

Table S2. Representation of the entire set of ligand – protein – protein Interaction entries results from this study. (Cα–Cα distance ≤ 3 Å)

	Uniprot Groups	PDBref [PDBref][resolution]	Ligand [affinity]	Surface residues	Dissimilarity mean values	Highest dissimilarity value	Uniprot descriptive names
1	P62152,Q29122	2vas[4dbq][2.4]	ADP[5.408]	12	0,403	0,73	Calmodulin Unconventional myosin-VI
2	P45983,Q9UQF2	4izy[2.3]	1J2[8.160]	4	0,39	0,55	Mitogen-activated protein kinase 8 C-Jun-amino-terminal kinase-interacting protein 1
3	P45983,Q9UQF2	4hyu[2.15]	1BK[8.209]	4	0,38	0,56	Mitogen-activated protein kinase 8 C-Jun-amino-terminal kinase-interacting protein 1
4	P45983,Q9WVI9	3o2m[2.7]	46A[4.800]	6	-0,35	-0,43	Mitogen-activated protein kinase 8 C-Jun-amino-terminal kinase-interacting protein 1
5	P45983,Q9UQF2	4g1w[2.45]	G1W[7.045]	4	0,33	0,41	Mitogen-activated protein kinase 8 C-Jun-amino-terminal kinase-interacting protein 1
6	P45983,Q9UQF2	4e73[2.27]	0NR[5.985]	5	0,32	0,44	Mitogen-activated protein kinase 8 C-Jun-amino-terminal kinase-interacting protein 1
7	P0A786,P0A7F3	4at1[7at1][2.6]	ATP[4.990]	10	0,284	0,5	Aspartate carbamoyltransferase catalytic chain Aspartate carbamoyltransferase regulatory chain
8	P01724,P01751	1oax[2.66]	ANQ[5.064]	4	-0,24	-0,69	Ig lambda-1 chain V regions MOPC 104E/RPC20/J558/S104 Ig heavy chain V region B1-8/186-2
9	P01724,P01751	2bjm[2.15]	ANF[4.350]	5	0,238	0,51	Ig lambda-1 chain V regions MOPC 104E/RPC20/J558/S104 Ig heavy chain V region B1-8/186-2
10	P01834,P01857	1d6v[2.0]	HOP[6.172]	4	-0,233	-0,4	Ig kappa chain C region Ig gamma-1 chain C region
11	P45983,Q9WVI9	1uki[2.7]	537[6.324]	4	-0,21	-0,32	Mitogen-activated protein kinase 8 C-Jun-amino-terminal kinase-interacting protein 1
12	P45983,Q9WVI9	3v3v[2.7]	MYU[5.837]	3	-0,21	-0,35	Mitogen-activated protein kinase 8 C-Jun-amino-terminal kinase-interacting protein 1
13	P0A786,P0A7F3	2h3e[2.3]	6PR[5.699]	9	0,186	0,27	Aspartate carbamoyltransferase catalytic chain Aspartate carbamoyltransferase regulatory chain
14	P01724,P01751	1oar[2.22]	AZN[7.399]	3	-0,18	-0,31	Ig lambda-1 chain V regions MOPC 104E/RPC20/J558/S104 Ig heavy chain V region B1-8/186-2
15	P11142,Q99933	3fzk[2.1]	3BK[5.470]	7	0,177	0,31	Heat shock cognate 71 kDa protein BAG family molecular chaperone regulator 1
16	P15873,Q12306	3v61[2.8]	NEQ[4.028]	1	-0,17	-0,17	Proliferating cell nuclear antigen Ubiquitin-like protein SMT3
17	P0A786,P0A7F3	1acm[8ate,1f1b,1q95,4f04,1xjw,1tth,1d09][2.8]	PAL[7.569]	10	0,161	0,26	Aspartate carbamoyltransferase catalytic chain Aspartate carbamoyltransferase regulatory chain
18	Q65ZC0,Q91Z05	1i9j[2.6]	TES[7.367]	9	-0,152	-0,42	Recombinant monoclonal anti-testosterone fab fragment light chain   Recombinant monoclonal anti-testosterone fab fragment heavy chain
19	Q08602,Q08603	3dst[3pz2][1.9]	GRG[9.080]	14	0,132	0,27	Geranylgeranyl transferase type-2 subunit alpha Geranylgeranyl transferase type-2 subunit beta
20	P40337,Q15369,Q15370	4b95[2.8]	UCK[4.280]	7	-0,093	-0,27	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
21	Q96E14,Q9H9A7	3mxn[1.55]	BEN[4.386]	7	-0,087	-0,23	RecQ-mediated genome instability protein 2 RecQ-mediated genome instability protein 1
22	P04483,P04483-P0ACT4,P0ACT4	3fk7[2.06]	4DM[9.125]	11	0,085	0,44	Tetracycline repressor protein class B from transposon Tn10 Tetracycline repressor protein class D
23	P40337,Q15369,Q15370	4bkt[2.35]	QD0[3.620]	5	-0,076	-0,14	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
24	P08559,P11177	1ni4[3exe,3exh,2ozl][1.95]	TPP[6.104]	19	0,068	0,44	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial Pyruvate dehydrogenase E1 component subunit beta
25	P20618,P21242,P21243,P22141,P23638,P23639,P23724,P25043,P25451,P28062,P30656,P30657,P32379,P38624	515f[2.5]	BO2[6.459]	15	0,064	0,82	Proteasome subunit beta type-1 Probable proteasome subunit alpha type-7 Proteasome subunit alpha type-1
26	P63104,Q93SQ3	5j31[2.4]	BEZ[3.873]	10	-0,061	-0,2	14-3-3 protein zeta/delta
27	P9WHT9,P9WHU1	3krd[2.5]	FEB[8.170]	16	0,061	0,17	Proteasome subunit beta Proteasome subunit alpha
28	P40337,Q15369,Q15370	4awj[2.5]	V6F[2.155]	4	-0,06	-0,09	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
29	P40337,Q15369,Q15370	4bks[2.2]	X6C[3.822]	6	-0,06	-0,1	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2

30	P40337,Q15369,Q15370	4w9c[2.2]	3JG[4.652]	5	-0,06	-0,1	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
31	P53762,P97481	4zph[2.8]	PRL[5.639]	13	-0,059	-0,31	Aryl hydrocarbon receptor nuclear translocator Endothelial PAS domain-containing protein 1
32	P07291,P13543,P24733	1b7t[112o,1qvi,1kk8][2.5]	ADP[5.408]	17	0,059	0,67	Myosin essential light chain, striated adductor muscle Myosin regulatory light chain, striated adductor muscle Myosin heavy chain, striated muscle
33	P40337,Q15369,Q15370	4w9j[2.2]	3JH[6.230]	6	-0,058	-0,09	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
34	P27540,Q99814	4xt2[1.7]	43L[7.100]	21	0,055	0,31	Aryl hydrocarbon receptor nuclear translocator Endothelial PAS domain-containing protein 1
35	P40337,Q15369,Q15370	4w9e[2.6]	3JT[5.150]	5	-0,054	-0,1	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
36	P04637,Q9WYW0	1yc5[2h4j][1.4]	NCA[4.209]	3	-0,053	-0,08	Cellular tumor antigen p53 NAD-dependent protein deacetylase
37	P40337,Q15369,Q15370	4w9h[2.1]	3JF[6.731]	6	-0,053	-0,12	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
38	P00734,P28504	1d9i[2.3]	00P[9.108]	3	0,053	0,07	Prothrombin Hirudin-2
39	P40337,Q15369,Q15370	4w9f[2.1]	3JU[5.488]	5	-0,052	-0,08	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
40	P40337,Q15369,Q15370	3ztd[2.79]	ZTD[4.020]	6	-0,05	-0,1	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
41	P40337,Q15369,Q15370	4w9g[2.7]	3JV[5.212]	5	-0,05	-0,07	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
42	P40337,Q15369,Q15370	4w9l[2.2]	3JJ[5.021]	5	-0,05	-0,1	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
43	P01834,P01857	1gaI[1.95]	NPE[5.247]	13	-0,04	-0,39	Ig kappa chain C region Ig gamma-1 chain C region
44	P00734,P28504	1sl3[1.81]	170[11.852]	1	0,04	0,04	Prothrombin Hirudin-2
45	P01958,P02062	1iwh[1.55]	PEM[4.360]	4	0,04	0,06	Hemoglobin subunit alpha Hemoglobin subunit beta
46	P40337,Q15369,Q15370	4w9i[2.4]	3JS[5.959]	6	-0,038	-0,09	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
47	P40337,Q15369,Q15370	3zrc[2.9]	L8B[5.303]	6	-0,037	-0,07	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
48	P00125,P00126,P00129,P00130,P00157,P07552,P13271,P13272,P23004,P31800	1ntk[2.6]	AY1[10.490]	19	-0,036	-0,22	Cytochrome c1, heme protein, mitochondrial Cytochrome b-c1 complex subunit 6, mitochondrial Cytochrome b-c1 complex subunit 7
49	P06730,Q13541	2v8w[2.3]	MGO[7.234]	10	-0,035	-0,08	Eukaryotic translation initiation factor 4E Eukaryotic translation initiation factor 4E-binding protein 1
50	P40337,Q15369,Q15370	4w9d[2.2]	3JK[4.991]	5	-0,032	-0,1	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
51	P18465,P61769	3upr[2.0]	1KX[6.481]	17	0,032	0,26	HLA class I histocompatibility antigen, B-57 alpha chain Beta-2-microglobulin
52	O13828,Q9P805	2qkm[2.8]	ATP[4.990]	13	-0,03	-0,62	mRNA decapping complex subunit 2 mRNA-decapping enzyme subunit 1
53	P27540,Q99814	4ghi[1.5]	0X3[7.069]	18	-0,03	-0,35	Aryl hydrocarbon receptor nuclear translocator Endothelial PAS domain-containing protein 1
54	P00734,P28504	1nm6[1.8]	L86[7.992]	1	0,03	0,03	Prothrombin Hirudin-2
55	P40337,Q15369,Q15370	3ztc[2.65]	TR0[4.560]	7	-0,029	-0,09	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
56	P00734,P01050	3egk[2.2]	M18[4.659]	9	0,029	0,06	Prothrombin Hirudin variant-1
57	P06730,Q13541	2v8x[2.3]	MGQ[4.984]	10	-0,028	-0,1	Eukaryotic translation initiation factor 4E Eukaryotic translation initiation factor 4E-binding protein 1
58	P11987,P18798,P22869	1xu5[1.96]	IPH[4.548]	55	-0,028	-0,17	Methane monooxygenase component A gamma chain Methane monooxygenase component A beta chain Methane monooxygenase component A alpha chain
59	P84887,P84888	2q7q[1.6]	C2B[3.585]	10	-0,028	-0,07	Aralkylamine dehydrogenase light chain Aralkylamine dehydrogenase heavy chain
60	P06730,Q13541	2v8y[2.1]	MGV[5.708]	9	-0,027	-0,07	Eukaryotic translation initiation factor 4E Eukaryotic translation initiation factor 4E-binding protein 1
61	P00734,P28504	1fpc[2.3]	0ZI[7.000]	9	0,027	0,09	Prothrombin Hirudin-2
62	P00734,P01050	2zfp[2.25]	19U[5.098]	13	0,026	0,06	Prothrombin Hirudin variant-1
63	P27540,Q99814	3h7w[1.65]	018[6.229]	4	-0,025	-0,07	Aryl hydrocarbon receptor nuclear translocator Endothelial PAS domain-containing protein 1
64	P04049,P31947	3iqv[1.2]	FSC[5.181]	6	0,025	0,06	RAF proto-oncogene serine/threonine-protein kinase 14-3-3 protein sigma

65	P00734,P01050	2zgx[1.8]	29U[6.851]	11	0,024	0,06	Prothrombin Hirudin variant-1
66	Q55389,Q55781	2puo[1.7]	NEQ[4.028]	3	-0,023	-0,04	Ferredoxin-thioredoxin reductase, catalytic chain Ferredoxin-thioredoxin reductase, variable chain
67	P07739,P07740	3fge[2.3]	FMN[3.920]	12	0,023	0,41	Alkanal monooxygenase beta chain Alkanal monooxygenase alpha chain
68	P84887,P84888	2agl[1.4]	PHZ[6.244]	13	-0,022	-0,07	Aralkylamine dehydrogenase light chain Aralkylamine dehydrogenase heavy chain
69	P31947,Q9NPC2	4fr3[1.9]	0V4[7.155]	4	0,022	0,05	14-3-3 protein sigma Potassium channel subfamily K member 9
70	P11987,P18798,P22869	1xu3[2.3]	BML[4.260]	48	-0,021	-0,17	Methane monooxygenase component A gamma chain Methane monooxygenase component A beta chain Methane monooxygenase component A alpha chain
71	P00734,P01050	2zhq[1.96]	27U[6.391]	12	0,021	0,07	Prothrombin Hirudin variant-1
72	P00734,P09945	3tu7[2.49]	0BM[7.714]	11	0,021	0,09	Prothrombin Hirudin variant-2
73	P00044,P00431	5cie[2.6]	ANL[3.696]	3	-0,02	-0,05	Cytochrome c iso-1 Cytochrome c peroxidase, mitochondrial
74	P84887,P84888	2agw[2iuq][1.45]	TSS[5.701]	11	-0,02	-0,07	Aralkylamine dehydrogenase light chain Aralkylamine dehydrogenase heavy chain
75	P00734,P01050	2zgb[1.6]	21U[6.268]	12	0,02	0,05	Prothrombin Hirudin variant-1
76	P00734,P28504	1ta6[1.9]	177[6.762]	3	0,02	0,05	Prothrombin Hirudin-2
77	P00734,P09945	2c8x[2.17]	C5M[6.659]	12	-0,019	-0,15	Prothrombin Hirudin variant-2
78	P00734,P09945	3f68[1.75]	91U[5.060]	12	-0,019	-0,11	Prothrombin Hirudin variant-2
79	P00734,P01050	2zo3[1.7]	33U[9.682]	12	0,019	0,07	Prothrombin Hirudin variant-1
80	P00125,P00126,P00129,P00130,P00157,P07552,P13271,P13272,P23004,P31800	1sqb[2.69]	AZO[7.950]	17	0,019	0,2	Cytochrome c1, heme protein, mitochondrial Cytochrome b-c1 complex subunit 6, mitochondrial Cytochrome b-c1 complex subunit 7
81	P03252,P03274	4pid[1.59]	2UQ[4.620]	15	-0,018	-0,08	Protease Pre-protein V1
82	O87798,O87799,O87802	1t0s[2.2]	BML[4.260]	40	0,018	0,12	
83	P00734,P28504	1c1v[1.98]	BAB[6.596]	46	0,018	-0,14	Prothrombin Hirudin-2
84	P00734,P09945	2zg0[1.75]	50U[5.932]	14	-0,017	-0,09	Prothrombin Hirudin variant-2
85	P01724,P01751	1oay[2.66]	FUR[5.920]	3	-0,017	-0,25	Ig lambda-1 chain V regions MOPC 104E/RPC20/J558/S104 Ig heavy chain V region B1-8/186-2
86	P00734,P01050	2zff[1.47]	53U[5.339]	14	-0,016	-0,17	Prothrombin Hirudin variant-1
87	P84887,P84888	2ok6[1.45]	BEZ[3.873]	14	-0,016	-0,06	Aralkylamine dehydrogenase light chain Aralkylamine dehydrogenase heavy chain
88	P00734,P01050	3dux[1.6]	64U[7.000]	13	0,016	0,06	Prothrombin Hirudin variant-1
89	Q08602,Q08603	4ehm[2.2]	PJA[5.850]	13	0,016	0,09	Geranylgeranyl transferase type-2 subunit alpha Geranylgeranyl transferase type-2 subunit beta
90	P00734,P09945	1w7g[1.65]	MIU[5.357]	13	-0,015	-0,06	Prothrombin Hirudin variant-2
91	P00734,P09945	2c8y[2.2]	C3M[4.000]	12	-0,015	-0,06	Prothrombin Hirudin variant-2
92	P36238,Q84BQ9	3cjr[2.05]	SFG[4.235]	4	-0,015	-0,32	50S ribosomal protein L11 Ribosomal protein L11 methyltransferase
93	P38182,P38862	3vh4[2.65]	ATP[4.990]	8	0,015	0,08	Autophagy-related protein 8 Ubiquitin-like modifier-activating enzyme ATG7
94	P00734,P09945	1way[2.02]	L02[3.399]	12	-0,014	-0,06	Prothrombin Hirudin variant-2
95	P00734,P09945	2bvr[1.25]	4CP[3.700]	14	-0,014	-0,06	Prothrombin Hirudin variant-2
96	P00734,P01050	2zda[1.73]	32U[8.610]	13	0,014	0,06	Prothrombin Hirudin variant-1
97	Q45871,Q45878	5bp5[2.18]	IPT[4.119]	7	0,014	0,03	
98	P00734,P09945	2bvs[1.4]	2CE[4.100]	13	-0,013	-0,07	Prothrombin Hirudin variant-2
99	P00760,P00974	2tpi[2.1]	ILE-VAL[4.310]	7	0,013	0,04	Cationic trypsin Pancreatic trypsin inhibitor

100	P00734,P01050	1aht[1.6]	APA[6.210]	13	0,013	0,06	Prothrombin Hirudin variant-1
101	P20371,P20372	2buq[2buy][1.8]	CAQ[4.366]	29	0,013	0,19	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
102	Q08602,Q08603	3dsu[1.9]	FPP[8.028]	15	-0,012	-0,03	Geranylgeranyl transferase type-2 subunit alpha Geranylgeranyl transferase type-2 subunit beta
103	P00734,P09945	2c8w[1.96]	C7M[8.443]	12	-0,012	-0,06	Prothrombin Hirudin variant-2
104	P20371,P20372	1eob[2buu,2bv0][2.2]	DHB[5.508]	27	0,012	0,04	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
105	P00734,P28504	1ype[1.81]	UIP[8.098]	14	-0,011	-0,05	Prothrombin Hirudin-2
106	P00734,P09945	2bxt[1.83]	C2D[8.520]	12	-0,011	-0,03	Prothrombin Hirudin variant-2
107	P00734,P28504	1c5o[1.9]	BAM[4.854]	46	0,011	-0,15	Prothrombin Hirudin-2
108	P00734,P28504	1c5n[1.5]	ESI[5.547]	44	-0,01	-0,19	Prothrombin Hirudin-2
109	P00734,P09945	1wbq[2.2]	L03[3.000]	11	-0,01	-0,06	Prothrombin Hirudin variant-2
110	P00734,P28504	1nt1[2.0]	T76[9.143]	1	-0,01	-0,01	Prothrombin Hirudin-2
111	P84887,P84888	2hj4[1.8]	PNZ[5.369]	13	-0,01	-0,05	Aralkylamine dehydrogenase light chain Aralkylamine dehydrogenase heavy chain
112	P00436,P00437	3pck[3pcm][2.13]	NNO[6.699]	46	0,01	0,12	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
113	P00436,P00437	3pcb[2.19]	3HB[4.706]	40	0,01	0,01	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
114	P00436,P00437	3pcc[1.98]	PHB[4.545]	38	0,01	0,01	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
115	P00436,P00437	3pce[2.06]	3HP[2.000]	42	0,01	0,01	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
116	P00436,P00437	3pcf[2.15]	FHB[6.048]	42	0,01	0,01	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
117	P00436,P00437	3pcg[1.96]	4HP[4.018]	40	0,01	0,01	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
118	P00436,P00437	3pch[2.05]	CHB[5.399]	43	0,01	0,01	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
119	P00734,P28504	1ta2[2.3]	176[8.521]	1	0,01	0,01	Prothrombin Hirudin-2
120	P01834,P01857	1i7z[2.3]	COC[6.326]	9	0,01	0,01	Ig kappa chain C region Ig gamma-1 chain C region
121	P09883,P13479	2vln[2vlp,2vlq][1.6]	MLA[4.159]	8	0,01	-0,09	Colicin-E9 Colicin-E9 immunity protein
122	P40337,Q15369,Q15370	4b9k[2.0]	TG0[6.089]	5	0,01	0,16	Von Hippel-Lindau disease tumor suppressor Transcription elongation factor B polypeptide 1 Transcription elongation factor B polypeptide 2
123	Q65ZC0,Q91Z05	1t66[2.3]	FLU[4.219]	3	0,01	0,01	
124	P20371,P20372	1eoc[2buz,2buu][2.25]	4NC[6.048]	26	0,009	0,04	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
125	P00436,P00437	3t67[3mi5][1.67]	CAQ[4.366]	29	0,009	0,22	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
126	P00734,P28504	1c4u[2.1]	IH1[10.368]	19	0,009	0,07	Prothrombin Hirudin-2
127	P00734,P28504	1ypg[1.8]	UIR[8.000]	12	-0,008	-0,05	Prothrombin Hirudin-2
128	P00734,P28504	1gj5[1.73]	130[4.890]	46	-0,008	-0,16	Prothrombin Hirudin-2
129	P00734,P01050	1bcu[2.0]	PRL[4.540]	11	-0,008	-0,04	Prothrombin Hirudin variant-1
130	P00436,P00437	3mi5[3t67][1.78]	CAQ[4.366]	29	0,008	0,11	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
131	Q00456,Q00457,Q00459,Q00460	3q14[1.75]	PCR[7.027]	51	0,008	0,19	Toluene-4-monooxygenase system protein A Toluene-4-monooxygenase system protein B Toluene-4-monooxygenase system protein D
132	P0A110,P0A112	1eg9[1uuv,1o7n][1.6]	IND[4.340]	14	-0,007	-0,03	Naphthalene 1,2-dioxygenase subunit alpha Naphthalene 1,2-dioxygenase subunit beta
133	P0A110,P0A112	1o7g[1.7]	NPY[4.124]	14	-0,007	-0,03	Naphthalene 1,2-dioxygenase subunit alpha Naphthalene 1,2-dioxygenase subunit beta
134	P84887,P84888	2hjb[1.85]	PZM[3.548]	14	-0,007	0,1	Aralkylamine dehydrogenase light chain Aralkylamine dehydrogenase heavy chain

135	P00734,P09945	1vzq[1.54]	SHY[7.442]	13	-0,007	-0,03	Prothrombin Hirudin variant-2
136	P00734,P28504	1qbv[1.8]	PPX[5.389]	12	-0,007	-0,05	Prothrombin Hirudin-2
137	Q08602,Q08603	3pz1[1.95]	3PZ[6.140]	15	0,007	-0,06	Geranylgeranyl transferase type-2 subunit alpha Geranylgeranyl transferase type-2 subunit beta
138	P20371,P20372	2bur[2buw][1.8]	PHB[4.619]	26	0,007	-0,16	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
139	Q7SID2,Q7SID3	4ob1[4ob2][1.63]	BUB[4.853]	31	-0,006	-0,03	Cobalt-containing nitrile hydratase subunit alpha Cobalt-containing nitrile hydratase subunit beta
140	P00734,P09945	2c93[2.2]	C4M[4.920]	9	-0,006	-0,03	Prothrombin Hirudin variant-2
141	P00436,P00437	3pcj[3pcl][2.13]	INO[7.221]	42	0,006	0,04	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
142	P00436,P00437	1ykl[3pca,3mv6,1ykn,3lmx,1ykp][2.25]	DHB[5.265]	39	-0,005	-0,14	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
143	P00734,P01050	2zc9[1.58]	22U[6.297]	15	-0,005	-0,04	Prothrombin Hirudin variant-1
144	Q7SID2,Q7SID3	1ugp[1.63]	BUA[2.890]	31	-0,004	-0,03	Cobalt-containing nitrile hydratase subunit alpha Cobalt-containing nitrile hydratase subunit beta
145	P00734,P28504	1ghw[1ghx][1.75]	BMZ[4.619]	44	0,004	-0,17	Prothrombin Hirudin-2
146	P00734,P09945	2bxu[2.8]	C1D[7.150]	9	0,004	-0,15	Prothrombin Hirudin variant-2
147	P00734,P28504	1c1u[1.75]	BAI[7.133]	46	-0,003	-0,18	Prothrombin Hirudin-2
148	P00734,P01050	3ldx[2.25]	NLI[8.890]	9	-0,003	-0,04	Prothrombin Hirudin variant-1
149	P00734,P01050	2znk[1.8]	31U[7.699]	13	-0,003	-0,04	Prothrombin Hirudin variant-1
150	P00734,P01050	1qj1[2.0]	166[8.050]	11	-0,003	-0,04	Prothrombin Hirudin variant-1
151	P00734,P01050	1qj6[2.2]	167[7.740]	11	-0,003	-0,04	Prothrombin Hirudin variant-1
152	P00734,P28504	1yp1[1.85]	RA8[4.975]	11	-0,003	-0,04	Prothrombin Hirudin-2
153	P00734,P28504	1ghy[1.85]	121[8.098]	44	-0,003	-0,17	Prothrombin Hirudin-2
154	P00734,P01050	1qj7[2.2]	GR1[8.100]	12	0,003	-0,04	Prothrombin Hirudin variant-1
155	P27540,Q99814	3h82[1.5]	020[5.824]	4	0,003	-0,02	Aryl hydrocarbon receptor nuclear translocator Endothelial PAS domain-containing protein 1
156	P00734,P09945	2c90[2.25]	C1M[3.481]	13	-0,002	0,06	Prothrombin Hirudin variant-2
157	P00734,P28504	1o2g[1.58]	696[6.960]	45	-0,002	-0,16	Prothrombin Hirudin-2
158	P00734,P01050	1qhr[2.2]	157[6.890]	11	-0,002	-0,04	Prothrombin Hirudin variant-1
159	P00734,P01050	3dhk[1.73]	23U[7.526]	13	-0,002	-0,04	Prothrombin Hirudin variant-1
160	P00734,P28504	1sb1[1.9]	165[6.891]	13	0,002	0,09	Prothrombin Hirudin-2
161	Q7SID2,Q7SID3	4ob0[1.2]	PBC[3.798]	32	0,002	0,06	Cobalt-containing nitrile hydratase subunit alpha Cobalt-containing nitrile hydratase subunit beta
162	P00734,P28504	1ypm[1.85]	RA4[5.721]	11	0,002	-0,05	Prothrombin Hirudin-2
163	P00734,P09945	2c8z[2.14]	C2A[3.856]	11	-0,001	-0,03	Prothrombin Hirudin variant-2
164	P00734,P01050	1bb0[2.1]	0IV[8.084]	12	-0,001	-0,04	Prothrombin Hirudin variant-1
165	P00734,P09945	2r2m[2.1]	I50[7.329]	14	0,001	-0,12	Prothrombin Hirudin variant-2
166	P00436,P00437	3pcn[3mfl][2.4]	DHY[3.659]	37	0,001	-0,05	Protocatechuate 3,4-dioxygenase alpha chain Protocatechuate 3,4-dioxygenase beta chain
167	P00734,P01050	1ca8[2.1]	0KV[8.355]	12	0,001	-0,04	Prothrombin Hirudin variant-1
168	P00734,P28504	1gj4[1.81]	132[5.802]	37	0,001	-0,16	Prothrombin Hirudin-2
169	P00734,P01050	1ad8[2.0]	MDL[6.600]	11	0	-0,04	Prothrombin Hirudin variant-1

170	P06213,P81122	3bu5[2.1]	ATP[4.990]	0	0	0	Insulin receptor Insulin receptor substrate 2
171	P53762,P97481	4zqd[2.87]	0X3[7.046]	0	0	0	Aryl hydrocarbon receptor nuclear translocator Endothelial PAS domain-containing protein 1
172	P00734,P28504	1ghv[1.85]	120[4.348]	44	0	-0,18	Prothrombin Hirudin-2
173	P00734,P01050	2zi2[2ziq,3d49][1.65]	BEN[4.522]	12	0	0,05	Prothrombin Hirudin variant-1
174	P00734,P09945	2zht[1.98]	49U[5.928]	11	0	0,03	Prothrombin Hirudin variant-2
175	P00734,P28504	1ypj[1.78]	UIB[7.021]	10	0	0,07	Prothrombin Hirudin-2