

Protein-Profiling of Genomic Instability in Endometrial Cancer

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S12

SSP 215

OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	
	14-3-3	sp P62258 1433E_HUMAN	protein epsilon OS Homo sapiens GN YWHAE PE 1 SV 1	29155	4.4355	9.9628	100	2	8.6275	2.6988		3.177	
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool
	628.8022		2	1255.5887	1255.5833	0.005483164	4.37489	66.6667	133.6922	131	141 (R)YLAEFATGNDNR(K)	22.39	PLGS Databank Search
	597.8048		2	1193.594	1193.5928	0.001220703	1.0227133	52.381	100.7239	143	153 (K)EAAENSLVAYK(A)	20.36	PLGS Databank Search

SSP 1501

OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	
	Vimentin	sp P08670 VIME_HUMAN	OS Homo sapiens GN VIM PE 1 SV 4	53619	4.8629	9.8356	100	8	17.382	17.784		18.7326	
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool
	558.2982		2	1114.5808	1114.5619	0.01904	17.08561	66.6667	97.0703	105	113 (K)VELQELNDR(F)	20.98	PLGS Databank Search
	585.3666		2	1168.7175	1168.7067	0.01086	9.29597	71.9298	67.0881	130	139 (K)ILLAELEQLK(G)	29.14	PLGS Databank Search
	538.7625		2	1075.5094	1075.4967	0.0127	11.80414	62.7451	75.5171	176	184 (R)DNLAEEDIMR(L)	26	PLGS Databank Search
	662.326		2	1322.6364	1322.6101	0.02625	19.84343	55.5556	18.7562	197	207 (K)EEAENLQSF(R)(Q)	22.11	PLGS Databank Search
	544.7871		2	1087.5586	1087.5258	0.03284	30.19415	78.9474	153.5165	208	217 (R)QDVNLSLAR(L)	17.52	PLGS Databank Search
	547.2772		2	1092.5388	1092.5199	0.01892	17.31858	71.9298	111.5425	295	304 (K)FADLSAANR(N)	20.55	PLGS Databank Search
	745.8955		2	1489.7754	1489.7448	0.03064	20.56705	38.6667	18.5221	322	334 (R)QVQSLTCEVDALK(G)	24.93	PLGS Databank Search
	559.7887		2	1117.5618	1117.5437	0.01807	16.16617	88.2353	64.5908	365	373 (R)LDIQNMK(E)	19.96	PLGS Databank Search
													Carbamidomethyl C (7)

SSP 1607

OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)
	Protein	sp P07237 PDIA1_HUMAN	disulfide isomerase OS Homo sapiens GN P4HB PE 1 SV 3	57980	4.5643	9.8356	100	8	16.3386	4.7348		5.2125	12.5
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool
	496.2795		2	990.5434	990.5386	0.004821777	4.867834	66.6667	110.7623	223	230 (K)ENLLDFIK(H)	30.13	PLGS Databank Search
	611.9745		3	1832.9	1832.9058	-0.005737305	-3.1301692	63.2184	91.0543	286	300 (K)ILFIFDSDHDTDNGR(I)	29.69	PLGS Databank Search
	483.792		2	965.56936	965.5596	0.009765625	10.113964	73.3333	108.9123	301	308 (R)ILEFFGLK(K)	30.5	PLGS Databank Search
	603.8211		2	1205.6266	1205.6213	0.005249023	4.353791	71.9298	153.577	317	326 (R)LTLEEEMTK(Y)	25.07	PLGS Databank Search
	484.5702		3	1450.6871	1450.694	-0.006835938	-4.7121844	37.6812	39.5022	327	338 (K)YKPESELTAER(I)	18.07	PLGS Databank Search
	607.2743		2	1212.533	1212.5298	0.003173828	2.617526	73.6842	88.7031	376	385 (K)NFEDVAFDEK(K)	24.04	PLGS Databank Search
	607.2693		2	1212.523	1212.5298	-0.006835938	-5.6377482	75.4386	162.737	376	385 (K)NFEDVAFDEK(K)	23.8	PLGS Databank Search
	485.7731		2	969.5306	969.5283	0.002258301	2.3292778	62.2222	120.3209	402	409 (K)QLAPIWDLK(L)	24.7	PLGS Databank Search
	655.3043		2	1308.593	1308.5867	0.006347656	4.850773	71.0145	190.5702	425	436 (K)MDSTANEVAVK(V)	17.89	PLGS Databank Search
													Oxidation M (1)

SSP 2327

OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)
	Thioredoxin-like	sp O43396 TXNL1_HUMAN	protein 1 OS Homo sapiens GN TXNL1 PE 1 SV 3	32230	4.6432	9.8356	100	4	9.3428	10.4205		11.7745	25
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool
	572.7806		2	1143.5455	1143.5308	0.01477	12.91658	61.9048	90.3991	182	192 (K)FQPDNGQGPK(Y)	16.93	PLGS Databank Search
	436.7725		2	871.52936	871.5279	0.00146	1.68078	58.9744	15.1555	196	202 (K)IFINLPR(S)	26.69	PLGS Databank Search
	557.2359		2	1112.4562	1112.4445	0.01172	10.53423	68.6274	56.4203	203	211 (R)SMDFEEAER(S)	20.78	PLGS Databank Search
	565.2368		2	1128.458	1128.4393	0.01868	16.55096	45.098	10.0545	203	211 (R)SMDFEEAER(S)	18.02	PLGS Databank Search
													Oxidation M (2)

SSP 2811														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	Heat	sp P07900 HSP90A_HUMAN	shock protein HSP 90 alpha OS Homo sapiens GN HSP90AA1 PE 1 SV 5	84606	4.747	9.8348	89.92	2	3.1421	9.0965		9.2505		
	Putative	sp Q58FF7 H90B3_HUMAN	heat shock protein HSP 90 beta 3 OS Homo sapiens GN HSP90AB3P PE 5 SV 1	68282	4.513	9.4553	68.36	2	3.6851	10.4574		10.8908		
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool	
	618.3115	2	2	1234.6074	1234.5941	0.01331	10.7736	33.3333	10.0572	500	510 (K)DQVANSAFVFER(L)	20.37	PLGS Databank Search	
	708.8282	2	2	1415.6407	1415.6302	0.0105	7.41581	60.8696	19.8509	547	558 (K)EGLLELPEDEEEK(K)	22.72	PLGS Databank Search	
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool	
	597.836	2	2	1193.6564	1193.6403	0.01611	13.4928	49.1228	22.5112	73	82 (K)DIHPNQER(T)	24.25	PLGS Databank Search	
	708.8282	2	2	1415.6407	1415.6302	0.0105	7.41581	60.8696	19.8509	412	423 (K)EGLLELPEDEEEK(K)	22.72	PLGS Databank Search	
SSP 5304														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	2 F-actin-capping	sp P52907 CAZA1_HUMAN	protein subunit alpha 1 OS Homo sapiens GN CAPZA1 PE 1 SV 3	32902	5.3258	9.8357	100	1	2.7972	5.0189		5.0189	100	
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Retention Time (min)	Query Tool
	469.2087	2	2	936.4018	936.3971	0.004699707	5.018925	33.3333	93.5765	122	129 (R)ECSDSLRLA(A)	Carbamidomethyl C (3)		15.54 PLGS Databank Search
SSP 5322														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	2 60S	sp P05388 RLA0_HUMAN	acidic ribosomal protein P0 OS Homo sapiens GN RPLP0 PE 1 SV 1	34251	5.6049	9.8355	99.99	8	32.4921	9.4361		12.3615	37.5	
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Retention Time (min)	Query Tool
	609.3349	2	2	1216.6542	1216.6702	-0.01599	-13.14342	57.8947	82.7807	17	26 (K)IILLDDYPK(C)		27.24	PLGS Databank Search
	633.8206	2	2	1265.6256	1265.6074	0.01819	14.37134	71.0145	63.9052	27	38 (K)CFIVGADNVGSK(Q)	Carbamidomethyl C (1)	24.22	PLGS Databank Search
	633.8161	2	2	1265.6166	1265.6074	0.00916	7.2339	39.1304	33.814	27	38 (K)CFIVGADNVGSK(Q)	Carbamidomethyl C (1)	22.91	PLGS Databank Search
	633.8053	2	2	1265.595	1265.6074	-0.01245	-9.8381	73.913	200.7681	27	38 (K)CFIVGADNVGSK(Q)	Carbamidomethyl C (1)	22.71	PLGS Databank Search
	484.765	2	2	967.5144	967.5127	0.00171	1.76637	76.4706	177.7671	84	92 (K)GNVGFVTK(E)		25.05	PLGS Databank Search
	438.2291	2	2	874.44257	874.4396	0.00299	3.42016	69.2308	60.6649	93	99 (K)EDLTEIR(D)		20.48	PLGS Databank Search
	727.3734	3	3	2179.0967	2179.0945	0.0022	1.00834	56.5891	230.7153	113	134 (R)AGAIAPCEVTPAQTGLGPEK(T)	Carbamidomethyl C (7)	23.76	PLGS Databank Search
	657.3662	2	2	1312.7168	1312.7028	0.01404	10.69403	76.8116	229.4973	135	146 (K)TSFFQALGITT(K)		30.69	PLGS Databank Search
	657.3591	2	2	1312.7025	1312.7028	0	-0.18598	43.4783	-4.5313	135	146 (K)TSFFQALGITT(K)		30.81	PLGS Databank Search
	657.8704	2	2	1313.7252	1313.6868	0.03845	29.27041	53.6232	166.3408	135	146 (K)TSFFQALGITT(K)	Deamidation Q (5)	30.69	PLGS Databank Search
	918.1728	3	3	2751.4949	2751.4959	0.0354	12.86604	38.7978	-0.0574	267	297 (K)AFLADPSAFVAAPVAATAAPAAAAAPAK(V)		29.89	PLGS Databank Search
SSP 8101														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	2 Protein	sp Q99497 PARK7_HUMAN	DJ 1 OS Homo sapiens GN PARK7 PE 1 SV 2	19878	6.3717	9.8357	100	5	19.5767	17.0567		19.3274	60	
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Retention Time (min)	Query Tool
	838.4333	2	2	1674.851	1674.7955	0.05542	33.09056	50.5747	52.0468	13	27 (K)GAEMETVIPDVMR(R)		28.28	PLGS Databank Search
	846.4155	2	2	1690.8154	1690.7905	0.0249	14.72823	36.7816	17.7256	13	27 (K)GAEMETVIPDVMR(R)	Oxidation M (14)	25.92	PLGS Databank Search
	854.4175	2	2	1706.8193	1706.7854	0.03394	19.88273	31.0345	33.8745	13	27 (K)GAEMETVIPDVMR(R)	Oxidation M (5), Oxidation M (14)	23.8	PLGS Databank Search
	766.3777	2	2	1530.7397	1530.7236	0.01611	10.52658	44.4444	0.0921	49	62 (R)DVVICPDASLEDK(K)	Carbamidomethyl C (5)	24.05	PLGS Databank Search
	437.7569	2	2	873.49817	873.492	0.00616	7.05736	68.8889	42.3717	149	156 (K)DGLLTSR(G)		23.14	PLGS Databank Search
SSP 1222														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	2 Heat	sp P08107 HSP71_HUMAN	shock 70 kDa protein 1 OS Homo sapiens GN HSPA1A PE 1 SV 5	70009	5.3187	9.8352	99.96	2	2.4961	9.2219		9.2255		
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool	
	402.7236	2	2	803.4316	803.4388	-0.007202148	-8.964153	64.1026	91.857	501	507 (K)ITTTNDK(G)		16.91	PLGS Databank Search
	474.2427	2	2	946.4698	946.4608	0.008972168	9.479703	78.4314	100.3472	551	559 (K)SVEDEGLK(G)		17.2	PLGS Databank Search
SSP 1313														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	2 Actin,	sp P60709 ACTB_HUMAN	cytoplasmic 1 OS Homo sapiens GN ACTB PE 1 SV 1	41709	5.142	9.1424	50	5	15.2	2.755		3.2615		
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool	
	488.7295	2	2	975.44336	975.441	0.002380371	2.4403026	50.8772	53.302	19	28 (K)AGFAGDDAPR(A)		17.72	PLGS Databank Search
	599.766	2	2	1197.5164	1197.5149	0.001464844	1.2232363	52.381	90.9453	51	61 (K)DSYVGDDEAGSK(R)		16.34	PLGS Databank Search
	652.0263	3	3	1953.0554	1953.0571	-0.001708984	-0.8750304	49.5238	88.4173	96	113 (R)VAPEEHPVLLTEAPLNPK(A)		24.54	PLGS Databank Search
	498.7504	2	2	997.48517	997.4791	0.006042481	6.057751	33.3333	42.5124	184	191 (R)DLTLYMK(I)		27.05	PLGS Databank Search
	566.7697	2	2	1131.8238	1131.5195	0.004272461	3.7758615	29.8246	19.5496	197	206 (R)GYSFTTAE(R)		20.45	PLGS Databank Search
	566.7688	2	2	1131.522	1131.5195	0.002441406	2.157635	57.8947	123.0299	197	206 (R)GYSFTTAE(R)		20.2	PLGS Databank Search

SSP 1342														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	2	Keratin,	sp P08729 K2C7_HUMAN	51386	5.311	9.8356	100	5	11.9403	5.3699	5.5967			
Description: type II cytoskeletal 7 OS Homo sapiens GN KRT7 PE 1 SV 3														
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool	
	2	721.907	2	1441.7983	1441.793	0.005371094	3.725288	61.3333	53.0113	137	149 (R)LPDIFEAQIAGLR(G)	30.61	PLGS Databank Search	
	2	610.8341	2	1219.6526	1219.6448	0.0078125	6.4055533	68.254	64.4997	188	198 (R)TAENEFVLK(K)	24.7	PLGS Databank Search	
	2	709.8701	2	1417.7246	1417.72	0.004638672	3.271924	65.2174	54.1568	215	226 (K)VDALNDEINFLR(T)	28.39	PLGS Databank Search	
	2	546.7923	2	1091.569	1091.561	0.00793457	7.2690125	56.1404	40.2093	287	296 (K)FETLQAAQAG(H)	19.27	PLGS Databank Search	
	2	593.8109	2	1185.6062	1185.5989	0.007324219	6.1776533	50.8772	24.4728	354	363 (K)QEELEALQRI(A)	22.02	PLGS Databank Search	
SSP 2509														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	2		60 sp P10809 CH60_HUMAN	61016	5.5503	9.8357	100	4	8.9005	3.6777	4.0263		25	
Description: kDa heat shock protein mitochondrial OS Homo sapiens GN HSPD1 PE 1 SV 2														
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Retention Time (min)	Query Tool
	2	752.8868	2	1503.7579	1503.749	0.008911133	5.9259443	53.3333	74.5803	206	218 (K)TLNDELEIEIGMK(F)		29.35	PLGS Databank Search
	2	617.3032	2	1232.5908	1232.5884	0.002441406	1.980715	72.4638	75.5546	406	417 (K)VGGSDEVVEVNEK(K)		16.91	PLGS Databank Search
	2	480.7607	2	959.5058	959.5036	0.002197266	2.2900023	72.549	115.3987	421	429 (R)VDALNATRI(A)		17.69	PLGS Databank Search
	2	842.9591	2	1683.9026	1683.8978	0.004760742	2.8272157	44.4444	114.1761	430	446 (R)AAVEEGIVLGGGCALLR(C)	Carbamidomethyl C (13)	27.9	PLGS Databank Search
	2	562.3041	3	1683.8888	1683.8978	-0.009033203	-5.3644605	36.3636	26.6871	430	446 (R)AAVEEGIVLGGGCALLR(C)	Carbamidomethyl C (13)	27.9	PLGS Databank Search
SSP 3301														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	2	ATP	sp P06576 ATPB_HUMAN	56524	5.0955	9.8357	100	4	10.586	6.1849	9.321		25	
Description: synthase subunit beta mitochondrial OS Homo sapiens GN ATP5B PE 1 SV 3														
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Retention Time (min)	Query Tool
	2	519.7918	2	1037.568	1037.569	-0.019920898	-18.235483	59.6491	107.1699	134	143 (K)IPVGPETLGR(I)		22.03	PLGS Databank Search
	2	737.4204	2	1472.8252	1472.8273	-0.002075195	-1.4089876	58.6667	23.8625	213	225 (K)YLVIELNNVAK(K)	Oxidation M (5)	31.36	PLGS Databank Search
	2	718.3793	2	1434.7429	1434.7467	-0.00378418	-2.6375246	60.4938	61.0572	311	324 (R)FQTAGSEVALLGR(I)		26.64	PLGS Databank Search
	2	994.5184	2	1987.0211	1987.026	-0.004882813	-2.4573472	53.1532	67.9976	388	406 (R)AIAELGYTPAVDPLDISTR(I)		29.25	PLGS Databank Search
SSP 3806														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	2		78 sp P11021 GRP78_HUMAN	72288	4.8748	9.8356	100	5	9.0214	1.5216	1.9284		20	
Description: kDa glucose regulated protein OS Homo sapiens GN HSPA5 PE 1 SV 2														
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Retention Time (min)	Query Tool
	2	715.85	2	1429.6943	1429.6938	4.89E-04	0.3415992	46.3768	25.3887	102	113 (R)WNPSPVQQDIK(F)		21.78	PLGS Databank Search
	2	768.9054	2	1535.7952	1535.7905	0.004638672	3.0203605	60.4938	79.9421	139	152 (K)TFARPEEISAMVLT(KM)		29.67	PLGS Databank Search
	2	665.3112	2	1328.6068	1328.6069	-1.22E-04	-0.09187843	66.6667	45.4201	327	336 (K)FEELNMLFR(S)	Oxidation M (6)	26.85	PLGS Databank Search
	2	730.8856	2	1459.7556	1459.7517	0.00390625	2.6759686	62.963	139.0804	354	367 (K)FDEIVLVGSTR(I)		26.4	PLGS Databank Search
	2	537.7818	2	1073.548	1073.5464	0.001586914	1.4781979	66.6667	147.1207	524	532 (K)ITTDGNLR(L)		17.28	PLGS Databank Search
SSP 4315														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	2	Protein	sp Q15084 PDIA6_HUMAN	48091	4.7615	9.8356	100	3	8.4091	3.4036	4.8502			
Description: disulfide isomerase A6 OS Homo sapiens GN PDIA6 PE 1 SV 1														
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool	
	2	693.8848	2	1385.754	1385.7513	0.002685547	1.3379718	66.6667	181.5525	119	132 (R)TGEAIVDAALSALR(Q)		31.29	PLGS Databank Search
	2	693.8841	2	1385.7526	1385.7513	0.001220703	0.8808962	54.321	75.4092	119	132 (R)TGEAIVDAALSALR(Q)		31.41	PLGS Databank Search
	2	698.8281	2	1395.6406	1395.6405	1.22E-04	0.08746544	56.5217	62.7468	161	172 (K)IDVLDLDSFDK(N)		26.2	PLGS Databank Search
	2	576.2579	2	1150.5001	1150.489	0.011108398	9.655372	60.3175	121.3447	246	256 (K)GESVVDYDGGRT(T)		18.14	PLGS Databank Search
	2	576.2549	2	1150.4941	1150.489	0.005126953	4.4563255	55.5556	45.7493	246	256 (K)GESVVDYDGGRT(T)		18.26	PLGS Databank Search
SSP 5104														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	2	Actin,	sp P06709 ACTB_HUMAN	41709	5.142	9.1425	50	11	25.0667	15.9678	26.2064		18.1818	6
Description: cytoplasmic 1 OS Homo sapiens GN ACTB PE 1 SV 1														
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Retention Time (min)	Query Tool
	2	488.7314	2	975.4472	975.441	0.00623	6.38233	47.3684	25.8068	19	28 (K)AGFAGDADAPR(A)		18.28	PLGS Databank Search
	2	599.7677	2	1197.5198	1197.5149	0.00488	4.07745	76.1905	68.5301	51	61 (K)DYSYVGEAAGSK(R)		17.11	PLGS Databank Search
	2	499.7475	2	997.4794	997.4791	0	0.24476	77.7778	163.9015	184	191 (R)DLTDVLMK(I)		27.29	PLGS Databank Search
	2	499.7472	2	997.47876	997.4791	0	-0.36714	55.5556	28.1325	184	191 (R)DLTDVLMK(I)		27.49	PLGS Databank Search
	2	507.7375	2	1013.45935	1013.4739	-0.01453	-14.33324	64.4444	110.3209	184	191 (R)DLTDVLMK(I)	Oxidation M (7)	24.83	PLGS Databank Search
	2	566.7739	2	1131.5322	1131.5195	0.01227	11.2197	42.1053	21.6452	197	206 (R)GYSFTTAE(R)		19.7	PLGS Databank Search
	2	566.7672	2	1131.5188	1131.5195	-0.001	-0.64729	68.4211	55.6962	197	206 (R)GYSFTTAE(R)		20.83	PLGS Databank Search
	2	566.7262	2	1131.4368	1131.5195	-0.08276	-73.14383	70.1754	244.1406	197	206 (R)GYSFTTAE(R)		20.6	PLGS Databank Search
	2	895.9587	2	1789.9017	1789.8846	0.01709	9.54801	56.9892	40.2347	239	254 (K)SYLVDPDGVITIGNER(F)		27.12	PLGS Databank Search
	2	389.1848	2	776.354	776.34875	0.00525	6.76117	75.7576	111.1564	285	290 (K)CDVDIR(K)	Carbamidomethyl C (1)	17.97	PLGS Databank Search
	2	581.3212	2	1160.6268	1160.6111	0.01575	13.56791	76.1905	234.7007	316	326 (K)EITALPSTMK(I)		22.5	PLGS Databank Search
	2	581.2773	2	1160.539	1160.6111	-0.07214	-62.15998	73.0159	207.1623	316	326 (K)EITALPSTMK(I)		22.67	PLGS Databank Search
	2	518.8332	2	1035.6508	1035.6439	0.00684	6.60066	19.6078	-8.6127	327	335 (K)KIAPPER(K)		24.53	PLGS Databank Search
	2	398.2333	2	794.451	794.465	-0.01404	-17.66996	61.5385	116.008	329	335 (K)IAPPER(K)		18.82	PLGS Databank Search
	2	758.8572	2	1515.6987	1515.6953	0.00342	2.25505	42.6667	41.368	360	372 (K)QYDESGPSIVHR(K)		19.24	PLGS Databank Search
	2	506.2262	3	1515.6552	1515.6953	-0.04016	-26.49684	77.3333	106.7073	360	372 (K)QYDESGPSIVHR(K)		19.24	PLGS Databank Search
SSP 5230														
OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error	Modified (%)	Missed Cleavages (%)	
	2	Annexin	sp P07355 ANXA2_HUMAN	38579	7.784	9.1424	50	2	6.1947	2.5099	2.9833			
Description: A2 OS Homo sapiens GN ANXA2 PE 1 SV 2														
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool	
	2	457.7685	2	913.52136	913.5233	-0.001953125	-2.1380134	56.8627	155.932	75	83 (R)NVPIVTSK(D)		19.44	PLGS Databank Search
	2	722.835	2	1443.6544	1443.6517	0.002685547	1.8602457	59.4203	37.4272	106	117 (R)FTSGEDYDER(V)		23.87	PLGS Databank Search
	2	531.7589	2	1061.8022	1061.4989	0.003295898	3.1049476	64.7059	151.4019	149	157 (R)QVSDDLTER(A)		18.12	PLGS Databank Search

SSP 6113

OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error		
	2 Heat	sp P04792 HSPB1_HUMAN	shock protein beta 1 OS Homo sapiens GN HSPB1 PE 1 SV 2	22768	5.9588	9.8356	100	3	17.0732	2.9634		4.0497	
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool
	2	582.319	2	1162.6223	1162.6134	0.008911133	7.664743	73.6842	146.0217	28	37 (R)LFDDQAFGLPR(L)	27.7	PLGS Databank Search
	2	582.3154	2	1162.6152	1162.6134	0.001831055	1.5749472	71.9298	80.0376	28	37 (R)LFDDQAFGLPR(L)	27.8	PLGS Databank Search
	2	595.3125	3	1782.9141	1782.9152	-0.001098633	-0.61620027	61.2903	22.4163	97	112 (R)VSLDYNHFAPDELTVK(T)	26.1	PLGS Databank Search
	2	459.252	2	916.4884	916.4866	0.001831055	1.9979068	70.5882	114.4933	115	123 (K)DGVVEITGK(H)	20.08	PLGS Databank Search

SSP 7123

OK	Accession	Entry	Description	mW (Da)	pI (pH)	PLGS Score	Probability (%)	Peptides	Coverage (%)	Mean Error	RMS Error		
	2 Growth	sp P62993 GRB2_HUMAN	factor receptor bound protein 2 OS Homo sapiens GN GRB2 PE 1 SV 1	25190	5.857	9.8357	100	2	7.8341	5.5098		5.6555	
OK	m/z	Charge	Peak mW	Peptide mW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Retention Time (min)	Query Tool
	2	548.7643	2	1095.513	1095.5083	0.004638672	4.2342644	42.1053	21.504	11	20 (K)ATADDELSFK(R)	21.9	PLGS Databank Search
	2	459.7588	2	917.50195	917.5082	-0.006225586	-6.7853193	64.1026	58.5613	143	149 (R)NQIFLR(D)	22.07	PLGS Databank Search