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Table 1S, Protein table.

Accession*	Score**	Mw (Da)	pI	Peptides#	Theoretical Peptides##	Coverage (%)§
Q15029	447	109366	4.6	18	74	29
P61247	348	29925	10.1	7	28	28
P62081	159	22113	10.5	4	21	25
P08865	345	32833	4.5	5	26	45
P06576	256	56524	5.0	13	38	33
P68133	755	42023	5.0	7	34	26
P12814	930	102992	5.0	4	27	77
Q16352	357	55357	5.1	17	51	38
P07355	854	38579	7.7	18	32	55
P68104	322	50109	9.3	12	32	30
P26641	376	50087	6.2	15	37	41
P08107	625	69995	5.3	13	49	29
P34931	794	70331	5.6	16	48	30
P17066	884	70984	5.7	19	57	39
P61978	303	50944	5.2	8	39	28
P00338	538	36665	8.3	12	33	37
P22234	635	47049	6.9	18	36	52
P23284	167	22728	9.7	3	21	24
Q13162	118	30520	5.8	6	20	32
P06454	371	12195	3.4	4	12	36
P38646	466	73634	5.7	17	69	37
P55072	528	89265	4.9	20	69	33
Q13748	1030	49927	4.7	11	35	41
Q71U36	1212	50103	4.7	11	35	34
Q9BQE3	1338	49863	4.7	12	35	41
P68363	1391	50119	4.7	12	35	37
P07437	901	49638	4.5	8	31	41
Q13885	606	49874	4.5	6	31	26
Q9BVA1	632	49920	4.5	7	31	26
P68371	638	49799	4.6	7	31	27
Q13509	511	50400	4.6	7	31	21
P04350	647	49553	4.5	10	31	38
Q9BUF5	412	49825	4.5	10	31	39

* Accession number according to SwissProt database; ** PLGS score; # numbers of identified peptides; ## number of calculated theoretical peptides; § percentage of sequence coverage

Table 2S, Peptides table.

Accession*	Score**	Precursor MH+ (Da)#	z##	Score§	Start[a]	End[b]	Sequence[c]
Q15029	447	969.53	2	132	804	813	(R)GGGQIIPTAR(R)
		1017.55	2	73	251	259	(R)LAVTVCINK(I)
P61247	348	1951.99	2	59	66	82	(R)VFEVSLADLQNDEVAFR(K)
		791.42	2	42	20	27	VVDPFSK
P62081	159	1337.85	2	290	59	70	(K)AIIIFVPVPQLK(S)
		2367.28	3	48	120	142	TLTAVHDAILEDLVFPSEIVGK
P08865	345	1698.86	2	50	103	117	(R)FTPGTFTNQIQAAFR(E)
		1740.95	2	83	64	80	(R)AIVAIENPADVSVISSR(N)
P06576	256	1435.75	2	120	311	324	(R)FTQAGSEVSALLGR(I)
		1988.03	2	60	225	239	(R)AIAELGIYPAVDPLDSTSR(L)
		1406.68	3	21	462	480	(R)FLSQPFQVAEVFTGHMGK(L)
P68133	755	795.45	2	1719	331	337	(K)IIAPPER(K)
		976.43	2	793	21	30	(K)AGFAGDDAPR(A)
		1198.52	2	2273	53	63	(K)DSYVGDEAQSK(R)
		1790.89	2	1939	241	256	(K)SYELPDGQVITIGNER(F)
P12814	930	1215.66	2	45	282	291	(K)LASDLLEWIR(R)
		1561.74	2	57	851	863	(R)ELPPDQAEYCIAR(M)
Q16352	357	949.48	2	25	29	39	(R)LSGAGGAGGFR(S)
		1544.76	2	22	92	104	(R)TNEKEQLQGLNDR(F)
P07355	854	1111.55	2	275	69	77	(R)QDIAFAYQR(R)
		1222.59	2	378	105	115	(K)TPAQYDASELK(A)
		1908.89	2	279	180	196	(R)AEDGSVIDYELIDQDAR(D)
		2064.98	3	65	179	196	(R)RAEDGSVIDYELIDQDAR(D)
P68104	322	914.55	2	71	431	439	(R)QTVAVGVIK(A)
		1314.74	2	84	135	146	(R)EHALLAYTLGVK(Q)
P26641	376	821.44	2	107	150	156	(R)TFLVGER(V)
		1609.79	2	44	190	201	(R)WFLTCINQPQFR(A)
P08107	625	1315.6	2	30	302	311	(R)FEELCSDLFR(S)
		1487.7	2	938	37	49	(R)TTPSYVAFTDTER(L)
P34931	794	804.43	2	195	503	509	(K)ITITNDK(G)

		1197.69	2	255	162	173	(K)DAGVIAGLNVLR(I)
		1228.62	2	659	28	38	(K)VEIIANDQGNR(T)
		1487.69	2	1595	39	51	(R)TTPSYVAFTDTER(L)
P17066	884	804.43	2	195	503	509	(K)ITITNDK(G)
		902.47	2	44	314	321	(R)STLEPVEK(A)
		1315.6	2	1346	304	313	(R)FEELCSDLFR(S)
		1487.69	2	1595	39	51	(R)TTPSYVAFTDTER(L)
		1675.7	3	67	223	238	(K)ATAGDTHLGGEDFDNR(L)
P61978	303	1780.8	2	65	70	86	(R)TDYNASVSVPDSSGPER(I)
		1340.8	2	104	208	220	(K)IILDLISESPIK(G)
P00338	538	742.44	2	60	107	112	(R)LNLVQR(N)
		1248.6	2	104	158	169	(R)VIGSGCNLDSAR(F)
		1657.85	2	95	43	57	(K)DLADELALVDVIEDK(L)
P22234	635	1016.5	2	243	37	46	(K)DQITAGNAAR(K)
		1249.63	2	38	20	30	(K)EVYELLDSPGK(V)
		1850.93	2	123	314	331	(K)AEYEGDGIPTVFVAVAGR(S)
P23284	167	860.4	2	43	44	51	(R)IGDEDVGR(V)
		1364.7	2	64	64	76	(K)TVDNFVALATGEK(G)
Q13162	118	819.41	2	91	224	230	(R)SVDETLR(L)
		2845.39	3	28	140	164	(R)SINTEVVACSVDSQFTHLAWINTPR
P06454	371	1565.62	3	249	91	104	(R)AAEDDEDDDVDTKK(Q)
		1437.55	2	637	91	103	(R)AAEDDEDDDVDTK(K)
P38646	466	1361.74	2	143	349	360	(R)AQFEGIVTDLIR(R)
		1694.84	2	31	188	202	(K)NAVITVPAYFNDSQR(Q)
		1231.66	2	34	635	646	(R)QAASSLQQASLK(L)
P55072	528	1116.5	2	30	587	599	(R)GGNIGDGGGAADR(V)
		1556.85	2	44	639	651	(R)LDQLIYIPLPDEK(S)
Q13748	1030	1410.7	2	36	85	96	(R)QLFHPEQLITGK(E)
		1598.77	2	390	340	352	(R)TIQFVDWCPTGFK(V)
		1718.89	3	84	216	229	(R)NLDIERPTYTNLNR(L)
		1824.99	2	170	353	370	(K)VGINYQPPTVVPGGDLAK(V)
		2007.9	2	87	41	60	(K)TIGGGDDSFNTFFSETGAGK(H)
Q71U36	1212	1085.615	2	64	113	121	(K)EIIDLVLDR(I)
		1410.77	2	36	85	96	(R)QLFHPEQLITGK(E)

		1598.77	2	390	340	352	(R)TIQFVDWCPTGFK(V)
		1701.9	2	604	65	79	(R)AVFVDLEPTVIDEVR(T)
		1718.86	3	84	216	229	(R)NLDIERPTYTNLNR(L)
		1824.99	2	170	353	370	(K)VGINYQPPTVVPGGDLAK(V)
		2007.9	2	87	41	60	(K)TIGGGDDSFNTFFSETGAGK(H)
Q9BQE3	1371	781.4	2	44	157	163	(R)LSVDYGK(K)
		1085.61	2	39	113	121	(K)EIIDLVLDR(I)
		1487.87	2	473	230	243	(R)LISQIVSSITASLR(F)
		1701.91	2	1827	65	79	(R)AVFVDLEPTVIDEVR(T)
		1718.86	3	108	216	229	(R)NLDIERPTYTNLNR(L)
		1824.99	2	606	353	370	(K)VGINYQPPTVVPGGDLAK(V)
		2007.9	2	183	41	60	(K)TIGGGDDSFNTFFSETGAGK(H)
		2409.23	2	96	244	264	(R)FDGALNVDLTEFQTNLVPYPR(I)
P68363	1391	1085.61	2	64	113	121	(K)EIIDLVLDR(I)
		1410.77	2	36	85	96	(R)QLFHPEQLITGK(E)
		1487.87	2	876	230	243	(R)LISQIVSSITASLR(F)
		1584.75	2	817	340	352	(R)SIQFVDWCPTGFK(V)
		1701.9	2	604	65	79	(R)AVFVDLEPTVIDEVR(T)
		1718.86	3	84	216	229	(R)NLDIERPTYTNLNR(L)
		1824.99	2	170	353	370	(K)VGINYQPPTVVPGGDLAK(V)
		2007.9	2	87	41	60	(K)TIGGGDDSFNTFFSETGAGK(H)
P07437	901	1301.63	2	240	47	58	(R)ISVYYNEATGGK(Y)
		1696.83	2	1679	337	350	(K)NSSYFVEWIPNNVK(T)
		1822.9	3	50	3	19	(R)EIVHIQAGQCGNQIGAK(F)
Q13885	606	1077.52	2	70	155	162	(K)IREEYPDR(I)
		1696.83	2	1485	337	350	(K)NSSYFVEWIPNNVK(T)
		1822.9	3	95	3	19	(R)EIVHIQAGQCGNQIGAK(F)
		2798.33	3	61	78	103	(R)SGPFGQIFRPDNFVFGQSGAGNNWAK(G)
Q9BVA1	632	1077.52	2	70	155	162	(K)IREEYPDR(I)
		1696.83	2	1485	337	350	(K)NSSYFVEWIPNNVK(T)
		1822.9	3	95	3	19	(R)EIVHIQAGQCGNQIGAK(F)
		2798.33	3	61	78	103	(R)SGPFGQIFRPDNFVFGQSGAGNNWAK(G)
P68371	638	1077.52	2	70	155	162	(K)IREEYPDR(I)
		1696.83	2	1485	337	350	(K)NSSYFVEWIPNNVK(T)
		2798.33	3	61	78	103	(R)SGPFGQIFRPDNFVFGQSGAGNNWAK(G)
Q13509	511	1696.87	2	655	337	350	(K)NSSYFVEWIPNNVK(V)

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* Accession number according to SwissProt database; ** PLGS score; # numbers of identified peptides; ## number of calculated theoretical peptides; § percentage of sequence coverage