

SUPPLEMENTARY MATERIAL

The RNA-Binding Protein PCBP1 Functions as a Tumor Suppressor in Prostate Cancer by Inhibiting Mitogen Activate Protein Kinase 1

Yingying Zhang^a Lin Meng^b Lin Xiao^b Ruiwang Liu^b Zhonghai Li^b
Ying-lei Wang^b

^aDepartment of Paediatrics, Affiliated Hospital of Jining Medical University, Jining, ^bUrology Department, Affiliated Hospital of Jining Medical University, Jining, China

Supplementary Table 1: COS M6_shRNA-GLB1

Protein Group	Protein ID	Accession	-10lgP	Coverage (%)	#Peptides	#Unique	PTM	Avg. Mass	Description
3	2860	XP_001094100.2	40,35	0	3	1		417938	PREDICTED: protein bassoon [Macaca mulatta]
32	1272	XP_001094596.2	33,78	1	2	0		80157	PREDICTED: transforming acidic coiled-coil-containing protein 1 [Macaca mulatta]
14	2866	XP_002808150.1	33,37	0	2	0		360539	PREDICTED: LOW QUALITY PROTEIN: vacuolar protein sorting-associated protein 13A-like [Macaca mulatta]
8	39	XP_002799249.1	31,26	1	6	3		480342	PREDICTED: baculoviral IAP repeat-containing protein 6-like [Macaca mulatta]
27	2955	XP_002808305.1	31,17	0	2	0		606386	PREDICTED: LOW QUALITY PROTEIN: hemicentin-1-like [Macaca mulatta]
7	2435	XP_001107299.2	30,3	1	2	0		131866	PREDICTED: isoleucyl-tRNA synthetase cytoplasmic [Macaca mulatta]
15	142	XP_002803600.1	29,86	7	6	6		75172	PREDICTED: LIM domain kinase 1-like [Macaca mulatta]
22	2855	XP_001088655.2	26,93	0	3	0		313208	PREDICTED: mucin-19 [Macaca mulatta]
21	46	XP_001113107.2	26,58	3	5	4		326975	PREDICTED: fibrillin-1-like [Macaca mulatta]
13	1245	XP_002808342.1	24,32	1	3	1		185275	PREDICTED: LOW QUALITY PROTEIN: histone-lysine N-methyltransferase SETD1A-like [Macaca mulatta]
31	655	XP_001089508.1	23,88	2	2	1		60326	PREDICTED: shugoshin-like 1 isoform 7 [Macaca mulatta]
70	119	XP_001097677.2	23,63	2	2	2		148040	PREDICTED: zinc finger protein 521-like isoform 1 [Macaca mulatta]
23	305	XP_002804508.1	21,75	1	1	1		89077	PREDICTED: peptidyl-glycine alpha-amidating monooxygenase isoform 3 [Macaca mulatta]
33	1870	XP_001117691.1	21,29	0	1	1		342577	PREDICTED: zinc finger ZZ-type and EF-hand domain-containing protein 1-like [Macaca mulatta]
97	1194	XP_002808183.1	20,61	0	1	1		174129	PREDICTED: LOW QUALITY PROTEIN: ATP-binding cassette sub-family A member 10-like [Macaca mulatta]
5	4	XP_001102519.2	20,53	1	1	1		46959	PREDICTED: transcription factor Sp8 isoform 1 [Macaca mulatta]
39	38	XP_001107053.2	20,28	1	5	3		352508	PREDICTED: protein eyes shut homolog [Macaca mulatta]
84	1	XP_001083243.1	20,15	2	1	1		47194	PREDICTED: uncharacterized protein C9orf50-like isoform 2 [Macaca mulatta]
17	144	XP_002802066.1	19,96	2	3	2		86354	PREDICTED: ral guanine nucleotide dissociation stimulator-like 1-like isoform 4 [Macaca mulatta]
48	121	XP_002805569.1	19,4	3	5	4		166488	PREDICTED: hypothetical protein LOC100429127 [Macaca mulatta]
75	246	XP_001108760.2	19,35	1	2	2		257234	PREDICTED: bromodomain and WD repeat-containing protein 1 isoform 2 [Macaca mulatta]
95	586	XP_001099227.1	19,2	6	1	1		27290	PREDICTED: aquaporin-8 [Macaca mulatta]
85	348	XP_001086134.2	19,12	1	1	1		178753	PREDICTED: PHD and RING finger domain-containing protein 1 [Macaca mulatta]
11	1725	NP_001106130.1	18,9	1	1	1		74528	proprotein convertase subtilisin/kexin type 9 precursor [Macaca mulatta]
57	363	XP_002808005.1	18,82	1	1	1		98599	PREDICTED: LOW QUALITY PROTEIN: e3 ubiquitin-protein ligase Itchy homolog [Macaca mulatta]
12	58	XP_001088212.1	18,76	1	4	4		532326	PREDICTED: plectin-1 isoform 1 [Macaca mulatta]
83	1971	XP_002800675.1	18,46	1	1	1		55290	PREDICTED: galectin-3-binding protein isoform 2 [Macaca mulatta]
35	103	XP_002799588.1	18,22	2	1	1		43287	PREDICTED: leupaxin-like isoform 2 [Macaca mulatta]
77	358	XP_001091687.1	17,94	1	2	2		460087	PREDICTED: midasin [Macaca mulatta]
65	1524	NP_001035239.1	17,69	1	2	2		119676	proline- glutamic acid- and leucine-rich protein 1 [Macaca mulatta]
51	1334	XP_001116366.1	17,55	2	2	1		65264	PREDICTED: sialic acid-binding Ig-like lectin 12-like isoform 3 [Macaca mulatta]
37	16	XP_001101705.1	17,29	4	7	7		271512	PREDICTED: talin-2-like isoform 2 [Macaca mulatta]
19	2743	XP_001097543.1	17,08	0	1	1		158903	PREDICTED: Bloom syndrome protein [Macaca mulatta]
101	2171	XP_002804455.1	17,01	0	1	1		294193	PREDICTED: transcription factor TFIIIB component B'' homolog isoform 2 [Macaca mulatta]
50	519	XP_002808534.1	16,99	0	1	1		460855	PREDICTED: LOW QUALITY PROTEIN: fibrocystin-L-like [Macaca mulatta]
81	1331	XP_002808411.1	16,96	1	2	1		288425	PREDICTED: LOW QUALITY PROTEIN: filamin-C-like [Macaca mulatta]
16	397	XP_001111844.1	16,59	1	1	1		114349	PREDICTED: synaptonemal complex protein 1-like isoform 3 [Macaca mulatta]
47	92	XP_001117994.2	16,51	1	4	4		519037	PREDICTED: low-density lipoprotein receptor-related protein 1B [Macaca mulatta]
59	1200	XP_001116216.2	16,38	1	2	2		129950	PREDICTED: protein jagged-1 [Macaca mulatta]
58	380	XP_001083490.1	16,26	2	2	1		46679	PREDICTED: uncharacterized protein C17orf97-like isoform 1 [Macaca mulatta]
55	212	XP_002804790.1	15,92	1	2	2		135806	PREDICTED: tau-tubulin kinase 2-like [Macaca mulatta]
94	431	XP_001086980.1	15,68	2	1	1		50382	PREDICTED: iroquois-class homeodomain protein IRX-5 isoform 2 [Macaca mulatta]
67	1311	XP_002808426.1	15,65	0	2	2		458469	PREDICTED: LOW QUALITY PROTEIN: tenascin-X-like [Macaca mulatta]
74	233	XP_001118617.2	15,6	1	2	2		337562	PREDICTED: laminin subunit alpha-1-like [Macaca mulatta]
68	1611	XP_001114797.1	15,59	1	1	1		59514	PREDICTED: cochlin-like isoform 4 [Macaca mulatta]
25	381	XP_002801676.1	15,57	2	1	1		42404	PREDICTED: heterogeneous nuclear ribonucleoprotein G-like isoform 1 [Macaca mulatta]
40	1102	XP_002798233.1	15,56	3	2	2		69261	PREDICTED: GDP-fucose protein O-fucosyltransferase 1-like [Macaca mulatta]
34	570	XP_001107670.2	15,42	1	1	1		57628	PREDICTED: hypothetical protein LOC716754 [Macaca mulatta]

54	139 XP_001114113.2	15,4	2	3	3	227161 PREDICTED: dynein heavy chain 9 axonemal [Macaca mulatta]
64	209 XP_002800001.1	15,24	2	3	3	239325 PREDICTED: protein BAT2-like 1-like [Macaca mulatta]
45	2867 XP_001109429.2	15,06	0	3	0	526985 PREDICTED: probable E3 ubiquitin-protein ligase HERC2-like [Macaca mulatta]
42	291 XP_001110265.1	15,06	0	2	1	479350 PREDICTED: protocadherin Fat 2-like [Macaca mulatta]

Supplementary Table 2: COS M6_shRNA-GLB1

Protein Group	Protein ID	Protein Accession	Peptide	Unique	-10lgP	Mass	Length	ppm	m/z	z	RT	Area	Scan	#Spec	Start	End
3	2860	XP_001094100.2	P.APASD.M	N	30,64	459,1965	5	29,1	460,2172	1	43,86		F3:8528	11	1485	1489
3	2860	XP_001094100.2	G.YILDD.S	N	19,4	637,2959	5	66,4	638,3455	1	58,81		F2:5041	1	3535	3539
3	2860	XP_001094100.2	G.EEPGR.R	Y	13,41	586,2711	5	-39,3	587,2553	1	73,83		F4:15489	1	3637	3641
5	4	XP_001102519.2	A.ALVSD.S	Y	20,53	503,2591	5	-21,1	504,2558	1	45,78		F3:8656	6	99	103
7	2435	XP_001107299.2	L.VLASD.G	N	20,56	503,2591	5	-17,6	504,2575	1	76,75		F4:15785	3	483	487
7	2435	XP_001107299.2	P.VSPSD.K	N	19,47	503,2227	5	-45,8	504,207	1	64,9		F4:13998	3	936	940
8	39	XP_002799249.1	R.NCAASGSD.P	Y	21,18	723,2494	8	-17,7	724,2438	1	58,11		F4:13106	4	2961	2968
8	39	XP_002799249.1	I.GVQSD.E	N	20,17	504,218	5	-5,7	505,2224	1	46,15		F3:8682	1	1518	1522
8	39	XP_002799249.1	R.AMCFTCSV.C	Y	7,65	860,3231	8	86,7	431,2061	2	74,96		F2:7541	1	326	333
8	39	XP_002799249.1	S.TAHLVSD.P	Y	7,32	854,4498	8	70,5	428,2623	2	65,38		F4:14073	12	2306	2313
8	39	XP_002799249.1	I.TGAPP.L	N	5,19	441,2223	5	70,5	442,2607	1	70,33		F4:14924	2	2027	2031
8	39	XP_002799249.1	L.NSSSS.G	N	5,12	480,1816	5	45,7	481,2108	1	69,25		F1:2797	1	2228	2232
11	1725	NP_001106130.1	T.SIQSD.H	Y	18,9	548,2442	5	77,9	549,2942	1	99,66		F1:3607	4	188	192
12	58	XP_001088212.1	L.ADPSD.D	Y	18,76	503,1863	5	-32,7	504,1772	1	47,28		F2:3944	5	2980	2984
12	58	XP_001088212.1	K.EQELQQTLQQEQSVLDRLRSEAEAAAR.R	Y	12,31	3054,533	26	60,8	510,127	6	45,65		F1:322	1	2198	2223
12	58	XP_001088212.1	R.QAEAEALALRVKAEAEAAAREK.Q	Y	11,29	2182,17	20	68,6	546,5873	4	50,41		F1:762	1	1648	1667
12	58	XP_001088212.1	R.TGSRTGSR.A	Y	9,43	820,4151	8	-45,3	411,1963	2	72,78		F2:7258	1	4627	4634
13	1245	XP_002808342.1	E.DEESD.S	N	16,68	593,1816	5	-54,8	594,1564	1	51,35		F1:915	2	1002	1006
13	1245	XP_002808342.1	G.GGGPSP.E	Y	15,27	470,2125	6	59	471,2475	1	64,25		F4:13881	4	440	445
13	1245	XP_002808342.1	P.PPAPAN.F	N	13,21	565,286	6	-24	566,2797	1	51,21		F4:12361	1	536	541
14	2866	XP_002808150.1	G.ITSSD.V	N	23,63	521,2333	5	74,6	522,2794	1	46,31		F1:415	1	2549	2553
14	2866	XP_002808150.1	S.VSPSD.S	N	19,47	503,2227	5	-45,8	504,207	1	64,9		F4:13998	3	1890	1894
15	142	XP_002803600.1	R.CCDCSASLSH.Q	Y	19,99	1024,341	10	45,1	513,201	2	72,55		F3:11277	4	97	106
15	142	XP_002803600.1	R.CCDCSA.S	Y	19,72	600,1342	6	56,8	601,1756	1	48,53		F3:8894	1	97	102
15	142	XP_002803600.1	R.CCDCSASLSHQYYEKDGQLFC.K	Y	9,42	2398,933	21	-63,5	600,7023	4	50,7		F2:4201	1	97	117
15	142	XP_002803600.1	K.GCFGQAIVKTHRETGEVMMVK.E	Y	8,03	2320,149	21	-81,4	580,9973	4	56,56		F4:12953	1	378	398
15	142	XP_002803600.1	R.CCDCSASLSHQYYEKDGQLFCKKDYW.A	Y	7,1	3119,292	26	-66,7	624,8241	5	59,15		F4:13231	1	97	122
15	142	XP_002803600.1	R.CCDCSASLSHQYYEKDGQLF.C	Y	5,87	2295,923	20	15,7	574,9971	4	57,93		F4:13080	1	97	116
16	397	XP_001111844.1	K.NGENIDSD.P	Y	16,59	862,3304	8	78,2	432,2062	2	67,33		F4:14399	8	58	65
17	144	XP_002802066.1	R.MMPGSD.P	Y	19,96	636,2247	6	42,3	637,2589	1	53,68		F2:4545	4	176	181
17	144	XP_002802066.1	K.KNCMEEQVK.L	Y	12,42	1107,505	9	68,1	554,7976	2	53,95		F7:16896	1	731	739
17	144	XP_002802066.1	M.MPGSD.P	N	11,71	505,1842	5	46,7	506,2151	1	45,95		F2:3863	1	177	181
19	2743	XP_001097543.1	D.AQESD.S	Y	17,08	548,2078	5	66,6	549,2516	1	48,78		F2:4066	4	252	256
21	46	XP_001113107.2	R.HRMDACCS.V	Y	18,67	1024,335	9	65,6	513,2083	2	72,73		F2:7251	1	1125	1133
21	46	XP_001113107.2	R.CMNGGSCSD.D	Y	15,81	872,2463	9	96,5	437,1725	2	60,28		F1:1714	3	273	281
21	46	XP_001113107.2	R.STCYGGYKRGQCIKPLFGAVTK.S	Y	7,77	2376,208	22	41,5	595,084	4	51,63		F4:12439	1	809	830
21	46	XP_001113107.2	R.EGYCFTEVLQNMCMQIGSSNRNPVTKSECCCDGG.R	Y	5,88	3571,46	33	81,7	596,2993	6	51,08		F4:12341	1	2486	2518
21	46	XP_001113107.2	Q.NIIGG.Y	N	5,11	472,2645	5	-81,1	473,2335	1	54,45		F3:9391	1	2733	2737
22	2855	XP_001088655.2	G.YLLDD.I	N	19,4	637,2959	5	66,4	638,3455	1	58,81		F2:5041	1	176	180
22	2855	XP_001088655.2	P.CESSG.N	N	15,06	481,1479	5	51,3	482,1798	1	62,98		F3:10220	1	195	199
22	2855	XP_001088655.2	Q.NNEGN.C	N	6,14	546,2034	5	40,1	547,2325	1	50,78		F1:818	4	540	544
23	305	XP_002804508.1	K.DCSGVSLHLTR.L	Y	21,75	1186,576	11	71,3	594,3378	2	56,38		F3:9510	5	181	191
27	2955	XP_002808305.1	P.LTSSD.K	N	23,63	521,2333	5	74,6	522,2794	1	46,31		F1:415	1	2765	2769
27	2955	XP_002808305.1	L.CESSG.I	N	15,06	481,1479	5	51,3	482,1798	1	62,98		F3:10220	1	2165	2169
31	655	XP_001089508.1	R.VGFLD.P	Y	16,34	549,2798	5	90,3	550,3367	1	55,53		F1:1226	1	226	230
31	655	XP_001089508.1	L.CESSG.S	N	15,06	481,1479	5	51,3	482,1798	1	62,98		F3:10220	1	368	372
32	1272	XP_001094596.2	T.LTSSD.F	N	23,63	521,2333	5	74,6	522,2794	1	46,31		F1:415	1	364	368
32	1272	XP_001094596.2	G.TLSSD.T	N	20,28	521,2333	5	79,6	522,282	1	45,83		F2:3851	1	226	230

33	1870	XP_001117691.1	R.CCGHSD.L	Y	21,29	620,1683	6	60,2	621,2129	1	59,23	F1:1570	2	2964	2969
35	103	XP_002799588.1	K.CGGCNRPV.L	Y	18,22	804,3371	8	86,7	403,2107	2	59,53	F7:17067	9	270	277
37	16	XP_001101705.1	K.LGAASLGSDD.P	Y	17,29	904,4138	10	82,8	453,2516	2	70,61	F1:2951	1	2065	2074
37	16	XP_001101705.1	K.SIAAATSALVK.S	Y	13,82	1030,602	11	-48,7	516,2833	2	68,11	F2:6460	2	2352	2362
37	16	XP_001101705.1	R.GQSGELAAASGK.F	Y	11,67	1074,531	12	41,3	538,2947	2	69	F4:14700	1	1264	1275
37	16	XP_001101705.1	K.ACEFGGFQAQIQFGPHVEHKHKPGFLDLKEFLPK.E	Y	7,35	3878,972	34	8,8	555,1509	7	48,25	F3:8848	1	237	270
37	16	XP_001101705.1	K.ADDDD.V	Y	6,54	549,1554	5	-77,4	550,1202	1	48,65	F3:8910	1	2483	2487
37	16	XP_001101705.1	A.FGECVGIASK.A	Y	6,54	1009,49	10	92,6	505,7991	2	68,35	F2:6493	1	1424	1433
37	16	XP_001101705.1	R.SLAINPKD.P	Y	6,47	856,4654	8	57,7	429,2647	2	63,4	F8:17690	1	1621	1628
39	38	XP_001107053.2	Q.TISSD.L	N	20,28	521,2333	5	79,6	522,282	1	45,83	F2:3851	1	1673	1677
39	38	XP_001107053.2	R.NGGECTVNGTTFSCR.C	Y	11,48	1544,635	15	-48,1	773,2875	2	65,63	F4:14130	2	2917	2931
39	38	XP_001107053.2	R.GCILDQLIN.N	Y	9,47	987,5059	9	85,2	494,8023	2	72,8	F2:7260	2	2307	2315
39	38	XP_001107053.2	S.GFTGK.N	N	9,44	508,2645	5	-25,7	509,2588	1	66,56	F2:6177	1	399	403
39	38	XP_001107053.2	R.CSCSLSYIGR.L	Y	5,38	1087,479	10	17,9	544,7565	2	50,46	F3:9033	1	590	599
40	1102	XP_002798233.1	L.RIGSD.W	Y	15,56	546,2761	5	27,1	547,2982	1	106,16	F2:8328	1	534	538
40	1102	XP_002798233.1	R.SAAAPGTGRAD.P	Y	6,41	972,4624	11	14,5	487,2455	2	42,8	F1:149	1	195	205
42	291	XP_001110265.1	K.VLQLILSD.P	Y	15,06	899,5328	8	13,9	450,7799	2	64,81	F2:5891	5	3445	3452
42	291	XP_001110265.1	E.VPVTCD.K	N	8,53	632,2839	6	20,7	633,3043	1	53,51	F7:16866	1	666	671
45	2867	XP_001109429.2	I.CESSG.K	N	15,06	481,1479	5	51,3	482,1798	1	62,98	F3:10220	1	998	1002
45	2867	XP_001109429.2	W.KFISD.G	N	13,38	608,317	5	8	609,3291	1	84,65	F4:16182	1	3721	3725
45	2867	XP_001109429.2	G.NEESD.L	N	10	592,1976	5	-62,2	593,1681	1	51,36	F4:12392	4	1574	1578
47	92	XP_001117994.2	R.CYCENG.F.E	Y	16,51	834,2676	7	93,8	418,1802	2	73,13	F3:11319	1	176	182
47	92	XP_001117994.2	C.PDDSD.E	Y	12,06	547,1761	5	78,1	548,2261	1	50,18	F1:752	2	97	101
47	92	XP_001117994.2	R.CDSQNDCSDNSDEENCKP.Q	Y	7,02	2001,662	18	-15,3	501,4152	4	78,21	F4:15890	1	3533	3550
47	92	XP_001117994.2	R.TCMCTVGYL.Q	Y	5,06	1152,465	10	46,8	577,2669	2	68,88	F2:6635	1	1896	1905
48	121	XP_002805569.1	P.YLLDD.T	N	19,4	637,2959	5	66,4	638,3455	1	58,81	F2:5041	1	1541	1545
48	121	XP_002805569.1	Q.GHAER.R	Y	14,19	568,2717	5	-5,1	569,2761	1	52	F1:985	1	1435	1439
48	121	XP_002805569.1	K.ACAFSSACSR.F	Y	9,3	1001,406	10	-11,5	501,7044	2	47,81	F4:12036	1	824	833
48	121	XP_002805569.1	R.CSSSAASCR.C	Y	9,08	870,3324	9	27	436,1852	2	66,81	F1:2435	1	898	906
48	121	XP_002805569.1	X.CCSSSWMLRF.C	Y	5,54	1218,498	10	56,1	610,2906	2	59,13	F4:13227	1	1197	1206
50	519	XP_002808534.1	K.CSGDCGFTWDS.D	Y	16,99	1176,385	11	79,2	589,2465	2	67,93	F4:14530	5	1010	1020
51	1334	XP_001116366.1	A.GSHTD.R	Y	17,55	515,1976	5	-39,7	516,1844	1	60,55	F4:13435	1	67	71
51	1334	XP_001116366.1	G.WNDSD.P	N	9,27	635,2187	5	-40,5	636,2003	1	53,36	F4:12561	4	53	57
54	139	XP_001114113.2	R.CAGTAEAEQLLQAFLDRDAAEG.P	Y	15,4	2278,054	22	-53,1	570,4904	4	51,63	F7:16836	1	46	67
54	139	XP_001114113.2	R.MMGLCCGYR.S	Y	8,61	1032,401	9	-73,3	517,1701	2	61,81	F1:1850	1	999	1007
54	139	XP_001114113.2	R.MMGLCCGYRST.F	Y	6,79	1220,481	11	45,1	611,2753	2	68,91	F2:6644	2	999	1009
55	212	XP_002804790.1	T.LEPKPD.T	Y	15,92	697,3646	6	9	698,3782	1	55,95	F4:12861	2	442	447
55	212	XP_002804790.1	K.TFGVIESD.P	Y	11,8	866,4022	8	85,8	434,2455	2	76,61	F2:7717	2	271	278
57	363	XP_002808005.1	R.LSTNGSDD.P	Y	18,82	807,3246	8	57,6	404,6928	2	65,98	F2:6069	4	175	182
58	380	XP_001083490.1	K.GFHTD.P	Y	16,26	575,2339	5	49,1	576,2695	1	56,53	F2:4815	3	206	210
58	380	XP_001083490.1	L.LYLS.D.K	N	8,4	609,301	5	49,1	610,3381	1	51,38	F3:9173	1	383	387
59	1200	XP_001116216.2	R.DECDTYFK.V	Y	16,38	1019,391	8	67,6	510,737	2	66,58	F4:14261	1	69	76
59	1200	XP_001116216.2	K.TCHSR.D	Y	6,47	602,2595	5	-83,6	603,2164	1	65,85	F4:14160	3	702	706
64	209	XP_002800001.1	S.GTGCR.S	Y	15,24	492,2115	5	22,9	493,23	1	64,18	F1:2087	1	717	721
64	209	XP_002800001.1	V.CSEDHSGLDAKSRGPRAFGR.A	Y	9,97	2145,013	20	42,7	430,0283	5	67,1	F2:6278	1	1185	1204
64	209	XP_002800001.1	R.HGLQSLGK.V	Y	9,74	838,4661	8	-56	420,2168	2	66,78	F1:2431	1	43	50
65	1524	NP_001035239.1	K.EEASD.V	Y	17,69	549,1918	5	-76	550,1573	1	49,25	F2:4113	1	771	775
65	1524	NP_001035239.1	R.ACGSLKGK.L	Y	8,98	762,4058	8	-69,9	763,3597	1	61,86	F4:13578	1	209	216
67	1311	XP_002808426.1	R.ACPGD.C	Y	15,65	461,158	5	50,8	462,1887	1	42,7	F1:138	1	496	500
67	1311	XP_002808426.1	W.GGPTCSD.P	Y	9,15	635,2221	7	-11,5	636,222	1	53,55	F3:9323	2	163	169

68	1611	XP_001114797.1	W.FGTTK.Y	Y	15,59	552,2908	5	-22,8	553,2855	1	68,63	F3:10940	1	337	341
70	119	XP_001097677.2	H.VANHMIDEGLNHECK.L	Y	23,63	1708,766	15	96,3	570,6508	3	60,26	F7:17147	1	1214	1228
70	119	XP_001097677.2	K.THTSNKPYK.C	Y	5,39	1074,546	9	94,8	538,3311	2	71,53	F2:7071	1	195	203
74	233	XP_001118617.2	R.KLVLIKRPQVQSFDfsRAFEWHGV.F	Y	15,6	2886,566	24	3,5	722,6512	4	57,86	F7:17016	1	3046	3069
74	233	XP_001118617.2	T.DEGQCHCVPGVAGKR.C	Y	5,45	1554,703	15	93,1	519,2899	3	74,35	F4:15547	1	969	983
75	246	XP_001108760.2	R.YHDGDDDR.S	Y	19,35	991,3631	8	87,6	496,7323	2	64,76	F1:2149	1	2249	2256
75	246	XP_001108760.2	R.EDGKCHK.M	Y	7,98	815,3596	7	21	408,6956	2	59,85	F1:1628	1	1833	1839
77	358	XP_001091687.1	K.CCFEVLTSWR.A	Y	17,94	1329,585	11	66,9	665,8441	2	53,55	F4:12596	1	1538	1548
77	358	XP_001091687.1	R.GMIDGSTPTITPNPNFRLFLSMD.P	Y	10,38	2523,214	23	63,1	505,6819	5	47,16	F4:12002	1	740	762
81	1331	XP_002808411.1	K.SPFRVGVTEGCD.P	Y	16,96	1265,571	12	44,3	422,883	3	73,58	F4:15450	1	1319	1330
81	1331	XP_002808411.1	E.GGLVN.K	N	7,18	458,2489	5	-57,2	459,2299	1	64,43	F3:10382	1	1343	1347
83	1971	XP_002800675.1	F.QAPSD.Y	Y	18,46	516,218	5	-50,2	517,1993	1	60,71	F4:13447	1	355	359
84	1	XP_001083243.1	R.SSDPRLPK.L	Y	20,15	898,4872	8	52,6	450,2745	2	64,63	F6:16665	1	27	34
85	348	XP_001086134.2	K.GPVRDASPAPLAQGEPGQED.L	Y	19,12	1989,939	20	-6,8	664,3158	3	41,35	F7:16769	1	1191	1210
94	431	XP_001086980.1	D.PEGPEAGGAEQK.A	Y	15,68	1168,536	12	77,1	585,3203	2	61,98	F7:17237	1	213	224
95	586	XP_001099227.1	Y.WLGPLLAGLLVGLLIR.C	Y	19,2	1703,086	16	47,7	568,7297	3	50,11	F1:749	1	231	246
97	1194	XP_002808183.1	K.EYYDTK.K	Y	20,61	817,3494	6	96,4	409,7214	2	67,38	F2:6343	1	1194	1199
101	2171	XP_002804455.1	K.NQDSSD.P	Y	17,01	664,23	6	32,8	665,259	1	61,36	F4:13511	1	2558	2563

Supplementary Table 3: COS M6_shRNA-PCBP1

Protein Group	Protein ID	Accession	-10lgP	Coverage (' #Peptides	#Unique	PTM	Avg. Mass	Description
81	2	XP_002804842.1	46,42	5	1	1	38604	PREDICTED: annexin A2 isoform 5 [Macaca mulatta]
3	88	XP_001089600.2	40,76	22	8	8	40421	PREDICTED: mitogen-activated protein kinase 1 [Macaca mulatta]
2	49	XP_002803800.1	36,49	2	3	2	108518	PREDICTED: uncharacterized protein KIAA0240-like [Macaca mulatta]
17	7	XP_001103956.1	36,05	2	1	1	68874	PREDICTED: serum albumin [Macaca mulatta]
5	241	XP_002802257.1	32,92	1	4	2	572123	PREDICTED: e3 ubiquitin-protein ligase UBR4-like [Macaca mulatta]
15	89	XP_001105471.1	32,55	10	2	2	35982	PREDICTED: glyceraldehyde-3-phosphate dehydrogenase [Macaca mulatta]
83	119	XP_002802772.1	32,42	5	1	1	38671	PREDICTED: actin cytoplasmic 1-like isoform 4 [Macaca mulatta]
65	23	XP_001115664.1	31,76	1	2	2	95594	PREDICTED: rab effector MyRIP-like isoform 4 [Macaca mulatta]
24	57	XP_001116949.2	31,74	1	2	0	76742	PREDICTED: nucleolin-like [Macaca mulatta]
22	448	XP_002801457.1	31,54	1	2	0	165691	PREDICTED: paternally-expressed gene 3 protein isoform 2 [Macaca mulatta]
14	8	XP_001112479.2	31,49	5	2	2	42586	PREDICTED: elongation factor 1-alpha 1 isoform 1 [Macaca mulatta]
7	1738	XP_002806302.1	31,46	1	2	1	160755	PREDICTED: lysine-specific demethylase 5C [Macaca mulatta]
6	1685	XP_001099166.2	30,26	1	2	1	142062	PREDICTED: ubiquitin-conjugating enzyme E2 O-like [Macaca mulatta]
82	16	XP_002799056.1	29,38	2	1	1	58673	PREDICTED: 60 kDa heat shock protein mitochondrial isoform 5 [Macaca mulatta]
11	91	XP_001113811.2	28,16	6	6	5	99688	PREDICTED: epidermal growth factor receptor substrate 15-like 1-like [Macaca mulatta]
27	1595	XP_001111650.2	28,16	1	2	0	74090	PREDICTED: uncharacterized protein C17orf56-like [Macaca mulatta]
23	1888	XP_001103691.1	26,86	1	3	0	152580	PREDICTED: zinc finger protein 804B-like [Macaca mulatta]
1	366	XP_001107670.2	25,42	1	1	1	57628	PREDICTED: hypothetical protein LOC716754 [Macaca mulatta]
25	173	XP_001106040.1	25,07	7	2	2	24734	PREDICTED: elongation factor 1-beta isoform 1 [Macaca mulatta]
33	29	XP_002801635.1	23,94	3	2	0	42078	PREDICTED: nucleosome assembly protein 1-like 1 isoform 2 [Macaca mulatta]
61	1007	XP_001087590.1	23,94	0	2	1	337747	PREDICTED: dmX-like protein 1-like isoform 2 [Macaca mulatta]
21	38	XP_002802064.1	23,78	1	2	2	83382	PREDICTED: ral guanine nucleotide dissociation stimulator-like 1-like isoform 2 [Macaca mulatta]
16	976	XP_001115747.1	23,02	1	1	1	56580	PREDICTED: NGFI-A-binding protein 2 isoform 3 [Macaca mulatta]
28	132	XP_002805234.1	22,8	1	1	1	73586	PREDICTED: cleavage and polyadenylation specificity factor subunit 2 [Macaca mulatta]
85	304	XP_002808280.1	21,53	1	1	1	113925	PREDICTED: LOW QUALITY PROTEIN: ankyrin repeat domain-containing protein 35-like [Macaca mulatta]
105	1861	XP_001104857.2	21,29	1	1	1	111897	PREDICTED: erythrocyte membrane protein band 4.1-like 2 [Macaca mulatta]
44	143	XP_002803160.1	21,27	1	1	1	95308	PREDICTED: serine/threonine-protein kinase SIK1-like [Macaca mulatta]
71	323	XP_001114282.2	20,66	1	2	2	229564	PREDICTED: myosin-IXb-like [Macaca mulatta]
9	310	XP_002805024.1	20,66	5	1	1	25230	PREDICTED: heterogeneous nuclear ribonucleoproteins C1/C2-like [Macaca mulatta]
13	75	XP_001104371.1	20,62	3	3	2	93253	PREDICTED: caldesmon isoform 14 [Macaca mulatta]
53	258	XP_002798870.1	20,29	1	3	3	494564	PREDICTED: dynein heavy chain 10 axonemal-like [Macaca mulatta]
91	893	XP_002802392.1	19,92	1	1	1	203343	PREDICTED: WD repeat-containing protein 90-like [Macaca mulatta]
26	896	XP_001100571.1	19,86	1	1	1	62101	PREDICTED: keratin type I cytoskeletal 10-like isoform 2 [Macaca mulatta]
34	324	XP_001093008.2	19,45	1	1	1	106539	PREDICTED: uncharacterized protein C9orf172-like [Macaca mulatta]
86	326	XP_002805894.1	19,06	2	1	1	52954	PREDICTED: hypothetical protein LOC100429153 [Macaca mulatta]
37	477	XP_001097911.2	18,45	2	2	1	123082	PREDICTED: ubiquitin conjugation factor E4 A isoform 3 [Macaca mulatta]
59	930	XP_002800014.1	18,15	0	1	1	282393	PREDICTED: spectrin alpha chain brain-like isoform 4 [Macaca mulatta]
84	293	XP_001111527.2	18,04	2	1	1	22455	PREDICTED: uncharacterized protein C20orf29-like isoform 1 [Macaca mulatta]
30	388	XP_001104133.1	17,78	1	2	0	97588	PREDICTED: spermatogenesis-associated protein 5-like isoform 3 [Macaca mulatta]
41	297	XP_002808529.1	17,78	2	2	2	91090	PREDICTED: LOW QUALITY PROTEIN: zinc finger and BTB domain-containing protein 10-like [Macaca mulatta]
77	852	XP_001094936.2	17,77	2	2	2	69319	PREDICTED: hypothetical protein LOC706559 [Macaca mulatta]
62	247	XP_002803268.1	17,75	2	2	2	64154	PREDICTED: zinc finger CW-type PWWP domain protein 1-like [Macaca mulatta]
70	189	XP_002800547.1	17,6	3	2	2	70009	PREDICTED: hypothetical protein LOC703932 [Macaca mulatta]
87	370	XP_002805862.1	17,59	4	1	1	17878	PREDICTED: hypothetical protein LOC100430719 [Macaca mulatta]
63	575	XP_001108337.1	17,56	1	1	1	48037	PREDICTED: trans-acting T-cell-specific transcription factor GATA-3-like isoform 3 [Macaca mulatta]
20	235	XP_001084293.1	17,41	2	3	3	99935	PREDICTED: PHD finger protein 14 isoform 1 [Macaca mulatta]
40	277	XP_001091310.1	17,08	1	3	3	256714	PREDICTED: probable JmjC domain-containing histone demethylation protein 2C isoform 3 [Macaca mulatta]
72	328	XP_001108724.2	17,08	5	2	2	54733	PREDICTED: hypothetical protein LOC717331 [Macaca mulatta]

66	151	XP_002805567.1	16,9	6	2	2	67193	PREDICTED: zinc finger protein 7 isoform 4 [Macaca mulatta]
51	228	XP_001103740.2	16,61	1	2	1	235094	PREDICTED: pecanex-like protein 2-like isoform 3 [Macaca mulatta]
103	1825	XP_002801580.1	16,43	1	1	1	65203	PREDICTED: actin-binding protein IPP [Macaca mulatta]
54	339	XP_002799471.1	16,38	10	2	2	42631	PREDICTED: tubulin alpha-3C/D chain-like isoform 2 [Macaca mulatta]
106	2251	XP_001087527.1	16,36	0	1	1	130688	PREDICTED: inactive dual specificity phosphatase 27 [Macaca mulatta]
45	890	XP_002799078.1	16,28	1	3	2	360978	PREDICTED: protein unc-80 homolog isoform 2 [Macaca mulatta]
55	348	XP_002799872.1	16,21	4	2	2	60508	PREDICTED: heat shock cognate 71 kDa protein isoform 6 [Macaca mulatta]
58	649	XP_001100797.1	16,13	0	2	2	356135	PREDICTED: protocadherin-16-like [Macaca mulatta]
75	392	XP_002808187.1	16,06	0	2	1	351200	PREDICTED: LOW QUALITY PROTEIN: protein furry homolog [Macaca mulatta]
95	961	XP_001091048.2	15,97	2	1	1	67582	PREDICTED: zinc finger protein 131 isoform 3 [Macaca mulatta]
48	128	XP_001094742.2	15,96	4	3	3	109345	PREDICTED: tubulin polyglutamylase TTL4 isoform 3 [Macaca mulatta]
56	371	XP_001098486.1	15,91	3	2	2	65502	PREDICTED: keratin type II cytoskeletal 2 epidermal-like [Macaca mulatta]
79	1883	XP_001085372.1	15,9	1	2	1	125751	PREDICTED: FH2 domain-containing protein 1 [Macaca mulatta]
76	416	XP_001097452.1	15,84	1	1	1	137027	PREDICTED: transcription initiation factor TFIID subunit 2 [Macaca mulatta]
80	1903	XP_002808518.1	15,73	0	1	1	388055	PREDICTED: LOW QUALITY PROTEIN: CUB and sushi domain-containing protein 1-like [Macaca mulatta]
64	2252	XP_001099384.2	15,68	0	1	1	153746	PREDICTED: DNA repair protein RAD50-like [Macaca mulatta]
57	378	XP_001084262.2	15,57	1	1	1	110079	PREDICTED: transmembrane protein 132A isoform 3 [Macaca mulatta]
38	177	XP_002808355.1	15,5	2	3	3	119402	PREDICTED: LOW QUALITY PROTEIN: zinc finger and BTB domain-containing protein 11-like [Macaca mulatta]
97	970	XP_001089429.1	15,39	7	1	1	24895	PREDICTED: ras-related protein Rab-27A-like isoform 2 [Macaca mulatta]
94	959	XP_001084586.2	15,38	1	1	1	76316	PREDICTED: x-ray repair cross-complementing protein 5 [Macaca mulatta]
36	379	XP_001118598.2	15,37	1	1	1	92036	PREDICTED: tyrosine-protein kinase ABL1-like [Macaca mulatta]
29	85	XP_002799249.1	15,35	1	3	3	480342	PREDICTED: baculoviral IAP repeat-containing protein 6-like [Macaca mulatta]
67	156	XP_001085960.2	15,34	1	2	2	170749	PREDICTED: protein KIAA0284-like isoform 2 [Macaca mulatta]
43	679	XP_002808390.1	15,3	1	2	2	259941	PREDICTED: LOW QUALITY PROTEIN: integrator complex subunit 1-like [Macaca mulatta]
99	972	XP_001093257.1	15,28	1	1	1	101791	PREDICTED: protein FAM40B-like [Macaca mulatta]
39	245	XP_001090498.2	15,12	1	2	2	190747	PREDICTED: laminin subunit beta-4 [Macaca mulatta]
49	198	XP_001100326.1	15,12	1	2	2	309280	PREDICTED: e3 ubiquitin-protein ligase UBR5 [Macaca mulatta]
46	1530	XP_001114534.2	15,08	1	2	2	164903	PREDICTED: cut-like 1 [Macaca mulatta]
100	984	XP_002800422.1	15,02	1	1	1	76234	PREDICTED: AP-1 complex subunit beta-1-like [Macaca mulatta]
118	79	XP_002808426.1	0	2	6	6	458469	PREDICTED: LOW QUALITY PROTEIN: tenascin-X-like [Macaca mulatta]
153	76	NP_001107827.1	0	8	5	5	93143	disrupted in schizophrenia 1 protein [Macaca mulatta]
154	87	XP_002805134.1	0	1	5	5	787218	PREDICTED: nesprin-2-like [Macaca mulatta]
156	118	XP_002808320.1	0	1	5	5	403256	PREDICTED: LOW QUALITY PROTEIN: msx2-interacting protein-like [Macaca mulatta]
131	160	XP_001117994.2	0	1	4	2	519037	PREDICTED: low-density lipoprotein receptor-related protein 1B [Macaca mulatta]
160	203	NP_001098005.1	0	1	4	3	410107	abnormal spindle-like microcephaly-associated protein homolog [Macaca mulatta]
179	141	XP_002802233.1	0	1	4	3	503581	PREDICTED: vacuolar protein sorting-associated protein 13D-like [Macaca mulatta]

mitogen-activated protein kinase 1 [Macaca mulatta]

1 MVR**GQVFDVG PR**YTNLSYIG EGAYGMVCSA YDNVNKVRVA IKK**ISPFEHQ TY**CQRTLREI KILLRFRHEN IIGINDIIRA
81 PTIEQMKDVY IVQDLMETDL YKLLKTQHLS NDHICYFLYQ ILRGLKYIHS ANVLHR**DLKP SNLLNNTT**CD LKICDFGLAR
161 VADPDHDHTG FLTEYVATRW YR**APEIMLNS K**GYTKSIDIW SVGCILAEML SNRPIFPGKH YLDQLNHILG ILGSPSQEDL
241 NCIINLKARN**YLLSLPHKNK** VPWNRLFPNA DSKALDLLDK MLTFNPHKR**I EVEQALAHPY LEQYYD**PSDE PIAEAPFKFD
321 MELDDLPEK**LKELIFEETA R**FQPGYRS

Supplementary Table 4: COS M6_shrRNA-PCBP1

Protein Group	Protein ID	Protein Accession	Peptide	Unique	-10lgP	Mass	Lengt	ppm	m/z	z	RT	Area	Scan	#Spec	Start	End
1	366	XP_001107670.2	R.GGPASD.P	Y	25,42	502,2023	6	-60,1	503,1794	1	47,76		F6:8212	38	435	440
2	49	XP_002803800.1	G.EGPSD.G	Y	24,51	503,1863	5	27,2	504,2073	1	46,35		F2:2320	10	70	74
2	49	XP_002803800.1	M.DDDDD.S	N	23,94	593,1453	5	-73,4	594,109	1	50,95		F1:623	1	2	6
2	49	XP_002803800.1	Y.FLHGPSNK.S	Y	6,21	898,4661	8	63,3	450,2687	2	80,51		F6:10691	1	22	29
3	88	XP_001089600.2	K.LKELIFEETAR.F	Y	20,65	1347,74	11	-8,6	450,25	3	53,9		F6:8442	3	331	341
3	88	XP_001089600.2	K.ELIFEETAR.F	Y	20,13	1106,561	9	60,3	554,321	2	54,73		F6:8499	6	333	341
3	88	XP_001089600.2	R.NYLLSLPHK.N	Y	17,75	1083,608	9	-5,3	542,8082	2	53,61		F6:8435	2	250	258
3	88	XP_001089600.2	R.GQVFDVGPR.Y	Y	16,49	973,4981	9	-11,6	487,7507	2	45,7		F6:8144	9	4	12
3	88	XP_001089600.2	R.APEIMLSNK.G	Y	12,91	1001,522	9	-42,9	501,7466	2	47,81		F6:8215	1	183	191
3	88	XP_001089600.2	R.IEVEQALAHYPYLEQYYD.P	Y	10,6	2079,979	17	-5,7	694,3296	3	70,85		F6:10034	1	290	306
3	88	XP_001089600.2	K.ISPFEHQTY.C	Y	9,24	1120,519	9	-0,7	561,2664	2	48,1		F6:8225	1	44	52
3	88	XP_001089600.2	R.DLKPSNLLNTT.C	Y	8,38	1327,735	12	-6,3	664,8705	2	62,98		F6:9275	1	137	148
5	241	XP_002802257.1	K.DDDDD.D	N	23,94	593,1453	5	-73,4	594,109	1	50,95		F1:623	1	2729	2733
5	241	XP_002802257.1	S.APASD.D	N	17,96	459,1965	5	1	460,2043	1	45,4		F4:3682	6	2864	2868
5	241	XP_002802257.1	R.HMACNEQQR.T	Y	8,35	1115,46	9	-30,6	558,7203	2	68,8		F4:5663	1	2218	2226
5	241	XP_002802257.1	D.PNSGLDESILEEC.L	Y	6,51	1404,608	13	-82,9	469,1711	3	66,9		F6:9680	1	1368	1380
6	1685	XP_001099166.2	A.SGPSSD.S	Y	21,28	548,2078	6	87,4	549,263	1	48,25		F1:404	1	44	49
6	1685	XP_001099166.2	P.APASD.S	N	17,96	459,1965	5	1	460,2043	1	45,4		F4:3682	6	37	41
7	1738	XP_002806302.1	M.EPGSD.D	Y	22,48	503,1863	5	33,5	504,2104	1	47,58		F1:333	1	2	6
7	1738	XP_002806302.1	A.APASD.P	N	17,96	459,1965	5	1	460,2043	1	45,4		F4:3682	6	1332	1336
9	310	XP_002805024.1	K.SEEEEQSSSVKK.D	Y	20,66	1323,615	12	50,2	662,8482	2	54,75		F4:4044	6	153	164
11	91	XP_001113811.2	D.PFESSD.P	Y	19,07	680,2653	6	80,9	681,3276	1	55,98		F1:910	1	704	709
11	91	XP_001113811.2	D.PFKSD.P	Y	18,18	592,2856	5	64,9	593,3314	1	52,06		F1:718	2	625	629
11	91	XP_001113811.2	R.VQLETIHK.S	Y	13,89	942,575	8	-84,3	472,255	2	64,48		F3:3429	2	524	531
11	91	XP_001113811.2	D.PFTSDPFMKNPSPSKLD.P	Y	8,22	2019,998	18	52	506,0329	4	48,05		F4:3754	1	686	703
11	91	XP_001113811.2	D.PFSSSSVSSKGSD.P	Y	7,5	1270,568	13	74,7	636,3386	2	100,33		F6:11151	1	710	722
11	91	XP_001113811.2	F.TSFGN.E	N	5,29	524,2231	5	87,3	525,2761	1	66,75		F6:9661	1	861	865
13	75	XP_001104371.1	K.PAASD.L	Y	20,62	459,1965	5	76,1	460,2387	1	42,31		F2:2158	3	697	701
13	75	XP_001104371.1	R.DAEENKKEDK.E	Y	9,86	1204,557	10	-29,7	603,2679	2	58,01		F4:4329	1	179	188
13	75	XP_001104371.1	L.EEEEQRR.K	N	6,41	974,4417	7	4,7	488,2304	2	42,5		F1:92	1	580	586
14	8	XP_001112479.2	K.IGGIGTVPVGR.V	Y	31,49	1024,603	11	-5,7	513,3058	2	46,16		F5:6963	3	189	199
14	8	XP_001112479.2	R.QTVAVGVIK.A	Y	8,75	913,5596	9	-6	457,7844	2	40,98		F5:6849	1	364	372
15	89	XP_001105471.1	R.GALQNIIPASTGAAK.A	Y	32,55	1410,783	15	-5,5	706,395	2	55,28		F6:8518	3	201	215
15	89	XP_001105471.1	K.AENGKLVINGSPITIFQERD.P	Y	6,8	2200,149	20	96,2	551,0974	4	49,36		F5:7155	1	62	81
16	976	XP_001115747.1	S.TPESD.V	Y	23,02	547,2125	5	61,5	548,2535	1	51,51		F4:3883	3	190	194
17	7	XP_001103956.1	K.VPQVSTPTLVEVSR.N	Y	36,05	1510,835	14	-4,5	756,4216	2	55,1		F5:7433	3	439	452
20	235	XP_001084293.1	K.ECSFCED.P	Y	17,41	831,2415	7	38,4	416,644	2	57,63		F4:4305	6	439	445
20	235	XP_001084293.1	E.CATCK.G	Y	7,84	524,2087	5	17,2	525,225	1	67,81		F4:5539	1	870	874
20	235	XP_001084293.1	K.YGAKECSFCED.P	Y	5,65	1250,458	11	-95,4	626,1768	2	42,43		F2:2177	1	435	445
21	38	XP_002802064.1	R.MMPGSD.P	Y	23,78	636,2247	6	46,4	637,2615	1	53,73		F2:2588	4	178	183
21	38	XP_002802064.1	I.PDSAN.V	Y	6,7	502,2023	5	59,6	503,2395	1	51,28		F5:7254	1	682	686
22	448	XP_002801457.1	E.DDDDD.D	N	23,94	593,1453	5	-73,4	594,109	1	50,95		F1:623	1	1232	1236
22	448	XP_002801457.1	S.IYISD.L	N	15,19	609,301	5	68,3	610,3499	1	51,33		F3:3103	4	733	737
23	1888	XP_001103691.1	S.SGPSD.T	N	19,27	461,1758	5	30,9	462,1973	1	44,08		F6:8097	1	905	909
23	1888	XP_001103691.1	C.LYLSD.E	N	15,19	609,301	5	68,3	610,3499	1	51,33		F3:3103	4	763	767
23	1888	XP_001103691.1	G.IIHLV.T	N	10,14	593,3901	5	86,9	594,4489	1	51,13		F3:3090	1	1030	1034
24	57	XP_001116949.2	E.DDDDD.E	N	23,94	593,1453	5	-73,4	594,109	1	50,95		F1:623	1	247	251
24	57	XP_001116949.2	K.KEDSD.E	N	15,6	592,234	5	91,8	593,2957	1	51,48		F2:2538	3	142	146

25	173	XP_001106040.1	K.LVPVGYGIK.K	Y	17,44	944,5695	9	3,7	473,2937	2	49,76	F4:3792	1	177	185
25	173	XP_001106040.1	R.WYNHIK.S	Y	15,26	859,4341	6	-44,8	430,705	2	61,51	F3:3343	1	55	60
26	896	XP_001100571.1	R.VLDELTTLK.A	Y	19,86	1030,591	9	16,3	516,3112	2	53,28	F5:7362	2	247	255
27	1595	XP_001111650.2	K.SGPSD.C	N	19,27	461,1758	5	30,9	462,1973	1	44,08	F6:8097	1	649	653
27	1595	XP_001111650.2	V.VALSD.C	N	17,78	503,2591	5	-3,6	504,2646	1	68,46	F6:9835	1	429	433
28	132	XP_002805234.1	V.DAPSD.S	Y	22,8	503,1863	5	-19,6	504,1837	1	46,26	F1:286	1	531	535
29	85	XP_002799249.1	R.NCAASGSD.P	Y	15,35	723,2494	8	92,5	724,3235	1	57,85	F2:2650	3	2961	2968
29	85	XP_002799249.1	K.HQSNKGYSLLAKVAAGK.E	Y	8,29	2042,127	20	79,1	409,465	5	62,2	F6:9183	1	1243	1262
29	85	XP_002799249.1	S.TAHLVSD.P	Y	6,45	854,4498	8	57,7	428,2568	2	95,01	F6:11002	7	2306	2313
30	388	XP_001104133.1	D.VALSD.K	N	17,78	503,2591	5	-3,6	504,2646	1	68,46	F6:9835	1	146	150
30	388	XP_001104133.1	L.YGPPGT.G	N	11,65	590,27	6	46,7	591,3049	1	72,68	F4:6056	8	392	397
33	29	XP_002801635.1	E.DDDDD.Y	N	23,94	593,1453	5	-73,4	594,109	1	50,95	F1:623	1	322	326
33	29	XP_002801635.1	E.PDDSD.P	N	12,73	547,1761	5	-3,4	548,1816	1	48,28	F2:2375	4	212	216
34	324	XP_001093008.2	R.TLQVAPPSD.P	Y	19,45	926,4709	9	60,3	464,2707	2	72,88	F4:6073	5	411	419
36	379	XP_001118598.2	K.GQGESD.P	Y	15,37	591,2136	6	-92,2	592,1664	1	51,18	F2:2518	5	278	283
37	477	XP_001097911.2	K.ETCLIPAVQEPK.F	Y	18,45	1326,685	12	38	664,3751	2	62,8	F6:9258	1	495	506
37	477	XP_001097911.2	S.PDDSD.N	N	12,73	547,1761	5	-3,4	548,1816	1	48,28	F2:2375	4	47	51
38	177	XP_002808355.1	S.ILTAD.M	Y	15,5	531,2904	5	-80,4	532,2549	1	53,71	F1:813	1	966	970
38	177	XP_002808355.1	K.AAACYVVR.G	Y	8,25	851,4323	8	-51,2	426,7016	2	59,98	F6:8871	1	36	43
38	177	XP_002808355.1	K.DWYSHVK.S	Y	6,05	933,4344	7	-12,6	467,7186	2	61,53	F4:4722	2	807	813
39	245	XP_001090498.2	R.TSLSASCSCN.S	Y	15,12	971,3688	10	84	486,7325	2	43,51	F5:6888	3	301	310
39	245	XP_001090498.2	R.CREGVSGQRCDR.C	Y	7,87	1364,604	12	11,5	455,8804	3	65,81	F6:9582	1	1124	1135
40	277	XP_001091310.1	R.SMPALHR.A	Y	17,08	810,4171	7	65,3	406,2422	2	100,45	F6:11158	2	980	986
40	277	XP_001091310.1	K.EQGLEVLPEHD.P	Y	7,68	1264,594	11	-0,5	633,3037	2	53,41	F2:2559	1	2174	2184
40	277	XP_001091310.1	K.NGGSSPESD.V	Y	5,5	848,3148	9	-70,2	425,1349	2	63,33	F6:9303	1	1747	1755
41	297	XP_002808529.1	E.LLLPQD.A	Y	17,78	697,401	6	-20,6	698,3939	1	56,1	F1:916	1	56	61
41	297	XP_002808529.1	K.YGLIPGTSN.D	Y	7,64	920,4603	9	54,6	461,2626	2	65,21	F6:9492	3	637	645
43	679	XP_002808390.1	L.EGNDD.R	Y	15,3	548,1714	5	-88,4	549,1302	1	48,5	F2:2410	3	258	262
43	679	XP_002808390.1	R.CGVLVGCTLESH.A	Y	6,19	1216,558	12	43,2	609,3126	2	74,11	F4:6158	1	868	879
44	143	XP_002803160.1	A.CSPVR.L	Y	21,27	560,274	5	50	561,3093	1	49,55	F2:2455	1	631	635
45	890	XP_002799078.1	K.TLVVHGQNECDIPTQLPVHEDTQFEALLK.E	Y	16,28	3273,634	29	88	546,6609	6	48,1	F1:377	1	1992	2020
45	890	XP_002799078.1	K.CGCPFALK.M	Y	8,84	837,3877	8	-54,1	419,6785	2	63,13	F3:3398	2	1330	1337
45	890	XP_002799078.1	I.LHPED.S	N	6,65	609,2758	5	91,9	610,3391	1	51,01	F2:2499	1	2194	2198
46	1530	XP_001114534.2	P.LSQSD.I	Y	15,08	548,2442	5	-70,4	549,2129	1	49,78	F1:527	1	733	737
46	1530	XP_001114534.2	R.KQVAPLLK.S	Y	5,68	895,5854	8	84,5	448,8379	2	65,56	F5:7877	1	51	58
48	128	XP_001094742.2	K.LNHFPGSFQIGR.K	Y	15,96	1371,705	12	91,7	458,2841	3	44,75	F1:150	1	494	505
48	128	XP_001094742.2	R.RPLLVR.Y	Y	10,09	880,5607	7	93,5	441,3288	2	70,98	F6:10049	1	579	585
48	128	XP_001094742.2	K.EFSFFPQSFILPQDAK.L	Y	9,91	1899,941	16	66,6	634,363	3	54,66	F4:4026	1	524	539
49	198	XP_001100326.1	K.DCMGGIRD.P	Y	15,12	865,3422	8	74,5	433,7106	2	65,76	F4:5238	2	825	832
49	198	XP_001100326.1	K.GHTSLMQR.L	Y	9,45	1029,503	9	-35,1	515,7405	2	65,35	F6:9517	1	2321	2329
51	228	XP_001103740.2	K.LLSWIKNESLLKSLQPF.K.W	Y	16,61	2214,278	19	36,8	554,597	4	48,36	F2:2391	1	1531	1549
51	228	XP_001103740.2	R.GCCCC.K	N	6,48	487,0688	5	-29	488,062	1	50,46	F1:554	2	1455	1459
53	258	XP_002798870.1	L.TLNSD	Y	20,29	548,2442	5	44	549,2756	1	49,38	F5:7161	1	4282	4286
53	258	XP_002798870.1	K.TLDARNTLK.L	Y	10,84	1030,577	9	25,4	516,309	2	71,41	F6:10092	1	454	462
53	258	XP_002798870.1	D.ELLSILGSSD.P	Y	5,5	1032,534	10	80	517,3156	2	70,35	F4:5843	1	1557	1566
54	339	XP_002799471.1	K.DVNAAIATIK.T	Y	16,38	1014,571	10	0,3	508,2929	2	48,5	F5:7099	2	261	270
54	339	XP_002799471.1	K.VGINYQPPTVPGGDLAKVQRAVCMLS.N	Y	5	2811,478	27	-21,3	563,2908	5	72,05	F6:10143	1	287	313
55	348	XP_002799872.1	K.EIAEAYLGK.T	Y	16,21	992,5178	9	-34,8	497,2489	2	44,78	F5:6943	2	37	45
55	348	XP_002799872.1	K.GPAVGIDLGTTY.S	Y	5,88	1162,587	12	86,2	582,3508	2	72,98	F6:10221	1	4	15
56	371	XP_001098486.1	K.IEISELNR.V	Y	15,91	972,524	8	-9,8	487,2645	2	45,71	F5:6955	2	401	408

56	371	XP_001098486.1	G.GYSSGSGSYGSGGR.G	Y	5,23	1277,527	14	76,2	639,8196	2	49,41	F5:7174	1	538	551
57	378	XP_001084262.2	K.EPPDSATD.P	Y	15,57	830,3293	8	-71,6	416,1422	2	60,05	F4:4532	3	880	887
58	649	XP_001100797.1	V.TITVR.D	Y	16,13	588,3595	5	81,5	589,4147	1	51,41	F1:683	1	2035	2039
58	649	XP_001100797.1	R.HQLVVQAAD.P	Y	11,05	979,5087	9	27,6	980,543	1	53,41	F2:2558	1	2761	2769
59	930	XP_002800014.1	R.DVDETISWIK.E	Y	18,15	1204,598	10	24,2	603,3206	2	57,91	F5:7506	3	263	272
61	1007	XP_001087590.1	S.DDDDD.D	N	23,94	593,1453	5	-73,4	594,109	1	50,95	F1:623	1	2459	2463
61	1007	XP_001087590.1	K.TASQVHLMK.F	Y	13,75	1013,533	9	68	507,8081	2	65,13	F5:7853	2	167	175
62	247	XP_002803268.1	G.MIESD.P	Y	17,75	593,2367	5	8	594,2487	1	52,5	F4:3906	1	335	339
62	247	XP_002803268.1	K.TDPTLPICK.Q	Y	7,01	986,5106	9	75,1	494,2996	2	71,11	F4:5918	1	450	458
63	575	XP_001108337.1	R.NANGD.P	Y	17,56	489,1819	5	-67,4	490,1562	1	50,61	F2:2466	1	332	336
64	2252	XP_001099384.2	K.CAEID.R	Y	15,68	549,2104	5	-74,1	550,177	1	50,48	F4:3844	2	133	137
65	23	XP_001115664.1	K.SCCSYQK.H	Y	31,76	817,3099	7	49,6	409,6825	2	67,05	F4:5433	1	91	97
65	23	XP_001115664.1	D.QGPMA.A	Y	8,21	502,2209	5	37,3	503,2469	1	61,96	F4:4784	1	433	437
66	151	XP_002805567.1	K.CDECGKAFRWISRLSQHQLIHTGEKPYK.C	Y	16,9	3329,655	28	38,1	555,9709	6	48,3	F2:2380	1	319	346
66	151	XP_002805567.1	I.HTGEKPFK.C	Y	12,61	942,4923	8	63,2	472,2832	2	70,69	F6:10016	1	176	183
67	156	XP_001085960.2	Q.DGDAVLPR.K	Y	15,34	841,4293	8	88,2	421,7591	2	41,03	F2:2085	1	803	810
67	156	XP_001085960.2	R.KRAGSFTGT.S	Y	8,2	923,4824	9	-73,7	462,7145	2	63,6	F4:4991	1	1175	1183
70	189	XP_002800547.1	R.QEYEQLIAK.N	Y	17,6	1120,576	9	1,8	561,2965	2	44,88	F5:6946	1	341	349
70	189	XP_002800547.1	K.DQIVDLTVGNK.T	Y	12,16	1314,678	12	-24,1	439,2227	3	62,91	F4:4879	1	226	237
71	323	XP_001114282.2	R.RISFSTD.V	Y	20,66	911,4348	8	80,9	912,5159	1	52,61	F4:3920	1	1352	1359
71	323	XP_001114282.2	C.PDNSD.P	Y	6,81	546,1921	5	-89,6	547,1505	1	49,63	F5:7198	1	1858	1862
72	328	XP_001108724.2	R.SPEDPAAAGARSPR.G	Y	17,08	1380,675	14	-37,4	691,3187	2	42,2	F5:6863	1	128	141
72	328	XP_001108724.2	G.GPGPTDDCR.S	Y	8,18	916,3708	9	63	459,2216	2	58,56	F5:7544	1	119	127
75	392	XP_002808187.1	R.KAVDNILR.H	Y	16,06	927,5501	8	-95,3	464,7381	2	71,68	F4:5971	1	561	568
75	392	XP_002808187.1	S.SSLKD.S	N	10,22	548,2806	5	-59,8	549,2551	1	49,06	F2:2445	1	2022	2026
76	416	XP_001097452.1	K.NGHVPSD.P	Y	15,84	724,314	7	17,8	725,3342	1	59,23	F4:4445	2	864	870
77	852	XP_001094936.2	P.THVED.D	Y	17,77	599,2551	5	-48,7	600,2332	1	49,23	F2:2449	1	76	80
77	852	XP_001094936.2	S.GCHGDS.S	Y	5,79	574,1805	6	54,3	575,219	1	56,83	F1:965	1	120	125
79	1883	XP_001085372.1	M.AKPVR.T	Y	15,9	569,3649	5	35,4	570,3923	1	50,26	F4:3830	1	887	891
79	1883	XP_001085372.1	S.ILHLV.L	N	10,14	593,3901	5	86,9	594,4489	1	51,13	F3:3090	1	294	298
80	1903	XP_002808518.1	R.VVNCSD.P	Y	15,73	635,2585	6	-81,9	636,2137	1	54,7	F6:8497	2	2787	2792
81	2	XP_002804842.1	K.LSLEGDHSTPPSAYGSVK.A	Y	46,42	1843,895	18	-2,3	615,6376	3	45,16	F6:8130	1	11	28
82	16	XP_002799056.1	K.NAGVEGLIVEK.I	Y	29,38	1214,651	12	-6,8	608,3285	2	46,01	F5:6959	1	459	470
83	119	XP_002802772.1	R.VAPEEHPVLLTEAPLNPK.A	Y	32,42	1953,057	18	-7,9	652,0211	3	56,08	F6:8542	1	68	85
84	293	XP_001111527.2	P.HGAER.D	Y	18,04	568,2717	5	-15,4	569,2703	1	50,28	F2:2461	1	41	45
85	304	XP_002808280.1	R.DQKLEAVQR.G	Y	21,53	1198,667	10	5,8	600,3442	2	52,26	F4:3896	1	53	62
86	326	XP_002805894.1	R.EFGGPWGTGR.R	Y	19,06	1062,488	10	44,6	532,2751	2	50,01	F4:3799	1	62	71
87	370	XP_002805862.1	R.APPPPD.P	Y	17,59	592,2856	6	60,5	593,3287	1	54	F4:4007	1	48	53
91	893	XP_002802392.1	R.VPGSGVPGSR.V	Y	19,92	911,4824	10	88,8	456,789	2	48,16	F5:7092	1	46	55
94	959	XP_001084586.2	K.TLFPLIEAK.K	Y	15,38	1030,606	9	-2,2	516,3093	2	69,98	F5:7961	1	475	483
95	961	XP_001091048.2	R.ESSQADAAK.A	Y	15,97	905,409	9	19,5	453,7206	2	60,85	F6:9048	1	546	554
97	970	XP_001089429.1	S.MDQLSEEKEKGACGC	Y	15,39	1626,669	15	-4,1	407,6728	4	62,23	F6:9188	1	207	221
99	972	XP_001093257.1	R.VTFPKGLPWAPK.V	Y	15,28	1339,765	12	-57,8	670,8511	2	55,33	F6:8520	1	471	482
100	984	XP_002800422.1	K.VFFVKYND.P	Y	15,02	1030,512	8	96	516,3129	2	74	F6:10312	1	60	67
103	1825	XP_002801580.1	K.EYCEVCK.S	Y	16,43	872,3408	7	91,4	437,2176	2	59,96	F1:1181	1	258	264
105	1861	XP_001104857.2	K.FYPPD.P	Y	21,29	637,2747	5	-89,2	638,2252	1	55,11	F4:4095	1	289	293
106	2251	XP_001087527.1	P.PFQSD.W	Y	16,36	592,2493	5	91,1	593,3105	1	53,2	F6:8426	1	954	958
118	79	XP_002808426.1	R.DGQPQAVRVGGEE.S	Y	12,72	1340,632	13	6,5	671,3276	2	50,2	F6:8321	4	3203	3215
118	79	XP_002808426.1	K.DGQPQAVPVAADQQEVTIYNL.E	Y	12,72	2255,107	21	9,3	752,7166	3	59,93	F4:4526	2	1553	1573
118	79	XP_002808426.1	R.SPVSVEAK.T	Y	9,47	815,4388	8	-91,3	408,6895	2	60,75	F5:7669	1	1691	1698

118	79 XP_002808426.1	R.SCPRGCSQRGRCEDGR.C	Y	8,76	1765,752	16	92,2	883,9646	2	63,65	F6:9352	1	248	263
118	79 XP_002808426.1	R.AVPVAADQHTVTIEDLEPGK.K	Y	8,23	2089,069	20	36,7	1045,58	2	55,61	F1:871	1	3491	3510
118	79 XP_002808426.1	D.PGYAGEDCGM.R	Y	7,66	998,3474	10	-90,4	500,1358	2	67,91	F4:5559	1	268	277
131	160 XP_001117994.2	K.CWPGFQLK.D	Y	13,59	977,4793	8	25,3	489,7593	2	61,71	F1:1323	1	2991	2998
131	160 XP_001117994.2	C.PDDSD.E	N	12,73	547,1761	5	-3,4	548,1816	1	48,28	F2:2375	4	97	101
131	160 XP_001117994.2	S.NHCSVVPGR.G	Y	6,91	967,4658	9	-88,2	484,6975	2	64,15	F4:5038	1	1223	1231
131	160 XP_001117994.2	A.CDGDND.C	N	5,01	637,165	6	-95	638,1117	1	54,71	F4:4037	1	1063	1068
153	76 NP_001107827.1	R.GEAEGCPPSR.E	Y	13,17	1001,424	10	-73,5	501,6823	2	46,33	F2:2319	1	224	233
153	76 NP_001107827.1	K.YMETLKDCLCCKCPLLK.V	Y	12,48	2172,082	19	-56	543,9973	4	48,26	F2:2371	1	671	689
153	76 NP_001107827.1	K.WEPVLR.D	Y	11,87	798,4388	6	7,3	400,2296	2	67,63	F6:9745	1	333	338
153	76 NP_001107827.1	R.SLTSEREGLEGLSK.L	Y	11,44	1617,857	15	95,6	405,5103	4	61,56	F3:3347	1	613	627
153	76 NP_001107827.1	R.LHSEDKRKTPQLALEEWK.A	Y	8,88	2207,17	18	-2,8	552,7982	4	48,35	F3:3024	1	736	753
154	87 XP_002805134.1	K.IVSALWEK.W	Y	10,28	944,5331	8	24,1	473,2852	2	49,58	F4:3787	1	3409	3416
154	87 XP_002805134.1	K.VSKIKTILLSK.E	Y	8,44	1228,812	11	97,2	410,651	3	56,51	F4:4166	1	3851	3861
154	87 XP_002805134.1	K.IGLRDPTVPAVK.H	Y	7,93	1264,75	12	84,5	633,4359	2	54,13	F5:7372	1	1419	1430
154	87 XP_002805134.1	K.DSLGNLKI.W	Y	7,63	986,576	9	1,4	494,296	2	69,71	F6:9947	1	2538	2546
154	87 XP_002805134.1	K.MEESQKELESYM.T	Y	6,64	1502,627	12	96,7	752,3933	2	58,28	F6:8719	1	816	827
156	118 XP_002808320.1	R.VHSIIESD.P	Y	13,51	898,4396	8	97,3	450,2708	2	70,16	F6:9978	1	2449	2456
156	118 XP_002808320.1	X.ERTGCSPSVRHGSFHEDED.P	Y	10,67	2143,898	19	-98,2	429,7447	5	64,16	F6:9424	1	1256	1274
156	118 XP_002808320.1	R.YYDDPR.E	Y	10,24	827,345	6	3,3	414,6811	2	57,31	F4:4272	1	673	678
156	118 XP_002808320.1	T.PPQSCTSD.P	Y	9,49	833,3225	8	73,7	417,6992	2	60,03	F1:1195	1	2393	2400
156	118 XP_002808320.1	K.TAAGGGPQGKK.G	Y	8,78	970,5195	11	33,6	486,2833	2	72,43	F3:3554	1	1989	1999
160	203 NP_001098005.1	D.LLIFK.T	N	13,61	632,4261	5	63,3	633,4734	1	53,48	F3:3127	1	642	646
160	203 NP_001098005.1	R.AAVLIQATFR.M	Y	9,4	1088,634	10	70,2	545,3625	2	48,28	F1:409	1	2486	2495
160	203 NP_001098005.1	K.HQAILLGNAEK.Q	Y	8,82	1192,656	11	54,4	597,3679	2	51,08	F2:2509	1	132	142
160	203 NP_001098005.1	K.MAAIVNQSALCCYR.S	Y	7,67	1541,715	14	39,4	771,8953	2	57,25	F4:4267	2	2769	2782
179	141 XP_002802233.1	R.KPRCCTGPQGILLPR.Y	Y	11,16	1524,802	14	-12,6	509,2681	3	79,86	F6:10669	1	4356	4369
179	141 XP_002802233.1	R.SDHYPAAD.P	Y	10,19	874,3457	8	-84,3	438,1433	2	60,45	F6:8979	1	795	802
179	141 XP_002802233.1	T.NTQDN.S	N	6,27	590,2296	5	96,8	591,294	1	52,03	F2:2546	1	942	946
179	141 XP_002802233.1	P.ATSGDPCVRVPASTPGTGSELAEPLGTPTSVSWGAR.A	Y	5,45	3510,705	36	27,8	586,141	6	71,96	F6:10135	1	102	137