31.80
416	Structural maintenance of chromosomes protein 2	O95347	141	23.30	27/41	8.54	136.09
417	Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	Q8HXW3	160	16.00	10/12	7.56	73.95
418	SUN domain-containing protein 2	Q8BJS4	65	12.40	9/15	6.54	81.73
419	Superkiller viralicidic activity 2-like 2	Q9CZU3	59	13.10	14/19	6.01	118.59
420	Synaptic vesicle membrane protein VAT-1 homolog	Q99536	102	13.20	4/14	5.88	42.12
421	Synaptotagmin-like protein 3	Q99N48	37	11.40	8/23	9.54	69.72
422	Syntaxin-binding protein 2	Q28288	57	5.60	3/4	6.38	66.91
423	Talin-1	Q9Y490	42	9.00	21/28	5.77	271.77
424	TAR DNA-binding protein 43	Q5R5W2	77	5.60	2/2	5.85	45.03
425	Targeting protein for Xklp2	Q9ULW0	162	22.20	16/28	9.29	86.23
426	TATA box-binding protein-like protein 2	A6H907	45	11.70	4/6	6.05	41.82
427	Tax1-binding protein 1 homolog	Q2KJE0	90	14.40	11/21	5.34	94.86
428	T-complex protein 1 subunit beta	Q5XIM9	147	28.40	12/33	6.01	57.76
429	T-complex protein 1 subunit eta	Q99832	257	27.40	16/30	7.55	59.84
430	T-complex protein 1 subunit zeta	Q3MHL7	63	19.60	11/19	6.32	58.38
431	T-complex protein 1 subunit zeta-2	Q3T084	53	11.50	6/10	7.60	58.51
432	Testin	Q2QLG8	48	22.60	11/18	7.96	49.66
433	TOM1-like protein 2	Q6ZVM7	62	12.80	5/6	4.69	55.86
434	TRAF2 and NCK-interacting protein kinase	Q9UKE5	43	5.80	9/60	6.70	155.36
435	Transcription termination factor 2	Q5NC05	35	5.80	8/88	9.08	126.71
436	Transducin beta-like protein 3	Q12788	59	4.30	3/7	6.44	90.35
437	Transketolase-like protein 1	Q99MX0	54	8.20	3/3	5.67	66.34
438	Translocon-associated protein subunit alpha	Q5R4X4	59	2.70	1/2	4.44	32.84
439	Transportin-3	Q9Y5L0	98	8.20	8/14	5.35	105.96

440	Trifunctional enzyme subunit beta, mitochondrial	Q99JY0	263	17.50	8/26	9.43	51.64
441	tRNA-splicing ligase RtcB homolog	Q5E9T9	246	27.30	13/22	6.77	55.68
442	Tropomodulin-1	P28289	138	11.10	4/31	5.03	40.66
443	Tropomodulin-2	Q9JKK7	613	9.40	3/48	5.28	39.49
444	Tubulin alpha chain-like 3	A6NHL2	380	11.70	5/40	5.68	50.68
445	Tubulin alpha-3 chain	Q68FR8	2855	40.00	15/112	4.97	50.61
446	Tubulin beta-2A chain	Q4R5B3	6253	45.60	21/223	4.78	50.27
447	Tubulin beta-8 chain-like protein LOC260334	A6NNZ2	2407	22.30	9/102	4.75	50.17
448	Tubulin gamma-1 chain	Q0VCD2	77	14.60	6/11	5.75	51.46
449	Tubulin gamma-2 chain	Q8VCK3	43	8.40	4/9	5.80	51.43
450	Tumor protein p53-inducible protein 13	B0BN44	117	8.00	2/10	11.40	43.14
451	Tyrosine-protein kinase HCK	P08631	271	10.60	6/32	6.27	60.08
452	Tyrosine-protein kinase JAK1	P23458	62	9.40	10/12	7.48	135.02
453	U3 small nucleolar RNA-associated protein 15 homolog	A2RRU3	42	13.40	8/17	9.15	59.88
454	U3 small nucleolar RNA-associated protein 18 homolog	Q9Y5J1	61	10.80	4/4	8.93	62.42
455	U4/U6 small nuclear ribonucleoprotein Prp3	Q2KIA6	101	14.20	14/42	9.43	77.57
456	Ubiquitin carboxyl-terminal hydrolase 26	Q99MX1	52	8.90	6/8	7.95	96.48
457	Ubiquitin carboxyl-terminal hydrolase 7	Q6A4J8	59	7.80	9/12	5.29	129.48
458	Ubiquitin-40S ribosomal protein S27a	P62978	1041	41.00	8/55	9.68	18.30
459	Ubiquitin-like modifier-activating enzyme 1	Q29504	67	10.40	11/15	5.51	118.70
460	Uncharacterized protein C2orf57 homolog	Q9DA60	41	3.00	2/10	4.22	56.65
461	Unconventional myosin-Ih	Q8N1T3	41	16.00	18/36	9.19	120.05
462	Uridine 5’-monophosphate synthase	Q5R514	45	10.80	5/7	6.40	52.55
463	Uromodulin	P07911	67	11.60	8/16	5.05	72.45
464	Urotensin-2	O95399	71	31.50	3/8	7.66	14.52
465	Vacuolar protein sorting-associated protein 26A	Q0VD53	137	26.00	8/23	6.13	38.25
466	Vacuolar protein sorting-associated protein 35	Q2HJG5	188	4.60	4/11	5.32	92.49
467	Vasodilator-stimulated phosphoprotein	P50551	101	32.60	9/13	7.77	40.50
468	Vesicle-fusing ATPase	Q9QUL6	44	10.30	8/16	6.55	83.17
469	Vitronectin	P48819	72	8.50	5/16	5.60	53.34
470	Voltage-dependent anion-selective channel protein 1	Q9Z2L0	88	23.70	5/5	8.62	30.85
471	V-type proton ATPase catalytic subunit A	Q5R5H2	93	12.00	5/12	5.35	68.63
472	WD repeat-containing protein 1	Q2KJH4	70	11.20	8/10	6.24	66.90
473	X-ray repair cross-complementing protein 5	P13010	97	9.80	9/19	5.55	83.22
474	YTH domain-containing family protein 2	Q0VCZ3	108	8.10	5/8	8.87	62.58

UniProt = Universal protein resource
%Cov = %Sequence coverage [(number of the matched residues/total number of residues in the entire sequence) x 100%]