Hit 1

ACC	Charge	Peak mH	Particle mH	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Mods/Localizations	Protein	Query Tool
9VAL_SAV	2	1496,763	1496,763	+0,0000	+0,0000	86,9870	292,7287	1	14	VIGFRAAMVSYSYSLK	Oxidation M	0	De-novo
9VAL_SAV	2	1496,763	1496,763	+0,0000	+0,0000	86,9870	292,7287	1	14	VIGFRAAMVSYSYSLK	Oxidation M	0	De-novo
9VAL_SAV	2	1496,763	1496,763	-0,0001	-0,7700	92,5276	179,6919	1	14	VIGFCAMSVSYSYSLK	Carbamidomethyl C /	0 / 7	De-novo
7VAL_SATS	2	1410,6740	1410,6740	+0,0000	+0,0000	75,5333	205,2150	1	12	LEGIMLSFTSYR	Carbamidomethyl C	4	De-novo
7VAL_SATS	2	1410,6740	1410,6740	+0,0004	+0,1200	75,5333	205,2150	1	12	LEGIMLCFTSYR	Carbamidomethyl C	4	De-novo
7VAL_SATS	2	1410,6740	1410,6740	+0,0004	+0,1200	75,6667	152,7352	1	12	TEGIMLCFTSYR	Carbamidomethyl C	4	De-novo
8VAL_SAAA	2	1474,7172	1474,7172	+0,0000	+0,0000	93,1313	195,1147	1	14	SAATTAMSYSYSTLR	Carbamidomethyl C	5	De-novo
8VAL_SAAA	2	1474,7172	1474,7172	+0,0002	+0,5200	93,1313	195,1147	1	14	SAATTAMSYSYSTLR	Carbamidomethyl C	5	De-novo
8VAL_SAAA	2	1474,7172	1474,7172	+0,0002	+0,5200	94,8276	125,157	1	14	SAATCAMSYSYSTLR	Carbamidomethyl C	5	De-novo
9VAL_SATA	2	1796,8132	1796,8132	+0,0000	+0,0000	86,5714	0	1	16	GSLGSMMAVLPGAAMTGR			De-novo
9VAL_SATA	2	1796,8132	1796,8132	+0,0752	+41,9100	86,5714	109,4923	1	16	GSLGSMMAVLPGAAMTGR			De-novo
9VAL_SATA	2	1796,8132	1796,8054	+0,0782	+43,5400	66,4668	125,1974	1	17	WSLGTSMLPGAAMTGR			De-novo
9VAL_SAVA	2	1793,7866	1793,8311	+0,0445	+24,8100	66,4668	0	1	17	VSLGSLCSLPGAAMTGR	Deamidation N /	5 / 7	De-novo
9VAL_SAVA	2	1793,7866	1793,8311	+0,0445	+24,8100	66,4668	301,5174	1	17	VSLGSLCSLPGAAMTGR	Deamidation N /	5 / 7	De-novo
9VAL_SAVA	2	1793,7866	1793,8311	+0,0445	+24,8100	66,5161	361,6739	1	18	RSSVLCSLPGAAMTGR	Deamidation N /	2 / 9	De-novo
10VAL_SAVT	3	1276,6747	1276,5571	+0,0864	+67,7000	36,9815	346,3994	1	20	MSTSTSAVSGSLCSTSTSTSLCSTSTSTSLR	Deamidation N	2 / 4	De-novo
10VAL_SAVT	3	1276,6747	1276,5571	+0,0864	+67,7000	36,9815	346,3994	1	20	MSTSTSAVSGSLCSTSTSTSLCSTSTSTSLR	Deamidation N	2 / 4	De-novo
10VAL_SAVT	3	1276,6747	1276,5576	+0,0897	+70,4400	36,9815	346,3952	1	20	MSTSTSAVSGSLCSTSTSTSLCSTSTSTSLR	Deamidation N	2 / 4	De-novo
9VAL_SAVA	2	1327,6892	1327,6892	+0,0000	+0,0000	75,9667	273,2169	1	14	GSTCAMSYSYSTLR	Carbamidomethyl C	4	De-novo
9VAL_SAVA	2	1327,6892	1327,691	+0,0014	+1,1000	75,9667	273,2169	1	14	GSTCAMSYSYSTLR	Carbamidomethyl C /	4 / 6	De-novo
9VAL_SAVA	2	1327,6892	1327,6909	+0,0017	+1,3200	75,9877	275,9312	1	14	GSTCAMSYSYSTLR	Oxidation M	7	De-novo
9VAL_SAVA	2	1327,6892	1327,6909	+0,0017	+1,3200	75,9877	275,9312	1	14	GSTCAMSYSYSTLR	Carbamidomethyl C /	4	De-novo
9VAL_SAVA	2	1311,6942	1311,6942	+0,0000	+0,0000	93,5172	246,3558	1	14	GSTCAMSYSYSTLR	Carbamidomethyl C / /	4 / 11	De-novo
9VAL_SAVA	2	1311,6942	1311,6942	+0,0002	+0,1482	93,5172	246,3558	1	14	GSTCAMSYSYSTLR	Carbamidomethyl C	4	De-novo
9VAL_SAVA	2	1311,6942	1311,6942	+0,0002	+0,1482	70,1149	246,3554	1	14	GSTCAMSYSYSTLR	Carbamidomethyl C	4	De-novo
9VAL_SAVA	2	1311,6942	1311,6942	+0,0002	+0,1482	70,1149	246,3554	1	14	GSTCAMSYSYSTLR	Deamidation N /	4 / 11	De-novo
9VAL_SATS	2	1793,8231	1793,8311	+0,0003	+1,6414	56,5253	151,7314	1	17	VSSVCLSVLPGAAMTGR			De-novo
9VAL_SATS	2	1793,8231	1793,8311	+0,0003	+1,6414	52,5253	151,2944	1	17	VSSVCLSVLPGAAMTGR			De-novo
9VAL_SATS	2	1793,8231	1793,8311	+0,0003	+1,6414	56,5253	151,7314	1	17	VSSVCLSVLPGAAMTGR	Deamidation N	1	De-novo
8VL_STTR	2	1320,7403	1320,7401	+0,0001	+0,0918	66,6667	261,6508	1	14	QTSTRGALSTTR	Deamidation Q	1	De-novo
8VL_STTR	2	1320,7403	1320,7401	+0,0001	+0,0918	66,6667	276,147	1	13	TQSTRGALSTTR	Deamidation Q	2	De-novo
8VL_STTR	2	1320,7403	1320,7401	+0,0001	+0,0918	66,6667	291,127	1	14	KTQSTRGALSTTR			De-novo

MS2 [Spectrum Viewer](#)

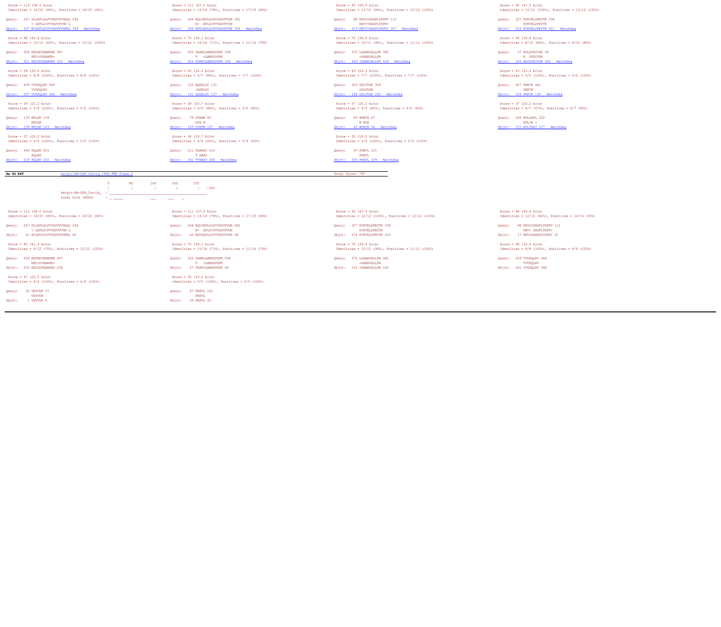
Hit 2 [Spectrum Viewer](#)

ACX	Charge	Mass_MH	Negative_MH	Tanimoto_CDK	Tanimoto_jaccard	Sumhex_Score	log_kimoto_score	Stereo	Name	Inchikey	Molecularformula	Molecularweight	Adduct	Compound_Source
2344.5600	2	2872.5120	2871.5042	-0.0000	-0.0000	-0.0000	-0.0000	1	24	BSQLWYYPPPSLLTBHSBSLLYYWB	C1H2N2O2S2	122.0132	[M+H]+	De-novo
2419.5600	2	2871.5120	2871.5042	-0.0492	-0.0492	-0.0492	31.4149	1	24	BSQLWYYPPPSLLTBHSBSLLYYWB	C1H2N2O2S2	122.0132	[M+H]+	De-novo
2494.5600	2	2870.5120	2869.5042	-0.0492	-0.0492	-0.0492	31.4149	1	24	BSQLWYYPPPSLLTBHSBSLLYYWB	C1H2N2O2S2	122.0132	[M+H]+	De-novo
599.7802	2	1197.2448	1197.2770	-0.0101	-0.0101	-0.0101	71.9208	1	12	QDYXYZCLGN	C6H8N2O2S2	204.0033	[M+H]+	De-novo
599.7802	2	1197.5648	1197.5770	-0.0101	-0.0101	-0.0101	71.9208	1	11	BAXRXYZCLGN	C6H8N2O2S2	204.0033	[M+H]+	De-novo
599.7802	2	1197.5648	1197.5770	-0.0101	-0.0101	-0.0101	71.9208	1	11	BAXRXYZCLGN	C6H8N2O2S2	204.0033	[M+H]+	De-novo
924.7878	2	1847.5610	1847.5851	-0.0001	-0.0001	-0.0001	75.7734	1	10	LAEYPPPYLN	C9H9N3O2	191.0659	[M+H]+	De-novo
924.7878	2	1847.5610	1847.5851	-0.0001	-0.0001	-0.0001	75.7734	1	10	LAEYPPPYLN	C9H9N3O2	191.0659	[M+H]+	De-novo
1224.897	2	2447.7940	2447.8701	-0.1138	-0.1138	-0.1138	192.785	1	16	YCLPXLEEPTPQNWPJPKTDTXAEPYZLFTBPE	C8H8N2O2S2	228.0033	Deamidation Q / Oxidation	6 / 1 [M-H]-

Spot 3

ACC	Charge	Mass OM	Negative OM	Delta ppm	Delta ppm	Ladder score	Score	log Likelihood	Start	End	Sequence	Modification	Rdbs	Query Seq.
[illegible]	2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	14	[illegible]		1	De-novo
845.2734	2	1296.7332	1296.7288	0.2954	4.4170	52	132.1957		1	13	QYSYHHCPCYCHH		1	De-novo
845.2734	2	1296.7332	1296.7288	0.2954	4.4170	52	132.1957		1	13	QYSYHHCPCYCHH	Deamidation Q	1	De-novo
845.2734	2	1296.7332	1296.7293	0.2957	4.0399	54.4897	162.2117		1	12	YSYHHCPCYCHH			De-novo
561.8422	2	1123.6688	1123.6713	-0.6925	-2.2462	98.234	96.6193		1	11	LSHHPCYLLM			De-novo
561.8422	2	1123.6688	1123.6713	-0.6925	-2.2462	98.234	96.6193		1	11	LSHHPCYLLM			De-novo
561.8422	2	1123.6688	1123.6713	-0.6925	-2.2462	98.234	91.9519		1	11	HLHHPCYLLM			De-novo
864.5403	2	1731.8750	1731.9132	-0.2390	-221.9549	51.4919	118.1949		1	14	FLWFTFTCQTQLQ			De-novo
864.5403	2	1731.8750	1731.9132	-0.2390	-221.9549	51.4919	118.1949		1	14	FLWFTFTCQTQLQ			De-novo
864.5403	2	1731.8750	1731.9132	-0.2390	-221.9549	51.4919	114.1944		1	14	LWFTFTCQTQLQ			De-novo
749.4230	2	1495.8432	1495.8407	-0.0327	-1.8272	63.2599	91.1914		1	14	SYLLHCSCFCYLQ			De-novo
749.4230	2	1495.8432	1495.8407	-0.0327	-1.8272	63.2599	91.1914		1	14	YLLHCSCFCYLQ			De-novo
749.4230	2	1495.8432	1495.8407	-0.0327	-1.8272	63.2599	84.9667		1	14	YLLHCSCFCYLQ			De-novo
864.5895	2	1496.7224	1496.725	-0.0914	-0.9571	62.9858	261.1572		1	14	TSYLHTRTHSYHKTK			De-novo
864.5895	2	1496.7224	1496.725	-0.0914	-0.9571	62.9858	261.1572	Carbamidomethyl C /	11 / 13	14	TSYLHTRTHSYHKTK			De-novo
865.7342	2	1329.6928	1329.5295	-0.1397	-27.4218	63.4921	75.9918	Carbamidomethyl C /	11 / 13	14	TRHSYHSWHK		4	De-novo
865.7342	2	1329.6928	1329.5295	-0.1397	-27.4218	63.4921	75.9918	Deamidation N	4	14	TRHSYHSWHK			De-novo
865.7342	2	1329.6928	1329.5295	-0.1397	-27.4218	63.4921	74.9322		1	11	TRHSYHSWHK			De-novo
865.7342	2	1329.6928	1329.5295	-0.1397	-27.4218	63.4921	74.9322	Deamidation N	1	11	TRHSYHSWHK			De-novo
473.2326	2	1346.6856	1346.6875	-0.2011	-1.5193	59.4203	131.6422		1	12	QLFHEGCHLGGR			De-novo
473.211	2	904.4988	904.4988	-0.0824	-48.5173	50.9824	112.1973		4	12	ELGHFHCGR			De-novo
561.3403	2	1146.6750	1146.6764	-0.2014	-1.2220	51.1728	142.2588	Deamidation N	1	12	SLLLLSLTNNFR	Deamidation N	9	De-novo
561.3403	2	1146.6750	1146.6764	-0.2014	-1.2220	51.1728	142.2588	Deamidation N	1	12	SLLLLSLTNNFR	Deamidation N	9	De-novo
561.3403	2	1146.6750	1146.6764	-0.2014	-1.2220	51.1728	141.1589	Deamidation N	1	12	ASLLLSLTNNFR	Deamidation N	9	De-novo

NCBI [illegible] Score Scale (%)



Ms 86 EGF [illegible] Score Scale (%)

qcl	Charge	Peak AR	Begin/End AR	Delta rtx	Delta ppm	Ladder score	log Likelihood	Start	End	Sequence	Modification	Score	Rank
705.3138	2	1414.9114	1414/1417	-0.0014	-1.0010	1.7333	-10.7333	1	12	GGGGGGGGGGGG	Deamidation Q	1	1
705.3138	2	1414.9114	1414/1417	-0.0014	-1.0010	1.7333	-10.7333	1	12	GGGGGGGGGGGG	Deamidation Q	1	2
705.3138	2	1414.9114	1414/1417	-0.0014	-1.0010	1.7333	-10.7333	1	12	GGGGGGGGGGGG	Deamidation Q	1	3
702.8398	2	1403.8440	1403/1404	0.0051	3.6158	3.1718	-10.8408	1	12	GGQGGGGGGGGN	Deamidation Q	1	1
785.3808	2	1516.7050	1516/1522	-0.0144	-9.6292	1.0000	111.0000	1	13	LQPWVRDEDGLK	Deamidation Q	0	1
785.3808	2	1516.7050	1516/1522	-0.0144	-9.6292	1.0000	111.0000	1	13	LQPWVRDEDGLK	Deamidation Q	0 / 0	2
785.3808	2	1516.7050	1516/1522	-0.0144	-9.6292	1.0000	111.0000	1	13	LQPWVRDEDGLK	Deamidation Q	0 / 0	3
813.8124	2	1315.9050	1315/4058	0.0058	4.7205	66.6667	141.4758	1	12	NAAGGGCNEPR	Deamidation Q	1	1
813.8124	2	1315.9050	1315/4058	0.0058	4.7205	66.6667	141.4758	1	12	NAAGGGCNEPR	Deamidation Q /	1 / 10	2
729.9286	2	1471.8514	1471/1477	0.0059	4.0049	59.3500	216.6552	1	14	YSYTGLEPSLLL	Deamidation Q		1
729.9286	2	1471.8514	1471/1477	0.0059	4.0049	59.7983	216.6142	1	14	YSYTGLEPSLLL			
729.8723	2	1471.7230	1471/1245	0.0043	3.5498	66.4008	226.0310	1	14	NSSAGLYNEPPR	Deamidation Q		1
729.8723	2	1471.7230	1471/1245	0.0043	3.5498	66.4008	226.0310	1	14	NSSAGLYNEPPR	Deamidation Q		2
729.8723	2	1471.7230	1471/1245	0.0043	3.5498	58.6597	215.6952	1	14	NSSAGLYNEPPR	Deamidation Q		3
414.8254	2	1151.9922	1151/1403	0.0047	3.7947	51.8518	191.7552	1	14	GSSHSGLSNNTR	Deamidation Q		1
414.8254	2	1151.9922	1151/1403	0.0047	3.7947	51.8518	191.7552	1	14	GSSHSGLSNNTR	Deamidation Q		2
478.2192	2	874.4818	874/4818	0.0010	1.1135	61.0323	71.1353	1	8	LEEAGCTR			
478.2192	2	874.4818	874/4818	0.0010	1.1135	61.0323	71.1353	1	8	LEEAGCTR			
841.4090	2	1481.8618	1481/1504	0.1049	5.2748	61.7284	147.1737	1	14	GAYLLPNYYSGAK			
841.4090	2	1481.8618	1481/1504	0.1049	5.2748	61.7284	147.1737	1	14	GAYLLPNYYSGAK			
841.4090	2	1481.8618	1481/1504	0.1049	5.2748	61.7284	147.1737	1	14	GAYLLPNYYSGAK			
815.5263	2	1344.6773	1344/4451	-0.0151	-10.5165	66.1135	81.0754	1	12	YTSTYLAAGFL			
815.5263	2	1344.6773	1344/4451	-0.0151	-10.5165	66.1135	81.0754	1	12	YTSTYLAAGFL	Deamidation Q	10	
815.5263	2	1344.6773	1344/4451	-0.0151	-10.5165	66.1135	94.7	1	12	YTSTYLAAGFL	Deamidation Q	9	
815.5263	2	1344.6773	1344/4451	-0.0151	-10.5165	66.1135	91.7893	1	12	YTSTYLAAGFL	Deamidation Q		4

NCBI gi|169234578|dbj|BAC4 Total Score: 1.5

Score = 83 (43.1 bits)
Identities = 10/12 (83%), Positives = 11/12 (92%)

Query: 39 DNQLGVNNQGFR 50
D+QLGVNNQGFR
Sbjct: 96 DHQLGVNNQGFR 107 Mm10356

Score = 42 (21.8 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 57 NDGDLLQ 63
NDGDLLQ
Sbjct: 102 NDGDLLQ 108 Mm10356

Score = 42 (21.8 bits)
Identities = 10/14 (71%), Positives = 13/14 (92%)

Query: 41 PLQPWVRDEDGLK 54
P+QPWV+DEDGLK LP
Sbjct: 84 PMQPWVKDEDGLK 96 Mm10356

Score = 34 (17.7 bits)
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 270 YPGDRL 275
YPGDRL
Sbjct: 93 YPGDRL 98 Mm10356

Score = 50 (25.2 bits)
Identities = 9/10 (90%), Positives = 9/10 (90%)

Query: 160 AAMGLNQLK 169
AAMGLN K
Sbjct: 476 AAMGLNSMK 485 Mm10356

Score = 42 (21.7 bits)
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 126 GNPPPL 131
GNPPPL
Sbjct: 116 GNPPPL 121 Mm10356

Score = 34 (17.5 bits)
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 14 QPHDD 18
QPHDD
Sbjct: 14 QPHDD 18 Mm10356

Sp 04 EDC tanqir|Mr0GR_Dating_ Total Score: 40

Score = 107 (55.6 bits)
Identities = 12/14 (86%), Positives = 14/14 (100%)

Query: 228 DAPLLPNDTRDAM 241
DAPLLPNDTRDAM
Sbjct: 119 DAPLLPNDTRDAM 132

Score = 103 (53.5 bits)
Identities = 12/13 (92%), Positives = 13/13 (100%)

Query: 244 PLLPNDTRDAMDD 256
PLLPNDTRDAMDD
Sbjct: 121 PLLPNDTRDAMDD 133

Score = 79 (39.6 bits)
Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 203 DAMDAPLLPNE 214
D DAPLLPNE
Sbjct: 114 DRDDAPLLPNE 127

Hpr: 5

ACC	Charge	Mass OM	Negative OM	Delta ppm	Delta ppm	Sadduc Score	Log Likelihood	Start	End	Sequence	Modification	Rdbe	Query Desc.
464.7312	2	929.4623	929.4550	+0.0786	+84.5	0.0000	-Infinity	1	8	YSIYRGDF		4	De-novo
463.7312	2	925.4470	925.4508	-0.0196	-42.0	66.6667	-141.4194	1	8	YTSIYGDF		4	De-novo
505.2943	2	1008.5886	1008.5828	+0.0575	+57.0	66.6667	-170.4259	1	8	YSYRYRDF	Deamidation Q	6	De-novo
505.2943	2	1008.5132	1008.5128	+0.0392	+3.9	75.549	-174.6519	1	8	YTYRYRDF	Deamidation N	6	De-novo
505.2943	2	1008.5132	1008.5128	+0.0392	+3.9	75.4786	-172.7477	1	8	YRYRYRDF		6	De-novo
505.2943	2	1008.5132	1008.5128	+0.0392	+3.9	75.4786	-172.7477	1	8	YRYRYRDF		6	De-novo
451.8203	2	1355.6410	1355.6416	-0.0054	-4.0229	66.6667	-254.6707	1	11	YRLAYRYLQK	Deamidation N	2 / 7	De-novo
451.8203	2	1355.6410	1355.6416	-0.0054	-4.0229	66.6667	-255.6759	1	11	YRLAYRYLQK	Deamidation N	2 / 7	De-novo
451.8203	2	1355.6410	1355.6416	-0.0054	-4.0229	66.6667	-255.6759	1	11	YRLAYRYLQK	Deamidation Q	2 / 7	De-novo
836.4137	2	1674.8030	1674.8077	-0.0512	-30.7268	83.7616	282.1319	1	14	MLYRLRAILCLGAMPR	Oxidation M /	7 / 7 / 7	De-novo
836.4137	2	1674.8030	1674.8077	-0.0512	-30.7268	83.7616	282.1319	1	14	MLYRLRAILCLGAMPR	Oxidation M /	7 / 7 / 7	De-novo
836.4137	2	1674.8030	1674.8077	-0.0512	-30.7268	83.7616	282.1319	1	14	MLYRLRAILCLGAMPR	Oxidation M /	7 / 7 / 7	De-novo
792.9056	2	1583.7956	1583.8156	-0.1284	-126.2601	66.6667	221.2448	1	14	MLYRLRAILCLYGLPR	Oxidation M / Deamidation	2 / 14	De-novo
792.9056	2	1583.7956	1583.8156	-0.1284	-126.2601	66.6667	221.2448	1	14	MLYRLRAILCLYGLPR		2 / 14	De-novo
984.8555	2	1171.4954	1171.4968	-0.0552	-0.8739	51.785	55.5972	1	11	LAQLCYRALF			De-novo
984.8555	2	1171.4954	1171.4968	-0.0552	-0.8739	51.785	55.5972	1	11	LAQLCYRALF			De-novo
984.8555	2	1171.4954	1171.4968	-0.0552	-0.8739	66.2503	76.117	1	11	LAQFCYRALF			De-novo
763.7122	3	2226.1132	2226.1200	-0.0197	-7.5122	65.9897	251.2969	1	20	TRYLRNAAPSYCSYRQLK	Deamidation Q /	5 / 13	De-novo
763.7122	3	2226.1132	2226.1200	-0.0197	-7.5122	65.9897	251.2969	1	20	TRYLRNAAPSYCSYRQLK	Deamidation Q /		De-novo
1171.6318	2	2351.2480	2351.2519	-0.0349	-12.0924	56.5995	168.6318	1	21	YLARYSLCLSLRYLSRTYQRW	Deamidation Q /	3 / 16	De-novo
1171.6318	2	2351.2480	2351.2519	-0.0349	-12.0924	56.5995	165.422	1	21	YLARYSLCLSLRYLSRTYERW	Deamidation Q /	3 / 9	De-novo
894.4406	2	1786.8158	1786.8197	-0.0341	-19.1041	66.6667	225.5564	1	14	YSYYLRLTSRTRFLQ	Deamidation Q	7 / 13	De-novo
894.4406	2	1786.8158	1786.8197	-0.0341	-19.1041	66.6667	225.5564	1	14	YSYYLRLTSRTRFLQ	Deamidation Q	7 / 13	De-novo
894.4406	2	1786.8158	1786.8197	-0.0341	-19.1041	66.6667	224.2473	1	14	YSYYLRLTSRTRFLQ	Deamidation Q	7	De-novo
451.8271	2	1355.6396	1355.6416	-0.0053	-3.8529	66.6667	255.1202	1	14	AFYRDERAFYAYAAKRF	Deamidation N	2	De-novo
451.8271	2	1355.6396	1355.6416	-0.0053	-3.8529	66.6667	65.5102	1	14	AFYRDERAFYAYAARRF	Deamidation N	2	De-novo
451.8271	2	1355.6396	1355.6416	-0.0144	-8.6453	66.6667	65.545	1	14	AFYRDERAFYAYAARRF		2	De-novo
1171.6318	2	2351.2480	2351.2519	-0.0349	-12.0924	56.5995	165.422	1	21	YLARYSLCLSLRYLSRTYERW	Deamidation Q	3	De-novo
785.4210	2	2355.2440	2355.2519	-0.0394	-13.7344	56.5995	415.5219	1	21	YLSRWSLCLSLRYLSRTYERW	Deamidation Q	5	De-novo
785.4210	2	2355.2440	2355.2519	-0.0394	-13.7344	56.5995	415.214	1	21	TRRLYRLLSLRYLSRTYERW	Deamidation Q	3	De-novo

MSms [illegible]

Extra/Fighes	None

Ex RS ESF	Sample-SM-DLW Delta 1ppm PMF Score 0	Total Score: 518

ACC	Change	Peak QM	Negative QM	Delta chi	Delta ggm	Leader score	log Likelihood	Start	Gap	Sequence	Mode/Confidence	Joins	Query Seq.
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	1	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	10	[illegible]	Deadbolton M /	2	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	1	[illegible]	Deadbolton M /	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	4	[illegible]	Deadbolton Q	4	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	4	[illegible]	Deadbolton Q	4	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	1	[illegible]	Deadbolton M	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	11	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	11	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	12	[illegible]	Deadbolton N	7	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	11	[illegible]	Deadbolton Q	3	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	11	[illegible]	Deadbolton M /	2 / 3	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	14	[illegible]	Deadbolton M /	2 / 5	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	17	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	17	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	17	[illegible]	Deadbolton Q	13	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	15	[illegible]	Oscillation M /	1 / 5 / 13	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	15	[illegible]	Oscillation M /	1 / 5 / 13	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	14	[illegible]	Oscillation M /	1 / 7 / 12	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	16	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	16	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	14	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	16	[illegible]	Deadbolton Q	18	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	16	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	16	[illegible]	Cochonderbolton Q /	1 / 2	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	16	[illegible]	Deadbolton N	5	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	11	[illegible]	Deadbolton N	7	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	11	[illegible]	Deadbolton N	7	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	11	[illegible]	Deadbolton N	7	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	11	[illegible]	Deadbolton Q	3	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	10	[illegible]	Cochonderbolton Q /	4 / 8	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	10	[illegible]	Cochonderbolton Q /	4 / 9	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	10	[illegible]	Cochonderbolton Q /	4	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	10	[illegible]	Deadbolton Q	8	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	10	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	22	[illegible]	Deadbolton N	1	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	22	[illegible]	Deadbolton N	1	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	22	[illegible]	Deadbolton N	1	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	14	[illegible]	Deadbolton Q	7 / 13	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	16	[illegible]	Deadbolton Q	5	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	16	[illegible]	Deadbolton Q	5	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	16	[illegible]	Deadbolton Q	5	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	4	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	16	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	16	[illegible]	[illegible]	[illegible]	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	22	[illegible]	Deadbolton Q	1	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	22	[illegible]	Deadbolton Q	1	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	22	[illegible]	Deadbolton Q	1	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	15	[illegible]	Cochonderbolton Q /	3 / 8	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	15	[illegible]	Cochonderbolton Q /	3 / 8	De-novo
[illegible]	I	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	15	[illegible]	Cochonderbolton Q /	3 / 8	De-novo

NEW: [illegible] Score: [illegible]

Interfaces [illegible] Score: [illegible]

Ex NS EGF [illegible] Score: [illegible]

ACA	Charge	Mass MH	Negative MH	Delta ppm	Delta Spec	Sample Score	Log Likelihood	Start	End	Sequence	Modification	Rank	Query Scan
[illegible]	2	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	10	[illegible]		[illegible]	[illegible]
[illegible]	2	[illegible]	[illegible]	-0.2430	-83.9977	32.2752	[illegible]	1	12	MAGGALSRGGGAQFMRSYVRNSLGSLSSLRNA		13	De-novo
[illegible]	2	[illegible]	[illegible]	-0.2430	-83.9977	32.2752	[illegible]	1	12	MAGGALSRGGGAQFMRSYVRNSLGSLSSLRNA	Deamidation Q	14	De-novo
[illegible]	2	[illegible]	[illegible]	-0.2053	-0.2268	62.7601	[illegible]	1	4	ASFFMGLY		1	De-novo
[illegible]	2	[illegible]	[illegible]	-0.2053	-0.2268	62.7601	[illegible]	1	4	ASFFMGLY	Deamidation Q	7	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1930	-0.2131	78.1223	[illegible]	1	4	YYYYYLEN		1	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1930	-0.2131	78.1223	[illegible]	1	4	YYYYYLEN		4	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1930	-0.2131	78.1223	[illegible]	1	4	YYYYYLEN		7	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1930	-0.2131	78.1223	[illegible]	1	4	YYYYYLEN		10	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1494	-26.9699	73.5133	[illegible]	1	11	AFMGLAEEFKD		1	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1494	-26.9699	73.5133	[illegible]	1	11	MFGALAEEFKD		2	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1494	-26.9699	73.5133	[illegible]	1	11	MFGALAEEFKD		3	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1244	-112.7202	98.254	[illegible]	1	11	GYSPRLSYIGR	Oxidation M	1	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1244	-112.7202	98.254	[illegible]	1	11	GYSPRLSYIGR	Deamidation Q / Oxidation	1 / 9	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1244	-112.7202	98.254	[illegible]	1	11	GYSPRLSYIGR	Deamidation Q	2 / 9	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1052	-16.7717	31.8019	[illegible]	1	14	SEYSRYTLTRNVVTSSEE	Deamidation N	6	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1052	-16.7717	31.8019	[illegible]	1	14	SEYSRYTLTRNVVTSSEE	Deamidation N	9	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1052	-16.7717	31.8019	[illegible]	1	14	SEYSRYTLTRNVVTSSEE	Deamidation N	10	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1033	-131.9895	45.9659	[illegible]	1	14	RRFQQRRRDYLAATAA	Deamidation R	1	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1033	-131.9895	45.9659	[illegible]	1	14	RRFQQRRRDYLAATAA	Deamidation R	2 / 9	De-novo
[illegible]	2	[illegible]	[illegible]	-0.1033	-131.9895	45.9659	[illegible]	1	14	RRFQQRRRDYLAATAA	Deamidation R	7 / 9	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0897	-47.1133	71.4206	[illegible]	1	11	ELFYFGLLLR		1	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0897	-47.1133	71.4206	[illegible]	1	11	LEFYFGLLLR		2	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0897	-47.1133	71.4206	[illegible]	1	11	LEFYFGLLLR		3	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0624	-32.5654	50.4065	[illegible]	1	21	RGGSFGGFLRGVWGFFRGQ	Deamidation R	14	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0624	-32.5654	50.4065	[illegible]	1	21	RGGSFGGFLRGVWGFFRGQ		2	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0624	-32.5654	50.4065	[illegible]	1	21	RGGSFGGFLRGVWGFFRGQ		3	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0219	-111.1269	44.144	[illegible]	1	14	RNAQGMRYDFFRQLDFR		1	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0197	-12.1652	49.5405	[illegible]	1	19	RNAQGMRYDFFRQLDFR		5	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0044	-17.4199	62.2222	[illegible]	1	23	ERSGNEGFSYRVLTYFFFQED	Deamidation R	5 / 12	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0044	-17.4199	62.2222	[illegible]	1	23	ERSGNEGFSYRVLTYFFFQED	Deamidation R /	5 / 23	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0044	-17.4199	62.2222	[illegible]	1	23	ERSGNEGFSYRVLTYFFFQED	Deamidation R	5 / 23	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0149	-13.3234	98.254	[illegible]	1	11	YRAEFFNLLR		1	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0149	-13.3234	98.254	[illegible]	1	11	YRAEFFNLLR	Deamidation Q	9	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0149	-13.3234	98.254	[illegible]	1	11	YRAEFFNLLR		10	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0075	4.8017	73.6667	[illegible]	1	13	GLFYAEFFNLLR		1	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0075	4.8017	73.6667	[illegible]	1	13	GLFYAEFFNLLR		2	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0075	4.8017	73.6667	[illegible]	1	13	GLFYAEFFNLLR		3	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0075	4.8017	73.6667	[illegible]	1	13	AYYAEFFNLLR		1	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0075	4.8017	73.6667	[illegible]	1	13	AYYAEFFNLLR		2	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0075	4.8017	73.6667	[illegible]	1	13	AYYAEFFNLLR		3	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0014	0.8940	56.4907	[illegible]	1	14	SRYTLTRNVVTSSEE	Deamidation N	7	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0014	0.8940	56.4907	[illegible]	1	14	SRYTLTRNVVTSSEE	Deamidation N	8	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0075	4.8017	73.6667	[illegible]	1	13	LLFYAEFFNLLR		1	De-novo
[illegible]	2	[illegible]	[illegible]	-0.0075	4.8017	73.6667	[illegible]	1	13	LLFYAEFFNLLR		2	De-novo

NCBI [illegible] Total Score: 1.76

Scorpion [illegible] Total Score: 87

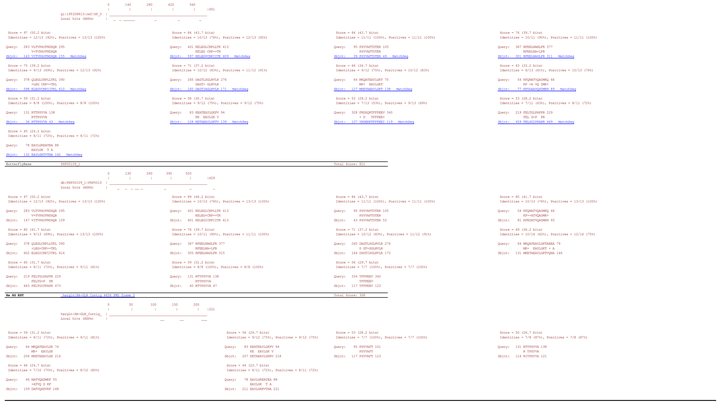
Ex RX EDF - **Sarcoplasmic Calcium-ATPase Isoform 1** Total Score: 444

Spec 8

m/z	Charge	Peak MH	Peptide MH	Delta ppm	Delta Spec	Sadder Score	Log Likelihood	Start	End	Sequence	Modifications	Rate	Query Scan
1511.8665	2	1441.8779	1441.8967	-0.6973	-0.0107	56,290	-71,1767	1	14	DDPGPPLPVNNEEGEP		0.0000	0e+scns
1511.8665	2	1441.8779	1441.8967	-0.6973	-0.0107	56,290	-71,1767	1	14	DDPGPPLPVNNEEGEP		0.0000	0e+scns
635.7872	2	1269.5580	1269.5947	-0.2941	-0.2108	66,6667	141,9974	1	11	EFPATFQLEWE	Deamidation @ 7 / Oxidation 3 / 10	0.0000	0e+scns
635.7872	2	1269.5580	1269.5947	-0.2941	-0.2108	66,6667	144,9955	1	11	EFPATFQLEWE	Deamidation @ 7 / Oxidation 3 / 10	0.0000	0e+scns
635.7872	2	1269.5580	1269.5947	-0.2941	-0.2108	66,6667	141,9974	1	11	EFPATFQLEWE	Deamidation @ 7 / 3 / 10	0.0000	0e+scns
635.7872	2	1269.5580	1269.5947	-0.2941	-0.2108	66,6667	144,9955	1	11	EFPATFQLEWE	Deamidation @ 7 / 3 / 10	0.0000	0e+scns
851.2486	2	981.4814	981.4814	-0.0000	-0.0245	56,902	126,0327	1	9	TAEAVCLLK		0.0000	0e+scns
851.2486	2	981.4814	981.4814	-0.0001	-0.0775	55,9834	125,4317	1	9	EATAVCLLK		0.0000	0e+scns
851.2486	2	981.4814	981.4814	-0.0001	-0.0775	55,9834	125,4317	1	9	EATAVCLLK		0.0000	0e+scns
761.6128	2	1481.8560	1481.7138	0.1862	56,1387	56,6667	271,6557	1	13	FYYYYYNTNTEYR	Deamidation @ 10	12	0e+scns
761.6128	2	1481.8560	1481.7138	0.1862	56,1387	56,6667	272,5162	1	13	FYYYYYNTNTEYR	Deamidation @ 12	12	0e+scns
761.6128	2	1481.8560	1481.7138	0.1862	56,1387	56,6667	271,6557	1	13	FYYYYYNTNTEYR	Deamidation @ 10 / 12	12	0e+scns
761.6128	2	1481.8560	1481.7138	0.1862	56,1387	56,6667	272,5162	1	13	FYYYYYNTNTEYR	Deamidation @ 10 / 12	12	0e+scns
764.3581	2	1496.7512	1496.656	0.1070	4,4923	66,6667	112,2217	1	13	TTYYYYNTNERYR	Deamidation @ 4 / 9 / 11	0.0000	0e+scns
764.3581	2	1496.7512	1496.656	0.1070	4,4923	66,6667	111,1719	1	13	TTYYYYNTNERYR	Deamidation @ 4	9	0e+scns
764.3581	2	1496.7512	1496.656	0.1070	4,4923	66,6667	112,2217	1	13	TTYYYYNTNERYR	Deamidation @ 9		0e+scns
596.5187	2	1190.6238	1190.6656	-0.2148	-14,1202	55,7196	215,5143	1	12	EQLEEEQEAVFR	Deamidation @ 1	1	0e+scns
596.5187	2	1190.6238	1190.6656	-0.2148	-14,1202	55,7196	215,9959	1	12	EQLEEEQEAVFR		1	0e+scns
596.5187	2	1190.6238	1190.6656	-0.2148	-14,1202	55,7196	215,5143	1	12	EQLEEEQEAVFR		1	0e+scns
596.5187	2	1190.6238	1190.6656	-0.2148	-14,1202	55,7196	215,9959	1	12	EQLEEEQEAVFR		1	0e+scns
596.5187	2	1190.6618	1190.6553	0.0545	5,6218	66,6667	241,5518	1	11	EELTELEAVFR		1	0e+scns
596.5187	2	1190.6618	1190.6553	0.0545	5,6218	66,6667	241,5518	1	11	EELTELEAVFR		1	0e+scns
596.5187	2	1190.9618	1190.9552	0.0556	5,4953	63,4921	240,9993	1	11	QETLTELEAVFR	Deamidation @ 1	1	0e+scns
596.5187	2	1190.9618	1190.9552	0.0556	5,4953	63,4921	241,4809	1	11	QETLTELEAVFR	Deamidation @ 1	1	0e+scns
808.3412	2	1214.6668	1214.6619	0.2043	4,2143	66,7734	121,6959	1	10	AEETLELEFLK	Deamidation @ 1	1	0e+scns
808.3412	2	1214.6668	1214.6619	0.2043	4,2143	66,7734	121,152	1	10	AEETLELEFLK		1	0e+scns
1511.8245	2	2022.2154	2022.217	-0.0794	0,1848	56,7568	241,5212	1	18	GAAPTFLTTTPNTPNTQQK		0.0000	0e+scns
1511.8245	2	2022.2154	2022.217	-0.0794	0,1848	56,7568	241,5212	1	18	GAAPTFLTTTPNTPNTQQK	Deamidation @ 10	10	0e+scns
1511.8245	2	2022.2154	2022.217	-0.0794	0,1848	56,7568	239,7257	1	18	GAAPTFLTTTPNTPNTQQK			0e+scns
1511.8245	2	2022.2154	2022.217	-0.0794	0,1848	56,7568	241,5212	1	18	GAAPTFLTTTPNTPNTQQK			0e+scns
927.5128	2	1352.8596	1352.8386	0.2013	5,7742	63,1379	86,9662	1	14	FEQLEMRLCR	Deamidation @ 5	0	0e+scns
927.5128	2	1352.8596	1352.8386	0.2013	5,7742	63,1379	87,369	1	14	FEQLEMRLCR	Deamidation @ 2 / 8	0	0e+scns
927.5128	2	1352.8596	1352.8386	0.2013	5,7742	63,1379	86,9662	1	14	FEQLEMRLCR	Deamidation @ 2 / 5	0	0e+scns
855.488	2	1385.7224	1385.7215	-0.0651	-1,5329	66,8088	275,8874	1	12	GLEELCNPLLCR	Deamidation @ 2	1 / 6	0e+scns
855.488	2	1385.7224	1385.7215	-0.0651	-1,5329	63,7481	276,373	1	12	GLEELCNPLLCR	Carbamidomethyl C	6	0e+scns
561.786	2	1085.5514	1085.4994	0.1138	105,2265	66,6667	195,7555	1	10	GAPPMEEGE	Deamidation @ 7	7 / 8	0e+scns
561.786	2	1085.5514	1085.4994	0.1138	105,2265	66,6667	195,7555	1	10	GAPPMEEGE	Deamidation @ 7 / Oxidation	3 / 8	0e+scns

MS2: [illegible]

Total Scans: 1[illegible]



Distillate 1[illegible]

Total Scans: 1[illegible]

Sa_Ba_RKP

Total Scans: 1[illegible]

m/z	Charge	Peak MH	Neutral MH	Delta ppm	Delta Amu	Sample Score	Log Likelihood	Start	End	Sequence	Modifications	Rank	Query Scan
534.7558	2	1067.4842	1067.4769	-0.2737	-0.2920	56.8423	-52.2127	1	10	PYYYYYYYYR	Deamidation N /	1	De-novo
534.7558	2	1067.4842	1067.4769	-0.2737	-0.2920	56.8423	-52.7477	1	10	PYYYYYYYYR	Deamidation N /	2	De-novo
613.2773	2	836.5340	836.5267	-0.8729	-0.7300	55.7170	-51.1112	1	7	LLQYFYR	Deamidation N / Deamidation	1 /	De-novo
613.2773	2	836.5340	836.512	0.6270	0.5170	55.7170	-51.1112	1	7	LLQYFYR			De-novo
613.2773	2	836.5340	836.5267	-0.8729	-0.7300	55.7170	-51.1112	1	7	LLQYFYR			De-novo
501.7745	2	1115.5274	1115.5201	-0.6513	-1.1375	56.6887	-54.7514	1	10	YSFYNMYMYQR			De-novo
501.7745	2	1115.5274	1115.526	0.0514	0.0469	56.7953	-55.1512	1	11	YSFYNMYMYQR			De-novo
501.7745	2	1115.5274	1115.5201	-0.6513	-1.1375	56.6887	-55.1512	1	11	YSFYNMYMYQR			De-novo
984.2885	2	1176.5614	1176.5538	0.1859	0.7635	56.4013	-121.1522	1	10	YYGGFGGYYR	Deamidation N	5	De-novo
984.2885	2	1176.5614	1176.5557	0.4957	0.2909	56.9413	-121.157	1	11	YYGGFGGYYR	Deamidation N	5	De-novo
984.2885	2	1176.5614	1176.5538	0.1859	0.7635	56.4013	-121.1522	1	11	YYGGFGGYYR	Deamidation N	5	De-novo
774.3514	2	1446.6876	1446.6858	-0.0512	-0.8345	57.4563	419.6738	1	14	LGNGNGNLYYYR	Deamidation N	3 / 8	De-novo
774.3514	2	1446.6876	1446.6888	-0.0512	-0.8345	57.4563	418.1937	1	14	LGNGNGNLYYYR	Deamidation N	2 / 9	De-novo
674.8204	2	1347.6262	1347.6186	-0.5224	-0.7037	56.2500	215.7414	1	14	NNGGGGGQLFLYR	Deamidation N	2	De-novo
674.8204	2	1347.6262	1347.6186	-0.5224	-0.7037	56.2500	215.7414	1	14	NNGGGGGQLFLYR	Deamidation N	2	De-novo
674.8204	2	1347.6262	1347.6186	-0.5224	-0.7037	56.2500	211.2944	1	14	NNGGGGGQLFLYR	Deamidation N	2	De-novo
541.2622	2	1078.5408	1078.5408	0.0000	0.0000	56.7009	195.5514	1	9	EGEYQEGLK		4	De-novo
541.2622	2	1078.5408	1078.5408	-0.0110	-11.5988	56.7009	195.5514	1	9	EGEYQEGLK	Deamidation Q	4	De-novo
541.2622	2	1078.5408	1078.5408	-0.0110	-11.5988	56.7009	194.6111	1	9	EGEYQEGLK		4	De-novo
541.2622	2	1078.5408	1078.5408	-0.0110	-11.5988	56.7009	194.6111	1	9	EGEYQEGLK	Deamidation Q	1 / 4	De-novo
872.3345	2	1742.6518	1742.663	-0.2896	-7.1278	56.8116	261.7949	1	12	MGNNQQLFLYR	Deamidation N	2	De-novo
872.3345	2	1742.6518	1742.663	-0.2896	-7.1278	56.8116	261.7952	1	12	MGNNQQLFLYR			De-novo
872.3345	2	1742.6518	1742.663	-0.2896	-7.1278	56.8116	261.7952	1	12	MGNNQQLFLYR	Deamidation N		De-novo
921.9801	2	1841.9448	1841.9424	0.2022	1.2014	63.6304	245.1757	1	17	YYGNFYGGNGFGMLR			De-novo
921.9801	2	1841.9448	1841.9424	0.2022	1.2014	63.6304	245.1757	1	17	YYGNFYGGNGFGMLR	Deamidation Q	9	De-novo
921.9801	2	1841.9448	1841.9424	0.2022	1.2014	63.6304	244.2742	1	17	YYGNFYGGNGFGMLR			De-novo
744.3925	2	1485.7694	1485.7719	-0.2035	-1.5639	67.8142	369.6664	1	14	GSYYLGSGNGMLR	Deamidation N	13	De-novo
744.3925	2	1485.7694	1485.7719	-0.2035	-1.5639	67.8142	369.6664	1	15	GSYYLGSGNGMLR	Deamidation N	13	De-novo
744.3925	2	1485.7694	1485.7719	-0.2035	-1.5639	67.8142	365.3552	1	15	GSYYLGSGNGMLR	Deamidation N	13	De-novo
513.7746	2	1025.5332	1025.5256	-0.2052	-0.2104	52.1111	47.1778	1	8	LSYYYGGY			De-novo
513.7746	2	1025.5332	1025.5256	-0.2052	-0.2104	52.1111	47.1778	1	8	LSYYYGGY	Deamidation N		De-novo
513.7746	2	1025.5332	1025.5256	-0.2052	-0.2104	52.1111	47.1218	1	8	LSYYYGGY			De-novo
562.5099	2	1122.4942	1122.4873	-0.6151	-0.7828	76.9398	236.6918	1	9	LFYYCQGFR		7	De-novo
562.5099	2	1122.4942	1122.4873	-0.6151	-0.7828	76.9398	236.6918	1	9	LFYYCQGFR	Deamidation Q	7	De-novo
562.5099	2	1122.4942	1122.4873	-0.6151	-0.7828	76.9398	236.6914	1	9	LFYYCQGFR			De-novo
501.2631	2	1000.5016	1000.5015	-0.0119	-11.8982	56.902	51.1714	1	9	LQYGTEYAK			De-novo
501.2631	2	1000.5016	1000.5015	-0.0119	-11.8982	56.902	51.1714	1	9	LQYGTEYAK			De-novo
501.2631	2	1000.5016	1000.5015	-0.0119	-11.8982	56.902	51.1714	1	9	LQYGTEYAK			De-novo
501.2631	2	1000.5016	1000.5015	-0.0119	-11.8982	56.902	50.9941	1	9	LQYGTEYAK			De-novo
501.305	2	1104.5944	1104.5915	0.2619	11.6949	56.9894	96.9598	1	9	LYQYCEKFR		7	De-novo
501.305	2	1104.5944	1104.5915	0.2619	11.6949	56.9894	96.9598	1	9	LYQYCEKFR	Deamidation Q	7	De-novo
501.305	2	1104.5944	1104.5915	0.2619	11.6949	56.9894	96.292	1	9	LYQYCEKFR			De-novo
492.8277	2	1983.9368	1983.9369	-0.0051	-0.1041	61.4287	51.1278	1	13	MRLNNEEGRFGGR		7	De-novo
492.8277	2	1983.9368	1983.9369	-0.0051	-0.1041	61.4287	51.1278	1	13	MRLNNEEGRFGGR	Oxidation M / Deamidation	2 / 7	De-novo
492.8277	2	1983.9368	1983.9369	-0.0051	-0.1041	61.4287	51.1278	1	13	MRLNNEEGRFGGR	Oxidation M / Deamidation	1 / 7	De-novo

m/z	Charge	Peak MH	Neutral Mr	Delta ppm	Delta Da	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rank	Query Pos.
1214.6161	2	1415.6441	1413.6441	-0.4290	-0.6065	5.0000	-0.0000	1	12	KLFVRGDFRMLQ	Deamidation Q	1	De-novo
1213.8301	2	1415.6444	1413.6444	-0.4290	-0.6065	57.0000	251.6919	1	12	KLFVRGDFRMLQ	Deamidation Q; M	2 / 10	De-novo
1213.8301	2	1415.6444	1413.6444	-0.4290	-0.6065	57.0000	251.6919	1	12	KLFVRGDFRMLQ	Deamidation Q	3	De-novo
762.3586	2	1482.7512	1480.7512	-0.0513	-0.0760	55.0000	199.9453	1	12	GLFTGERTFTLK	Oxidation M	4	De-novo
762.3586	2	1482.7512	1480.7512	-0.0513	-0.0760	55.0000	127.1142	1	12	GLFTGERTFTLK	Oxidation M	5	De-novo
762.3586	2	1482.7512	1480.7512	-0.0513	-0.0760	55.0000	127.1142	1	12	GLFTGERTFTLK	Oxidation M / Deamidation N	6	De-novo
803.8461	2	1765.7766	1765.7766	-0.1019	-0.5689	29.7669	105.6171	1	16	HRVVGLAFSYAHGRYR			De-novo
803.8461	2	1765.7766	1765.7766	-0.0910	-0.5027	51.4200	98.993	1	16	SSFRVEGSSLGLGNGRFR	Deamidation R	4	De-novo
803.8461	2	1765.7766	1765.7766	-0.0910	-0.5027	51.4200	98.993	1	16	SSFRVEGSSLGLGNGRFR			De-novo
574.2419	2	1146.9482	1146.9714	-0.2042	-0.4522	50.6667	253.8414	1	12	ARYFFGLGAGAR	Deamidation R	2 / 12	De-novo
574.2419	2	1146.9482	1146.9714	-0.0942	-0.4522	50.6667	203.7867	1	12	RAYFFGLGAGAR	Deamidation R	1 / 12	De-novo
574.2419	2	1146.9482	1146.9714	-0.0942	-0.4522	50.6667	203.7867	1	12	RAYFFGLGAGAR	Deamidation R	3 / 12	De-novo
725.8787	2	1449.7618	1449.7618	-0.0958	-0.5089	60.8696	146.6412	1	12	RELLYEFYLALK	Deamidation R	1	De-novo
725.8787	2	1449.7618	1449.7618	-0.0958	-0.5089	60.8696	146.6412	1	12	RELLYEFYLALK	Deamidation R	2	De-novo
725.8787	2	1449.7618	1449.7618	-0.0958	-0.5089	60.8696	146.6412	1	12	RELLYEFYLALK	Deamidation R	3	De-novo
801.9274	2	1601.8532	1601.8774	-0.1184	-0.5269	63.1538	327.1479	1	14	FTEGSFLFLSTRYNNF	Oxidation M	1	De-novo
801.9274	2	1601.8532	1601.8774	-0.1184	-0.5269	63.1538	327.1479	1	14	FTEGSFLFLSTRYNNF			De-novo
801.9274	2	1601.8532	1601.8774	-0.1184	-0.5269	58.9077	316.4917	1	14	FTEGSFLFLSTRYNNF			De-novo
801.9274	2	1601.8532	1601.8774	-0.1184	-0.5269	58.9077	316.4917	1	14	FTEGSFLFLSTRYNNF			De-novo
662.8403	2	1323.7650	1323.7649	0.0991	0.0574	71.2145	205.5527	1	12	LFTLFLTRYLGR	Deamidation Q	1	De-novo
662.8403	2	1323.7650	1323.7649	0.0991	0.0574	71.2145	207.1959	1	12	LFTLFLTRYLGR	Deamidation R	4	De-novo
662.8403	2	1323.7650	1323.7649	0.0991	0.0574	71.2145	207.1959	1	12	LFTLFLTRYLGR			De-novo
647.1406	2	1293.7964	1293.7966	0.1858	0.2404	76.5669	241.1318	1	12	LFTLFLTRYLLR			De-novo
647.1406	2	1293.7964	1293.7966	0.1858	0.2404	76.5669	241.1318	1	12	LFTLFLTRYLLR			De-novo
647.1406	2	1293.7964	1293.7966	0.1858	0.2404	69.9452	241.1342	1	12	TFLLFLTRYLLR			De-novo
647.1406	2	1293.7964	1293.7966	0.1858	0.2404	69.9452	241.1342	1	12	TFLLFLTRYLLR			De-novo
682.8709	2	1363.7202	1363.7217	0.2035	0.3121	69.9452	113.6304	1	12	FFYAFFGFGFGR	Deamidation Q	4	De-novo
682.8709	2	1363.7202	1363.7217	0.2035	0.3121	69.9452	120.767	1	12	FFYAFFGFGQFR			De-novo
682.8709	2	1363.7202	1363.7217	0.2035	0.3121	69.9452	120.767	1	12	FFYAFFGFGQFR			De-novo
723.3828	2	1402.7522	1402.7474	0.2040	3.1249	72.4828	176.9413	1	12	FGLFNMRMLLLF	Deamidation Q / Oxidation M	3 / 7	De-novo
723.3828	2	1402.7522	1402.7474	0.2040	3.1249	72.4828	176.9413	1	12	FGLFNMRMLLLF	Oxidation M	7	De-novo
723.3828	2	1402.7522	1402.7474	0.2040	3.1249	66.6667	177.1912	1	12	GFLFNMRMLLLF	Deamidation N	1	De-novo
804.8406	2	1607.7134	1607.7139	0.0517	1.0425	63.4609	282.4397	1	14	RGGGFGLGTGFLQGF	Deamidation Q	4	De-novo
804.8406	2	1607.7134	1607.7139	0.0517	1.0425	63.4609	282.4397	1	14	RGGGFGLGTGFLQGF	Deamidation R /	1 / 14	De-novo
804.8406	2	1607.7134	1607.7139	0.0517	1.0425	63.4609	291.3159	1	14	RGGGFGLGTGFLQGF	Deamidation R /	1 / 14	De-novo
621.3541	2	1240.6926	1240.6187	0.2739	59.5477	66.6667	187.1852	1	11	GRYCWDYR	Deamidation R	1	De-novo
621.3541	2	1240.6926	1240.6187	0.2739	59.5477	66.6667	187.1852	1	11	GRYCWDYR			De-novo
621.3541	2	1240.6926	1240.6187	0.2739	59.5477	66.6667	186.5722	1	11	GQCWDYR	Deamidation Q	3	De-novo
694.8209	2	1387.5962	1387.5930	0.2023	1.6402	65.5333	235.2918	1	14	GCRNNRYRGAGLR	Carbamidomethyl C /	1 / 14	De-novo
694.8209	2	1387.5962	1387.5930	0.2023	1.6402	65.5333	235.2918	1	14	GCRNNRYRGAGLR	Carbamidomethyl C /	2 / 14	De-novo
694.8209	2	1387.5962	1387.5930	0.2023	1.6402	71.2145	236.3944	1	14	CGRNNRYRGAGLR	Carbamidomethyl C /	1 / 14	De-novo
716.351	2	1430.6954	1430.6985	-0.2021	-1.4794	56.7544	215.5988	1	12	RGFGGGRFFGVR			De-novo
716.351	2	1430.6954	1430.6985	-0.2021	-1.4794	56.7544	215.5988	1	12	RGFGGGRFFGVR	Deamidation Q	2	De-novo
716.351	2	1430.6954	1430.6985	-0.2021	-1.4794	56.7544	217.5175	1	12	RGFGGQRFFGVR			De-novo

NCBI gi|224972549|gb|ACI72 [ ] Homo sapiens(human) [ ] Hemoglobin subunit beta [ ] 146 aa, chain 1, Primate [ ] [Uniprot=P68871]

Total Score: 384

```
                    0        30       60       90      120      150
                    |        |        |        |        |        |
gi|224972549|gb|ACI72 [ ]
Local Score (MSMS)  [ ]
```

Score = 101.2(5.7 bits)
Identities = 12/13 (92%), Positives = 13/13 (100%)

Query: 407 EFEQFMNAWSALK 419
EFEQFMNAWSALK
Sbjct: 135 EFEQFMNAWSALK 147 [Mass=1508]

Score = 88.2(5.7 bits)
Identities = 13/16 (81%), Positives = 15/16 (94%)

Query: 26 KLGFNMRMRMQEGK 41
KLGFNMRMRMVQAK M
Sbjct: 130 KLGFNMRMRMLGAK 143 [Mass=1508]

Score = 92.2(5.8 bits)
Identities = 12/13 (92%), Positives = 12/13 (100%)

Query: 328 GCNNAMRYGRRLK 340
GCNNAMRYGRRLK
Sbjct: 146 GCNNAMRYGRRLK 158 [Mass=1508]

Score = 88.1(5.5 bits)
Identities = 7/7 (71%), Positives = 7/7 (100%)

Query: 458 PLEVEER 465
PLEVEER
Sbjct: 273 PLEVEER 279 [Mass=1508]

Score = 88.1(5.5 bits)
Identities = 8/12 (80%), Positives = 8/12 (80%)

Query: 443 RRGGGRLAF 452
R GGGRLAF
Sbjct: 92 RGGGRLAF 100 [Mass=1508]

Mr 80 KDP [ ] [ ] [ ]

Hpt 11

ACC	Change	Peak mM	Peptide mM	Inclin. Chg	Inclin. Ggmn	Ladder Score	Log Likelihood	Start	End	Sequence	Modification	Score	Query Succ.
814,2777	2	824,5346	824,5346	-0,0496	-111,6293	60,8489	116,7997	1	4	LLQGFFM			De-novo
814,2777	2	824,5346	824,5346	-0,0496	-111,6293	60,8489	116,7997	1	4	LLQGFFM			De-novo
876,3918	2	916,5345	916,519	-0,0513	-119,1273	70,5333	131,8710	1	4	KGTFTQR	Deamidation N	7	De-novo
734,3588	2	1446,9020	1446,8988	-0,0498	-159,1973	87,6543	401,3674	1	14	LSRCRNNCSSLFTCR	Deamidation N	5	De-novo
734,3588	2	1446,9020	1446,8988	-0,0498	-159,1973	87,6543	401,3674	1	14	LSRCRNNCSSLFTCR	Deamidation N	5 + 8	De-novo
734,3588	2	1446,9020	1446,8988	-0,0498	-159,1973	87,6543	404,6894	1	14	LSRCRNNCSSLFTCR	Deamidation N	5 + 8	De-novo
799,401	3	2235,5696	2235,5566	0,0252	11,2785	50,4965	276,3542	1	21	RRSAFRSFRFSFQTLLRSCGR	Deamidation R	27	De-novo
799,401	3	2235,5696	2235,5566	0,0252	11,2785	50,4965	276,3542	1	21	RRSAFRSFRFSFQTLLRSCGR	Deamidation R	4 + 27	De-novo
799,401	3	2235,5696	2235,5566	0,0252	11,2785	50,4965	277,5857	1	21	RRSAFRSFRFSFQTLLRSCGR	Deamidation R	4 + 27	De-novo
873,5352	2	1342,8548	1342,863	-0,0392	-6,1251	72,0145	101,256	1	12	RRGRRQLFLFLM	Deamidation R	2	De-novo
873,5352	2	1342,8548	1342,863	-0,0392	-6,1251	72,0145	101,256	1	12	RRGRRQLFLFLM	Deamidation R	2	De-novo
873,5352	2	1342,8548	1342,8628	-0,0392	-6,9742	48	317,4553	1	12	RRGRRQLFLFLM		1	De-novo
921,8738	3	2841,9560	2841,9624	-0,0394	-3,4874	75,7676	555,6152	1	17	YRSRFYLRSAAQFPRLR			De-novo
921,8738	3	2841,9560	2841,9624	-0,0394	-3,4874	75,7676	556,7437	1	17	YRSRFYLRSAAQFPRLR			De-novo
921,8738	3	2841,9560	2841,9624	-0,0394	-3,4874	69,5238	556,343	1	18	YRSRFYLRSAAFQRRLR			De-novo
745,3843	2	1490,7530	1490,7729	-0,0199	-13,9649	65,5172	312,1792	1	15	TYSRGLSERVRLRLR	Deamidation R	13	De-novo
745,3843	2	1490,7530	1490,7729	-0,0199	-13,9649	65,5172	312,1792	1	15	TYSRGLSERVRLRLR	Deamidation R	13	De-novo
745,3843	2	1490,7530	1490,7729	-0,0199	-13,9649	65,5172	179,7564	1	15	TYSRGLSERVRLRLR			De-novo
745,3843	2	1490,7530	1490,7729	-0,0199	-13,9649	65,5172	312,1779	1	15	TYSRGLSERWRRLR			De-novo
745,3843	2	1490,7530	1490,7729	-0,0199	-13,9649	65,5172	312,1779	1	15	TYSRGLSERWRRLR	Deamidation Q /	8	De-novo
962,2307	2	1123,5758	1123,4773	-0,0515	-16,2611	76,5698	231,9712	1	4	LFTFCTQPK			De-novo
962,2307	2	1123,5758	1123,4773	-0,0515	-16,2611	76,5698	249,6911	1	4	LFTFCTQPK	Deamidation Q	7	De-novo
962,2307	2	1123,5758	1123,4773	-0,0515	-16,2611	76,5698	249,6911	1	4	LFTFCTQPK			De-novo
745,3602	2	1476,7048	1476,7261	-0,0347	-5,1422	55,5556	211,6549	1	14	RRSCGLGCLFSTCRR	Deamidation Q	2	De-novo
745,3602	2	1476,7048	1476,7261	-0,0347	-5,1422	55,5556	211,5983	1	14	RRSCGLGCLFSTCRR	Deamidation Q	2	De-novo
745,3602	2	1476,7048	1476,7261	-0,0347	-5,1422	55,5556	211,5983	1	14	RRSCGLGCLFSTCRR	Deamidation Q	2	De-novo
949,5195	2	1126,4219	1126,423	-0,0054	-5,1268	66,5138	47,4748	1	4	LFTFCQTCK	Deamidation Q	4	De-novo
949,5195	2	1126,4219	1126,423	-0,0054	-5,1268	66,5138	47,4748	1	4	LFTFCQTCK	Deamidation Q	4	De-novo
949,5195	2	1126,4219	1126,423	-0,0054	-5,1268	66,5138	52,9612	1	4	LFTFCQTCK			De-novo
949,5195	2	1126,4219	1126,423	-0,0054	-5,1268	66,5138	52,9612	1	4	LFTFCQTCK			De-novo
816,3491	2	1156,5966	1156,5944	0,0022	17,7713	61,5172	76,7974	1	10	RQTRTCSRRR			De-novo
816,3491	2	1156,5966	1156,6065	0,0221	17,8859	45,614	71,2759	1	10	RQTRTCSRRR	Deamidation R	9	De-novo
816,3491	2	1156,5966	1156,6065	0,0221	17,8859	45,614	71,2759	1	10	RQTRTCSRRR	Deamidation R	9	De-novo
816,3491	2	1156,6549	1156,6065	0,0221	17,7348	47,5884	69,6589	1	10	RQTRTCSRRR			De-novo
774,3472	2	1546,8788	1546,8796	-0,0008	-0,5329	66,9878	158,2514	1	15	YRFLGSCCRRGCRRF	Oxidation M	7	De-novo
774,3472	2	1546,8788	1546,8796	-0,0008	-0,5329	66,9878	158,2514	1	15	YRFLGSCCRRGCRRF	Oxidation M	7	De-novo
774,3472	2	1546,8788	1546,8797	-0,0019	-0,5974	64,1375	115,5138	1	14	RFYLGSCCRRGCRF	Oxidation M	7	De-novo
1114,5281	2	2231,5456	2231,4264	0,0192	7,2505	62,7967	351,6322	1	22	RRGRAFGFGFGFQTLLRSCGR	Deamidation R	2 + 18	De-novo
1114,5281	2	2231,5456	2231,4264	0,0192	7,2505	62,7967	351,6322	1	22	RRGRAFGFGFGFQTLLRSCGR	Deamidation R	2 + 18	De-novo
1114,5281	2	2231,5456	2231,4264	0,0192	7,2505	62,7967	369,5597	1	22	RRGRAFGFGFGFQTLLRSCGR	Deamidation R	2 + 7 + 18	De-novo
535,283	3	1056,5554	1056,5608	-0,0154	-8,9473	66,6276	192,2779	1	9	QSLETQSLF	Deamidation Q	1 + 8	De-novo
535,283	3	1056,5554	1056,5608	-0,0154	-8,9473	66,6276	192,2779	1	9	QSLETQSLF	Deamidation Q	1 + 8	De-novo
535,283	3	1056,5554	1056,5608	-0,0154	-8,9473	66,6276	195,7514	1	9	QSLETQSLF	Deamidation Q	1	De-novo
855,8301	2	1196,6650	1196,651	0,0196	7,9623	48,254	135,491	1	11	TLLSLEAQLLA			De-novo
855,8301	2	1196,6650	1196,651	0,0196	7,9623	48,254	135,491	1	11	TLLSLEAQLLA	Deamidation Q	9	De-novo
553,2388	2	1106,5653	1106,5564	0,0259	23,1550	66,5697	47,4588	1	10	TSSQCTLQFR	Deamidation Q	6	De-novo
553,2388	2	1106,5653	1106,5564	0,0259	23,1550	70,1734	96,3987	1	10	TSSQCTLQFR	Deamidation Q	6	De-novo
553,2388	2	1106,5653	1106,5564	0,0259	23,1550	70,1734	96,3987	1	10	TSSQCTLQFR			De-novo
899,3417	2	1374,6679	1374,6561	0,0117	6,6938	48	201,5168	1	13	RRSRRQLFLFLM	Deamidation R	2	De-novo
899,3417	2	1374,6679	1374,6561	0,0117	6,6938	48	201,5168	1	13	RRSRRQLFLFLM			De-novo
899,3417	2	1374,6679	1374,6561	0,0117	6,6938	48	290,1414	1	13	RRSRRQLFLFLM			De-novo
745,3846	2	1490,7729	1490,7729	-0,0193	-13,9623	55,9513	176,7147	1	15	TYSRGLSERVRRLR	Deamidation R	13	De-novo
745,3846	2	1490,7729	1490,7729	-0,0193	-13,9623	55,9513	176,7147	1	15	TYSRGLSERVRRLR	Deamidation R	13	De-novo
745,3846	2	1490,7729	1490,7729	-0,0193	-13,9623	55,9513	175,1966	1	15	TYSRGLSERVRRLR	Deamidation R	13	De-novo

MCMC [illegible]

Hpt 12 [illegible]

Hpt 13

ACC	Change	Peak mM	Peptide mM	Inclin. Chg	Inclin. Ggmn	Ladder Score	Log Likelihood	Start	End	Sequence	Modification	Score	Query Succ.
765,3747	2	1532,8873	1532,8873	-0,0002	-0,0777	59,5455	266,6653	1	13	YSSQGFMRRGF			De-novo
765,3747	2	1532,8873	1532,8873	-0,0002	-0,0777	59,5455	266,6653	1	13	YSSQGFMRRGF			De-novo
876,3227	2	1356,6528	1356,6365	-0,0447	-5,6873	78	324,6923	1	13	YSSYCFLRRGFRR	Deamidation N	5	De-novo
876,3227	2	1356,6528	1356,6365	-0,0447	-5,6873	78	324,6923	1	13	YSSYCFLRRGFRR	Deamidation N	5 + 8	De-novo
876,3227	2	1356,6528	1356,6365	-0,0447	-5,6873	78	352,8958	1	13	YSSYCFLRRGFRR	Deamidation N	5	De-novo
994,5002	2	1104,5870	1104,5872	-0,0002	-0,1502	66,6667	134,7793	1	11	YRSRYYNAGFR			De-novo
994,5002	2	1104,5870	1104,5872	-0,0002	-0,1502	66,6667	134,7793	1	11	YRSRYYNAGFR			De-novo
513,765	3	1023,5168	1023,5389	-0,0245	-15,9660	61,2222	196,2555	1	9	YSFQFTN			De-novo
513,765	3	1023,5168	1023,5389	-0,0245	-15,9660	61,2222	196,2555	1	9	YSFQFTN			De-novo
513,765	3	1023,5168	1023,5389	-0,0245	-15,9660	61,2222	185,3369	1	9	YSFQFTN	Deamidation Q	5	De-novo
671,3115	2	852,4779	852,413	0,0650	-6,5977	49,4848	136,6877	1	6	YAMFLR			De-novo
671,3115	2	852,4779	852,413	0,0650	-6,5977	49,4848	136,6877	1	6	YAMFLR			De-novo
671,3115	2	852,4779	852,413	0,0650	-6,5977	49,4848	135,4949	1	6	YAMFLR			De-novo
763,3504	3	2287,4278	2287,483	-0,0552	-24,2313	59,1206	324,8588	1	21	RRRAAMYSYSFRSYRAFR	Deamidation R	1 + 8	De-novo
763,3504	3	2287,4278	2287,483	-0,0552	-24,2313	59,1206	324,8588	1	21	RRRAAMYSYSFRSYRAFR	Deamidation R / Deamidation	1 + 8	De-novo
763,3504	3	2287,4278	2287,483	-0,0552	-24,2313	59,5096	343,9483	1	21	RRRAAMYSYSFRSYRAFR	Deamidation R / Deamidation	1 + 7	De-novo
763,3504	3	2287,4278	2287,483	-0,0552	-24,2313	59,5096	343,9483	1	21	RRRAAMYSYSFRSYRAFR	Deamidation R / Deamidation	1 + 7	De-novo
574,409	3	1726,8036	1726,8167	-0,0131	-7,5876	52,4862	201,3973	1	16	TASSFRSYLRTDFRAM	Deamidation R	12	De-novo
574,409	3	1726,8036	1726,8167	-0,0131	-7,5876	52,4862	241,2163	1	16	TASSFRSYLRTDFRAM			De-novo
574,409	3	1726,8036	1726,8167	-0,0131	-7,5876	56,5274	256,9974	1	16	ATSSFRSYLRTDFRAM			De-novo

MCMC [illegible]

Hpt 22 [illegible]

Hpt 23

Query 12

m/s	Charge	Peak mH	Particle mH	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbs	Query Tool
981.2268	2	1961.4535	1961.4535	0.0000	0.0000	96.000	98.000	1	16	TTSSFSLLLLFR			De-novo
981.2268	2	1961.4535	1961.4535	0.0000	0.0000	96.000	98.000	1	16	TTSSFSLLLLFR	Carbamidomethyl 2	0 / 0	De-novo
981.9973	2	1963.9945	1963.9958	0.0012	0.6133	76.474	232.079	1	4	RYSFLFTPR		4	De-novo
981.9973	2	1963.9945	1963.9958	0.0012	0.6133	76.474	232.079	1	4	RYSFLFTPR	Deamidation Q	0	De-novo
981.5070	2	1962.0140	1962.0170	0.0012	0.6119	86.562	219.852	1	4	RYVTCEGR		4	De-novo
981.5095	2	1962.0190	1962.0170	0.0012	0.6119	86.562	219.852	1	4	RYVTCEGR		4	De-novo
981.5095	2	1962.0190	1962.0201	0.0010	0.5081	73.871	112.763	1	12	RYEEGVSSLGLR			De-novo
981.5095	2	1962.0190	1962.0201	0.0010	0.5081	73.871	112.763	1	12	RYEEGVSSLGLR			De-novo
671.2197	2	952.4238	952.413	-0.0090	-10.8210	66.668	151.184	1	4	YWFGK	Deamidation N	2	De-novo
671.2197	2	952.4238	952.413	-0.0090	-10.8210	66.668	151.663	1	4	YWFGK		2	De-novo
931.8772	2	1861.4908	1861.4907	-0.1814	-97.7098	51.314	311.949	1	16	TSSFSSFSSFLLFRAGA	Deamidation N	15	De-novo
931.8772	2	1861.4908	1861.4907	-0.1814	-97.7098	51.314	311.949	1	16	TSSFSSFSSFLLFRAGA	Deamidation N	16	De-novo
931.8772	2	1861.4908	1861.4907	-0.1814	-97.7098	47.462	331.438	1	20	TSSFSSFSSFLLFRAGAA	Deamidation N	16	De-novo
931.8772	2	1861.4908	1861.4907	-0.1814	-97.7098	47.462	331.438	1	20	TSSFSSFSSFLLFRAGAA	Deamidation N	16	De-novo
786.3698	4	3144.4460	3144.5314	-0.1436	-45.7071	38.517	426.673	1	29	QAAAFFQQIGCLEEFSTFFSTLQTR	Deamidation Q	1	De-novo
786.3698	4	3144.4460	3144.5314	-0.1436	-45.7071	38.517	427.193	1	29	QAAAFFQQIGCLEEFSTFFSTLQTR	Deamidation Q	1 / 28	De-novo
512.7790	2	1023.5428	1023.5389	0.0039	3.7669	75.504	121.152	1	4	YSYLQTER		4	De-novo
512.7790	2	1023.5428	1023.5389	0.0039	3.7669	75.504	121.152	1	4	YSYLQTER	Deamidation Q	5	De-novo
512.7790	2	1023.5428	1023.5389	0.0039	3.7669	75.504	121.152	1	4	YSYLQTER		4	De-novo
512.7790	2	1023.5428	1023.5389	0.0039	3.7669	75.504	121.152	1	4	YSYLQTER	Deamidation Q	5	De-novo
737.7106	3	2210.1284	2210.1969	0.0111	5.0171	47.462	263.622	1	20	RGSAQLFIGRMQFLAAAK		4	De-novo
737.7106	3	2210.1284	2210.1969	0.0111	5.0171	47.462	263.622	1	20	RGSAQLFIGRMQFLAAAK	Deamidation R	4 / 7	De-novo
737.7106	3	2210.1284	2210.1969	0.0111	5.0171	47.462	261.972	1	20	RGSAQLFIGRMQFLAAAK	Deamidation Q	4 / 7	De-novo
888.913	2	1775.8116	1775.8556	0.0450	2.8847	70.967	286.814	1	16	FSTTTEGTLSTMTRSK		12	De-novo
888.913	2	1775.8116	1775.8556	0.0450	2.8847	70.967	285.693	1	16	FSTTTEGTLSTMTRSK	Deamidation R	7 / 12	De-novo
888.913	2	1775.8116	1775.8556	0.0450	2.8847	70.967	285.693	1	16	FSTTTEGTLSTMTRSK	Deamidation R	7 / 12	De-novo
771.5305	3	2310.2561	2310.2737	-0.0176	-15.2248	45.028	287.633	1	23	TTRRSEQRMLRSFRRFFTTT			De-novo
771.5305	3	2310.2561	2310.2737	-0.0190	-15.9911	43.707	281.697	1	23	TTRRSEQRMLRSFRRFFTTT			De-novo
771.5305	3	2310.2561	2310.2737	-0.0190	-15.9911	43.707	281.697	1	23	TTRRSEQRMLRSFRRFFTTT			De-novo
974.8085	3	2775.8221	2775.8147	-0.2144	-16.6318	49.424	251.556	1	24	STTRRRTLSTMTRSKT	Deamidation R	4 / 12	De-novo
974.8085	3	2775.8221	2775.8147	-0.2144	-16.6318	49.424	251.556	1	24	STTRRRTLSTMTRSKT	Deamidation R	4 / 12	De-novo
974.8085	3	2775.8221	2775.8147	-0.2144	-16.6318	51.623	251.556	1	24	STTRRRTLSTMTRSKT	Deamidation R	4 / 12	De-novo
419.7601	4	1671.0266	1671.0273	0.0013	1.5216	66.989	26.108	1	4	LSYVLQR			De-novo
419.7601	4	1671.0266	1671.0273	0.0013	1.5216	66.989	26.108	1	4	LSYVLQR			De-novo
490.1108	2	976.5220	976.5287	-0.0147	-121.4795	60.0222	151.174	1	8	SELMFCR			De-novo
490.1108	2	976.5220	976.5287	-0.0147	-121.4795	60.0222	151.174	1	8	SELMFCR			De-novo
490.1108	2	976.5220	976.5287	-0.0147	-121.4795	61.533	151.393	1	8	SELMFCR			De-novo

MSMS [ms_ms_12_0000001.mgf.0000001.1.1.1

Spot 12

m/z	Charge	Peak ab	Particle ab	Delta (Da)	Delta (ppm)	Lookbac Score	Log Likelihood	Start	End	Sequence	Mods/Localizat	Protein(s)	Query Scan
504.8411	2	1972.4778	1972.4778	-0.0000	-0.0000	50.9274	136.1937	1	9	GSSVMGGF			6e-nonc
504.8411	2	1411.8988	1411.8978	0.0098	19.5148	66.6487	191.1977	1	13	YGMYYCLMGGCR			6e-nonc
504.8411	2	1411.8988	1411.8978	0.0098	19.5148	66.6487	191.1977	1	13	YGMYYCLMGGCR			6e-nonc
505.3343	2	1180.6773	1180.6778	-0.0004	-0.7120	72.549	123.4922	1	9	HYYCQTGM	Deamidation Q		6e-nonc
505.3343	2	1180.6773	1180.6778	-0.0004	-0.7120	72.549	123.4922	1	9	HYYCQTGM			6e-nonc
981.5563	2	2166.5970	2166.5978	-0.0008	-0.7220	72.549	121.7469	1	8	HYYCQTGM	Deamidation Q	8	6e-nonc
981.5563	2	2166.5970	2166.5978	-0.0008	-0.7220	72.549	121.7469	1	8	HYYCQTGM			6e-nonc
473.211	2	852.4564	852.4517	-0.0046	-5.7759	66.4561	125.0773	1	6	YWFCQ	Deamidation Q	2	6e-nonc
473.211	2	852.4564	852.4517	-0.0046	-5.7759	66.4561	118.7617	1	6	YWFCQ			6e-nonc
848.8758	2	1705.7340	1705.8513	-0.1173	-137.6323	51.461	87.2159	1	18	TAKVNAAVLLATGYRVR	Deamidation N	3 / 17	6e-nonc
848.8758	2	1705.7340	1705.8513	-0.1173	-137.6323	51.461	87.2159	1	18	TAKVNAAVLLATGYRVR	Deamidation N	3	6e-nonc
848.8758	2	1705.7340	1705.8513	-0.1173	-137.6323	66.4987	107.2912	1	18	TAKVNAAVLLATGYRVR	Deamidation N	3 / 18	6e-nonc
516.9179	3	1547.7303	1547.7207	0.0096	17.1435	48.478	126.6999	1	14	DSYMDLGRQAQR	Deamidation R / Deamidation	3 / 11	6e-nonc
516.9179	3	1547.7303	1547.7207	0.0096	17.1435	48.478	126.6999	1	14	DSYMDLGRQAQR	Deamidation R / Deamidation	3 / 11	6e-nonc
516.9179	3	1547.7303	1547.7207	0.0096	17.1435	48.1485	136.1962	1	14	DSYMDLGRQAQR	Deamidation R / Deamidation	3 / 11	6e-nonc
516.9179	3	1547.7303	1547.7207	0.0096	17.1435	48.1485	136.1962	1	14	DSYMDLGRQAQR			6e-nonc
574.6201	3	1720.8519	1720.8147	-0.3129	-181.8948	52.4882	241.4922	1	14	EMFEAMYLGTRNEW	Deamidation N	3 / 12	6e-nonc
574.6201	3	1720.8519	1720.8147	-0.3129	-181.8948	52.4882	241.4922	1	14	EMFEAMYLGTRNEW			6e-nonc
574.6201	3	1720.8519	1720.8147	-0.3129	-181.8948	52.4882	241.4922	1	14	EMFEAMYLGTRNEW	Deamidation N	3	6e-nonc
574.6201	3	1720.8519	1720.8147	-0.3129	-181.8948	52.4882	241.4922	1	14	EMFEAMYLGTRNEW			6e-nonc
727.4163	2	1452.8170	1452.7765	0.0405	27.8611	40	61.2177	1	13	GLFAQMTPTLYYR			6e-nonc
727.4163	2	1452.8170	1452.7765	0.0405	27.8611	40	61.2177	1	13	GLFAQMTPTLYYR			6e-nonc
512.8183	2	1023.6418	1023.6265	-0.0153	-14.8329	62.7665	91.7004	1	9	YYYTCQAA			6e-nonc
512.8183	2	1023.6418	1023.6265	-0.0153	-14.8329	62.7665	91.7004	1	9	YYYTCQAA			6e-nonc
512.7787	2	1023.5418	1023.5369	0.0019	2.8699	70.1111	91.2033	1	8	YYYLQTGM	Deamidation Q	5	6e-nonc
512.7787	2	1023.5418	1023.5369	0.0019	2.8699	70.1111	91.2033	1	8	YYYLQTGM			6e-nonc
512.7787	2	1023.5418	1023.5369	0.0019	2.8699	70.1111	73.4969	1	8	YYYLQTGM			6e-nonc

MSV: ID=1242024|SF=0|NS=1|1:Tryptic|M:Carbamidomethylation|Q:Deamidation|Q:Deamidation|Q:Deamid

Spot 14

ACX	Charge	Peak mM	Peptide mM	Delta Obs	Delta Ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbe	Query Scan
594,7268	2	1,214,1212	1,214,1212	0,0000	0,0000	0,0000	0,0000	1	8	GGGGGGGR		3	De-novo
889,7268	2	875,4380	875,4609	-0,0229	-12,9876	56,1474	77,4957	1	10	GGRAGRRGRR		5	De-novo
889,7268	2	875,4380	875,4609	-0,0229	-12,9876	56,1474	77,4957	1	10	GGRAGRRGRR	Deamidation N	5	De-novo
705,3326	2	1498,6446	1498,6624	-0,0129	-8,5375	40	204,5304	1	12	RDGCGCGRCGLGR	Deamidation N	7	De-novo
705,3326	2	1498,6446	1498,6624	-0,0129	-8,5375	40	202,7992	1	12	RDGCGCGRCGLGR	Deamidation N	7	De-novo
705,3326	2	1498,6446	1498,6624	-0,0129	-8,5375	40	202,7992	1	12	RDGCGCGRCGLGR	Deamidation N	7	De-novo
514,8021	2	1027,5860	1027,5927	-0,0067	-6,5123	76,4214	196,7510	1	9	PTGCGRGPR		4	De-novo
814,9047	2	1851,7838	1851,7966	-0,0128	-2,8250	52,8736	195,4723	1	15	RSGPGLCTCGSRPCR	Carbamidomethyl C	14	De-novo
594,7268	2	1214,1212	1214,1212	0,0000	0,0000	0,0000	0,0000	1	8	GGGGGGGR		3	De-novo
560,7476	2	1119,2146	1119,2197	-0,0051	-4,5288	56,9123	119,5519	1	10	YGVFTGCGR		5	De-novo
560,7476	2	1119,2146	1119,2197	-0,0051	-4,5288	56,9123	119,5519	1	10	YGVFTGCGR		5	De-novo
560,7476	2	1119,2146	1119,2197	-0,0051	-4,5288	56,9123	119,551	1	10	YGVFTGCGR	Deamidation Q	5	De-novo
560,7476	2	1119,2146	1119,2197	-0,0051	-4,5288	56,9123	119,551	1	10	YGVFTGCGR	Deamidation Q	5	De-novo
756,8565	2	1511,8974	1511,9053	-0,0011	-1,3697	40	81,1348	1	14	QEYEEGCGFCFR	Deamidation N	7	De-novo
756,8565	2	1511,8974	1511,9053	-0,0011	-1,3697	55,5036	81,892	1	14	QEYEEGCGFCFR	Deamidation N	7	De-novo
756,8565	2	1511,8974	1511,9053	-0,0011	-1,3697	55,5036	81,892	1	14	QEYEEGCGFCFR	Deamidation N	7	De-novo
473,2730	2	945,5418	945,5444	-0,0013	-1,0841	52,9412	89,5922	1	9	AGYFGCLGR		4	De-novo
473,2730	2	945,5418	945,5444	-0,0013	-1,0841	52,9412	89,7552	1	9	AGYFGCLGR		4	De-novo
473,2730	2	945,5418	945,5444	-0,0013	-1,0841	52,9412	90,7552	1	9	AGYFGCLGR		4	De-novo

MGRC gi|197627725|pdb|3BMO|D Total Score = 41

```
                                   0        40       80      120      160
                                   |         |        |        |        |
                                   ---------------------------------------
gi|197627725|pdb|3BMO|D            ---------------------------------------
Local Score 3BMO                   * ** *    ***      ***      ****
```

Score = 75 (39.4 bits)
Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 110 TEEGCGTTTGCGR 124
TEEGCGTTT +R
Sbjct: 145 TEEGCGTTTGCGT 157 Deaminase

Score = 70 (36.8 bits)
Identities = 9/10 (90%), Positives = 10/10 (100%)

Query: 174 AEYEGCGLR 183
AEYEGCGLR
Sbjct: 15 AEYEGCGLR 24 Deaminase

Score = 48 (26.8 bits)
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 3 YYGEAQGR 11
YYGEAQGR
Sbjct: 16 YYGEAQGR 23 Deaminase

Score = 45 (26.4 bits)
Identities = 8/9 (89%), Positives = 9/9 (100%)

Query: 75 PRGLYGAER 79
PRGLYGAER
Sbjct: 35 PRGLYGAER 43 Deaminase

Score = 44 (26.4 bits)
Identities = 10/13 (76%), Positives = 10/13 (76%)

Query: 110 TEEGCGTTTGCGR 124
TEEGCGTTT +R
Sbjct: 102 TEEGCGTTTGRGR 114

Score = 41 (25.6 bits)
Identities = 9/14 (64%), Positives = 9/14 (64%)

Query: 174 AEYEGCGLRGLAER 187
A Y+ G+GLR+ A+
Sbjct: 15 AGYKGIGLRNFAKR 28

Score = 41 (25.6 bits)
Identities = 7/12 (58%), Positives = 9/12 (75%)

Query: 11 RGAPAGRRAERRAP 24
R PAGRAER P
Sbjct: 74 RAGRRNLAERAAP 85

Score = 40 (25.2 bits)
Identities = 7/12 (58%), Positives = 9/12 (75%)

Query: 75 PRGLYGAER 86
R+ +GAER RCP I+
Sbjct: 1 RAGRRCLGAERARCPIIR 12

Da 60 EDF Protein:CBP/EP300 CTAD (KIX) Domain 2

Total Score = 34

```
                                   0        40       80      120      160
                                   |         |        |        |        |
                                   ---------------------------------------
hsa|p2c-ON-EQK_Cbp/p3_             ---------------------------------------
Local Score 3BMO                   *  **   *    ***      ***      ****
```

Score = 71 (37.4 bits)
Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 110 TEEGCGTTTGCGR 124
TEEGCGTTT +R
Sbjct: 102 TEEGCGTTTGRGR 114

Score = 70 (36.8 bits)
Identities = 9/10 (90%), Positives = 10/10 (100%)

Query: 174 AEYEGCGLR 183
AEYEGCGLR
Sbjct: 16 AEYEGCGLR 25

Score = 48 (26.8 bits)
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 3 YYGEAQGR 11
YYGEAQGR
Sbjct: 35 YYGEAQGR 42

Score = 45 (26.4 bits)
Identities = 8/9 (89%), Positives = 9/9 (100%)

Query: 75 PRGLYGAER 79
PRGLYGAER
Sbjct: 44 PRGLYGAER 52

Score = 41 (25.6 bits)
Identities = 10/14 (71%)

Query: 11 RGAPAGRRAERRAP 24
R PAGRAER P
Sbjct: 74 RAGRRNLAERAAP 85

Spot 15

ACX	Charge	Peak mM	Peptide mM	Delta Obs	Delta Ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbe	Query Scan
833,7862	2	815,5508	815,5508	0,0000	0,0000	0,0000	0,0000	1	8	GGGGGGGR		3	De-novo
833,7862	2	815,5508	815,587	-0,0362	-12,1913	40	141,9754	1	8	GRGGGGGR		3	De-novo
833,7862	2	815,5508	815,587	-0,0362	-12,1913	40	141,9754	1	8	GRGGGGGR	Deamidation N	3	De-novo
449,7909	2	897,5602	897,5530	0,0127	14,1228	66,9966	135,2262	1	8	GGLLGFGR	Deamidation N	3	De-novo
449,7909	2	897,5602	897,5530	0,0129	14,2342	66,9966	101,2778	1	8	GGLLGFGR	Deamidation N	2	De-novo
449,7909	2	897,5602	897,5530	0,0129	14,2342	66,9966	101,2	1	8	GGLLGFGR		2	De-novo
401,7906	2	801,5536	801,5738	-0,0202	-22,5848	39,5328	125,4263	1	7	RLLGFGR		2	De-novo
401,7906	2	801,5536	801,5585	-0,0049	-5,5858	66,9966	112,9425	1	8	GGLLGFGR	Deamidation N	3	De-novo
401,7906	2	801,5536	801,5585	-0,0049	-5,5858	40	112,9425	1	8	GGLLGFGR	Deamidation N	3	De-novo
473,3078	2	944,6020	944,5952	0,0068	7,2085	51,1111	84,5589	1	8	GRLLGFGR		3	De-novo
473,3078	2	944,6020	944,5952	0,0068	7,2085	53,5333	84,245	1	8	RGLLGFGR		3	De-novo
511,8395	2	1021,6634	1021,6535	0,0099	9,6667	55,9804	111,4919	1	9	GFTLLGFLR		4	De-novo
511,8395	2	1021,6634	1021,6535	0,0099	9,6667	55,9804	125,4919	1	9	GFTLLGFLR		4	De-novo
511,8395	2	1021,6634	1021,6535	0,0099	9,6667	55,9804	111,1763	1	9	GFTLLGFLR		4	De-novo
897,5120	2	1793,9210	1793,8256	-0,0946	-52,7148	40	125,2329	1	18	AARRRDDDLLDRRDER	Deamidation N / Deamidation	6 / 10	De-novo
897,5120	2	1793,9210	1793,8256	-0,0946	-52,7148	40	125,2329	1	18	AARRRDDDLLDRRDER	Deamidation N	6	De-novo
897,5120	2	1793,9210	1793,8256	-0,0946	-52,7148	40	125,2329	1	18	AARRRDDDLLDRRDER	Deamidation N	6	De-novo

MGRC gi|197627725|pdb|3BMO|D Total Score = 4

```
                                   0        40       80      120      160
                                   |         |        |        |        |
                                   ---------------------------------------
gi|197627725|pdb|3BMO|D            ---------------------------------------
Local Score 3BMO                   *  *  *  *  *  *  *  *  *  *  *  *
```

Score = 47 (25.7 bits)
Identities = 12/12 (47%), Positives = 16/12 (100%)

Query: 14 ARDLDLRDRRLLDRRDELLD 34
AR LLF. ALrrr A LrL
Sbjct: 192 ARRLDLRDRLFGDRRDLFL 204 Deaminase

Interfaces None

Da 85 EDF None

Da 85 EDF alone Protein:CBP/EP300 CTAD (KIX) Domain 2

Total Score = 34

```
                                   0        40       80      120      160      200
                                   |         |        |        |        |        |
                                   ---------------------------------------------
hsa|p2c_Ala-ON-EQL_Cbp/p3_         ---------------------------------------------
Local Score 3BMO                   *  *  *  *  *  *  *  *  *  *  *  *
```

Score = 40 (22.1 bits)
Identities = 8/12 (75%), Positives = 10/12 (83%)

Query: 77 PGRRGLLLRDF 88
PGRR L+ +RLRD
Sbjct: 27 PGRRGCFLRDF 38

Score = 41 (22.5 bits)
Identities = 7/10 (70%), Positives = 8/10 (80%)

Query: 198 RRGLLLRDR 177
R GLLLF R
Sbjct: 247 RRGLLLFGR 276

Score = 41 (22.5 bits)
Identities = 5/6 (83%), Positives = 6/6 (100%)

Query: 12 LLFLRR 17
LLFLRR
Sbjct: 119 LLFLRR 124

Score = 36 (20.0 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)

Query: 48 FLRRLLFL 56
FLRR L L
Sbjct: 188 FLRRLLFL 197

Spot 16

ACX	Charge	Peak mM	Peptide mM	Delta Obs	Delta Ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbe	Query Scan
514,2904	2	1026,5652	1026,5814	-0,0162	-15,7811	56,7878	114,9959	1	11	YGGYGGLGLGR		5	De-novo
514,2904	2	1026,5652	1026,5814	-0,0162	-15,7811	40,9524	114,7724	1	11	YGGYGGLGLGR		5	De-novo
514,2904	2	1026,5652	1026,5814	-0,0162	-15,7811	40,9524	114,7724	1	11	YGGYGGLGLGR	Deamidation Q	5	De-novo
474,3733	2	1046,7354	1046,7382	-0,0028	-2,6573	40,9524	135,4414	1	10	DGSCGCGRQGCFR	Deamidation Q	10	De-novo
474,3733	2	1046,7354	1046,7382	-0,0028	-2,6573	40,9524	135,4414	1	10	DGSCGCGRQGCFR	Deamidation Q	10	De-novo
441,7918	2	881,5680	881,5585	0,0095	10,7841	55,5333	85,7755	1	7	LRLLFLR		2	De-novo
441,7918	2	881,5680	881,5585	0,0095	10,7841	55,5333	85,7755	1	7	LRLLFLR	Deamidation N	2	De-novo
441,7918	2	881,5680	881,5585	0,0095	10,7841	55,5333	85,7755	1	8	RGLLGFLR		3	De-novo
566,8087	2	1130,4918	1130,4369	0,0549	48,5478	66,9825	81,2954	1	11	AAFFEGYLLR		6	De-novo
566,8087	2	1130,4918	1130,4369	-0,0231	-20,5478	66,9825	81,2954	1	11	AAFFEGYLLR		6	De-novo
566,8087	2	1130,4918	1130,4369	-0,0231	-20,5478	66,9825	81,2954	1	11	AAFFEGYLLR		6	De-novo
401,2487	2	800,4818	800,4796	0,0022	2,7194	55,5333	81,1111	1	7	RKLGLR		2	De-novo
401,2487	2	800,4818	800,4796	0,0022	2,7194	55,5333	81,1111	1	7	RKLGLR		2	De-novo
401,2487	2	800,4818	800,4796	0,0022	2,7194	55,5333	81,1919	1	7	YKLGLR		2	De-novo

MGRC gi|197627725|pdb|3BMO|D Total Score = 14

```
                                   0        40       80      120      160
                                   |         |        |        |        |
                                   ---------------------------------------
gi|197627725|pdb|3BMO|D            ---------------------------------------
Local Score 3BMO                   *  *  *  *  *  *  *  *  *  *  *  *
```

Score = 84 (25.5 bits)
Identities = 8/12 (66%), Positives = 9/12 (75%)

Query: 82 LLFLRRLLF 91
LLFLR RLLF
Sbjct: 30 LFLFRCLLF 39 Deaminase

Score = 37 (20.2 bits)
Identities = 8/12 (66%), Positives = 9/12 (75%)

Query: 210 LRLRLLFLRR 199
LRLR RLLF R
Sbjct: 15 LRLRRCLFGR 26 Deaminase

Score = 31 (17.7 bits)
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 95 RLLLF 99
RLLLF
Sbjct: 135 RLLLF 140 Deaminase

Interfaces None

Da 60 EDF Protein:CBP/EP300 CTAD (KIX) Domain 2

Total Score = 14

```
                                   0        40       80      120      160
                                   |         |        |        |        |
                                   ---------------------------------------
hsa|p2c-ON-EQK_Cbp/p3_             ---------------------------------------
Local Score 3BMO                   *  *  *  *  *  *  *  *  *  *  *  *
```

Score = 84 (26.4 bits)
Identities = 12/13 (92%), Positives = 12/13 (92%)

Query: 14 AGLRDRGDRRLRLFD 32
A+L R RGDRRLFLFD
Sbjct: 1 ALSDRRGDRRLFLFD 15

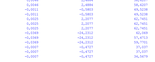
Score = 54 (19.5 bits)
Identities = 9/10 (90%), Positives = 10/10 (100%)

Query: 48 YGRRGLFLRR 40
Y RGRRGLFLRR
Sbjct: 6 YARRGLFLRR 17

Spot 17

m/z	Charge	Peak mH	Peptide mH	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rule	Query Scan
504.7487	2	1007.4828	1007.4828	+0.0000	+0.0000	96.0000	96.0000	1	8	MSSYNNER			De-novo
604.7487	2	1207.4828	1207.4903	+0.0085	+8.4408	88.6276	181.2762	1	9	YRSFRNDER	Deamidation Q	6	De-novo
677.3158	2	1353.6170	1353.6170	+0.0000	+0.0000	75.0000	75.0000	1	9	YGSSYNNER	Deamidation N	4	De-novo
691.7378	2	981.5010	981.5219	+0.0209	+21.3003	72.5349	97.4353	1	8	YQSSYEGR	Deamidation N	4	De-novo
691.7378	2	996.5000	996.5029	+0.0029	+2.9030	66.9623	97.1762	1	10	YGSLVEEGVR	Deamidation N	9	De-novo
691.7378	2	1381.7000	1381.7029	+0.0029	+2.1000	66.9623	97.1762	1	7	YGSLVEK			De-novo
691.2345	2	878.4534	878.4572	+0.0038	+4.3321	66.5328	94.5344	1	7	YRSLFR			De-novo
691.2345	2	878.4534	878.4572	+0.0038	+4.3321	61.0258	94.7968	1	7	QYRLFR	Deamidation Q	1	De-novo
512.7766	2	1023.5712	1023.5389	+0.0317	+31.0049	51.1111	71.9979	1	9	YYTLQFRK		5	De-novo
512.7766	2	1023.5712	1023.5389	+0.0317	+31.0049	51.1111	71.9979	1	9	YYTLQFRK	Deamidation Q	5	De-novo
868.9042	2	1735.7968	1735.8014	+0.0046	+2.6439	56.1905	111.1259	1	14	TASSVAAGSVTLATMTER	Deamidation N	14	De-novo
868.9042	2	1735.7968	1735.8014	+0.0046	+2.6439	56.1905	111.1259	1	14	TASSVAAGSVTLATMTER			De-novo
921.4808	2	1840.9461	1840.9614	+0.0153	+8.3099	56.1168	201.7518	1	16	TELLLYTSSVRLLAR			De-novo
921.4808	2	1840.9461	1840.9614	+0.0153	+8.3099	56.4207	276.1757	1	15	TELLLYTSSVRLLR			De-novo
921.4808	2	1840.9461	1840.9614	+0.0153	+8.3099	56.4207	276.1757	1	15	TELLLYTSSVRLLR	Deamidation Q	12	De-novo
965.5366	2	1927.2532	1927.2563	+0.0311	+16.0803	66.5228	181.7132	1	18	MYYYQNEYEELQSVTLER			De-novo
965.5366	2	1927.2532	1927.2563	+0.0311	+16.0803	66.5228	181.6232	1	18	YMYYQNEYEELQSVTLER			De-novo
965.5366	2	1927.2532	1927.2563	+0.0311	+16.0803	66.5228	181.6232	1	18	YMYYQNEYEELQSVTLER			De-novo
561.7787	2	1121.5478	1121.5553	+0.0555	+2.0277	62.7401	139.0918	1	9	YTSSVSLLR			De-novo
561.7787	2	1121.5478	1121.5553	+0.0555	+2.0277	62.7401	139.0918	1	9	YTSSVSLLR	Deamidation Q	5	De-novo
561.7787	2	1121.5478	1121.5553	+0.0555	+2.0277	62.7401	171.4772	1	9	YTSSVSLLR	Deamidation Q	8	De-novo
762.8991	2	1523.7828	1523.8140	+0.1349	+24.2212	57.4713	246.1613	1	15	LSEGFFNSLTTHAR			De-novo
762.8991	2	1523.7828	1523.8140	+0.1349	+24.2212	57.4713	246.1613	1	15	LSEGFFNSLTTHAR			De-novo
762.8991	2	1523.7828	1523.8140	+0.1349	+24.2212	55.7761	246.1987	1	15	ESEGFFNSLTTHAR			De-novo
762.8991	2	1523.7828	1523.8140	+0.1349	+24.2212	55.7761	246.1987	1	15	ESEGFFNSLTTHAR			De-novo
766.8014	2	1531.7874	1531.7883	+0.0057	+3.6737	35.2207	127.2077	1	14	GSYGMSVNSVLK			De-novo
766.8014	2	1531.7874	1531.7883	+0.0057	+3.6737	35.2207	127.2077	1	14	GSYGMSVNSVLK			De-novo

MSMS [Prev] [Next] [Spectrum] [Ladders] [Deamidation] [Mass Calc] [Modifications] Total Score: 181



Score = 107 (96.5 bits)
Identities = 13/16 (78%), Positives = 17/16 (88%)

Query: 165 RRYYYQNEYEELQSVTLER 181
RRYYYQN+YEELQ VTLER
Sbjct: 165 RRYYYQNDYEELQ VTLER 181 More\Hide

Score = 40 (15.9 bits)
Identities = 9/16 (56%), Positives = 11/16 (78%)

Query: 106 LYTSSVRLLAMMY 166
L+TSS RLLA M+
Sbjct: 106 LFTSSERLLAMMH 122 More\Hide

Score = 40 (15.9 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 208 LYTSSRS 246
LYTSSRS
Sbjct: 112 LFTSSRS 118 More\Hide

Score = 39 (15.6 bits)
Identities = 5/10 (50%), Positives = 8/10 (80%)

Query: 28 TQLSSSLSRT 37
T LSS +RT
Sbjct: 27 TRLSSALSRT 36 More\Hide

Score = 36 (14.4 bits)
Identities = 5/10 (50%), Positives = 7/10 (70%)

Query: 9 RYNSFRNDER 18
+Y NS R DER
Sbjct: 9 KYNSVRDDER 18 More\Hide

Mw MS EDF [Prev] [Next] [Spectrum] [Ladders] [Deamidation] [Mass Calc] [Modifications] Total Score: 181

Score = 70 (28.0 bits)
Identities = 10/11 (90%), Positives = 10/11 (90%)

Query: 109 AGYLATSATER 119
AGYLATSATER
Sbjct: 144 AGYLATSATER 154

Score = 42 (16.1 bits)
Identities = 7/8 (87%), Positives = 8/8 (100%)

Query: 8 YSYSNER 9
YSYSNER
Sbjct: 192 YSYSYSNR 299

Score = 34 (13.6 bits)
Identities = 4/5 (80%), Positives = 5/5 (100%)

Query: 3 SYSNER 9
SYSNER
Sbjct: 279 SSLNER 284

Spot 18

m/z	Charge	Peak mH	Peptide mH	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rule	Query Scan
703.8122	2	1406.6099	1406.6027	+0.0072	+5.1179	91.4147	291.2988	1	13	LNEGYSGAGR			De-novo
574.2722	2	1146.4999	1146.5027	+0.0270	+23.4767	91.414	291.2988	1	10	LNEGYSGAGR	Deamidation N	2 / Deamidation	De-novo
703.8122	2	1405.6088	1405.6027	+0.0439	+31.2928	76.6967	294.9022	1	13	MYSNGEGTTRQK	Deamidation N	M / TT	De-novo
703.8122	2	1405.6088	1405.6027	+0.0439	+31.2928	76.6967	294.9022	1	13	MYSNGEGTTRQK	Deamidation Q	R	De-novo
703.8122	2	1405.6088	1405.6027	+0.0439	+31.2928	76.6967	295.4059	1	13	MYSNGEGTTRQK	Deamidation N /	M / TT	De-novo
521.3004	2	1040.5879	1040.5878	+0.0002	+0.0153	65.5379	129.5565	1	10	YQATCYLTNR			De-novo
521.3004	2	1040.5879	1040.5878	+0.0002	+0.0153	65.5379	129.5565	1	10	YQATCYLTNR			De-novo
521.3004	2	1040.5879	1040.5878	+0.0002	+0.0153	65.5379	129.4889	1	10	YQATCYLTNR			De-novo
609.7890	2	1215.5620	1215.5833	+0.0205	+16.9462	71.4296	237.5373	1	11	YLAEFFCTGER	Deamidation N	10	De-novo
609.7890	2	1215.5620	1215.5833	+0.0205	+16.9462	71.4296	237.5373	1	11	YLAEFFCTGER			De-novo
609.7890	2	1215.5620	1215.5833	+0.0205	+16.9462	71.4296	251.113	1	11	YLAEFFCTGER	Deamidation Q	4	De-novo
691.3422	2	1381.6680	1381.7184	+0.1498	+38.6234	50.1739	46.941	1	12	MYNSYLCYCSSV			De-novo
691.7489	2	876.4622	876.4614	+0.0008	+0.9013	51.8775	35.4924	1	10	ANFNSWAGAF			De-novo
691.7489	2	876.4622	876.4614	+0.0008	+0.9013	51.8775	35.4924	1	10	ANFNSWAGAF			De-novo
691.7489	2	876.4622	876.4614	+0.0008	+0.9013	47.7894	45.1911	1	10	ANFNSWAGAF			De-novo
691.7489	2	876.4622	876.4614	+0.0008	+0.9013	47.7894	45.1911	1	10	ANFNSWAGAF			De-novo
896.8154	2	1791.6226	1791.6204	+0.0148	+5.6485	85.4558	61.4127	1	14	LSEAQQAGAFSFGG			De-novo
896.8154	2	1791.6226	1791.6204	+0.0148	+5.6485	85.4558	61.4127	1	14	LSEAQQAGAFSFGG	Deamidation N	8	De-novo
896.8154	2	1791.6226	1791.6204	+0.0148	+5.6485	85.4558	61.4127	1	14	LSEAQQAGAFSFGG	Deamidation Q	5	De-novo
661.2968	2	1320.5780	1320.6017	+0.0237	+17.9778	81.9896	125.4569	1	12	ELSYEQTEGSDR			De-novo
661.2968	2	1320.5780	1320.6017	+0.0237	+17.9778	81.9896	143.3524	1	12	ELSYEQTEGSDR			De-novo
661.2968	2	1320.5780	1320.6017	+0.0237	+17.9778	81.9896	143.3524	1	12	ELSYEQTEGSDR	Deamidation Q	10	De-novo
597.8502	2	1193.5988	1193.5928	+0.0059	+4.9503	55.7557	125.5962	1	11	QAAEGCCSCGR	Deamidation Q	1	De-novo
597.8502	2	1193.5988	1193.5928	+0.0059	+4.9503	55.7557	126.5364	1	11	EAAEGCCSCGR			De-novo
566.128	2	1130.4604	1130.4624	+0.0020	+1.7664	66.6667	145.7712	1	9	NSYRFEAAK	Deamidation N / Deamidation	2 / 8	De-novo
566.128	2	1130.4604	1130.4624	+0.0020	+1.7664	66.6667	145.7712	1	9	NSYRFEAAK	Deamidation N / Deamidation	2 / 8	De-novo
566.128	2	1130.4604	1130.4624	+0.0020	+1.7664	66.6667	146.7284	1	9	NSYRFEAAK	Deamidation N / Deamidation	2 / 8	De-novo
566.128	2	1130.4604	1130.4624	+0.0020	+1.7664	66.6667	146.7284	1	9	NSYRFEAAK	Deamidation N /	2 / 8	De-novo

MSMS [Prev] [Next] [Spectrum] [Ladders] [Deamidation] [Mass Calc] [Modifications] Total Score: 198

Score = 89 (45.8 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)

Query: 100 NYLAEFFCTGER 111
NYLAEFFCTGER
Sbjct: 10 NYLAEFFCTGER 20 More\Hide

Score = 38 (14.8 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

Query: 16 YNSNFRY 22
YNSNFRY
Sbjct: 16 YNSNRRY 22 More\Hide

Score = 36 (14.0 bits)
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 29 YRSFR 33
YRSFR
Sbjct: 29 YRSFR 33 More\Hide

Score = 34 (13.6 bits)
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query: 109 LLFTSSRSR 117
LLFTSSRSR
Sbjct: 111 LLFTSSRSR 119 More\Hide

Score = 32 (12.8 bits)
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 45 ELFTRGER 47
ELFTRGER
Sbjct: 36 ELFTRGER 39 More\Hide

Mw MS EDF [Prev] [Next] [Spectrum] [Ladders] [Deamidation] [Mass Calc] [Modifications] Total Score: 198

Score = 80 (40.4 bits)
Identities = 10/12 (83%), Positives = 10/12 (83%)

Query: 154 NAYRNYRNNAER 167
NAYRNYRNNAER
Sbjct: 155 NAYRNYRNNAER 166

Score = 76 (38.3 bits)
Identities = 11/12 (92%), Positives = 11/12 (92%)

Query: 314 AYGRTGTLFNR 324
AYGRTGTLFNR
Sbjct: 42 AYGRTGTLFNR 52

Score = 32 (16.0 bits)
Identities = 9/13 (69%), Positives = 10/13 (76%)

Query: 327 AFNSNNRNNAER 339
AFNSNNAR - 8+
Sbjct: 158 AFNSNNRNNQRD 170

Spot 19

ACX	Charge	Peak mz	Peptide mz	Delta ppm	Delta Spec	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rank	Query Scan
760.5000	2	1519.9927	1519.9927	0.0000	0.0000	52.0000	52.0000	1	14	GGGGGGGGGGGGGG	Deamidation(N)	1	De-novo
822.3529	2	1643.9910	1643.9905	0.0911	0.0479	72.4658	112.7267	1	12	KLKGKGFRQLLK	Deamidation Q	3	De-novo
822.3529	2	1643.9910	1643.9905	0.0911	0.0479	72.4658	112.7267	1	12	KLKGKGFRQLLK	Deamidation Q	4	De-novo
535.2896	2	1068.5432	1068.5408	0.2253	-2.2049	62.7601	171.4169	1	9	KLGCEQLLK	Deamidation Q	5	De-novo
535.2896	2	1068.5432	1068.5408	0.2253	-2.2049	62.7601	171.1769	1	9	KLGCEQLLK		6	De-novo
471.344	2	1940.6714	1940.6714	0.2093	-0.2179	69.9413	95.1519	1	17	DATTCLAWYR	Deamidation C	1 / 4	De-novo
471.344	2	1940.6714	1940.6714	0.2093	-0.2179	69.9413	95.1519	1	17	DATTCLAWYR		5	De-novo
471.344	2	1940.6714	1940.6714	0.2093	-0.2179	69.9413	95.967	1	17	DATTCLAWYR	Deamidation T	1	De-novo
471.344	2	1940.6714	1940.6714	0.2093	-0.2179	69.9413	95.967	1	17	DATTCLAWYR		2	De-novo
964.8812	2	1927.7448	1927.7438	0.5200	-1.8983	79.5123	262.1661	1	14	YVNEEGLLGAERFR	Oxidation M / Deamidation	3 / 4	De-novo
964.8812	2	1927.7448	1927.7438	0.5200	-1.8345	79.5123	261.9819	1	14	YVNEEGLLGAERFR	Oxidation M / Deamidation	3 / 9	De-novo
964.8812	2	1927.7448	1927.7438	0.5200	-1.8983	79.5123	261.9819	1	14	YVNEEGLLGAERFR	Oxidation M	4	De-novo
749.3963	2	1495.7770	1495.7728	0.2842	2.8012	48.1481	39.4143	1	14	GATTCLEGRFFLK		1	De-novo
749.3963	2	1495.7770	1495.7728	0.2842	2.8012	48.1481	91.123	1	14	GATTCLEGRFFLK	Deamidation Q	8	De-novo
805.3500	2	1606.7010	1606.7017	0.4311	1.0597	57.1469	227.1519	1	13	TEGYQLLELLK		1	De-novo
805.3500	2	1606.7010	1606.7017	0.4311	1.0597	57.1469	227.1519	1	13	TEGYQLLELLK		2	De-novo
805.3500	2	1606.7010	1606.7015	0.2911	0.2211	55.9594	235.8432	1	13	ETGYQLLELLK		1	De-novo
805.3500	2	1606.7010	1606.7015	0.2911	0.2211	55.9594	235.6032	1	13	ETGYQLLELLK	Deamidation N	2	De-novo
962.5125	2	1922.4970	1922.4973	0.1651	1.8493	66.6667	47.4594	1	4	LFTGQTFR		1	De-novo
962.5125	2	1922.4970	1922.4973	0.1651	1.8493	66.6667	97.7959	1	4	LFTGQTFR	Deamidation Q	8	De-novo
612.7028	2	823.4898	823.4914	-0.2003	-1.6378	55.5556	35.0553	1	4	VKVSLQR		1	De-novo
612.7028	2	823.4898	823.4914	-0.2003	-1.6378	55.5556	61.0553	1	4	VKVSLQR		2	De-novo
612.7028	2	823.4898	823.4914	-0.2003	-1.6378	55.5556	61.792	1	4	VQFSLQR		1	De-novo
612.7028	2	823.4898	823.4914	-0.2003	-1.6378	55.5556	61.792	1	4	VQFSLQR		2	De-novo
872.5605	2	1742.6854	1742.6856	-0.1350	-10.3610	26.6825	76.0557	1	15	TYSTFLLWRFR	Oxidation M	8	De-novo
872.5605	2	1742.6854	1742.6856	-0.1350	-10.3610	62.8571	76.0557	1	15	TYSTFLLWRFR	Oxidation M	9	De-novo
744.3622	2	1486.7008	1486.7052	0.2936	2.4053	51.1724	75.1724	1	15	FRAVGVSGTTRLLR		1	De-novo
744.3622	2	1486.7008	1486.7052	0.2936	2.4053	51.1724	171.4919	1	15	FRAVGVSGTTRLLR	Deamidation N	3	De-novo
744.3622	2	1486.7008	1486.7052	0.2936	2.4053	57.4713	171.252	1	15	AFRAVGVSGTTRLLR	Deamidation N	3	De-novo
744.3622	2	1486.7008	1486.7052	0.2936	2.5398	57.4713	171.252	1	15	FRAVGVSGTTRLLR		3	De-novo

MSMS [redacted]

Total Score: 114

Score = 78 (40.5 bits)
Identities = 10/14 (71%), Positives = 12/14 (85%)

Score = 42 (22.4 bits)
Identities = 10/17 (58%), Positives = 11/17 (64%)

Score = 49 (26.0 bits)
Identities = 9/12 (75%), Positives = 9/12 (75%)

Score = 35 (19.1 bits)
Identities = 5/9 (56%), Positives = 6/9 (67%)

Sp 40 EDT [redacted]

Total Score: 111

Score = 88 (45.4 bits)
Identities = 10/10 (100%), Positives = 10/10 (100%)

Score = 84 (43.4 bits)
Identities = 9/9 (100%), Positives = 9/9 (100%)

Score = 50 (26.5 bits)
Identities = 8/10 (80%), Positives = 8/10 (80%)

Score = 39 (21.1 bits)
Identities = 6/10 (60%), Positives = 9/12 (69%)

Spot 20

ACX	Charge	Peak mz	Peptide mz	Delta ppm	Delta Spec	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rank	Query Scan
760.5000	2	1519.9927	1519.9927	0.0000	0.0000	52.0000	52.0000	1	14	GGGGGGGGGGGGGG	Deamidation(N)	1	De-novo
822.3529	2	1643.9910	1643.9905	-0.1875	-48.2929	72.0145	101.9943	1	12	LARGFRQALQK	Deamidation R	3	De-novo
744.3626	2	1486.6714	1486.7053	-0.1337	-22.0837	47.8516	235.4888	1	15	FRAVGVSGTTRLLR		1	De-novo
744.3626	2	1486.6714	1486.7053	-0.1337	-22.0837	47.8516	235.4888	1	15	FRAVGVSGTTRLLR		2	De-novo
744.3626	2	1486.6714	1486.7053	-0.1337	-22.0837	72.4138	231.2919	1	15	FRAVGVSGTTRLLR		3	De-novo
744.3626	2	1486.6714	1486.7053	-0.1337	-22.0837	72.4138	231.2919	1	15	FRAVGVSGTTRLLR		4	De-novo
744.3626	2	1486.6714	1486.7053	-0.1337	-22.0837	45.5172	226.0922	1	15	AFRAVGVSGTTRLLR		1	De-novo
744.3626	2	1486.6714	1486.7052	-0.1338	-22.0240	47.8161	231.4193	1	15	FRAVGVSGTTRLLR	Deamidation R	3	De-novo
744.3626	2	1486.6714	1486.7052	-0.1338	-22.0240	47.8161	231.4193	1	15	FRAVGVSGTTRLLR	Deamidation R	4	De-novo
744.3626	2	1486.6714	1486.7052	-0.1338	-22.0240	72.4138	227.2213	1	15	FRAVGVSGTTRLLR		5	De-novo
385.2730	2	1148.5434	1148.5567	-0.0113	-9.8968	74.8252	136.2495	1	11	TGRGLFTACGK	Carbamidomethyl C	9	De-novo
385.2730	2	1148.5434	1148.5567	-0.0113	-9.8968	74.8252	136.1295	1	11	TGRGLFTACGK	Carbamidomethyl C	10	De-novo
385.2730	2	1148.5434	1148.5567	-0.0113	-9.8968	38.234	135.5295	1	11	TGRGLFTCGK	Carbamidomethyl C	9	De-novo
387.1882	2	1192.3828	1192.5783	-0.0137	-179.2132	61.4935	149.7963	1	10	GFEGYGFTK		1	De-novo
387.1882	2	1192.3828	1192.5783	-0.0137	-179.2132	61.4935	147.5563	1	10	GFEGYGFTK	Deamidation Q	2	De-novo
387.1882	2	1192.3828	1192.5783	-0.0137	-179.2132	61.4935	147.5563	1	10	GFQEGYGFTK	Deamidation Q	3	De-novo
401.8004	2	1241.7030	1241.8979	0.0997	8.5712	69.9413	134.6429	1	11	QTGFLEELEFR	Deamidation N	7	De-novo
401.8004	2	1241.7030	1241.8979	0.0997	8.5712	69.9413	134.4029	1	11	QTGFLEELEFR	Deamidation Q / Deamidation N	1	De-novo
401.8004	2	1241.7030	1241.8979	0.0997	8.5712	69.7581	133.4712	1	11	SGLLEELEFLR	Deamidation N	8	De-novo
1028.5138	2	2055.0220	2055.0180	-0.4875	-3.6613	58.7084	182.5851	1	18	CEYCFEEFEFCERLAGR	Carbamidomethyl C / Carbamidomethyl C	1 / 15	De-novo
1028.5138	2	2055.0220	2055.0180	-0.4875	-3.6613	58.7084	182.5851	1	18	CEYCFEEFEFCERLAGR	Carbamidomethyl C / Carbamidomethyl C	1 / 16	De-novo
1028.5138	2	2055.0220	2055.0180	-0.4875	-3.6613	58.7084	184.1918	1	18	CEYCFEEFEFCERLAGR	Carbamidomethyl C / Carbamidomethyl C	1 / 17	De-novo
763.434	2	1495.8566	1495.8527	0.2637	2.6408	78	206.6423	1	13	EAFTGFLLFLLLK		1	De-novo
763.434	2	1495.8566	1495.8527	0.2637	2.6408	78	206.6423	1	13	EAFTGFLLFLLLK		2	De-novo
763.434	2	1495.8566	1495.8527	0.2637	2.6408	78	208.6423	1	13	EAFTGFLLFLLLK	Deamidation N	1	De-novo
401.8013	2	921.3870	921.3898	-0.3028	-5.5443	77.7778	146.7113	1	8	LFLGFRLF		1	De-novo
401.8013	2	921.3870	921.3898	-0.3028	-5.5443	77.7778	146.4713	1	8	LFLGFRLF	Deamidation Q	2	De-novo
401.3329	2	1200.6162	1200.6179	-0.0917	-1.4359	61.4935	196.3267	1	11	EEFLLAERIR		1	De-novo
401.3329	2	1200.6162	1200.6179	-0.0917	-1.4359	66.9123	187.2719	1	10	EEFLLAERIR		2	De-novo
401.3329	2	1200.6162	1200.6179	-0.0917	-1.4359	66.9123	187.0319	1	10	EEFLLAERIR	Deamidation Q	3	De-novo
534.2589	2	1066.4982	1066.4967	-0.1515	-1.5847	76.982	176.2813	1	9	EGYGGTFS		1	De-novo
534.2589	2	1066.4982	1066.4966	-0.1612	-19.9612	62.7401	176.3963	1	9	EMKYGFTS		1	De-novo
534.2589	2	1066.4982	1066.4966	-0.1612	-19.9612	62.7401	176.1563	1	9	EMKYGFTS	Deamidation M	2	De-novo
576.2796	2	1134.5442	1134.5277	0.2136	-1.2738	61.4935	196.9863	1	10	QEGFTACIR	Deamidation Q / Carbamidomethyl C	1 / 8	De-novo
576.2796	2	1134.5442	1134.5278	0.2144	-16.1942	61.4935	196.8163	1	10	EEGFTACIR	Carbamidomethyl C	8	De-novo
576.2796	2	1134.5442	1134.5277	0.2136	-16.1942	61.4935	196.8163	1	10	EEGFTACIR	Deamidation Q /	1 / 2	De-novo
763.4396	2	1485.8626	1485.7513	-0.8877	-38.8515	65.5172	151.4273	1	15	ARRGKGAGSTTRLLR		1	De-novo
763.4396	2	1485.8626	1485.7513	-0.8877	-38.8515	65.5184	150.1593	1	15	ARRGKGAGSTTRLLR		2	De-novo
763.4396	2	1485.8626	1485.7513	-0.8877	-38.8515	65.5184	149.9193	1	15	ARRGKGAGSTTRLLR	Deamidation G	3	De-novo
874.4501	2	1747.8848	1747.87	-0.1539	-58.2847	26.5379	124.3255	1	16	LRRGYSTRRLRSLLLR		1	De-novo
763.3636	2	1486.6714	1486.7052	-0.2236	-22.4141	47.8161	235.4888	1	15	AFRAVGVSGTTRLLR	Deamidation N	3	De-novo

MSMS [redacted]

Total Score: 84

Score = 27 (12.6 bits)
Identities = 8/12 (66%), Positives = 8/12 (66%)

Score = 35 (16.4 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)

Score = 35 (16.4 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)

Score = 35 (16.4 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)

Score = 35 (16.4 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)

Score = 35 (16.4 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)

Score = 35 (16.4 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)

Score = 35 (16.4 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)

Score = 35 (16.4 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)

Sp 41 EDT [redacted]

Total Score: 90

Score = 72 (38.1 bits)
Identities = 12/15 (80%), Positives = 12/15 (80%)

Score = 42 (22.4 bits)
Identities = 9/16 (56%), Positives = 13/16 (75%)

Score = 42 (22.4 bits)
Identities = 7/12 (58%), Positives = 12/12 (92%)

Score = 49 (26.0 bits)
Identities = 8/12 (66%), Positives = 9/12 (75%)

Score = 42 (22.4 bits)
Identities = 7/9 (78%), Positives = 7/9 (78%)

Score = 35 (16.4 bits)
Identities = 6/11 (55%), Positives = 8/11 (73%)

Score = 35 (16.4 bits)
Identities = 6/11 (55%), Positives = 8/11 (73%)

Score = 35 (16.4 bits)
Identities = 6/11 (55%), Positives = 8/11 (73%)

Sp 35 EDT None

Sp EDT other [redacted]

Total Score: 384

Score = 109 (56.9 bits)
Identities = 14/14 (100%), Positives = 14/14 (100%)

Score = 98 (51.4 bits)
Identities = 13/13 (100%), Positives = 13/13 (100%)

Score = 88 (46.1 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)

Score = 76 (40.0 bits)
Identities = 11/11 (100%), Positives = 11/11 (100%)

Score = 72 (38.1 bits)
Identities = 10/10 (100%), Positives = 10/10 (100%)

Score = 72 (38.1 bits)
Identities = 10/10 (100%), Positives = 10/10 (100%)

Score = 72 (38.1 bits)
Identities = 10/10 (100%), Positives = 10/10 (100%)

Score = 67 (35.4 bits)
Identities = 9/9 (100%), Positives = 9/9 (100%)

Hpr: 21

ACC	Charge	Peak MH	Peptide MH	Delta.Obs	Delta.Ppm	Sadder Score	Log Likelihood	Stars	Mod	Sequence	Modifications	Rdbs	Query Desc.
5411.2440	2	2695.4718	2695.4718	0.0000	0.0000	78.6214	115.2467	1	4	YTQCFYYYN	Cysteine(Amethyl) C /	1 / 2	9 De-novo
5411.2440	2	2695.4718	2695.4718	0.0000	0.0000	78.6214	115.2467	1	4	YTQCFYYYN	Cysteine(Amethyl) C /	1 / 2	9 De-novo
796.1377	2	1590.2538	1590.1773	+0.0765	+48.1566	77.7778	426.6342	1	14	QYTFYYYCLGRRER	Deamidation Q	1	De-novo
796.1377	2	1590.2538	1590.1773	+0.0765	+48.1566	77.7778	426.2169	1	14	QYFFYYYCLGRRER	Deamidation Q	1 / 13	De-novo
796.1377	2	1590.2538	1590.1773	+0.0765	+48.1566	77.7778	426.2169	1	14	QYFFYYYCLGRRER	Deamidation Q	1 / 13	De-novo
805.5025	2	1608.9904	1608.4038	+0.5144	+11.5549	76.1565	256.2359	1	14	YLWYRTYCLN	Deamidation N	7	De-novo
571.2984	2	1140.5732	1140.5521	0.0951	4.4006	76.9098	235.1423	1	8	YAQLWWTR	Deamidation Q	2	De-novo
571.2984	2	1140.5732	1140.5521	0.0951	4.4006	76.9098	235.1423	1	8	YAQLWWTR	Deamidation Q /	2 / 7	De-novo
571.2984	2	1140.5732	1140.5521	0.0951	4.4006	76.9098	231.1179	1	8	YLQLWWTR			De-novo
595.3046	2	1178.5936	1178.5951	0.0995	5.4039	75.130	146.1391	1	10	YEELQCYNGR			De-novo
595.3046	2	1178.5936	1178.5951	0.0995	5.4039	75.130	146.1391	1	10	YEELQCYNGR			De-novo
595.3046	2	1178.5936	1178.5951	0.0995	5.4039	75.130	145.4997	1	10	YQELQCYNGR	Deamidation Q	2	De-novo
595.275	2	1176.5344	1176.5557	+0.0213	+18.0170	36.9079	175.1774	1	11	NKAAYRYSLW	Deamidation N	1	De-novo
595.275	2	1176.5344	1176.5557	+0.0213	+18.0170	36.9079	175.1774	1	11	NKAAYRYSLW	Deamidation N	1	De-novo
595.275	2	1176.5344	1176.5557	+0.0213	+18.0170	36.9079	174.2953	1	11	NKAFYRYSLW	Deamidation N	1	De-novo
454.1638	2	906.5123	906.5275	+0.0255	+9.3939	61.0222	173.1914	1	8	KLLYCCCN			De-novo
1042.9852	2	2081.9548	2081.8756	+0.0792	+38.0179	48.4688	247.3279	1	19	TEAWYSSWTRTQQLLKLK	Deamidation W	5	De-novo
1042.9852	2	2081.9548	2081.8756	+0.0792	+38.0179	48.4688	247.3279	1	19	TEAWYSSWTRTQQLLKLK	Deamidation W	5	De-novo
1042.9852	2	2081.9548	2081.8753	+0.0795	+38.0179	48.4688	247.1853	1	19	TEAWYSSWTRTQQLLKLK	Deamidation W	4 / 17	De-novo
1042.9852	2	2081.9548	2081.8753	+0.0795	+38.0179	48.4688	247.1853	1	19	TEAWYSSWTRTQQLLKLK	Deamidation W	4 / 17	De-novo
455.3102	2	1082.6018	1082.4815	+0.1207	+55.5313	76.5887	246.3858	1	12	SLWRGRRRTLGK	Deamidation R	12	De-novo
2779.4974	2	2136.9781	2136.9781	0.0961	1.8997	63.4140	316.1969	1	21	PRRRAAGAWLFLLEEEKCK	Deamidation R	7 / 7 / 20	De-novo
2779.4974	2	2136.9781	2136.9781	0.0961	1.8997	63.4140	316.1969	1	21	PRRRAAGAWLFLLEEEKCK	Deamidation R	7 / 7 / 20	De-novo
727.3480	2	1452.7222	1452.7885	+0.0455	+45.1023	56.6827	111.128	1	13	TLIGFCYCLLLGR			De-novo
727.3480	2	1452.7222	1452.7885	+0.0455	+45.1023	53.5333	111.4919	1	13	TLGFCYCLLLGR			De-novo
801.8420	2	1601.7114	1601.7078	0.0356	2.7472	81.1174	176.7513	1	12	ILLLGLLLWPR			De-novo
801.8420	2	1601.7114	1601.7078	0.0356	2.7472	81.1174	176.7513	1	12	ILLLGLLLWPR			De-novo
801.8420	2	1601.7114	1601.7078	0.0356	2.7472	79.913	198.2262	1	12	ILLLGLLLWQR	Deamidation Q	10	De-novo
801.8420	2	1601.7114	1601.7078	0.0356	2.7472	79.913	198.2262	1	12	ILLLGLLLWQR	Deamidation Q /	10 / 11	De-novo
714.3707	2	1426.7258	1426.7213	0.0555	2.4194	63.7481	141.0154	1	12	LGIYFCLLLGR	Deamidation Q	1 / 8	De-novo
714.3707	2	1426.7258	1426.7213	0.0555	2.4194	65.9402	141.4499	1	12	LGIYFCLLLGR	Cysteine(Amethyl) C /	7 / 9	De-novo
595.3348	2	1188.6560	1188.6536	0.0244	5.0815	96.4211	112.1349	1	10	RYYLWQLLR	Deamidation Q	7	De-novo
595.3348	2	1188.6560	1188.6536	0.0244	5.0815	96.4211	112.1349	1	10	RYYLWQLLR			De-novo
595.3348	2	1188.6560	1188.6536	0.0244	5.0815	96.4211	112.1347	1	10	RYYLWQLLR	Deamidation Q	7	De-novo
622.8313	2	1243.6470	1243.6407	0.0363	5.3445	73.9862	215.1564	1	10	RYYWRYLCQK			De-novo
622.8313	2	1243.6470	1243.6407	0.0363	5.3445	73.9862	215.1564	1	10	RYYWRYLCQK			De-novo
622.8313	2	1243.6470	1243.6407	0.0363	5.3445	98.374	215.1548	1	11	LRDYRRYLCQK	Deamidation R	2	De-novo
801.375	2	1599.7334	1599.7439	+0.0404	+25.2284	42.8571	115.3502	1	14	GRRLGRRRGRRQWQR			De-novo
801.375	2	1599.7334	1599.7439	+0.0404	+25.2284	42.8571	115.3502	1	14	GRRLGRRRGRRQWQR			De-novo
714.9995	2	2136.9781	2136.9781	+0.0234	+1.9350	57.145	218.7405	1	20	TLIGRRAAGLLFLLEEEKCK	Cysteine(Amethyl) C /	7 / 9 / 17	De-novo
714.9995	2	2136.9781	2136.9781	+0.0234	+1.9350	57.145	218.7405	1	20	TLIGRRAAGLLFLLEEEKCK	Cysteine(Amethyl) C /	7 / 9 / 17	De-novo
714.9995	2	2136.9781	2136.9781	+0.0234	+1.9350	51.1148	225.0503	1	20	TLIGRRAAGLLFLLEEEKCK	Cysteine(Amethyl) C /	7 / 17 / 20	De-novo
487.2304	2	972.5172	972.524	+0.0068	+7.0108	66.8969	75.452	1	8	LQLRCGRF	Deamidation Q	2	De-novo
487.2304	2	972.5172	972.524	+0.0068	+7.0108	66.8969	75.452	1	8	LQLRCGRF			De-novo
653.3288	2	1304.6422	1304.63	0.0122	9.3201	77.7778	136.8717	1	11	RTAQRFFLF	Deamidation Q	5	De-novo
854.3806	2	1706.7632	1706.7809	0.2023	1.1535	55.5051	114.7397	1	17	GSGLRFSRSRGRQGRR			De-novo
854.3806	2	1706.7632	1706.7809	0.2023	1.1535	55.5051	114.7397	1	17	GSGLRFSRSRGRQGRR			De-novo
854.3806	2	1706.7632	1706.7809	0.2023	1.1535	49.9949	115.5173	1	17	GSGLRFSRSRGRQGRR			De-novo

NCBI

Score = 106 (54.3 bits)
Identities = 19/57 (86%), Positives = 19/57 (86%)

Score = 77 (40.6 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)

Score = 51 (28.1 bits)
Identities = 8/12 (67%), Positives = 9/12 (75%)

Score = 51 (28.1 bits)
Identities = 8/12 (67%), Positives = 9/12 (75%)

Ncbi BLAST

Score = 106 (54.3 bits)
Identities = 19/57 (86%), Positives = 19/57 (86%)

Score = 77 (40.6 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)

Score = 51 (28.1 bits)
Identities = 8/12 (67%), Positives = 9/12 (75%)

Score = 51 (28.1 bits)
Identities = 8/12 (67%), Positives = 9/12 (75%)

Hpr: 22

ACC	Charge	Peak MH	Peptide MH	Delta.Obs	Delta.Ppm	Sadder Score	Log Likelihood	Stars	Mod	Sequence	Modifications	Rdbs	Query Desc.
1590.2538	2	3179.4931	3179.5076	0.1454	45.7192	78.7778	426.6342	1	28	QYTFYYYCLGRRERRRRRRRRRRR			De-novo
891.5278	2	1781.6400	1781.6558	0.1454	25.6236	56.5317	74.941	1	12	FRRDYRRYLLQK	Deamidation Q	12	De-novo
891.5278	2	1781.6400	1781.6558	0.1454	25.6236	56.5317	74.941	1	12	FRRDYRRYLLQK	Deamidation Q	12	De-novo
815.9229	2	1629.8302	1629.7898	0.3404	24.8734	52.5353	153.245	1	17	TRWFRSSRRTCLWLR	Deamidation R	15	De-novo
815.9229	2	1629.8302	1629.7898	0.3404	24.8734	52.5353	152.982	1	17	TRWFRSSRRTCLWLR			De-novo
815.9229	2	1629.8302	1629.7898	0.3404	24.8734	52.5353	152.982	1	17	TRWFRSSRRTCLWLR	Deamidation R	15	De-novo
714.8705	2	1425.7528	1425.727	0.2511	21.7345	25.2174	136.9924	1	12	TLGRGCYAGRF	Deamidation R	9	De-novo
413.2207	2	844.4328	844.429	0.1049	6.5244	65.5134	61.153	1	8	GRKTPRLS			De-novo
413.2207	2	844.4328	844.429	0.1049	6.5244	65.5134	61.153	1	8	GRKTPRLS			De-novo
555.3121	2	1094.6090	1094.6124	-0.0138	-12.6122	59.5895	205.5924	1	10	YLFYCCYLW			De-novo
555.3121	2	1094.6090	1094.6124	-0.0138	-12.6122	59.5895	196.1924	1	10	LYFYCCYLW			De-novo
555.3121	2	1094.6090	1094.5387	0.0703	65.0875	63.1379	156.9423	1	10	RFFYCCLLW	Deamidation R	1	De-novo

NCBI

Score = 76 (39.7 bits)
Identities = 15/51 (29%), Positives = 15/51 (29%)

Score = 42 (23.7 bits)
Identities = 6/9 (66%), Positives = 8/9 (88%)

Score = 32 (20.1 bits)
Identities = 5/9 (56%), Positives = 6/9 (66%)

Score = 32 (20.1 bits)
Identities = 5/9 (56%), Positives = 6/9 (75%)

Interactive

Score = 76 (39.7 bits)
Identities = 15/51 (29%), Positives = 15/51 (29%)

Score = 42 (23.7 bits)
Identities = 6/9 (66%), Positives = 8/9 (88%)

Score = 32 (20.1 bits)
Identities = 5/9 (56%), Positives = 7/9 (77%)

Ncbi BLAST

Score = 76 (39.7 bits)
Identities = 15/51 (29%), Positives = 15/51 (29%)

Score = 42 (23.7 bits)
Identities = 6/9 (66%), Positives = 8/9 (88%)

Score = 47 (25.4 bits)
Identities = 5/9 (56%), Positives = 6/9 (66%)

Score = 37 (23.0 bits)
Identities = 5/9 (56%), Positives = 5/9 (56%)

Hpt 23

ACC	Charge	Peak MH	Peptide MH	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbs	Query Scan
801,2976	2	1200,5746	1200,5667	+0,0791	+66,0979	5,1429	76,958	1	11	KTRRAGTEQAK			De-novo
801,2976	2	1200,5746	1200,5667	+0,0791	+66,0979	5,1429	76,958	1	11	KTRRAGTEQAK			De-novo
806,8308	2	1201,6540	1201,6461	+0,0792	+65,9207	75,1128	201,0957	1	10	KLSVSEQEAQKSFLK	Deamidation Q	7	De-novo
806,8308	2	1201,6540	1201,6461	+0,0792	+65,9207	75,1128	201,0957	1	10	KLSVSEQEAQKSFLK	Deamidation Q	7	De-novo
809,8118	2	1201,6090	1201,6090	+0,0013	+10,5178	61,9048	202,0797	1	11	HRVCRLMRCAK	Carbamidomethyl C	7	De-novo
809,8118	2	1201,6090	1201,6090	+0,0013	+10,5178	61,9048	202,0797	1	11	HRVCRLMRCAK	Carbamidomethyl C	7	De-novo
809,8118	2	1201,6090	1201,6090	+0,0013	+10,5178	61,9048	202,0797	1	11	HRVCRLMRCAK	Deamidation R 1 / 8		De-novo
809,8118	2	1201,6090	1201,6090	+0,0013	+10,5178	61,9048	202,0797	1	11	HRVCRLMRCAK	Deamidation R 1 / 8		De-novo
723,8619	2	1445,7302	1445,7208	+0,0914	+63,2203	73,3333	246,7579	1	13	FLGRSKSLCRAGN	Deamidation R	5	De-novo
723,8619	2	1445,7302	1445,7208	+0,0914	+63,2203	73,3333	247,1959	1	13	FLGRSKSLCRAGN	Deamidation R 2 / 9		De-novo
723,8619	2	1445,7302	1445,7208	+0,0914	+63,2203	73,3333	247,1959	1	13	FLGRSKSLCRAGN	Deamidation R	5	De-novo
598,3449	2	1196,6742	1196,6732	0,0952	1,8514	57,1429	75,1318	1	11	HSVTCTRLLF			De-novo
598,3449	2	1196,6742	1196,6732	0,0952	1,8514	62,9571	77,1952	1	11	HSVTCTRLLF			De-novo
735,3874	2	1470,7502	1470,7389	0,1093	74,3371	66,9667	286,1393	1	14	LTSTCGRETCTGRF	Oxidation M	9	De-novo
735,3874	2	1470,7502	1470,7389	0,1093	74,3371	66	286,1393	1	14	LTSTCGRETCTGRF	Oxidation M	9	De-novo
735,3874	2	1470,7502	1470,7389	0,1093	74,3371	66,9667	286,1713	1	14	TLSTCGRETCTGRF	Oxidation M	9	De-novo
735,3874	2	1470,7502	1470,7389	0,1093	74,3371	66,9667	286,1713	1	14	TLSTCGRETCTGRF	Oxidation M	9	De-novo
562,7609	2	1123,5122	1123,5140	-0,0014	-1,2375	57,8947	119,7669	1	10	GSSLSRLRGR	Deamidation R	7	De-novo
562,7609	2	1123,5122	1123,5140	-0,0014	-1,2375	57,8947	119,7669	1	10	GSSLSRLRGR	Deamidation R	8	De-novo
562,7609	2	1123,5122	1123,5140	-0,0014	-1,2375	56,1404	121,4172	1	10	GSSLSRLRGR	Deamidation R	8	De-novo
735,3897	2	1469,7638	1469,7561	+0,0002	+0,1538	76,9667	236,8213	1	14	TLSTCGRETCTGR			De-novo
735,3897	2	1469,7638	1469,7561	+0,0002	+0,1538	76,9667	236,8213	1	14	TLSTCGRETCTGR			De-novo
735,3897	2	1469,7638	1469,7561	+0,0002	+0,1538	77,3333	236,7913	1	13	LTSTCGRETCTGR	Deamidation Q	12	De-novo
735,3897	2	1469,7638	1469,7561	+0,0002	+0,1538	77,3333	236,7913	1	13	LTSTCGRETCTGR	Deamidation Q	12	De-novo
701,8308	2	1401,6616	1401,6572	0,0392	28,0733	26,7914	151,759	1	14	ARVTGHAGCGVGHR	Deamidation R	14	De-novo
874,2131	2	994,8168	994,4927	+0,3791	+81,4778	52,9824	155,9769	1	8	ESEFCTAH			De-novo
723,8620	2	1445,5958	1445,7071	-0,1113	-77,0155	26,5926	47,48	1	14	GSSLSLSRRCTGR			De-novo
723,8620	2	1445,5958	1445,7071	-0,1113	-77,0155	26,5926	47,48	1	14	GSSLSLSRRCTGR	Carbamidomethyl C	12	De-novo
723,8620	2	1445,5958	1445,7096	-0,1138	-81,5693	66,6667	84,922	1	13	RSSLSLSRRCRCR	Carbamidomethyl C	12	De-novo
723,8620	2	1445,5958	1445,7096	-0,1138	-81,5693	66,6667	84,922	1	13	RSSLSLSRRCRCR	Carbamidomethyl C	12	De-novo
804,3927	2	1605,7017	1605,7108	-0,0091	-5,6122	54,6667	141,9943	1	15	EGLPRSLSRLRGR	Deamidation R	2 / 8	De-novo
804,3927	2	1605,7017	1605,7108	-0,0091	-5,6122	54,6667	141,9943	1	15	EGLPRSLSRLRGR	Deamidation R	8	De-novo
703,8308	2	1405,6540	1405,6519	0,0202	14,3511	56,6207	276,5372	1	14	ARVTGHVGPGVGLQ			De-novo
703,8308	2	1405,6540	1405,6519	0,0202	14,3511	56,6207	276,5372	1	14	ARVTGHVGPGVGLQ			De-novo
703,8308	2	1405,6540	1405,6519	0,0202	14,3511	56,6207	276,5372	1	14	ARVTGHVGPGVGLQ	Deamidation R	14	De-novo

MSMS [p:1]:[0]:[0]:[0

Spot 26

ACY	Change	Peak HM	Peak% HM	Valley HM	Valley 2Sd	Valley Sigma	Sashimi Score	Log Likelihood	Stars	Hom	Sequence	Motif/Cutscore	Duke	Query Posi...
904.7420	2	1017.5102	100.0000	1017.5102	0.0000	0.0000	0.0000	-10.0000	1	12	CCGGGGGGCCGC		0	De-novo
904.7420	2	1017.5102	100.0000	1017.5102	-0.0000	-0.0000	0.0000	-10.0000	1	12	AGAGAGTCCGGG		0	De-novo
904.7420	2	1017.5102	100.0000	1017.5102	-0.0000	-0.0000	0.0000	-10.0000	1	12	CCGGGGGGCCGC		0	De-novo
927.8300	2	1255.8628	100.0000	1255.8628	-0.0000	-0.0000	-0.0000	-10.0000	1	12	CCGGGGGGCCGC	DeepLearcun 0	0	De-novo
927.8300	2	1255.8628	100.0000	1255.8628	-0.0000	-0.0000	-0.0000	-10.0000	1	12	CCGGGGGGCCGC	DeepLearcun 0	0	De-novo
927.8300	2	1255.8628	100.0000	1255.8628	-0.0000	-0.0000	-0.0000	-10.0000	1	12	CCGGGGGGCCGC	DeepLearcun 0	0	De-novo
925.8608	2	1949.7120	100.0000	1949.6768	0.1352	21.5230	53.0864	136.2124	1	14	CGCCGGCCGCCGCCGC	DeepLearcun 0	3 / 11	De-novo
925.8608	2	1949.7120	100.0000	1949.6768	0.1352	21.5230	53.0864	136.2124	1	14	CGCCGGCCGCCGCCGC	DeepLearcun 0	3 / 11	De-novo
925.8608	2	1949.7120	100.0000	1949.6768	0.1352	21.5230	53.0864	136.2124	1	14	CGCCGGCCGCCGCCGC	DeepLearcun 0	3 / 11	De-novo
917.9460	2	1455.7170	100.0000	1455.7181	-0.0011	-0.0005	67.9012	170.4869	1	14	CGCCGGGGGCCGCCGC	DeepLearcun 0		De-novo
917.9460	2	1455.7170	100.0000	1455.7181	-0.0011	-0.0005	67.9012	170.4869	1	14	CGCCGGGGGCCGCCGC	DeepLearcun 0		De-novo
917.9460	2	1455.7170	100.0000	1455.7181	-0.0011	-0.0005	67.9012	170.4869	1	14	CGCCGGGGGCCGCCGC	DeepLearcun 0		De-novo
896.8754	2	1391.7202	100.0000	1391.7256	0.0956	6.2040	75.5823	257.2144	1	12	CCGGCCGCCCGC	DeepLearcun 0	3 / 8	De-novo
896.8754	2	1391.7202	100.0000	1391.7256	0.0956	6.2040	75.5823	257.2144	1	12	CCGGCCGCCCGC	DeepLearcun 0	3 / 8	De-novo
896.8754	2	1391.7202	100.0000	1391.7256	0.0956	6.2040	75.5823	257.2144	1	12	CCGGCCGCCCGC	DeepLearcun 0	3 / 8	De-novo
702.8787	2	1403.7378	100.0000	1403.7404	-0.0371	-0.0750	26.9270	25.9782	1	11	CCGCCCACCCG	DeepLearcun 0	7	De-novo
702.8787	2	1403.7378	100.0000	1403.7404	-0.0371	-0.0750	26.9270	25.9782	1	11	CCGCCCACCCG		7	De-novo
702.8787	2	1403.7378	100.0000	1403.7404	-0.0371	-0.0750	26.9270	25.9782	1	11	CCGCCCACCCG		7	De-novo

NCBI [ref|NC_000070.6| [gi|89511947|ref|NC_00 ...] Score Score: 131

```
                                    0        40        80       120       160
                                    |         |         |         |         |     173
gi|89511947|ref|NC_00 Score Score 100%%
                        ------------ -----

Score = 114 (57.4 bits)
Identities = 14/14 (87%), Positives = 13/14 (92%)

Query:  110 UGCGGGGGGAGCGCGC 125
            UGCG GGGAGCGCGC
Sbjct:  ---- 4 UGCCGGGGGCGCGC 19  Matching

Score = 103 (52.0 bits)
Identities = 12/12 (75%), Positives = 12/12 (100%)

Query:  103 UGCGGGGGGCGCGCGC 125
            UGCG GGGCGCGCGC
Sbjct:  ---- 1 UGCCGGGGGCGCGCGC 16  Matching

Score = 42 (21.1 bits)
Identities = 9/13 (69%), Positives = 12/13 (92%)

Query:  129 GCGGGCGCGCGGCC 153
            GCG+GCGCGC G +
Sbjct:  ---- 21 GCGCGCGCGCGCG 35  Matching

Score = 40 (19.1 bits)
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query:  35 GCGGGCGGG 43
           GCGGGCGGG
Sbjct:  ---- 79 GCGGGCGGG 88  Matching
```

Spot 27

ACY	Change	Peak HM	Peak% HM	Valley HM	Valley 2Sd	Valley Sigma	Sashimi Score	Log Likelihood	Stars	Hom	Sequence	Motif/Cutscore	Duke	Query Posi...
932.7278	2	1031.9400	100.0000	1031.9400	0.0000	0.0000	0.0000	-10.0000	1	9	GAACCCGG		0	De-novo
932.7278	2	1031.9400	100.0000	1031.9400	-0.0000	-0.0000	0.0000	-10.0000	1	9	GAACCCGG	CustomCombo(Gc) C	0 / 5	De-novo
911.7605	2	1331.3594	100.0000	1331.3587	-0.0000	-0.0179	0.0000	31.2587	1	11	CGCGCGGCCGC	DeepLearcun 0	4	De-novo
911.8139	2	1245.6142	100.0000	1245.6136	-0.0016	-0.0023	0.0000	36.5070	1	11	CAAAGCGCCCG	DeepLearcun 0	7	De-novo

NCBI [ref|NC_000070.6| [gi|89511947|ref|NC_00 ...] Score Score: 1.1

```
                                    0        10        20
                                    |         |         |     20
gi|77753:GR:NBEDCHER Score Score 100%%
                        ------------

Score = 43 (23.7 bits)
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query:  1 GAACCCGG 8
          GAACCCGG
Sbjct:  ---- 1 GAACCCGG 8  Matching

Score = 43 (23.7 bits)
Identities = 8/8 (100%), Positives = 8/8 (100%)

Query:  1 GAACCCGG 8
          GAACCCGG
Sbjct:  ---- 10 GAACCCGG 17
```

Ex 03 EDF [ref|NC_000070.6| [gi|89511947|ref|NC_00 ...] Score Score: 14

```
                                    0        40        80       120       160
                                    |         |         |         |         |     203
hasgin:GR:EGK_Cerlia_ Score Score 100%%
                        ------------ -----

Score = 43 (23.7 bits)
Identities = 8/9 (100%), Positives = 9/9 (100%)

Query:  1 GAACCCGGG 9
          GAACCCGGG
Sbjct:  ---- 10 GAACCCGGG 109
```

Spot 28

ACY	Change	Peak HM	Peak% HM	Valley HM	Valley 2Sd	Valley Sigma	Sashimi Score	Log Likelihood	Stars	Hom	Sequence	Motif/Cutscore	Duke	Query Posi...
878.2274	2	934.4986	100.0000	934.4985	-0.1103	-0.0000	95.9000	95.9000	1	8	GCCCGCCG		0	De-novo
878.2274	2	934.4986	100.0000	934.4985	-0.1103	-0.0000	95.9000	95.9000	1	8	GCCCGCCG		0	De-novo
826.2720	2	1255.9310	100.0000	1255.9708	-0.1438	-35.0431	69.5310	235.2719	1	13	CCGGCCCGCGCCG	CustomCombo(Gc) C	3	De-novo
826.2720	2	1255.9310	100.0000	1255.9708	-0.1438	-35.0431	69.5310	235.2719	1	13	CCGGCCCGCGCCG	CustomCombo(Gc) C	3	De-novo
826.2720	2	1255.9310	100.0000	1255.9708	-0.1438	-35.0431	69.5310	235.2719	1	13	CCGGCCCGCGCCG		3	De-novo
501.8044	2	1181.5932	100.0000	1181.6136	-0.1284	-12.3247	81.5397	191.2722	1	11	GCGGGCGGCGC	DeepLearcun 0	5	De-novo
501.8044	2	1181.5932	100.0000	1181.6136	-0.1284	-12.3247	81.5397	191.2722	1	11	GCGGGCGGCGC	DeepLearcun 0	5 / 5	De-novo
501.8044	2	1181.5932	100.0000	1181.6136	-0.1284	-12.3247	81.5397	191.2722	1	11	GCGGGCGGCGC		5	De-novo
449.3714	2	1196.7282	100.0000	1196.7401	-0.1119	-9.1994	35.3333	91.1919	1	12	CCCCGGCGGGGG	DeepLearcun 0	0	De-novo
449.3714	2	1196.7282	100.0000	1196.7401	-0.1119	-9.1994	35.3333	91.1919	1	12	CCCCGGCGGGGG			De-novo
449.3714	2	1196.7282	100.0000	1196.7401	-0.1119	-9.1994	35.3333	91.1919	1	12	CCCCGGCGGGGG			De-novo
1271.5137	2	2544.0118	100.0000	2544.1969	-0.0231	-0.5895	95.1705	217.5254	1	25	PGQCGCGGCGGCCGGCCGCCGCCCC	DeepLearcun 0 /	7 / 23 / 25	De-novo
1271.5137	2	2544.0118	100.0000	2544.1969	-0.0231	-0.5895	95.1705	217.5254	1	25	PGQCGCGGCGGCCGGCCGCCGCCCC	DeepLearcun 0 /	7 / 23 / 25	De-novo
1271.5137	2	2544.0118	100.0000	2544.1969	-0.0231	-0.5895	95.1705	217.5254	1	25	PGQCGCGGCGGCCGGCCGCCGCCCC			De-novo
861.8964	2	1765.7772	100.0000	1765.7963	-0.0171	-0.6876	67.4767	175.3543	1	17	GGGGGCGCCGCGGCCCC			De-novo
861.8964	2	1765.7772	100.0000	1765.7963	-0.0171	-0.6876	67.4767	175.3543	1	17	GGGGGCGCCGCGGCCCC			De-novo
861.8964	2	1765.7772	100.0000	1765.7963	-0.0171	-0.6876	67.4767	175.3543	1	17	GGGGGCGCCGCGGCCCC			De-novo
813.2132	2	924.4108	100.0000	924.4102	0.1008	0.4997	38.6615	51.8208	1	7	GGTGCGC		0	De-novo
813.2132	2	924.4108	100.0000	924.4102	0.1008	0.4997	38.6615	51.8208	1	7	GGTGCGC	DeepLearcun 0 / DeepLearcun	3 / 5	De-novo
813.2132	2	924.4108	100.0000	924.4102	0.1008	0.4997	38.6615	51.8208	1	7	GGTGCGC	DeepLearcun 0 / DeepLearcun	3 / 5	De-novo
727.7045	2	2034.5901	100.0000	2034.6529	-0.0276	-16.5993	97.1984	97.7224	1	21	CGCGGCGCCGGCCGCCGCCGC	DeepLearcun 0	0	De-novo
727.7045	2	2034.5901	100.0000	2034.6529	-0.0276	-16.5993	97.1984	97.7224	1	21	CGCGGCGCCGGCCGCCGCCGC	DeepLearcun 0	0	De-novo
727.7045	2	2034.5901	100.0000	2034.6529	-0.0276	-16.5993	97.1984	97.7224	1	21	CGCGGCGCCGGCCGCCGCCGC		0	De-novo

NCBI [ref|NC_000070.6| [gi|89511947|ref|NC_00 ...] Score Score: 14

```
                                    0        40        80       120       160
                                    |         |         |         |         |     160
gi|1169852629:gp:GAEFAA Score Score 100%%
                        ------------ -----

Score = 77 (41.6 bits)
Identities = 14/15 (93%), Positives = 14/15 (93%)

Query:  70 RGRLGTGCLGRRGGCGTGCCGCA 84
           RGRL  L GRRGGCGTGCCGCA
Sbjct:  ---- 157 RGRLRGCLGRRGGCGTGCCGCA 143  Matching

Score = 38 (21.1 bits)
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query:  9 YRRRR 8
          YRRRR
Sbjct:  ---- 33 YRRRR 87
```

Ex 03 EDF [ref|NC_000070.6| [gi|89511947|ref|NC_00 ...] Score Score: 14

```
                                    0        40        80       120       160
                                    |         |         |         |         |     160
hasgin:GR:EGK_Cerlia_ Score Score 100%%
                        ------------ -----

Score = 77 (41.6 bits)
Identities = 14/15 (93%), Positives = 14/15 (93%)

Query:  70 RGRLGTGCLGRRGGCGTGCCGCA 84
           RGRL  L GRRGGCGTGCCGCA
Sbjct:  ---- 158 RGRLRGCLGRRGGCGTGCCGCA 144

Score = 38 (21.1 bits)
Identities = 5/5 (100%), Positives = 5/5 (100%)

Query:  9 YRRRR 8
          YRRRR
Sbjct:  ---- 83 YRRRR 87
```

Hpr 29

ACC	Change	Pos# AM	Neg#AM AM	Delta Obj	Delta Lgmv	Lambda Score	log Likelihood	Steps	Ins	Sequence	Modifications	Rdm	Query Seq.
815,2399	2	814,842	814,840	-0.0013	-0.0015	-0.0479	-14,2169	1	4	QSEVRLTCR	Cochaetomarius C	1	De-novo
815,2399	2	844,842	844,840	-0.0013	-0.0479	-0.0479	16,1917	1	4	QSEVRLTCR	Deadalnin Q	1	De-novo
815,3281	2	1224,4348	1224,4346	-0.0196	-0.0196	-0.0268	75,1122	1	12	EGYEFEWAAVR	Deadalnin H	1	De-novo
815,3281	2	1224,4348	1224,4346	-0.0196	-0.0268	-0.0268	216,1122	1	12	EGYEFEWAAVR		1	De-novo
815,3281	2	1224,4348	1224,4346	-0.0196	-0.0268	-0.0268	213,9977	1	12	EGYEFEWAAVR		1	De-novo
815,3281	2	1224,4348	1224,4346	-0.0196	-0.0268	-0.0268	213,9977	1	12	EGYEFEWAAVR		1	De-novo
817,7481	2	873,4816	873,4236	-0.2343	-0.7365	-0.5867	95,7714	1	4	GRWRSCLK		1	De-novo
817,7481	2	873,4816	873,4236	-0.2343	-0.7365	-0.5867	97,1111	1	4	GRWRSCLK		1	De-novo
826,8062	2	1071,4382	1071,4382	-0.0242	-0.0242	-0.0242	16,9889	1	12	CLAVLQLCLLSP		1	De-novo

MSMS [redacted] Total Score: 19

```
                    0        40        80       120       160
                    |         |         |         |         |
                    |         |         |         |         |
                    |         |         |         |         |
gi|194215767|gb|AC0M47 |
Local Score 0MPMs   |
                    |         |         |         |         |
                    0        40        80       120       160
```

Score = 88 (28.3 bits)
Identities = 12/18 (66%), Positives = 12/18 (66%)

```
Query:   54 SPLEPMMSPLPSPSMMSP 71
            SP EEP  MP EEP  SP
Sbjct:   [redacted]
```

Acetylation None

Ac 36 EEP [redacted] Total Score: 19

```
                    0        40        80       120       160       200
                    |         |         |         |         |         |
                    |         |         |         |         |         |
                    |         |         |         |         |         |
hanjin-Ub-EGK_Cerlig |
Local Score 0MPMs   |
                    |         |         |         |         |         |
                    0        40        80       120       160       200
```

Score = 34 (16.2 bits)
Identities = 7/9 (77%), Positives = 8/9 (88%)

```
Query:   56 SMLEPSTLS 64
            SMLEP  LS
Sbjct:   [redacted]
```

Score = 32 (15.2 bits)
Identities = 7/11 (63%), Positives = 8/11 (72%)

```
Query:   115 SMTMLEPSTLS 125
             S  MLEP  LS
Sbjct:   [redacted]
```

Hpr 30

ACC	Change	Pos# AM	Neg#AM AM	Delta Obj	Delta Lgmv	Lambda Score	log Likelihood	Steps	Ins	Sequence	Modifications	Rdm	Query Seq.
1224,8212	2	1223,4872	1223,4870	-0.0019	-0.0019	-0.0479	16,7969	1	4	EGYEFEYQAW	Cochaetomarius C	1	De-novo
871,8214	2	1223,4872	1223,4870	-0.0019	-0.0479	-0.0479	61,8948	1	12	EGYEFEYQAW	Deadalnin H	1	De-novo
871,8214	2	1223,4872	1223,4870	-0.0019	-0.0479	-0.0479	111,479	1	12	EGYEFEYQAW		1	De-novo
766,3981	2	1495,7746	1495,8050	-0.1947	-15.2920	-15.5207	35,4537	1	13	YSTGSQLEQSYLK	Deadalnin H	12	De-novo
766,3981	2	1495,7746	1495,8050	-0.1947	-15.2920	-15.5207	36,8948	1	13	YSTGSQLEQSYLK			De-novo
766,3981	2	1495,7746	1495,8050	-0.1947	-15.2920	-15.5207	37,1479	1	13	YSTGSQLEQSYLK			De-novo
945,5109	2	1122,4002	1122,4073	-0.0511	-0.0512	-0.0547	15,5414	1	4	LFTVCDRA	Deadalnin Q	1	De-novo
945,5109	2	1122,4002	1122,4073	-0.0511	-0.0512	-0.0547	44,4687	1	4	LFTVCDRA		1	De-novo
945,5109	2	1122,4002	1122,4073	-0.0511	-0.0512	-0.0547	46,7059	1	4	LFTVCDRA		1	De-novo
871,7562	2	913,5668	913,587	-0.2202	-0.2202	-0.2452	15,7778	1	4	GRLLCLK	Deidelin M	2	De-novo
871,7562	2	913,5668	913,587	-0.2202	-0.2202	-0.2452	15,7778	1	4	GRLLCLK		2	De-novo
871,7562	2	913,5668	913,587	-0.2202	-0.2202	-0.2452	30,448	1	4	GRLLCLK		2	De-novo
535,29	2	1208,5944	1208,5408	0.2036	3.3742	2.7742	15,7778	1	5	EGRCTEQLK	Deadalnin Q	1 / 6	De-novo
535,29	2	1208,5944	1208,5408	0.2036	3.3742	2.7742	24,752	1	5	EGRCTEQLK		1	De-novo
535,29	2	1208,5944	1208,5408	0.2036	3.3742	2.7742	44,7059	1	5	EGRCTEQLK		1	De-novo

MSMS [redacted] Total Score: 19

```
                    0        100       200       300       400
                    |         |         |         |         |
                    |         |         |         |         |
                    |         |         |         |         |
gi|194464287|gb|AM0YM |
Local Score 0MPMs   |
                    |         |         |         |         |
                    0        100       200       300       400
```

Score = 88 (28.3 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)

```
Query:   110 MMLEPMMLM 118
             MMLEPMMLM
Sbjct:   [redacted]
```

Acetylation None

Ac 40 EEP [redacted] Total Score: 114

```
                    0        100       200       300       400       500
                    |         |         |         |         |         |
                    |         |         |         |         |         |
                    |         |         |         |         |         |
hanjin-Ub-EGK_Cerlig |
Local Score 0MPMs   |
                    |         |         |         |         |         |
                    0        100       200       300       400       500
```

Score = 69 (36.4 bits)
Identities = 8/12 (75%), Positives = 11/12 (91%)

```
Query:   12 MSPSPSPQAW 23
            MSPSPSPQAW
Sbjct:   [redacted]
```

Score = 45 (24.3 bits)
Identities = 5/6 (83%), Positives = 6/6 (100%)

```
Query:   118 LLLFLRKL 125
             LLLFLRKL
Sbjct:   [redacted]
```

Score = 42 (22.8 bits)
Identities = 5/6 (83%), Positives = 6/6 (100%)

```
Query:   108 LLLFLRKL 115
             LLLFLRKL
Sbjct:   [redacted]
```

Hpr 31

ACC	Change	Pos# AM	Neg#AM AM	Delta Obj	Delta Lgmv	Lambda Score	log Likelihood	Steps	Ins	Sequence	Modifications	Rdm	Query Seq.
871,2104	2	936,4510	936,4532	-0.0513	-1.7365	-1.7365	33,5333	1	4	AFLFCTCY	Cochaetomarius C	1	De-novo
871,2104	2	936,4510	936,4532	-0.0513	-1.7365	-1.7365	46,6066	1	4	AFLFCTCY	Cochaetomarius C	1	De-novo
871,2104	2	936,4510	936,4532	-0.0513	-1.7365	-1.7365	48,9333	1	4	AFLFCTCY		1	De-novo
596,3458	2	1134,4750	1134,472	-0.1340	-1.5291	-1.5291	36,5667	1	13	QSSYPCCFNAGYR			De-novo
596,3458	2	1134,4750	1134,472	-0.1340	-1.5291	-1.5291	36,752	1	13	QSSYPCCFNAGYR			De-novo
596,3458	2	1134,4750	1134,472	-0.1340	-1.5291	-1.5291	38,6667	1	13	QSSYPCCFNAGYR			De-novo
894,5704	2	1366,7272	1366,7404	-0.1684	-6.1435	-7.7333	27,4667	1	13	YVVNCTSCLYCFR	Deadalnin H	6 / 12	De-novo
894,5704	2	1366,7272	1366,7404	-0.1684	-6.1435	-7.7333	28,7333	1	13	YVVNCTSCLYCFR		6 / 12	De-novo
894,5704	2	1366,7272	1366,7404	-0.1684	-6.1435	-7.7333	283,9016	1	13	YVVNCTSCLYCFR			De-novo
816,903	2	1655,7804	1655,8025	-0.0111	-0.2345	-0.2345	21,9333	1	13	TLCYCLEQCEQLQF			De-novo
816,903	2	1655,7804	1655,8025	-0.0111	-0.2345	-0.2345	71,248	1	13	TLCYCLEQCEQLQF			De-novo
816,903	2	1655,7804	1655,8025	-0.0111	-0.2345	-0.2345	78,532	1	13	TLCYCLEQCEQLQF	Deadalnin Q	8	De-novo
731,3917	2	1491,7276	1491,7022	0.0358	0.8172	18	211,2948	1	13	TCQNHCCYYFFPR	Deadalnin H	5	De-novo
731,3917	2	1491,7276	1491,7022	0.0358	0.8172	18	211,2948	1	13	TCQNHCCYYFFPR		5	De-novo
731,3917	2	1491,7276	1491,7022	0.0358	0.8172	18	211,2948	1	13	TCQNHCCYYFFPR	Deadalnin H	5	De-novo

MSMS [redacted] Total Score: 43

```
                    0        20        40        60        80
                    |         |         |         |         |
                    |         |         |         |         |
                    |         |         |         |         |
gi|747980|sp|P81171 |
Local Score 0MPMs   |
                    |         |         |         |         |
                    0        20        40        60        80
```

Score = 45 (24.4 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)

```
Query:   72 YVNNPPPNL 80
            YV NPPPN
Sbjct:   [redacted]
```

Score = 41 (22.8 bits)
Identities = 6/9 (66%), Positives = 6/9 (66%)

```
Query:   81 PPNAP 96
            PPNAP
Sbjct:   [redacted]
```

Score = 35 (19.4 bits)
Identities = 5/5 (100%), Positives = 5/5 (100%)

```
Query:   84 YPNAP 88
            YPNAP
Sbjct:   [redacted]
```

Score = 35 (19.4 bits)
Identities = 5/5 (100%), Positives = 5/5 (100%)

```
Query:   101 YNPPP 106
             YNPPP
Sbjct:   [redacted]
```

Score = 31 (18.4 bits)
Identities = 5/9 (55%), Positives = 5/9 (55%)

```
Query:   175 NAPPPP 180
             N PP PP
Sbjct:   [redacted]
```

Acetylation [redacted] Total Score: 48

```
                    0        40        80       120
                    |         |         |         |
                    |         |         |         |
                    |         |         |         |
dc|NP00109.1|MP0109 |
Local Score 0MPMs   |
                    |         |         |         |
                    0        40        80       120
```

Score = 85 (28.5 bits)
Identities = 16/17 (94%), Positives = 16/17 (94%)

```
Query:   46 YVDGTGSLSYMPPPVNGTMGLVPMPPPGSLQYP 100
            YVD  GTS  Y PP  N  MGLVPMPPPGSLQYP
Sbjct:   [redacted]
```

Score = 75 (25.3 bits)
Identities = 14/16 (88%), Positives = 17/16 (106%)

```
Query:   42 YVDGTGSLSYMPPPVNGTMGLVPMPPPGSLQYP 92
            YVD  GTS  Y PP  N  MGLVPMPPPGSLQYP
Sbjct:   [redacted]
```

Ac 41 EEP [redacted] Total Score: 45

```
                    0        40        80       120       160
                    |         |         |         |         |
                    |         |         |         |         |
                    |         |         |         |         |
hanjin_Ub-Ub-Ub-Ub_ |
Local Score 0MPMs   |
                    |         |         |         |         |
                    0        40        80       120       160
```

Score = 101 (32.6 bits)
Identities = 14/15 (93%), Positives = 15/15 (100%)

```
Query:   136 MTQQQQQQQYPPM 152
             MTQQQQQQQYPPM
Sbjct:   [redacted]
```

Score = 91 (47.4 bits)
Identities = 12/14 (85%), Positives = 13/14 (92%)

```
Query:   49 MYPPMMGQLPPMPM 62
            MYPPMMGQLPPMPM
Sbjct:   [redacted]
```

Score = 32 (21.6 bits)
Identities = 6/8 (100%), Positives = 8/8 (100%)

```
Query:   8 MPLMPPPM 16
           MPLMPPPM
Sbjct:   [redacted]
```

Hpr 32

ACC	Change	Pos# AM	Neg#AM AM	Delta Obj	Delta Lgmv	Lambda Score	log Likelihood	Steps	Ins	Sequence	Modifications	Rdm	Query Seq.
595,3074	2	1176,5992	1176,5901	0.0681	5,1553	75,5882	96,179	1	4	YMSLLQTQK			De-novo
595,3074	2	1176,5992	1176,5901	0.0681	5,1553	75,5882	96,914	1	5	YQFLSCTLK	Deadalnin Q	2	De-novo
595,3074	2	1176,5992	1176,5901	0.0681	5,1553	75,5882	102,649	1	5	YQFLSCTLK	Deadalnin A	2	De-novo
894,5525	2	1202,4366	1202,5296	-0.2038	-20,4277	61,538	152,649	1	12	GRLCRRCSLQPL			De-novo
894,5525	2	1202,4366	1202,5296	-0.2038	-20,4277	61,538	152,649	1	12	GRLCRRCSLQPL			De-novo
894,5525	2	1202,4366	1202,5296	-0.2038	-20,4277	61,538	152,649	1	12	GRLCRRCSLQPL			De-novo
894,5525	2	1202,4366	1202,5296	-0.2038	-20,4277	61,538	152,649	1	12	GRLCRRCSLQPL			De-novo
894,5525	2	1202,4366	1202,5296	-0.2038	-20,4277	61,538	152,649	1	12	GRLCRRCSLQPL	Deidelin M / Deadalnin	2 / 8	De-novo
894,5525	2	1202,4366	1202,5296	-0.2038	-20,4277	61,538	152,649	1	12	GRLCRRCSLQPL	Deidelin M / Deadalnin	2 / 8	De-novo

MSMS [redacted] Total Score: 16

```
                    0        20        40        60        80
                    |         |         |         |         |
                    |         |         |         |         |
                    |         |         |         |         |
gi|77942419|gb|AM0K00 |
Local Score 0MPMs   |
                    |         |         |         |         |
                    0        20        40        60        80
```

Score = 87 (26.4 bits)
Identities = 8/9 (88%), Positives = 9/9 (100%)

```
Query:   39 PLMMPCPM 47
            PLMMPCPM
Sbjct:   [redacted]
```

Score = 35 (19.4 bits)
Identities = 6/9 (66%), Positives = 8/9 (88%)

```
Query:   63 MPLMPPL 70
            MPLMPPL
Sbjct:   [redacted]
```

Ac 46 EEP [redacted] Total Score: 16

```
                    0        40        80       120       160       200
                    |         |         |         |         |         |
                    |         |         |         |         |         |
                    |         |         |         |         |         |
hanjin-Ub-EGK_Cerlig |
Local Score 0MPMs   |
                    |         |         |         |         |         |
                    0        40        80       120       160       200
```

Score = 87 (26.4 bits)
Identities = 8/9 (88%), Positives = 9/9 (100%)

```
Query:   79 PLMMPCPM 87
            PLMMPCPM
Sbjct:   [redacted]
```

Score = 35 (19.4 bits)
Identities = 6/9 (66%), Positives = 8/9 (88%)

```
Query:   93 MPLMPPL 100
            MPLMPPL
Sbjct:   [redacted]
```

Spot 32

ACX	Charge	Peak AM	Peak/Lim AM	Valle Abs	Valle Sgmt	Ladder Score	Log Likelihood	Start	Age	Sequence	Modification	Date	Query Seq.
504,7527	2	2147,4898	2147,4917	-0,0019	-0,0019	-0,0019	-72,2137	1	10	QEQQQQQQQK	Deamidation Q / Deamidation	2 / 9	De-novo
504,7527	2	2147,4898	2147,4917	-0,0019	-1,8024	57,6947	-72,2137	1	10	NYFGYYYYNN	Oxidation M / Deamidation	2 / 9	De-novo
504,7569	2	1051,4982	1051,4968	0,0014	0,0014	0,0014	126,1549	1	10	YNYYYYYYNN	Deamidation N	8	De-novo
504,7569	2	1051,4982	1051,4968	0,0014	-1,3389	70,1734	126,1549	1	10	YNYYYYYYNN	Deamidation N	8	De-novo
504,7569	2	1051,4982	1051,4968	0,0014	1,3389	70,1734	126,1549	1	10	YNYYYYYYNN	Deamidation N	9	De-novo
504,7569	2	1051,4982	1051,4968	0,0014	0,0014	0,0014	126,1549	1	10	YNYYYYYYNN	Deamidation N	9	De-novo
505,2262	2	994,4540	994,4552	-0,0011	-0,0019	73,1112	108,4294	1	9	MLYNYNLNK	Oxidation M	4	De-novo
505,281	2	1079,5664	1079,5658	0,0006	0,5565	69,9413	212,6752	1	11	QTLAPYAYRIR	Deamidation Q	1	De-novo
505,281	2	1079,5664	1079,5658	0,0006	-0,5565	69,9413	212,6752	1	11	QTLAPYAYRIR	Deamidation Q	1	De-novo
505,281	2	1079,5664	1079,5658	0,0006	0,5565	69,9413	212,6752	1	11	QTLAPYAYRIR	Deamidation Q	1	De-novo
505,3125	2	1225,6512	1225,6489	0,0177	-14,4609	68,9413	113,989	1	11	LRRLGNRYCR	Carbamidomethyl C	10	De-novo
505,3125	2	1225,6512	1225,6489	0,0177	14,4609	68,9413	113,989	1	11	LRRLGNRYCR	Carbamidomethyl C	10	De-novo
505,3125	2	1225,6512	1225,6489	0,0177	0,0177	0,0177	113,989	1	11	LRRLGNRYCR			De-novo
505,3125	2	1225,6512	1225,6489	0,0177	-14,3793	69,4915	113,989	1	11	LRRLGNRYCR	Carbamidomethyl C	10	De-novo
505,3125	2	1225,6512	1225,6489	0,0177	14,3793	69,4915	113,989	1	11	LRRLGNRYCR	Carbamidomethyl C	10	De-novo
505,3296	2	1096,5632	1096,5648	-0,0013	-0,1542	68,4274	95,1942	1	9	QLELAFRYF	Deamidation Q	1	De-novo
505,6987	2	1765,7818	1765,7862	-0,0125	-7,0926	65,4545	105,2138	1	17	RQEGGYEGCLGNCRKYE	Deamidation Q / Oxidation	2 / 3	De-novo
505,6987	2	1765,7818	1765,7862	-0,0125	7,0926	65,4545	105,2138	1	17	RQEGGYEGCLGNCRKYE	Deamidation Q / C	2 / 7	De-novo
505,6987	2	1765,7818	1765,7862	-0,0125	-7,1529	65,4545	105,6522	1	17	KSTQEGGYLGNCRNKTE	Deamidation Q	5	De-novo
505,7725	2	1025,5294	1025,5306	0,0190	28,2005	40	171,2969	1	8	EQIFYYIR	Oxidation M	3	De-novo
505,7725	2	1025,5294	1025,5306	0,0190	-28,2005	40,0000	171,2969	1	8	EQIFYYIR	Oxidation M	3	De-novo
505,7725	2	1025,5294	1025,4971	0,3323	31,4735	40	171,341	1	8	IYFYYEQK			De-novo
505,3138	2	1122,6123	1122,6073	0,0347	4,1053	62,7401	111,6969	1	8	LFFPLTEFR			De-novo
505,3138	2	1122,6123	1122,6073	0,0347	-4,1053	62,7401	111,6969	1	8	LFFPLTEFR	Deamidation Q		De-novo
505,3138	2	1122,6123	1122,6073	0,0347	4,1053	56,9844	109,6569	1	8	LFFPLQTFR	Deamidation Q	6	De-novo
505,7405	2	1145,5134	1145,5050	0,0191	8,6452	62,5597	154,1927	1	11	TEQAAQLAWRR	Deamidation Q /	7 / 10	De-novo
505,7405	2	1145,5134	1145,5050	0,0191	-8,6452	62,5597	154,1927	1	11	TEQAAQLAWRR	Deamidation Q		De-novo
494,7428	2	987,5120	987,5138	-0,0019	-1,8471	70,5882	147,169	1	9	ALSYQFQNR			De-novo
494,7428	2	987,5120	987,5138	-0,0019	-1,8483	70,5882	145,6152	1	9	LASFQFCNR			De-novo
505,3151	2	1225,6244	1225,6214	0,0032	0,0032	0,0032	109,4454	1	11	MLGYGELLCR			De-novo
505,3151	2	1225,6244	1225,6214	0,0032	-1,8519	69,2593	109,4454	1	11	MLGYGELLCR	Deamidation N	1 / 7	De-novo
505,8323	2	1225,6440	1225,6489	0,0051	0,0620	72,4618	366,1993	1	12	LRRLGNSSYCR	Carbamidomethyl C	11	De-novo
505,8323	2	1225,6440	1225,6489	0,0051	-0,0620	72,4618	366,1993	1	12	LRRLGNSSYCR	Carbamidomethyl C	11	De-novo

MS2: [illegible] [illegible] **Score:** [illegible]

Score = 82 (49.2 bits)
Identities = 11/12 (92%), Positives = 12/12 (100%)
Query: 274 RYQGQGGGGGRY 285
RYQGQGGGGGRY
Mr/z: 97 RYQGQGGGGGR [illegible]

Score = 74 (28.2 bits)
Identities = 9/12 (75%), Positives = 12/12 (100%)
Query: 30 RYNRYGLGGNRY 41
RYNRYGLGGNRY
Mr/z: 94 RYNRYGLGGNR [illegible]

Score = 62 (13.1 bits)
Identities = 8/11 (82%), Positives = 10/11 (90%)
Query: 74 RQTQTNRRGYR 84
RYTQTNRRGYR
Mr/z: 210 RYTQTNRRGYR [illegible]

Score = 60 (12.1 bits)
Identities = 7/11 (64%), Positives = 10/11 (90%)
Query: 136 LLGNRGYRNF 146
LIGNRGY NF
Mr/z: 272 LLGNRGYRNF [illegible]

Score = 57 (10.4 bits)
Identities = 7/11 (64%), Positives = 10/11 (90%)
Query: 150 RLRNLGNRNF 160
RLRNLGNRNF
Mr/z: 300 RLRNLGNRNF [illegible]

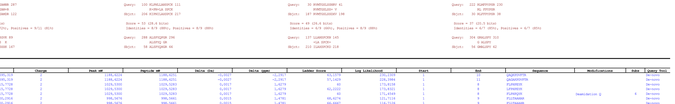
Score = 49 (6.8 bits)
Identities = 5/9 (55%), Positives = 6/9 (66%)
Query: 217 PYPPRR 222
PYPPRR
Mr/z: 433 PYPPRR [illegible]

Score = 43 (3.8 bits)
Identities = 7/9 (77%), Positives = 7/9 (77%)
Query: 248 NLGFRGRR 256
NLGFRGRR
Mr/z: 495 NLGFRGRR [illegible]

Score = 40 (2.2 bits)
Identities = 5/9 (55%), Positives = 6/9 (66%)
Query: 45 MRRGR 49
MRRGR
Mr/z: 127 MRRGR [illegible]

Score = 36 (0.5 bits)
Identities = 4/9 (44%), Positives = 6/9 (66%)
Query: 95 PRAERGRLR 103
PAER R R
Mr/z: 318 PAERLRTR [illegible]

Sp 40 EGF [illegible] **Total Score:** [illegible]



Score = 82 (49.2 bits)
Identities = 11/12 (92%), Positives = 12/12 (100%)
Query: 274 RYQGQGGGGGRY 285
RYQGQGGGGGRY
Mr/z: 111 RYQGQGGGGGR 122

Score = 75 (29.7 bits)
Identities = 9/12 (75%), Positives = 11/12 (92%)
Query: 30 RYNRYGLGGNRY 41
RYNRYGLGGNRY
Mr/z: 268 RLNRYGLGGNRY 257

Score = 71 (27.3 bits)
Identities = 10/12 (83%), Positives = 11/12 (92%)
Query: 30 RYNRYGLGGNRY 41
RYNRYGLGGNRY
Mr/z: 147 RYNRYGLGGNRY 198

Score = 58 (21.1 bits)
Identities = 6/9 (66%), Positives = 8/9 (88%)
Query: 122 RLRPPPPRR 130
RL PPPPRR
Mr/z: 35 RLPPPPRR 38

Score = 56 (20.1 bits)
Identities = 8/11 (72%), Positives = 9/11 (82%)
Query: 79 RQTLQTNRR 89
RYTLQTNRR
Mr/z: 197 RRTLQTNRR 187

Score = 53 (18.4 bits)
Identities = 6/9 (66%), Positives = 8/9 (88%)
Query: 298 RLGFRGRR 306
RLGFRGRR
Mr/z: 76 RLGFRGRR 68

Score = 49 (16.4 bits)
Identities = 6/9 (66%), Positives = 8/9 (88%)
Query: 137 LLGNRGYRN 145
LLGNRGY RN
Mr/z: 210 LLGNRGYRN 224

Score = 37 (10.5 bits)
Identities = 4/7 (57%), Positives = 4/7 (57%)
Query: 294 GRRLRT 313
GRRLRT
Mr/z: 56 GRRLRT 42

Spot 34

ACX	Charge	Peak AM	Peak/Lim AM	Valle Abs	Valle Sgmt	Ladder Score	Log Likelihood	Start	Age	Sequence	Modification	Date	Query Seq.
505,514	2	1108,6223	1108,6231	-0,0007	-0,0007	-0,0007	93,5153	1	11	QQQQYYYYYN			De-novo
505,514	2	1108,6223	1108,6231	-0,0007	-2,0927	57,5429	126,594	1	11	QQQQYYYYYN			De-novo
505,5159	2	1025,5300	1025,5283	0,0017	0,0017	0,0017	175,6522	1	8	LFYRYEYR			De-novo
505,5159	2	1025,5300	1025,5283	0,0017	-0,0179	40,5522	175,6522	1	8	LFYRYEYR			De-novo
505,5159	2	1025,5300	1025,5283	0,0017	0,0179	40	171,6549	1	8	FLFRYQYR	Deamidation Q	6	De-novo
505,2543	2	996,5476	996,5461	0,0015	0,1491	61,9207	119,7218	1	9	FLLTGAAAR			De-novo
505,2543	2	996,5476	996,5461	0,0015	-0,1491	61,9207	119,7218	1	9	FLLTGAAAR			De-novo
505,2543	2	996,5476	996,5461	0,0015	1,2782	60,7843	113,6543	1	9	LFLTGAAAV			De-novo
505,2543	2	996,5476	996,5461	0,0015	-1,2782	60,7843	113,6543	1	9	LFLTGAAAV	Carbamidomethyl C	7	De-novo
514,2502	2	1026,4708	1026,4692	0,0016	1,5334	57,7779	101,192	1	8	DFCGFCLF	Deamidation D /	1 / 3	De-novo
717,3874	2	1432,7506	1432,735	0,0148	17,1532	36,6667	87,6457	1	13	GSEFCLGFCGYCR			De-novo
717,3874	2	1432,7506	1432,735	0,0148	-17,1532	36,6667	87,6457	1	13	GSEFCLGFCGYCR			De-novo
505,8377	2	1191,6998	1191,7206	-0,0208	-11,4195	75,913	237,2202	1	10	FGSTQLCFLGR			De-novo
737,7509	2	1033,0913	1033,0969	-0,0058	-2,5561	46,9413	270,4977	1	21	RGNRCLGFCGFGRNAFYCRAA			De-novo
737,7509	2	1033,0913	1033,0969	-0,0058	2,5561	46,9413	270,4977	1	21	RGNRCLGFCGFGRNAFYCRAA	Deamidation N	3	De-novo
832,0608	3	2493,180	2493,177	-0,0190	-0,6243	51,0204	286,6252	1	25	TRGRQEGGGGGEGFLGTRNLFYCR	Deamidation Q	5	De-novo
832,0608	3	2493,180	2493,177	-0,0190	0,6243	51,0204	286,6252	1	25	TRGRQEGGGGGEGFLGTRNLFYCR	Deamidation Q	5	De-novo
832,0608	3	2493,180	2493,177	-0,0190	-1,9243	46,9413	286,9272	1	25	TRGRQEGGGGGEGFLGTRNLFYCR	Deamidation Q /	5 / 8	De-novo
505,8391	2	1489,7028	1489,7209	-0,0181	-12,5278	32,2898	252,1288	1	13	RYYRGYGGGYGGRF	Oxidation M	4	De-novo
505,8391	2	1489,7028	1489,7209	-0,0181	12,5278	32,2898	252,1288	1	13	RYYRGYGGGYGGRF	Oxidation M	4	De-novo
505,8391	2	1489,7028	1489,7209	-0,0181	-16,5278	63,2184	295,5517	1	13	RYYRGYGGGYGGRF			De-novo
836,8317	2	1673,6478	1673,6633	-0,0155	-0,5348	56,1264	75,5209	1	15	YLQLFCWCFR			De-novo
836,8317	2	1673,6478	1673,6633	-0,0155	0,5348	56,1264	75,5209	1	15	YLQLFCWCFR			De-novo
836,8317	2	1673,6478	1673,6633	-0,0155	-2,5348	56,1264	76,197	1	15	YLQLFCWCFR	Deamidation Q	3	De-novo
505,8402	2	1181,6768	1181,6927	-0,0159	-8,7632	59,9907	206,2254	1	12	LRRYYGGGGGRF	Oxidation M	3	De-novo
505,8402	2	1181,6768	1181,6927	-0,0159	8,7632	59,9907	206,2254	1	12	LRRYYGGGGGRF	Oxidation M	3	De-novo
505,5118	2	2005,0080	2005,0197	-0,0117	-0,8473	50,5253	187,1478	1	17	RYGLALLGYFYCFYCF			De-novo
505,5118	2	2005,0080	2005,0197	-0,0117	0,8473	50,5253	187,1478	1	17	RYGLALLGYFYCFYCF			De-novo
505,5118	2	2005,0080	2005,0197	-0,0117	-2,8473	50,5253	185,6544	1	17	RYGLALLGYFYCFYCF			De-novo

MS2: [illegible] [illegible] **Score:** [illegible]

Score = 76 (28.6 bits)
Identities = 10/17 (59%), Positives = 14/17 (82%)
Query: 342 RYGLALLGYFYCFYC 357
RYGLALLGYFYCFYC
Mr/z: 37 RYGLALLGYFYCFYC [illegible]

Score = 34 (8.8 bits)
Identities = 8/9 (100%), Positives = 8/9 (100%)
Query: 45 RYLFGRR 53
RYLFGRR
Mr/z: 105 RYLFGRR [illegible]

Score = 48 (15.8 bits)
Identities = 8/9 (66%), Positives = 11/9 (77%)
Query: 226 ALLGYFYCFYCF 240
ALLGYFYCFYCF
Mr/z: 226 ALLGYFYCFYCF [illegible]

Score = 40 (12.8 bits)
Identities = 6/9 (77%), Positives = 6/9 (77%)
Query: 27 RFLFGRQF 44
RF FGRQF
Mr/z: 209 RFFGRQF [illegible]

Spot 35 [illegible] **Total Score:** [illegible]

Score = 76 (28.6 bits)
Identities = 10/14 (71%), Positives = 12/14 (85%)
Query: 127 LLGNRGYRNNNRF 140
LLGNRGY NNNRF
Mr/z: 215 LLGNRGYRNNNR [illegible]

Score = 48 (16.3 bits)
Identities = 8/10 (80%), Positives = 9/10 (90%)
Query: 74 RQTQTNRRGY 83
RYTQTNRRGY
Mr/z: 234 RYTQTNRRGY [illegible]

Score = 52 (18.4 bits)
Identities = 8/10 (80%), Positives = 10/10 (100%)
Query: 114 RYGTQLALLGYFYCFYR 258
RYGTQLALLGYFYCFYR
Mr/z: 217 RYGTQLALLGYFYCFYR [illegible]

Score = 52 (17.8 bits)
Identities = 8/9 (88%), Positives = 7/9 (77%)
Query: 21 RFLFGRQFY 29
RF FGRQFY
Mr/z: 185 RFLFGRQFY [illegible]

Score = 48 (15.8 bits)
Identities = 7/8 (87%), Positives = 8/8 (100%)
Query: 311 RLGFRRRY 318
RLGFRRRY
Mr/z: 190 RLGFRRRY [illegible]

Score = 40 (12.8 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 49 YLGFRRR 55
YLGFRRR
Mr/z: 145 YLGFRRR [illegible]

Score = 39 (12.3 bits)
Identities = 5/7 (71%), Positives = 5/7 (71%)
Query: 34 RFLGFRR 40
RYLGFRR
Mr/z: 144 RFLGFRR [illegible]

Score = 36 (10.5 bits)
Identities = 4/9 (44%), Positives = 7/9 (77%)
Query: 71 RRRTQRTL 79
AR TLRTL
Mr/z: 61 ARRRTQRTL [illegible]

Score = 36 (10.5 bits)
Identities = 4/9 (44%), Positives = 6/9 (66%)
Query: 95 PRAERGRLR 103
PAER R R
Mr/z: 318 PAERLRTR [illegible]

Sp 40 EGF [illegible] **Total Score:** [illegible]

Score = 48 (15.8 bits)
Identities = 6/9 (66%), Positives = 8/9 (88%)
Query: 107 LRRYGRRL 115
LRRYGRRL
Mr/z: 14 LRRYGRRL [illegible]

Hpa: 35

ACC	Charge	Peak mz	Peptide mz	Delta Conc	Delta ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modification	Rank	Query Scan
92G/7G3	2	1344,5110	1344,5077	0,0033	2,4553	6,1215	81,7903	134,1412	1	13	LYSPRMEGR	Cysteine(Carbamidomethylation) 1	1 De-novo
92G/7G3	2	1344,5110	1344,5077	0,0033	2,4553	6,1215	81,7903	134,1412	1	9	LEGAAWCK	Cysteine(Carbamidomethylation) 8	6 De-novo
92G/7G3	2	1344,5110	1344,5077	0,0033	2,4553	6,1215	81,7903	134,1412	1	9	LEGAAWCK	Cysteine(Carbamidomethylation) 8	7 De-novo
91L/6J8	2	1335,5925	1335,6077	-0,0152	-14,2867	6,4211	105,4544	1	10	LYSYRVEGR	Deamidation N	1 De-novo
91L/6J8	2	1335,5925	1335,6077	-0,0152	-14,2867	6,4211	107,3752	1	10	LYSYRVEGR		2 De-novo
91L/6J8	2	1335,5925	1335,6077	-0,0152	-14,2867	6,4211	107,3752	1	10	LYSYRVEGR	Deamidation R	3 De-novo
49A/B4W	2	1197,5960	1197,5941	0,0019	1,5247	11,5209	66,9487	1	11	LLGMQEMSLLR	Oxidation M	1 De-novo
49A/B4W	2	1197,5960	1197,5941	0,0019	1,5247	11,5209	66,9487	1	11	LLGMQEMSLLR	Oxidation M / Deamidation	6 7 9 De-novo
49A/B4W	2	1197,5960	1197,5941	0,0019	1,5247	11,5209	66,9487	1	11	LLGMQEMSLLR		8 De-novo
5KS/77G	2	1125,5334	1125,5376	-0,0043	-3,8779	7,1,7754	105,1158	1	10	NELYSYRVGF	Deamidation N	7 De-novo
4KS/73B	2	995,4614	995,4617	-0,0003	-0,3208	9,1,2222	91,7919	1	8	LRYSRMER	Deamidation R	6 7 7 De-novo
4KS/73B	2	995,4614	995,4617	-0,0003	-0,3208	9,1,2222	91,7919	1	8	LRYSRMER	Deamidation R	8 De-novo
4KS/73B	2	995,4614	995,4617	-0,0003	-0,3208	9,1,2222	91,3144	1	8	LRYSRMER	Deamidation R	9 De-novo
81L/23S	2	835,4346	835,4333	0,0014	1,6059	9,4229	94,1326	1,1,2492	1	7	RYSRLLF	De-novo
81L/23S	2	835,4346	835,4333	0,0014	1,6059	9,4229	94,1326	1,1,2492	1	7	RYSRLLF	De-novo
81L/23S	2	835,4346	835,4333	0,0014	1,6059	9,4229	94,1326	1,1,2492	1	7	LRYSRLLF	Deamidation Q	De-novo
8CL/2P5	2	1205,5736	1205,5868	-0,0054	-4,5178	6,2157	66,0317	1,6,1492	1	11	RAFSYCTERR	De-novo
8CL/2P5	2	1205,5736	1205,5868	-0,0054	-4,5178	6,2157	66,0317	1,6,1492	1	11	RAFSYCTERR	De-novo
8CL/2P5	2	1205,5736	1205,5868	-0,0054	-4,5178	6,2157	66,0317	1,6,1492	1	11	YSFYCTERR	De-novo
8KS/3N6	2	1704,7652	1704,7592	0,0060	3,5035	7,5,2,2	75,243	1,1,1,1	1	14	QAYDAGYSYYCLRR	Deamidation Q	5 De-novo
8KS/3N6	2	1704,7652	1704,7592	0,0060	3,5035	7,5,2,2	75,243	1,1,1,1	1	14	QAYDAGYSYYCLRR	Deamidation Q	6 De-novo
8KS/3N6	2	1704,7652	1704,7592	0,0060	3,5035	7,5,2,2	75,243	1,1,1,1	1	14	QAYDAGYSYYCLRR	Deamidation Q	1 1 5 De-novo
5KL/B77	2	1155,5988	1155,5985	0,0030	2,6079	5,2,4114	121,572	1	10	RYSKSNDLR	Deamidation N	8 De-novo
5KL/B77	2	1155,5988	1155,5985	0,0030	2,6079	5,2,4114	121,572	1	10	RYSKSNDLR		9 De-novo
5KL/33G	2	985,5223	985,517	0,0053	5,4273	6,1,2,2	65,963	1,1,1,1	1	8	ATLGR	De-novo
5KL/33G	2	985,5223	985,517	0,0053	5,4273	6,1,2,2	65,963	1,1,1,1	1	8	ATLGR	Deamidation Q	8 De-novo
4KS/33B	2	1163,6940	1163,6938	0,0003	0,2269	7,1,2,2	76,6667	1,1,1,1	1	11	YSSTLEELRSLK	De-novo
4KS/33B	2	1163,6940	1163,6938	0,0003	0,2269	7,1,2,2	76,6667	1,1,1,1	1	11	YSSTLEELRSLK	De-novo
4KS/33B	2	1163,6940	1163,6938	0,0003	0,2269	7,1,2,2	76,6667	1,1,1,1	1	13	YSSTLEELRSLK	Deamidation Q	11 De-novo

NCBI gi|24399178|gb|AAB07[redacted]

Total Score: 54

Hu 01 EDT tanpin-SN-EGK_Cortex_[redacted]

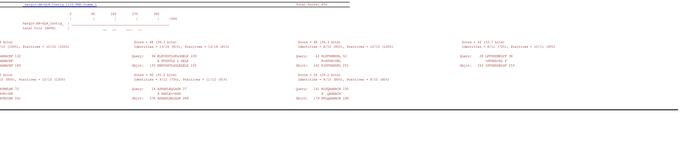
Total Score: 54

Hpa: 35

ACC	Charge	Peak mz	Peptide mz	Delta Conc	Delta ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modification	Rank	Query Scan
49L/7G1	2	1344,5110	1344,5077	0,0033	2,4553	6,1215	81,7903	134,1412	1	9	LEGAAWCK	Cysteine(Carbamidomethylation) 8	6 De-novo
49A/7G1	2	987,5560	987,5601	-0,0403	-0,5434	7,5,549	135,0343	1	9	KGLEGLGAK	De-novo
49A/7G1	2	987,5560	987,5601	-0,0403	-0,5434	7,5,549	135,0343	1	9	KGLEGLGAK	Deamidation Q	7 De-novo
49L/73T4	2	985,4822	985,4617	-0,0013	-1,5445	9,1,2222	113,7618	1	8	LRYSRMER	Deamidation R	7 De-novo
49L/73T4	2	985,4822	985,4617	-0,0013	-1,5445	9,1,2222	113,363	1	8	LRYSRMER	Deamidation R	6 7 7 De-novo
5KL/3N6	2	1155,5932	1155,6077	-0,0145	-12,5343	7,1,7,2	106,7595	1	11	LYSYRVEGLQF	Deamidation N	8 De-novo
5KL/3N6	2	1155,5932	1155,6077	-0,0145	-12,5343	7,1,7,2	106,7595	1	11	LYSYRVEGLQF	Deamidation N	9 De-novo
5KL/3N6	2	1155,5932	1155,6077	-0,0145	-12,5343	7,1,7,2	98,4311	1	11	LYSYRVEGLQF	Deamidation N	7 De-novo
4KS/2D6	2	1124,7036	1124,698	0,0056	4,5294	8,1,2,2	29,1857	1	11	YSSTSQLLRSLK	Deamidation Q	6 7 7 De-novo
4KS/2D6	2	1124,7036	1124,698	0,0056	4,5294	8,1,2,2	29,1857	1	11	YSSTSQLLRSLK	Deamidation Q	7 De-novo
4KS/2D6	2	1124,7036	1124,698	0,0056	4,5294	8,1,2,2	30,4667	1	11	YSSTSQLLRSLK		8 De-novo
5KS/7G1	2	1344,5040	1344,5077	-0,0037	-2,8748	6,1,2,2	81,7903	1,1,1,1	1	13	FLGAAWCKR	Cysteine(Carbamidomethylation) 8	7 7 De-novo
5KS/7G1	2	1344,5040	1344,5077	-0,0037	-2,8748	6,1,2,2	81,4035	1,1,1,1	1	13	FLGAAWCKR	Cysteine(Carbamidomethylation) 8	9 De-novo
5KS/7G1	2	1344,5040	1344,5077	-0,0037	-2,8748	6,1,2,2	81,7903	1,1,1,1	1	9	LEGAAWCK	Cysteine(Carbamidomethylation) 8	8 De-novo

NCBI gi|24399178|gb|AAB07[redacted]

Total Score: 49



Hu 01 EDT tanpin-SN-EGK_Cortex_[redacted]

Total Score: 49

Hpt 37

ACC	Charge	Peak mz	Peptide mz	Delta Obs	Delta Ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modification	Rdbe	Query Scan
723,8863	2	1453,5872	1453,5872	0,0000	0,0000	56,9000	101,1164	1	12	GSPRMEMRMLQE	Deamidation N	10	De-novo
723,8863	2	1453,5872	1453,5872	-0,0010	-0,7004	58,6667	102,2362	1	12	GSPRMEMRMLQE	Deamidation N	10	De-novo
533,2397	2	1066,4638	1066,4651	-0,0013	-1,2184	41,4000	64,4611	1	10	YDYGCGFFN		1	De-novo
533,2397	2	1066,4638	1066,4651	-0,0013	-1,2184	41,4000	64,4611	1	10	YDYGCGFFN	Carbamidomethyl C	1	De-novo
533,2397	2	1066,4638	1066,4651	-0,0013	-1,2184	41,4000	101,4615	1	10	YDYGCGFFN	Carbamidomethyl C	1	De-novo
533,2397	2	1066,4638	1066,4651	-0,0013	-1,2184	41,4000	101,4615	1	10	YDYGCGFFN	Carbamidomethyl C	1	De-novo
494,7966	2	1387,5656	1387,5559	+0,0097	+6,9893	105,6123	85,5174	1	12	YSHWMMYQLLK	Carbamidomethyl C /	1 / 10	De-novo
494,7966	2	1387,5656	1387,5559	+0,0097	+6,9893	105,6123	101,9973	1	12	YSHWMMYQLLK	Carbamidomethyl C	1	De-novo
494,7966	2	1387,5656	1387,5559	+0,0097	+6,9893	105,6123	101,9973	1	12	YSHWMMYQLLK	Carbamidomethyl C	1	De-novo
534,2423	2	1066,4930	1066,5063	-0,0067	-6,4338	31,7778	127,9827	4	12	GLYYPQGM	Deamidation N	7	De-novo
534,2423	2	1066,5030	1066,5063	-0,0067	-6,4338	56,4667	137,4944	4	12	GLYYPQGM	Deamidation N	7	De-novo
534,2423	2	1066,5030	1066,5063	-0,0067	-6,4338	56,4667	137,4944	4	12	GLYYPQGM	Deamidation N /	7 / 9	De-novo
562,3112	2	1122,6040	1122,6073	-0,0033	-2,9408	56,8125	82,4449	4	12	LPTYQLEFN	Deamidation Q	4	De-novo
562,3112	2	1122,6040	1122,6073	-0,0117	-10,4434	47,0588	91,07	4	12	LPTYQLEFN		4	De-novo
562,3112	2	1122,6040	1122,6073	-0,0117	-10,4434	47,0588	91,07	4	12	LPTYQLEFN	Deamidation Q	4	De-novo
571,8815	2	1402,7474	1402,7478	-0,0002	-0,1342	52,1739	102,8553	12	21	RQFMRMYQLLF	Oxidation M	7	De-novo
571,8815	2	1402,7474	1402,7478	-0,0002	-0,1342	52,1739	138,7254	12	21	RQFMRMYQLLF	Deamidation Q / Oxidation	7 / 7	De-novo
571,8815	2	1402,7474	1402,7478	-0,0002	-0,1342	52,1739	138,7254	12	21	RQFMRMYQLLF		7	De-novo
804,857	2	1607,6966	1607,7139	-0,0173	-10,6559	68,9655	404,5024	13	26	GGSGSGCCATLATLEW	Carbamidomethyl C /	9	De-novo
804,857	2	1607,6966	1607,7139	-0,0173	-10,6559	68,9655	403,9813	13	26	GGSGSGCCATLATLEW	Carbamidomethyl C /	9 / 14	De-novo
804,857	2	1607,6966	1607,7139	-0,0173	-10,6559	68,9655	403,9813	13	26	GGSGSGCCATLATLEW	Carbamidomethyl C /	9 / 14	De-novo
571,3718	2	1470,7200	1470,7218	-0,0020	-1,3617	66,5000	125,7510	14	23	NYATCTQQQFMM	Deamidation N	4	De-novo
571,3718	2	1470,7200	1470,7218	-0,0020	-1,3617	66,5000	125,7510	14	23	NYATCTQQQFMM	Deamidation N	4 / 10	De-novo
571,3718	2	1470,7200	1470,7218	-0,0020	-1,3617	66,5000	125,2502	14	23	NYATCTQQQFMM	Deamidation N	4	De-novo
789,396	2	1577,7934	1577,7719	+0,0215	+13,6202	45,4000	95,4328	14	24	TGLYGGSGLGLA	Deamidation G	2	De-novo
789,396	2	1577,7934	1577,7719	+0,0215	+13,6202	45,4000	95,4328	14	24	TGLYGGSGLGLA			De-novo
789,396	2	1577,7934	1577,7719	+0,0215	+13,6202	42,4667	87,7953	14	24	TGLYGGSGLGLA			De-novo
792,8517	2	1583,5872	1583,5922	-0,0049	-3,1013	44	201,1444	13	24	CGSMAMYQEQLK	Carbamidomethyl C /	1 / 12	De-novo
792,8517	2	1583,5872	1583,5922	-0,0049	-3,1013	44	201,1444	13	24	CGSMAMYQEQLK	Carbamidomethyl C /	1 / 12	De-novo
792,8517	2	1583,5872	1583,5922	-0,0049	-3,1013	44	248,9969	13	24	CGSMAMYQEQLK	Carbamidomethyl C	1	De-novo

MZRD gi|224972549:gb|ACCCC | Length: 1628 | Mass: 180.0934 | Sequence: MPPP

Spec 38

ACC	Charge	Mass obs	Mass/Calc obs	Delta Obs	Delta Ppm	Sadduc Score	Log Likelihood	Start	End	Sequence	Mods/Cleavage	Rdbs	Query Scan
XP_[illegible]	2	1329,[illegible]	1329,[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	1	[illegible]	[illegible]			[illegible]
WYL,WLC	2	1269,7584	1269,7582	+0.0008	+0.6389	52,1739	95,763	1	12	ERKFMYRRGLAF		9	3e-term
YYL,WLC	2	1462,7584	1462,7582	+0.0008	+0.5469	52,1739	97,1513	1	12	ERKFMYRRGLAF		9	3e-term
YYL,WLC	2	1462,7584	1462,7582	+0.0008	+0.5469	52,1739	97,1513	1	20	PRRACRRDDDGDLCMRTCM	Deamidation N	2 / 19	3e-term
YYL,WLC	2	1462,7584	1462,7582	+0.0008	+0.5469	52,2040	98,2894	1	21	PRRACRDDDGDLCMRTCM	Deamidation N	2 / 17	3e-term
YYL,WLC	2	1462,7584	1462,7582	+0.0008	+0.5469	52,2040	98,2894	1	21	PRRACRDDDGDLCMRTCM	Deamidation N	2 / 17	3e-term
SKL,SSG	2	1176,5772	1176,5771	+0.0009	+0.7654	52,1739	94,1842	1	10	CRGCYLLGCM		7	3e-term
RKR,RIG	2	1295,8346	1295,8350	-0.0004	-0.3454	4,1493	93,5170	1	11	CYGRQCYYYCR	Cysteinylation(1) C	1	3e-term
RKR,RIG	2	1295,8346	1295,8350	-0.0004	-0.3454	4,1493	93,5170	1	11	CYGRQCYYYCR	Cysteinylation(1) C	1	3e-term
RKR,RIG	2	1295,8346	1295,8350	-0.0004	-0.3454	4,1493	93,6232	1	12	GCYRQCYYYCR		1	3e-term
RKL,RWL	2	1745,7756	1745,7758	-0.0010	-0.5527	52,9742	126,1712	1	18	RSTRMQGRLGVSRCRFR	Deamidation Q	9	3e-term
RKL,RWL	2	1745,7756	1745,7758	-0.0010	-0.5527	52,9742	126,1712	1	18	RSTRMQGRLGVSRCRFR	Deamidation Q	9	3e-term
RKL,RWL	2	1745,7756	1745,7758	-0.0010	-0.5527	52,9742	126,1979	1	18	RSTRMQGRLGVSRCRFR		9	3e-term
RZL,RKY	2	1249,5858	1249,5859	-0.0001	-0.0997	51,8298	114,4993	1	10	MLRAMCRPLF	Deamidation R	3	3e-term
RLL,RWC	2	1320,7328	1320,7330	-0.0002	-0.1516	51,1549	95,1548	1	11	LRRILLLGRLF			3e-term
RLL,RWC	2	1320,7328	1320,7330	-0.0002	-0.1516	51,1549	95,1548	1	11	LRRILLLGRLF			3e-term
RLL,RWC	2	1320,7328	1320,7330	-0.0001	-0.1073	47,4139	95,9918	1	11	RLGRLLLGRLF			3e-term
RLL,RWC	2	1320,7328	1320,7330	-0.0001	-0.1073	47,4139	95,9918	1	11	RLGRLLLGRLF			3e-term
YYL,RZY	2	1473,8198	1473,8202	-0.0005	-0.3393	51,7324	86,6419	1	14	AYLGFRRYYGYCRM			3e-term
LYRL,LLG	2	2730,5198	2730,5217	0.0170	6,3077	97,2369	196,9417	1	27	FSEGGAGTGGTLGRVTGTRDEGGTTR			3e-term
LYRL,LLG	2	2730,5198	2730,5217	0.0170	6,3077	97,2369	196,9417	1	27	FSEGGAGTGGTLGRVTGTRDEGGTTR			3e-term
LYRL,LLG	2	2730,5198	2730,5217	0.0170	6,3077	97,2369	197,6588	1	27	FSEGGAGTGGTLGRVTGTRDEGGTTR	Deamidation Q	20	3e-term
KKL,DKW	2	1473,8274	1473,8302	-0.0028	-1,8242	46,9130	102,972	1	14	AKLAFYRVTFRW			3e-term
KKL,DKW	2	1473,8274	1473,8302	-0.0028	-1,8242	46,9130	102,972	1	14	AKLAFYRVTFRW			3e-term
KKL,DKW	2	1473,8274	1473,8302	-0.0028	-1,8242	46,9130	101,157	1	14	AKLAFYRVTFRW		13	3e-term
RRR,RKTS	2	1395,8756	1395,8783	0.0011	0,7710	56	117,417	1	13	LYSYRRSYLRRRW	Deamidation R	7	3e-term
RRR,RKTS	2	1395,8756	1395,8783	0.0011	0,7710	56	117,417	1	13	LYSYRRSYLRRRW	Deamidation R	7	3e-term
RRR,RKTS	2	1395,8756	1395,8783	0.0011	0,7710	56	125,034	1	13	LYSYRRSYLRRRW	Deamidation R /	7 / 10	3e-term

NCBI gi|261270971|gp|ELB1 [illegible] [Escherichia coli] Score: 1[illegible] Total Score: 3[illegible]

```
                    0        40       120       160       240
                    |         |         |         |         |      1298
gi|261270971|gp|ELB1 |
Local hits (BLAST)  |  ______                   _                 ____ _
```

Score = 89 (46.4 bits)
Identities = 12/14 (86%), Positives = 14/14 (100%)

```
Query:  43 RGSGGGLPWTGW 56
          RGSGGGLPWTGW
Sbjct:  [illegible]
```

Score = 75 (39.4 bits)
Identities = 11/16 (70%), Positives = 12/15 (80%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 45 (24.8 bits)
Identities = 7/10 (70%), Positives = 10/10 (100%)

```
Query:  198 MLRGSCRPLF 205
          MLRG RPLF
Sbjct:  [illegible]
```

Score = 42 (23.3 bits)
Identities = 4/5 (100%), Positives = 4/5 (100%)

```
Query:  113 LFYGW 117
          LFYGW
Sbjct:  [illegible]
```

Score = 37 (20.4 bits)
Identities = 3/4 (75%), Positives = 4/4 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Sp 85 EXP None

Sp 85 other [illegible] [Escherichia coli] Score: [illegible]

```
                    0        40       120       160       240
                    |         |         |         |         |      1298
[illegible] |
Local hits (BLAST)  |  ____ ____ __ _____
```

Score = 89 (46.4 bits)
Identities = 12/14 (86%), Positives = 14/14 (100%)

```
Query:  43 RGSGGGLPWTGW 56
          RGSGGGLPWTGW
Sbjct:  [illegible]
```

Score = 47 (25.4 bits)
Identities = 9/12 (75%), Positives = 9/12 (75%)

```
Query:  353 ACRRRYPRER 362
          ACRR RER
Sbjct:  [illegible]
```

Score = 42 (23.4 bits)
Identities = 8/13 (61%), Positives = 9/13 (69%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 41 (23.0 bits)
Identities = 7/8 (87%), Positives = 8/8 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 41 (23.0 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 41 (23.0 bits)
Identities = 8/12 (67%), Positives = 9/12 (75%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 37 (20.8 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Sp 85 EXP None

Sp 85 other [illegible] [Escherichia coli] Score: [illegible]

```
                    0        40       120       160       240
                    |         |         |         |         |      1298
[illegible] |
Local hits (BLAST)  |  ____ ____ __ _____
```

Score = 89 (46.4 bits)
Identities = 12/14 (86%), Positives = 14/14 (100%)

```
Query:  43 RGSGGGLPWTGW 56
          RGSGGGLPWTGW
Sbjct:  [illegible]
```

Score = 47 (25.4 bits)
Identities = 9/12 (75%), Positives = 9/12 (75%)

```
Query:  353 ACRRRYPRER 362
          ACRR RER
Sbjct:  [illegible]
```

Score = 42 (23.4 bits)
Identities = 8/13 (61%), Positives = 9/13 (69%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 41 (23.0 bits)
Identities = 7/8 (87%), Positives = 8/8 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 41 (23.0 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 41 (23.0 bits)
Identities = 8/12 (67%), Positives = 9/12 (75%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 37 (20.8 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Sp 85 EXP None

Sp 85 other [illegible] [Escherichia coli] Score: [illegible]

```
                    0        40       120       160       240
                    |         |         |         |         |      1298
[illegible] |
Local hits (BLAST)  |  ____ ____ __ _____
```

Score = 89 (46.4 bits)
Identities = 12/14 (86%), Positives = 14/14 (100%)

```
Query:  43 RGSGGGLPWTGW 56
          RGSGGGLPWTGW
Sbjct:  [illegible]
```

Score = 47 (25.4 bits)
Identities = 9/12 (75%), Positives = 9/12 (75%)

```
Query:  353 ACRRRYPRER 362
          ACRR RER
Sbjct:  [illegible]
```

Score = 42 (23.4 bits)
Identities = 8/13 (61%), Positives = 9/13 (69%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 41 (23.0 bits)
Identities = 7/8 (87%), Positives = 8/8 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 41 (23.0 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 41 (23.0 bits)
Identities = 8/12 (67%), Positives = 9/12 (75%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 37 (20.8 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Spec 40

ACC	Charge	Mass obs	Mass/Calc obs	Delta Obs	Delta Ppm	Sadduc Score	Log Likelihood	Start	End	Sequence	Mods/Cleavage	Rdbs	Query Scan
HCL,RCW	2	1329,5860	1329,5859	0,0011	0,8042	49,1529	[illegible]	1	12	GRDFCTQFRRCW			3e-term
HCL,RCW	2	1329,5860	1329,5859	0,0011	0,8042	49,1529	76,1518	1	12	GRDFCTQFRRCW			3e-term
HCL,RCW	2	1329,5860	1329,5859	0,0011	0,8042	52,1739	76,1518	1	12	GRDFCTQFRRCW			3e-term
YHR,IDGY	2	1014,4970	1014,4980	-0,0102	-10,7944	60,7451	85,693	1	9	EYRDAFMTY		7	3e-term
YHR,IDGY	2	1014,4970	1014,4980	-0,0102	-10,7944	60,7451	85,693	1	9	EYRDAFMTY	Oxidation M	7	3e-term
ELR,LHR	2	1234,5259	1234,5213	+0,0011	+0,8335	9	125,7326	1	12	FSSYGGGAGGSGF	Deamidation G / Oxidation	7 / 1	3e-term
ELR,LHR	2	1234,5259	1234,5213	+0,0011	+0,8335	50,6667	115,4797	1	12	FSSYGGGAGGSGF			3e-term
ELR,LHR	2	1234,5259	1234,5213	+0,0011	+0,8335	50,6667	115,4797	1	12	FSSYGGGAGGSGF			3e-term
SYL,LIR	2	1028,4230	1028,4451	-0,0221	-21,5121	73,549	225,0313	1	9	TSRGFYSSY	Deamidation R	3	3e-term
SYL,LIR	2	1028,4230	1028,4451	-0,0221	-21,5121	73,549	232,0468	1	9	TSRGFYSSY			3e-term
SYL,LIR	2	1028,4230	1028,4451	-0,0221	-21,5121	73,549	232,0468	1	9	TSRGFYSSY			3e-term
RRL,RLG	2	1787,8888	1787,8884	+0,0014	+0,7849	54,1583	108,5068	1	16	GYSFRQLLRGLFRRRFR	Deamidation R	10	3e-term
RRL,RLG	2	1787,8888	1787,8884	+0,0014	+0,7849	54,1583	107,1617	1	16	GYSFRQLLRGLFRRRFR		10	3e-term
RRL,RLG	2	1787,8888	1787,8884	+0,0014	+0,7849	54,1583	107,1617	1	16	GYSFRQLLRGLFRRRFR			3e-term
ETA,IGYS	2	1356,6454	1356,6885	-0,0431	-31,7862	81,3333	219,5555	1	14	LRSGRRLGRAQGR	Deamidation R	6	3e-term
ETA,IGYS	2	1356,6454	1356,6885	-0,0431	-31,7862	81,3333	219,5555	1	14	LRSGRRLGRAQGR	Deamidation R	6	3e-term
ETA,IGYS	2	1356,6454	1356,6885	-0,0431	-31,7862	81,3333	217,385	1	13	LRSGRRLGRAQGR	Deamidation R	6	3e-term
ATL,LMR	2	873,4810	873,4809	+0,0140	+16,0192	46,9969	121,4373	1	9	LARGCFRR	Deamidation R	3	3e-term
ATL,LMR	2	873,4810	873,4809	+0,0140	+16,0192	46,9969	121,4373	1	9	LARGCFRR	Deamidation R	3	3e-term
ATL,LMR	2	873,4810	873,486	-0,0140	-16,0192	46,9969	121,3131	1	8	LARGCFRR	Deamidation R	3	3e-term
ELL,DMR	2	1331,7042	1331,7079	-0,0037	-27,6219	49,3333	236,4874	1	11	MYLRLLFLFLR	Deamidation R	1	3e-term
ELL,DMR	2	1331,7042	1331,7079	-0,0037	-27,6219	49,3333	236,4874	1	11	MYLRLLFLFLR	Deamidation R	1	3e-term
ELL,RWG	2	1331,7128	1331,7079	+0,0050	+36,8227	95,5174	176,5311	1	12	ELSLCLCLLWFR			3e-term
ELL,RWG	2	1331,7128	1331,7079	+0,0050	+36,8227	95,5174	176,5311	1	12	ELSLCLCLLWFR			3e-term
ELL,RWG	2	1331,7128	1331,7079	+0,0050	+36,8227	95,5174	172,1739	1	12	ELSLCLCLLWFR	Deamidation Q	10	3e-term
KIL,LLR	2	894,4218	894,4161	+0,0123	+16,2347	46,9969	131,947	1	9	NLALCFFR			3e-term
KIL,LLR	2	894,4218	894,4161	+0,0123	+16,2347	46,9969	131,947	1	9	NLALCFFR	Deamidation N /	8 / 9	3e-term
HDL,SIG	2	1329,4510	1329,4511	-0,0011	-0,8440	65,9004	86,5388	1	12	YRQDRLRAQRQR	Deamidation Q /	8 / 9	3e-term
HDL,SIG	2	1329,4510	1329,4511	-0,0011	-0,8440	53,6232	87,8553	1	12	YRQDRLRAQRQR	Deamidation Q	9	3e-term
HDL,SIG	2	1329,4510	1329,4511	-0,0011	-0,8440	53,6232	86,5388	1	12	YRQDRLRAQRQR			3e-term
HDL,RKN	2	1296,5494	1296,5496	-0,0002	-0,1853	63,4921	212,1383	1	11	TSSQLFRTCR	Deamidation Q /	6 / 9	3e-term
HDL,RKN	2	1296,5494	1296,5496	-0,0002	-0,1853	63,4921	208,5971	1	11	TSSQLFRTCR	Cysteinylation(1) C	9	3e-term
HDL,RKN	2	1296,5494	1296,5496	-0,0002	-0,1853	63,4921	212,1383	1	11	TSSQLFRTCR	Deamidation Q	6	3e-term
HGL,RIG	2	1321,6066	1321,6017	0,0029	2,1719	49,2174	271,794	1	12	DRWRCRFLRR			3e-term
HGL,RIG	2	1321,6066	1321,6017	0,0029	2,1719	75,913	269,152	1	12	RRYCRTRFLRR			3e-term
HGL,RIG	2	1321,6066	1321,6017	0,0029	2,1719	75,913	271,794	1	12	RRYCRTRFLRR	Deamidation Q	1	3e-term
SKL,DRW	2	1164,5720	1164,5775	-0,0055	-4,7434	76,5208	86,8735	1	9	LSRSLCFTR			3e-term
SKL,DRW	2	1164,5720	1164,5775	-0,0055	-4,7434	76,5208	85,5614	1	10	LSRSLCFTRR			3e-term
RFL,RLG	2	1793,8128	1793,8226	-0,0128	-7,1495	52,4230	191,6173	1	16	GRFTRCRLLCLRRRFR	Deamidation R	4 / 10	3e-term
RFL,RLG	2	1793,8128	1793,8226	-0,0128	-7,1495	52,4230	191,6173	1	16	GRFTRCRLLCLRRRFR	Deamidation R	2 / 10	3e-term
RFL,RLG	2	1793,8128	1793,8226	-0,0128	-7,1495	52,4230	193,464	1	17	ARRCRGYCCLLCRRRFR	Cysteinylation(1) C /	5 / 15	3e-term

NCBI gi|261279443|gp|EDM[illegible] [Escherichia coli] Score: 1[illegible] Total Score: 1[illegible]

```
                    0       120       240       480       560
                    |         |         |         |         |      1376
gi|261279443|gp|EDM[illegible] |
Local hits (BLAST)  |  ____ _ ____ _
```

Score = 80 (42.2 bits)
Identities = 20/22 (90%), Positives = 21/22 (95%)

```
Query:  55 RFRSSSRRRRRRFSSSSRAAGRFGGGAGRGGGGGRGGGFT 95
          R SSSR  R RRRR  R SSSR  A +FT
Sbjct:  [illegible]
```

Score = 32 (16.9 bits)
Identities = 6/6 (100%), Positives = 6/6 (100%)

```
Query:  513 SSSRRRRSS 521
          SSSR R SS
Sbjct:  [illegible]
```

Spectrum [illegible] Total Score: [illegible]

```
                    0        50       100       150       200
                    |         |         |         |         |      1344
Scaffold[illegible] |
Local hits (BLAST)  |  ____ __ __ __
```

Score = 56 (29.4 bits)
Identities = 8/8 (100%), Positives = 8/8 (100%)

```
Query:  291 AFEGFLAR 298
          AFEGFLAR
Sbjct:  [illegible]
```

Score = 35 (18.4 bits)
Identities = 6/6 (100%), Positives = 6/6 (100%)

```
Query:  121 RGLRGLR 127
          RGLRGLR
Sbjct:  [illegible]
```

Score = 34 (18.0 bits)
Identities = 7/10 (70%), Positives = 7/10 (70%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 34 (18.0 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 34 (18.0 bits)
Identities = 8/11 (73%), Positives = 8/11 (73%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Sp 85 EXP None

Sp 85 other [illegible] [Escherichia coli] Score: [illegible]

```
                    0        40       120       180       240
                    |         |         |         |         |      1298
[illegible] |
Local hits (BLAST)  |  ____ ____ __ _____
```

Score = 89 (46.4 bits)
Identities = 12/14 (86%), Positives = 14/14 (100%)

```
Query:  43 RGSGGGLPWTGW 56
          RGSGGGLPWTGW
Sbjct:  [illegible]
```

Score = 47 (25.4 bits)
Identities = 9/12 (75%), Positives = 9/12 (75%)

```
Query:  353 ACRRRYPRER 362
          ACRR RER
Sbjct:  [illegible]
```

Score = 42 (23.4 bits)
Identities = 8/13 (61%), Positives = 9/13 (69%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 41 (23.0 bits)
Identities = 7/8 (87%), Positives = 8/8 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 41 (23.0 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 41 (23.0 bits)
Identities = 8/12 (67%), Positives = 9/12 (75%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Score = 37 (20.8 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

```
Query:  [illegible]
Sbjct:  [illegible]
```

Open 41

n/a	Change	Peak qM	Replicon ac	Locus (bp)	Locus (gpu)	Ladder Score	log Likelihood	Stars	Hot	Sequence	Modifications	Aln	Query Desc.
944,740	2	1127,8858	1127,9858	-0,0110	-18,7775	80,9509	-72,1152	1	10	TGAGTTTTGG	Cachaemlem(1) C	1	De-novo
944,740	2	1127,8858	1127,9858	-0,0110	-18,7775	80,9509	-72,1152	1	10	TGAGTTTTGG	Cachaemlem(1) C	4	De-novo
473,704	2	963,4532	963,4532	-0,0349	-59,2202	73,5202	21,7918	1	4	TGCgTTGG		1	De-novo
473,704	2	963,4532	963,4532	-0,0349	-59,2202	73,5202	21,7918	1	4	TGCgTTGG	Cachaemlem(1) C	2	De-novo
563,241	2	1094,9664	1094,9663	-0,0919	-11,7741	57,8947	131,9164	1	10	TCGACTTTGG	Cachaemlem(1) C	1	De-novo
563,241	2	1094,9664	1094,9663	-0,0919	-11,7741	57,8947	131,9164	1	10	TCGACTTTGG	Cachaemlem(1) C	2 2	De-novo
563,241	2	1094,9664	1094,9663	-0,0919	-11,7741	57,8947	131,9164	1	10	TCGACTTTGG	Cachaemlem(1) C	2 1	De-novo
865,8132	2	1319,8148	1319,814	0,0958	0,9881	66,4867	217,1074	1	12	TTCATCCCGACG	Dewakiolus B /	1 / 11	De-novo
865,8132	2	1319,8148	1319,814	0,0958	0,9881	66,4867	217,1074	1	12	TTCATCCCGACG	Dewakiolus B / Dewakiolus	2 / 9	De-novo
865,8132	2	1319,8148	1319,8139	0,0959	0,8839	66,4867	216,7865	1	12	TTCATCCCGACG	Dewakiolus B /	1 / 4 / 12	De-novo
864,2169	2	936,8182	936,8260	-0,0994	-8,9942	61,0222	142,6214	1	8	TTCTTCCCGA	Dewakiolus B	4	De-novo
864,2169	2	936,8182	936,8260	-0,0994	-8,9942	61,0222	142,6214	1	8	TTCTTCCCGA	Dewakiolus B	9	De-novo
864,2169	2	936,8182	936,8260	-0,0994	-8,9942	66,8889	128,5519	1	8	TTCTTCCCGA	Dewakiolus B	4	De-novo
480,235	2	936,8544	936,8565	-0,0992	-17,7828	66,5236	153,1994	1	8	CTCTCCCGTA	Dewakiolus B	9	De-novo
480,235	2	936,8544	936,8565	-0,0992	-17,7828	66,5236	153,1994	1	8	CTCTCCCGTA	Dewakiolus B /	2 / 9	De-novo
480,235	2	936,8544	936,8565	-0,0992	-17,7828	66,7452	154,7214	1	8	CTCTCCCGTA	Dewakiolus B	4	De-novo
487,7863	2	973,5570	973,5556	-0,0926	-12,4953	62,7431	138,4764	1	8	TTCCAACTCG			De-novo
487,7863	2	973,5570	973,5556	-0,0926	-12,4953	62,7431	138,4764	1	8	TTCCAACTCG			De-novo
487,7863	2	973,5570	973,5556	-0,0926	-12,4953	56,9844	130,264	1	8	TTCCAACGCG			De-novo

NCBI

Score = 80 (42.3 bits)
Identities = 8/12 (66%), Positives = 10/12 (83%)

Query: 89 TGGCCTCCGCCA 99
Sbjct: 141 TGGCCTCCGCCA 152
Score = 36 (19.4 bits)
Identities = 7/9 (78%), Positives = 8/9 (89%)

Query: 154 TTCCAACGC 162
Sbjct: 185 TTCCAACGC 193
Score = 31 (17.9 bits)
Identities = 7/7 (100%), Positives = 8/9 (88%)

Query: 148 CTCTTCCGTA 154
Sbjct: 191 CTCTTCCGTA 197
Score = 40 (22.2 bits)
Identities = 8/9 (88%), Positives = 7/9 (77%)

Query: 118 CTCTCCCGAC 126
Sbjct: 161 CTCTCCCGAC 169
Score = 27 (15.6 bits)
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 105 GCGTGG 110
GCGTGG 5
Sbjct: 173 GCGTGG 177
Score = 26 (14.8 bits)
Identities = 5/5 (100%), Positives = 4/5 (80%)

Query: 92 GTGTG 96
GT GG
Sbjct: 34 GCGCG 38

Ka 80 EDF Sequelle-DNA Locus 1700 MAC Locus 1

Score = 71 (38.1 bits)
Identities = 8/10 (80%), Positives = 10/10 (100%)

Query: 133 AATCCAACTC 142
AATCCAACTC
Sbjct: 202 AATCCAACTC 211
Score = 44 (24.5 bits)
Identities = 8/9 (88%), Positives = 8/9 (100%)

Query: 75 ATCCAGACA 83
ATCCAGACA
Sbjct: 167 ATCCAGACA 175
Score = 42 (23.5 bits)
Identities = 8/9 (88%), Positives = 8/9 (100%)

Query: 200 GGGTGGGAA 208
GGGTGGGAA
Sbjct: 240 GGGTGGGAA 248
Score = 37 (20.9 bits)
Identities = 7/8 (87%), Positives = 8/9 (100%)

Query: 14 CTTTTGGA 21
CTTTTGGA
Sbjct: 348 CTTTTGGA 355
Score = 42 (23.5 bits)
Identities = 8/10 (80%), Positives = 10/10 (100%)

Query: 109 CGCCGGCCAA 118
CGCCGGCCAA
Sbjct: 205 CGCCGGCCAA 214

Open 42

n/a	Change	Peak qM	Replicon ac	Locus (bp)	Locus (gpu)	Ladder Score	log Likelihood	Stars	Hot	Sequence	Modifications	Aln	Query Desc.
456,2509	2	914,4860	914,4860	-0,0935	-0,8717	62,7431	146,875	1	8	TGGCCTCCGC			De-novo
456,2509	2	914,4860	914,4860	-0,0935	-0,8717	62,7431	146,875	1	8	TGGCCTCCGC	Cachaemlem(1) C /	4 /	De-novo
591,2791	2	1185,5366	1185,5336	-0,0132	-2,5203	56,9927	76,1327	1	9	WTCACCGCA		5 / 6	De-novo
591,2791	2	1185,5366	1185,5336	-0,0132	-2,6953	56,992	76,363	1	9	WTCACCGCA	Cachaemlem(1) C /	6 / 7 / 8	De-novo
374,3623	2	1149,4670	1149,4667	-0,0922	-1,8649	51,8035	176,1588	1	12	TCCCTTTCGA			De-novo
374,3623	2	1149,4670	1149,4667	-0,0922	-1,8649	51,8035	176,1588	1	12	TCCCTTTCGA			De-novo
374,3623	2	1149,4670	1149,4668	-0,0922	1,8477	59,9495	176,1514	1	12	CTCATTTCGC			De-novo
374,3623	2	1149,4670	1149,4668	-0,0922	1,8477	59,9495	176,1514	1	12	CTCATTTCGC	Dewakiolus B	7	De-novo
808,5249	2	1615,8342	1615,8334	0,0938	1,5349	52,343	246,8562	1	14	TTCCTGGCCCTGT	Dewakiolus B	7	De-novo
808,5249	2	1615,8342	1615,8334	0,0938	1,5349	52,343	246,8562	1	14	TTCCTGGCCCTGT	Dewakiolus B	7	De-novo

NCBI

Score = 88 (45.2 bits)
Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 105 TCCTTTCGCCAG 116
TccttcgCCCAG
Sbjct: 35 TCCTTCGCCCAG 46
Score = 41 (21.8 bits)
Identities = 8/10 (80%), Positives = 9/10 (90%)

Query: 14 TCGGGGGGGTGGG 27
TC GG GATCGG
Sbjct: 19 TCAGGCATCATGG 31
Score = 32 (17.0 bits)
Identities = 6/11 (55%), Positives = 10/11 (90%)

Query: 44 GACCCTCTTCGC 54
GACCCTCTTCGC
Sbjct: 171 GACCCTCTTCGC 181

Ka 80 EDF Sequelle-DNA Locus 1700 MAC Locus 1

Score = 88 (45.2 bits)
Identities = 11/14 (79%), Positives = 14/14 (100%)

Query: 105 TCCTTTCGCCAGGG 118
TccttcgCCCAGGG
Sbjct: 35 TCCTTCGCCCAGGG 48
Score = 76 (40.5 bits)
Identities = 10/14 (71%), Positives = 12/14 (85%)

Query: 14 TCGGGGGGGTGGGG 27
TC GG GATCGGG
Sbjct: 34 TCAGGCATCATGGG 47
Score = 77 (39.6 bits)
Identities = 9/12 (75%), Positives = 12/12 (100%)

Query: 44 GACCCTCTTCGC 55
GACCCTCTTCGC
Sbjct: 201 GACCCTCTTCGC 212
Score = 47 (25.7 bits)
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 8 ATGACCTCGG 18
ATGACCTCGG
Sbjct: 188 ATGACCTCGG 197

Open 43

n/a	Change	Peak qM	Replicon ac	Locus (bp)	Locus (gpu)	Ladder Score	log Likelihood	Stars	Hot	Sequence	Modifications	Aln	Query Desc.
464,7200	2	897,4630	897,46	0,0930	0,9534	55,5203	242,1954	1	8	CCGGGCTC	Dewakiolus B	1	De-novo
464,7200	2	897,4630	897,46	0,0930	0,9534	55,5203	242,1954	1	8	CCGGGCTC		8	De-novo
464,7200	2	897,4630	897,46	0,0930	0,9534	51,1112	183,183	1	8	CCGGGCTC	Dewakiolus B	8	De-novo
425,3006	2	1249,1876	1249,188	-0,1084	-6,7447	61,8571	91,9677	1	11	GGGCATCTCGT	Dewakiolus B / Dewakiolus	2 / 9	De-novo
425,3006	2	1249,1876	1249,188	-0,1084	-6,7447	61,8571	91,9677	1	11	GGGCATCTCGT	Dewakiolus B	3	De-novo
425,3006	2	1249,1876	1249,188	-0,1084	-6,7447	66,0317	92,6949	1	11	GGGCATCTCGT	Dewakiolus B / Dewakiolus	2 / 9	De-novo
447,2583	2	1292,7022	1292,6975	0,0935	2,8890	71,5202	256,7877	1	13	TATCGCCGGGTTT	Dewakiolus B	10	De-novo
447,2583	2	1292,7022	1292,6975	0,0935	2,8890	71,5202	256,7877	1	13	TATCGCCGGGTTT	Dewakiolus B	10	De-novo
447,2583	2	1292,7022	1292,6975	0,0935	2,8890	69,5202	256,5024	1	13	CCATCCCGGGTTT	Dewakiolus B	10	De-novo
473,2407	2	946,5338	946,5179	-0,0933	-1,2488	61,8182	145,2888	1	8	GCCATCCA		8	De-novo
473,2407	2	946,5338	946,5179	-0,0933	-1,2488	56	145,2888	1	8	GCCATCCA			De-novo
434,7150	2	897,4230	897,424	-0,0910	-1,1895	66,5324	89,9329	1	7	GGTCGCA			De-novo
434,7150	2	897,4230	897,424	-0,0910	-1,1895	66,5324	89,9329	1	7	GGTCGCA			De-novo

NCBI

Score = 58 (30.4 bits)
Identities = 8/11 (73%), Positives = 8/11 (73%)

Query: 122 TTGTGCCGAAC 132
TtGCG G AC
Sbjct: 12 TCACCGGGGCC 22
Score = 54 (28.4 bits)
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 113 GATGCGGAG 121
G ATGCGGAG
Sbjct: 27 GCCATGCGG 35
Score = 34 (18.5 bits)
Identities = 5/11 (45%), Positives = 8/11 (73%)

Query: 70 ATGACCGCGGA 80
A ACCT GGA
Sbjct: 44 ACCCTCGGCGA 54

Ka 80 EDF Sequelle-DNA Locus 1700 MAC Locus 1

Score = 84 (43.2 bits)
Identities = 10/14 (71%), Positives = 12/14 (85%)

Query: 118 GAATGATGCGGAGG 131
G ATGACCGCGGA
Sbjct: 105 GGATGACCGCGGAG 118
Score = 77 (39.7 bits)
Identities = 11/13 (85%), Positives = 12/13 (92%)

Query: 73 ATGACCGCGGAGG 85
ATGACCGCGGA TE
Sbjct: 107 ATGACCGCGGATE 119
Score = 72 (37.1 bits)
Identities = 10/13 (76%), Positives = 10/13 (100%)

Query: 85 TGCGTGGGTTTTA 97
TGCGTGGG TTTA
Sbjct: 124 TGCGTGGGTTTTA 136
Score = 58 (30.4 bits)
Identities = 9/14 (64%), Positives = 10/14 (71%)

Query: 98 GAGGCATCTCGTCT 111
GGGCAT C
Sbjct: 11 TCACCATCGGCGA 24

Open 44

n/a	Change	Peak qM	Replicon ac	Locus (bp)	Locus (gpu)	Ladder Score	log Likelihood	Stars	Hot	Sequence	Modifications	Aln	Query Desc.
441,7391	2	897,4630	897,46	0,0930	0,9534	55,5203	242,1954	1	8	CCGGGCTC			De-novo
441,7391	2	897,4630	897,46	0,0930	0,9534	55,5203	242,1954	1	8	CCGGGCTC	Dewakiolus B	1	De-novo
441,7391	2	897,4630	897,46	0,0930	0,9534	51,1112	183,183	1	8	CCGGGCTC		8	De-novo
425,3006	2	1249,1876	1249,188	-0,1084	-6,7447	61,8571	91,9677	1	11	GGGCATCTCGT	Dewakiolus B / Dewakiolus	2 / 9	De-novo
425,3006	2	1249,1876	1249,188	-0,1084	-6,7447	61,8571	91,9677	1	11	GGGCATCTCGT	Dewakiolus B	3	De-novo
425,3006	2	1249,1876	1249,188	-0,1084	-6,7447	66,0317	92,6949	1	11	GGGCATCTCGT	Dewakiolus B / Dewakiolus	2 / 9	De-novo
447,2583	2	1292,7022	1292,6975	0,0935	2,8890	71,5202	256,7877	1	13	TATCGCCGGGTTT	Dewakiolus B	10	De-novo
447,2583	2	1292,7022	1292,6975	0,0935	2,8890	71,5202	256,7877	1	13	TATCGCCGGGTTT	Dewakiolus B	10	De-novo
447,2583	2	1292,7022	1292,6975	0,0935	2,8890	69,5202	256,5024	1	13	CCATCCCGGGTTT	Dewakiolus B	10	De-novo
473,2407	2	946,5338	946,5179	-0,0933	-1,2488	61,8182	145,2888	1	8	GCCATCCA		8	De-novo
473,2407	2	946,5338	946,5179	-0,0933	-1,2488	56	145,2888	1	8	GCCATCCA			De-novo
434,7150	2	897,4230	897,424	-0,0910	-1,1895	66,5324	89,9329	1	7	GGTCGCA			De-novo
434,7150	2	897,4230	897,424	-0,0910	-1,1895	66,5324	89,9329	1	7	GGTCGCA			De-novo

NCBI

Score = 58 (30.4 bits)
Identities = 8/11 (73%), Positives = 8/11 (73%)

Query: 122 TTGTGCCGAAC 132
TtGCG G AC
Sbjct: 12 TCACCGGGGCC 22
Score = 54 (28.4 bits)
Identities = 7/9 (77%), Positives = 8/9 (88%)

Query: 113 GATGCGGAG 121
G ATGCGGAG
Sbjct: 27 GCCATGCGG 35
Score = 34 (18.5 bits)
Identities = 5/11 (45%), Positives = 8/11 (73%)

Query: 70 ATGACCGCGGA 80
A ACCT GGA
Sbjct: 44 ACCCTCGGCGA 54

Ka 80 EDF Sequelle-DNA Locus 1700 MAC Locus 1

Score = 84 (43.2 bits)
Identities = 10/14 (71%), Positives = 12/14 (85%)

Query: 118 GAATGATGCGGAGG 131
G ATGACCGCGGA
Sbjct: 105 GGATGACCGCGGAG 118
Score = 77 (39.7 bits)
Identities = 11/13 (85%), Positives = 12/13 (92%)

Query: 73 ATGACCGCGGAGG 85
ATGACCGCGGA TE
Sbjct: 107 ATGACCGCGGATE 119
Score = 72 (37.1 bits)
Identities = 10/13 (76%), Positives = 10/13 (100%)

Query: 85 TGCGTGGGTTTTA 97
TGCGTGGG TTTA
Sbjct: 124 TGCGTGGGTTTTA 136
Score = 58 (30.4 bits)
Identities = 9/14 (64%), Positives = 10/14 (71%)

Query: 98 GAGGCATCTCGTCT 111
GGGCAT C
Sbjct: 11 TCACCATCGGCGA 24

Spot 82

ACA	Charge	Peak MM	Replicate MM	Delta Cha	Delta Ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Subs	Query Scan
1006.2012	2	1006.8012	1006.8012	0.0000	0.0000	0.0000	0.0000	1	9	VGGGGGGGG		0	De-novo
896.2513	2	896.8870	896.8865	0.0965	0.0965	6.5982	52.6319	1	10	WRRRRRQQQR			De-novo
1006.2012	2	1006.8012	1006.8012	0.0000	0.0000	0.0000	0.0000	1	9	VGGGGGGGG		0	De-novo
835.3046	2	1206.5436	1206.5893	0.2397	0.2397	5.3049	41.2208	1	11	PSSYSYSYSYR	Deamidation N	1	De-novo
835.3046	2	1206.5436	1206.5893	0.2397	0.2397	5.3049	41.2208	1	11	PSSYSYSYSYR	Deamidation N	1 / 10	De-novo
835.3046	2	1206.5436	1206.5893	0.2397	0.2397	5.3049	41.2208	1	11	PSSYSYSYSYR	Deamidation N	1 / 10	De-novo
825.3234	2	1196.6232	1196.6232	0.0000	0.0000	-0.0100	37.8367	1	10	YWHSSYSYW			De-novo

NCBI gi|194245779|ref|NP_0 Total Score: 268

```
                    0        90       180       270       360
                    |         |         |         |         |     >401
gi|194245779|ref|NP_0 |
Local hits 1000ms   |
                    ----  -  -  --
```

Score = 59 (22.2 bits)
Identities = 11/14 (80%), Positives = 11/14 (80%)

Query: 35 SPPPPPPPPPPPPP 48
SPPPPP+PPPPPPP
Sbjct: 122 SPPPPPPPPPPPPP 135 Mus musculus

Score = 44 (16.6 bits)
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 34 PPPPPPP 40
PPPPPP+
Sbjct: 79 PPPPPPP 85 Mus musculus

Score = 43 (16.1 bits)
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 78 PPPPPPP 84
PPPPPP+
Sbjct: 215 PPPPPPP 221 Mus musculus

Score = 41 (15.1 bits)
Identities = 6/7 (85%), Positives = 6/7 (85%)

Query: 37 PPPPPPP 43
PPPPPP+
Sbjct: 208 PPPPPPP 214 Mus musculus

Score = 38 (14.4 bits)
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 77 YPPPPP 82
Y PPPPP
Sbjct: 183 YPPPPP 188 Mus musculus

Score = 38 (14.4 bits)
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 39 PPPPPP 44
Y PPPPP
Sbjct: 198 YPPPPP 203 Mus musculus

Butterfly butterfly Total Score: 14

```
                    0        40       120       160       240
                    |         |         |         |         |     >255
butterfly|BM92367_2 |
                    ------------------------------------------
```

Score = 46 (16.5 bits)
Identities = 8/12 (66%), Positives = 8/12 (66%)

Query: 10 RHRRHRQQQR 20
RHR YR QQR
Sbjct: 243 RHRRYRQQR 253

Score = 44 (15.8 bits)
Identities = 7/7 (77%), Positives = 7/7 (77%)

Query: 3 RHRRQQR 11
R YR QQR
Sbjct: 248 RYRQQRR 254

Ha 60 EST [illegible] Total Score: 14

```
                    0        90       180       270       360
                    |         |         |         |         |     >450
hs|gi|60-QLK_Contig |
Local hits 1000ms   |
                    -
```

Score = 78 (28.4 bits)
Identities = 11/11 (100%), Positives = 11/11 (100%)

Query: 10 RHRRHRQQQR 20
RHRRHRQQQR
Sbjct: 275 RHRRHRQQQR 285

Score = 42 (15.5 bits)
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 3 RHRRQQQR 11
RHRRQQQR
Sbjct: 278 RHRRQQQR 286

Spot 85

ACA	Charge	Peak MM	Replicate MM	Delta Cha	Delta Ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Subs	Query Scan
1006.2012	2	1006.8012	1006.8012	0.0000	0.0000	0.0000	0.0000	1	9	VGGGGGGGG		0	De-novo
976.2561	2	1136.5680	1136.5650	-0.2658	-0.5461	5.7481	48.4211	1	10	YYSPRYRYMR			De-novo
976.2561	2	1136.5680	1136.5650	-0.2658	-0.5461	5.7481	48.4211	1	10	YYSPRYRYMR	Oxidation M	9	De-novo
965.2960	2	1122.5730	1122.5760	-0.2513	-1.1794	5.9495	125.8984	1	10	YYSPRYRYMR	Oxidation M	9	De-novo
965.2960	2	1122.5730	1122.5760	-0.2513	-1.1794	5.9495	142.9218	1	10	YYSPRYRYMR			De-novo
965.2960	2	1122.5730	1122.5760	-0.2513	-1.1794	5.9495	142.9218	1	10	YYSPRYRYMR			De-novo
781.391	2	1562.7554	1562.7077	-0.4973	-4.6868	36.5927	75.0257	1	13	YSSYRSYYSLQPR		2 / 10	De-novo
781.391	2	1562.7554	1562.7077	-0.4973	-4.6868	36.5927	72.6142	1	13	YSSYRSYYSLQPR	Deamidation Q /	2 / 10	De-novo
781.391	2	1562.7554	1562.7077	-0.4973	-4.6868	36.5927	72.6142	1	13	YSSYRSYYSLQPR	Deamidation Q /	2 / 10	De-novo
844.7403	2	871.3230	871.3178	-0.2628	-3.0147	26.7024	116.9979	1	9	SSYSPQRRR			De-novo
844.7403	2	871.3230	871.3178	-0.2628	-3.0147	26.7024	116.9911	1	9	SSYSPQRRR			De-novo
844.7403	2	871.3230	871.3178	-0.2628	-3.0147	26.7024	116.9911	1	9	SSYSPQRRR			De-novo
851.8307	2	1301.6458	1301.6462	-0.2034	-0.3257	40	128.6227	1	12	ARSYSSLSRRLR		1	De-novo
851.8307	2	1301.6458	1301.6462	-0.2034	-0.3257	40	128.6227	1	12	ARSYSSLSRRLR	Deamidation R	2	De-novo
851.8307	2	1301.6458	1301.6462	-0.2034	-0.3257	40	125.1542	1	12	ARSYSSLSRRLR	Deamidation R /	1 / 10	De-novo

NCBI gi|194245779|ref|NP_0 Total Score: 324

```
                    0        90       180       270       360
                    |         |         |         |         |     >272
gi|194245779|ref|NP_0 |
Local hits 1000ms   |
                    -  ---  --
```

Score = 76 (29.6 bits)
Identities = 9/10 (90%), Positives = 10/10 (100%)

Query: 30 YYLPRRYRMR 39
YYLPRRYRMR
Sbjct: 261 YYLPRRYRMR 270 Mus musculus

Score = 48 (18.7 bits)
Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 32 LPRRYRMRMRLR 43
+PRRYRMR R R
Sbjct: 263 +PRRYRMRRRLR 274 Mus musculus

Score = 42 (16.5 bits)
Identities = 6/9 (67%), Positives = 6/9 (67%)

Query: 108 LRLPRRR 116
LRLPL RR
Sbjct: 179 LRLPLRR 185 Mus musculus

Score = 42 (16.5 bits)
Identities = 6/9 (67%), Positives = 6/9 (67%)

Query: 166 LPRRRRR 174
LPL RRR
Sbjct: 178 LPLRRRR 184 Mus musculus

Score = 42 (16.5 bits)
Identities = 8/12 (67%), Positives = 7/12 (75%)

Query: 164 RRPRRRPRRR 173
RR R RRR R
Sbjct: 34 RRTRRRTRRR 45 Mus musculus

Score = 40 (15.8 bits)
Identities = 5/9 (56%), Positives = 5/9 (56%)

Query: 128 RRLRRRR 136
RRL RRR
Sbjct: 47 RRLRRRR 55 Mus musculus

Butterfly butterfly Total Score: 41

```
                    0        40       120       160       240
                    |         |         |         |         |     >256
ds|BM92367_1_Contig1 |
Local hits 1000ms   |
                    - -  ---  ---
```

Score = 76 (28.4 bits)
Identities = 10/10 (100%), Positives = 10/10 (100%)

Query: 30 YYLPRRYRMR 39
YYLPRRYRMR
Sbjct: 161 YYLPRRYRMR 170

Score = 48 (18.7 bits)
Identities = 9/12 (75%), Positives = 10/12 (83%)

Query: 32 LPRRYRMRMRLR 43
+PRRYRMR R R
Sbjct: 123 LPRRYRMRRRLR 134

Score = 48 (18.7 bits)
Identities = 7/10 (70%), Positives = 7/10 (70%)

Query: 108 LRLPRRRRLR 117
LRLPL RR R R
Sbjct: 176 LRLPLRRRLR 185

Score = 42 (16.5 bits)
Identities = 6/9 (67%), Positives = 6/9 (67%)

Query: 166 LPRRRRR 174
LPL RRR
Sbjct: 178 LPLRRRR 184

Score = 42 (16.5 bits)
Identities = 8/12 (67%), Positives = 7/12 (58%)

Query: 164 RRPRRRPRRR 173
RR R RRR R
Sbjct: 34 RRTRRRTRRR 45

Score = 40 (15.8 bits)
Identities = 5/9 (56%), Positives = 5/9 (56%)

Query: 128 RRLRRRR 136
RRL RRR
Sbjct: 47 RRLRRRR 55

Ha 60 other [illegible]

Ha 60 other [illegible] Total Score: 14

```
                    0        90       180       270       360
                    |         |         |         |         |     >450
hs|gi|60-NM-NM-NLL_Co |
Local hits 1000ms   |
                    -
```

Score = 60 (21.7 bits)
Identities = 9/12 (75%), Positives = 9/12 (75%)

Query: 42 LPRRYRMRQQR 52
LPRRYR R QQR
Sbjct: 436 LPRRYRRRQQR 446

Score = 35 (13.3 bits)
Identities = 5/7 (71%), Positives = 5/7 (71%)

Query: 79 YYRQQRR 85
YYR RR
Sbjct: 474 YYRRRRR 480

Spot 86

ACA	Charge	Peak MM	Replicate MM	Delta Cha	Delta Ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Subs	Query Scan
885.4350	2	1770.8860	1770.8860	0.0000	0.0000	0.0000	0.0000	1	16	LQSYSSTSQ-YSSYR		0	De-novo
885.4350	2	1770.8860	1770.8860	0.0000	0.0000	0.0000	0.0000	1	16	LQSYSSTSQ-YSSYR	Deamidation Q /	1	De-novo
885.4350	2	1770.8860	1770.8860	0.0000	0.0000	0.0000	0.0000	1	16	LQSYSSTSQ-YSSYR	Deamidation Q /	1 / 1	De-novo
844.5727	3	2535.1987	2535.1911	0.3458	0.3458	17.1840	43.5424	1	24	NQNHSNSSSSYSYSLLQNSSYR	Deamidation Q /	2 / 10	De-novo
844.5727	3	2535.1987	2535.1911	0.3458	0.3458	17.1840	43.5424	1	24	NQNHSNSSSSYSYSLLQNSSYR	Deamidation Q /	2 / 10	De-novo
844.5727	3	2535.1987	2535.1911	0.3458	0.3458	15.3119	46.2906	1	24	NQNHSNSSSSYSYSLLQNSSYR	Deamidation Q /	2 / 10	De-novo
885.8648	2	1326.4738	1326.4677	0.0459	0.0459	4.4141	55.0725	1	12	GSRNEYRRYRLR	Deamidation Q	2	De-novo
885.8648	2	1326.4738	1326.4677	0.0459	0.0459	4.4141	55.0725	1	12	GSRNEYRRYRLR			De-novo
885.8648	2	1326.4738	1326.4677	0.0459	0.0459	4.4141	46.5750	1	12	GSRNEYRRYRLR		0	De-novo
827.5292	2	1252.6366	1252.5909	0.3437	36.8885	55.8967	71.2442	1	10	RLYQYQRRYR	Deamidation Q	5	De-novo
827.5292	2	1252.6366	1252.5909	0.3437	36.8885	55.8967	70.9374	1	10	RLYQYQRRYR	Deamidation Q	5	De-novo

NCBI gi|194245779|ref|NP_0 Total Score: 432

```
                    0        90       180       270       360
                    |         |         |         |         |     >256
gi|194245779|ref|NP_0 |
Local hits 1000ms   |
                    ---  ----
```

Score = 97 (35.7 bits)
Identities = 12/13 (92%), Positives = 13/13 (100%)

Query: 132 RRQYRRRYRRYRR 144
RRQYRRRYRRYRR
Sbjct: 61 RRQYRRRYRRYRR 73 Mus musculus

Score = 74 (28.3 bits)
Identities = 9/11 (82%), Positives = 11/11 (100%)

Query: 18 RLRRRRYRQQR 28
RLRRRRYRQQR
Sbjct: 71 RLRRRRYRQQR 81 Mus musculus

Ha 60 EST [illegible] Total Score: 14

```
                    0        90       180       270       360
                    |         |         |         |         |     >450
hs|gi|60-QLK_Contig |
Local hits 1000ms   |
                    ---
```

Score = 68 (25.0 bits)
Identities = 9/11 (82%), Positives = 11/11 (100%)

Query: 42 RRLQRRRYRQR 52
RRLQRRRYRQR
Sbjct: 177 RRLQRRRYRQR 187

Span 47

ACC	Charge	Post MM	Replicm MM	Delta CMs	Delta Gaps	Ladder Score	Log Likelihood	Start	End	Sequence	Mode/Influence	Score	Query Seq.
473,760	2	945,474	945,474	-0,0000	-0,0000	-0,0000	0,0000	1	9	CTGCCGCAT	Deletion @	0	De-novo
473,760	2	945,474	945,474	-0,0000	-0,0000	66,6408	137,1914	1	9	CATCAGCA	Deletion @	0	De-novo
473,760	2	945,474	945,474	-0,0000	-0,0000	66,6408	137,1914	1	9	CATCAGCA	Deletion @	0	De-novo
845,236	2	876,645	876,645	-0,0342	-6,8285	61,5385	99,7413	1	7	TGCATCG	Deletion @	0	De-novo
845,236	2	876,645	876,645	-0,0342	-6,8285	61,5385	99,7413	1	7	TGCATCG			De-novo
845,236	2	876,645	876,645	-0,0342	-6,8285	61,5385	99,7413	1	7	TGCATCG	Deletion @	0	De-novo
514,515	2	1035,694	1035,673	-0,0013	-1,3419	57,8947	91,9618	1	10	TGCATGCAAG			De-novo
861,8960	2	1765,774	1765,8748	-0,0973	-19,1138	56,0902	76,6292	1	18	ACATCTCCCCCCCCCATCTC			De-novo
861,8960	2	1765,774	1765,8748	-0,0973	-19,1138	56,0902	76,6292	1	18	ACATCTCCCCCCCCCATCTC			De-novo
897,911	2	1765,8544	1765,814	-0,0114	-0,5685	55,5333	75,2544	1	17	CCAAGAGCCCCCCCCCC			De-novo
897,911	2	1765,8544	1765,814	-0,0114	-0,5685	55,5333	75,2544	1	17	CCAAGAGCCCCCCCCCC	Deletion @	10	De-novo
897,911	2	1765,8544	1765,814	-0,0114	-0,5685	55,5333	75,2544	1	17	CCAAGAGCCCCCCCCCC	Cachexia&Deep/Ill /	0	De-novo
895,3381	2	1386,7316	1386,7263	-0,0377	-0,5623	66,1139	75,5162	1	12	TCACCCTCTTCCC	Cachexia&Deep/Ill /	4 / 11	De-novo
895,3381	2	1386,7316	1386,7263	-0,0377	-0,5623	66,1139	75,5162	1	12	TCACCCTCTTCCC	Cachexia&Deep/Ill /	4 / 11	De-novo
895,3381	2	1386,7316	1386,7263	-0,0377	-0,5623	66,1139	75,5162	1	12	TCACCCTCTTCCC			De-novo
895,5260	2	1386,6412	1386,7283	-0,0878	-13,4756	65,0556	153,6449	1	12	CATCCTGCCATGAC			De-novo

Hit gi|155233|ref|NC_000913.3| Escherichia coli K12 substr. MG1655, complete genome Score: 141

```
                                   0        40        80       120       160
                                   |         |         |         |         |
gi|155233|ref|NC_000913.3|  ACCTCCTCCTC
```

Spot 32

ALN	Charge	Peak MH	Peptide MH	Delta Obs	Delta Ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modification	Pos.	Query Seq.
588,7402	2	1176,5220	1176,5174	+0,0046	+3,9102	56,7402	156,1217	1	10	MKKTTTSCAK	Cysteine(Reduced) C	10	De-novo
588,7402	2	1176,5220	1176,5178	+0,0042	+3,5750	56,7402	153,6074	1	11	KKKTTTSCAK	Cysteine(Reduced) C	10	De-novo
573,2927	2	1144,5708	1144,5714	-0,0006	-0,5245	46,6667	271,4122	1	10	QLPPTTTLQK	Deamidation Q /	1 / 9	De-novo
573,2927	2	1144,5708	1144,5714	-0,0006	-0,5245	46,6667	255,4122	1	10	QLPPTTTLQK	Deamidation Q /	1 / 9	De-novo
573,2927	2	1144,5708	1144,5714	-0,0006	-0,5245	46,6667	235,1158	1	10	QLPPTTTLQK	Deamidation Q	9	De-novo
573,2927	2	1144,5708	1144,5714	-0,0006	-0,5245	46,6667	231,1158	1	10	QLPPTTTLQK	Deamidation Q	1	De-novo
703,3542	2	1404,6940	1404,6950	-0,0009	-0,6539	46,9206	165,9843	1	12	MLYSSPPMLGR	Oxidation M / Deamidation	1 / 8	De-novo
703,3542	2	1404,6940	1404,7072	-0,0132	-9,4208	46,9206	149,4773	1	12	MLYSSPPMLGR	Oxidation M	1	De-novo
703,3542	2	1404,6940	1404,7072	-0,0132	-9,4208	46,9206	147,4773	1	12	MLYSSPPMLGR			De-novo
809,2185	2	1616,4261	1616,7239	-0,2978	-183,6973	56,5217	156,0243	1	12	SPSPSPSPLGR			De-novo
809,8815	2	1611,7474	1611,7617	0,0957	5,9217	42,963	247,1767	1	14	TKETQTQTSRLGW	Deamidation Q	10	De-novo
809,8815	2	1611,7474	1611,7617	0,0957	5,9217	42,963	231,1767	1	14	TKETQTQTSRLGW	Deamidation Q	5,10	De-novo
809,8815	2	1611,7474	1611,7617	0,0957	5,9217	42,963	205,2042	1	14	TKETQTQTSRLGW	Deamidation Q	10	De-novo
896,3542	2	1339,4828	1339,7558	-0,2236	-7,9857	36,9206	46,4282	1	11	YYYPPGGNGKR			De-novo
896,3542	2	1339,4828	1339,7558	-0,2236	-7,9857	36,9206	41,4282	1	11	YYYPPGGNGKR			De-novo
896,3542	2	1339,4828	1339,7558	-0,2236	-7,9857	36,9206	41,2888	1	11	YYYPPGGNGKR			De-novo

NCBI [gi|28347663|gb|AAH0788 | Protein [Homo sapiens] gi|28347663|gb|AAH0788 |] Total Score: 213

```
                    0        30        60        90       120
                    |         |         |         |         |
gi|28347663|gb|AAH0788  1 ------------------------------------------------------------ 120
Local hits (MSMs)        ---- -- --------                   ------
```

Score = 96 (48.4 bits)
Identities = 12/14 (86%), Positives = 14/14 (100%)

```
Query:  64 KMKLYSSPPMLGR  77
          KMKLYSSPPMLGR
Sbjct:  102 KMKLYSSPPMLGR  115
```

Score = 77 (38.8 bits)
Identities = 9/10 (90%), Positives = 10/10 (100%)

```
Query:  114 TKETQTQTSR  123
            TKETQTQTSR
Sbjct:  8   TKETQTQTSR  17
```

Score = 71 (37.8 bits)
Identities = 10/10 (100%), Positives = 10/10 (100%)

```
Query:  118 TQTQTSRLGW  127
            TQTQTSRLGW
Sbjct:  4   TQTQTSRLGW  13
```

Score = 39 (21.1 bits)
Identities = 7/11 (64%), Positives = 10/11 (90%)

```
Query:  188 PLQPPTTTQK  198
            PLQ+PTTTQK
Sbjct:  10  PLQSPTTTQK  20
```

Score = 57 (30.3 bits)
Identities = 9/11 (82%), Positives = 9/11 (82%)

```
Query:  13 AQPTTTSGK  23
           A+PTTTS+K
Sbjct:  7  ARPTTTSSK  17
```

Score = 48 (25.6 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)

```
Query:  95  PPGGNGS  101
            PPGGNGS
Sbjct:  11  PPGGNGS  17
```

Score = 47 (25.2 bits)
Identities = 6/6 (100%), Positives = 6/6 (100%)

```
Query:  174 WYYYP  180
            +Y+YP
Sbjct:  4   YYYYP  10
```

Spot 33

ALN	Charge	Peak MH	Peptide MH	Delta Obs	Delta Ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modification	Pos.	Query Seq.
667,3138	2	1332,6122	1332,6137	-0,0037	-2,7945	52,7903	276,6277	1	14	KLGSSPPMSSTPPW	Deamidation S	1	De-novo
734,3537	2	1466,6818	1466,6888	0,0930	2,6291	56,7903	137,2131	1	14	LGSSPPMSSTPPW	Deamidation S	9	De-novo
734,3537	2	1466,6818	1466,6888	0,0930	2,6291	56,7903	134,2131	1	14	LGSSPPMSSTPPW	Deamidation S /	8 / 9	De-novo
734,3537	2	1466,6818	1466,6888	0,0930	2,6291	56,7903	134,517	1	14	LGSSPPMSSTPPW	Deamidation S	8	De-novo
478,7181	2	955,4655	955,4651	-0,0043	-4,7349	46,9999	132,9073	1	8	YQAGFTK		2	De-novo
621,8147	2	1239,6138	1239,6340	-0,0208	-16,7985	49,5652	303,7018	1	12	SASPGFQLQSP		1 / 8	De-novo
621,8147	2	1239,6138	1239,6340	-0,0208	-16,7985	49,5652	303,5218	1	12	SASPGFQLQSP	Deamidation Q	1 / 8	De-novo
621,8147	2	1239,6138	1239,6340	-0,0208	-16,7985	49,5652	303,7093	1	12	SASPGFQLQSP			De-novo
621,8147	2	1239,6138	1239,6340	-0,0208	-16,7985	49,5652	303,5293	1	12	SASPGFQLQSP	Deamidation Q	7	De-novo
561,3132	2	1121,6208	1121,6072	0,0035	3,0944	76,5398	239,6174	1	9	LPTPCQCPR			De-novo
561,3132	2	1121,6208	1121,6072	0,0035	3,0944	76,5398	202,5893	1	9	LPTPCQCPR			De-novo
774,3276	2	1547,6336	1547,6363	0,0033	2,1219	61,569	228,5268	1	15	LQAGQPTTPGQPQK	Deamidation Q	12	De-novo
774,3276	2	1547,6336	1547,6363	0,0033	2,1219	61,569	226,5268	1	15	LQAGQPTTPGQPQK			De-novo
774,3276	2	1547,6336	1547,6363	0,0033	2,1219	61,569	215,9739	1	15	LQAGQPTTPGQPQK			De-novo
894,3851	2	1786,7556	1786,5924	-0,1758	-104,5272	35,303	156,1349	1	17	ATPLAGTAGCLPLIR			De-novo
894,3851	2	1786,7556	1786,5924	-0,1758	-104,5272	35,303	135,1349	1	17	ATPLAGTAGCLPLIR			De-novo
894,3851	2	1786,7556	1786,5924	-0,1758	-104,5272	35,303	130,1349	1	17	ATPLAGTAGCLPLIR			De-novo
621,7583	2	841,3510	841,3511	-0,0011	-1,2237	76,5504	70,9	1	8	YATPLGR			De-novo
621,7583	2	841,3510	841,3511	-0,0011	-1,2237	76,5504	55,569	1	8	YATPLGR			De-novo
526,2981	2	1054,5914	1054,5771	0,0093	8,6567	47,5084	84,1561	1	10	GGPGCTEGCR			De-novo

NCBI [gi|15902670|ref|NP_0 | Lamin A/C [Homo sapiens] gi|15902670|ref|NP_0 |] Total Score: 148

```
                    0       420       840       1260      1680
                    |         |         |         |         |
gi|15902670|ref|NP_0  1 ------------------------------------------------------------ 1679
Local hits (MSMs)        ---------------------------------------------------------
```

Score = 58 (29.6 bits)
Identities = 9/12 (88%), Positives = 11/12 (78%)

```
Query:  190 ATPLAGTAGCLP  201
            A PLAGTA GC+
Sbjct:  597 ASPLAGTAGCMP  608
```

Score = 52 (27.3 bits)
Identities = 7/10 (70%), Positives = 8/10 (80%)

```
Query:  173 ATPLAGTAGC  182
            A PLAGTA G
Sbjct:  612 ASPLAGTAGG  621
```

Score = 32 (16.9 bits)
Identities = 7/10 (70%), Positives = 8/10 (80%)

```
Query:  209 ATPLAGTGCP  218
            A PLAGTGCP
Sbjct:  883 ASPLAGTGCG  892
```

Spot 34

ALN	Charge	Peak MH	Peptide MH	Delta Obs	Delta Ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modification	Pos.	Query Seq.
781,3429	2	1560,6702	1560,6756	-0,0052	-3,3417	55,914	102,224	1	14	EGSYSHMSSSQMSP	Deamidation S /	1 / 12	De-novo
781,3429	2	1560,6702	1560,6756	-0,0052	-3,3417	55,914	100,224	1	14	EGSYSHMSSSQMSP	Deamidation S	1	De-novo
581,3044	2	1176,5936	1176,6066	-0,0129	-10,9285	43,1273	72,8898	1	9	YEELQKTK			De-novo
581,3044	2	1176,5936	1176,6066	-0,0129	-10,9285	56,992	70,4292	1	9	YEELQKTKK		7	De-novo
853,8508	2	1705,7720	1705,812	-0,0401	-23,4841	25,1203	195,9573	1	18	DSTNETSSLLLNMLNTR	Deamidation N	4	De-novo
853,8508	2	1705,7720	1705,812	-0,0401	-23,4841	25,1203	194,9573	1	18	DSTNETSSLLLNMLNTR	Deamidation N	4	De-novo
853,8508	2	1705,7720	1705,812	-0,0401	-23,4841	40	186,1719	1	18	DSTNETSSLLLNMLNTR	Deamidation N	4	De-novo
853,8508	2	1705,7720	1705,812	-0,0401	-23,4841	25,1203	41,8	1	18	DSTNETSSLLLNMLNTR	Deamidation N /	4 / 14	De-novo
897,9103	2	1793,8203	1793,8273	-0,0037	-2,0194	35,303	151,255	1	17	AANDNSSILLGNMSRK	Deamidation N	14	De-novo
897,9103	2	1793,8203	1793,8273	-0,0037	-2,0194	46,4669	130,4123	1	17	AANDNSSILLGNMSRK	Deamidation N	13	De-novo

NCBI [gi|15214968|ref|NP_0 | Protein [Homo sapiens] gi|15214968|ref|NP_0 |] Total Score: 93

```
                    0        30        60        90       120
                    |         |         |         |         |
gi|15214968|ref|NP_0  1 ------------------------------------------------------------ 120
Local hits (MSMs)        ------------------------------------
```

Score = 95 (48.0 bits)
Identities = 12/14 (86%), Positives = 13/14 (92%)

```
Query:  13 LGSSPPMSSTPPW  26
           LGSSPPMSSTPPW
Sbjct:  94 LGSSPPMSSTPPW  107
```

Score = 77 (38.8 bits)
Identities = 9/10 (90%), Positives = 10/10 (100%)

```
Query:  20 PPMSSTPPWR  29
           PPMSSTPPWR
Sbjct:  101 PPMSSTPPWR  110
```

Spot 35

ALN	Charge	Peak MH	Peptide MH	Delta Obs	Delta Ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modification	Pos.	Query Seq.
781,3429	2	1560,6702	1560,6756	-0,0052	-3,3417	55,914	102,224	1	14	EGSYSHMSSSQMSP	Deamidation S /	1 / 12	De-novo
781,3429	2	1560,6702	1560,6756	-0,0052	-3,3417	55,914	100,224	1	14	EGSYSHMSSSQMSP	Deamidation S	1	De-novo
581,3044	2	1176,5936	1176,6066	-0,0129	-10,9285	43,1273	72,8898	1	9	YEELQKTK			De-novo
581,3044	2	1176,5936	1176,6066	-0,0129	-10,9285	56,992	70,4292	1	9	YEELQKTKK		7	De-novo
853,8508	2	1705,7720	1705,812	-0,0401	-23,4841	25,1203	195,9573	1	18	DSTNETSSLLLNMLNTR	Deamidation N	4	De-novo
853,8508	2	1705,7720	1705,812	-0,0401	-23,4841	25,1203	194,9573	1	18	DSTNETSSLLLNMLNTR	Deamidation N	4	De-novo
853,8508	2	1705,7720	1705,812	-0,0401	-23,4841	40	186,1719	1	18	DSTNETSSLLLNMLNTR	Deamidation N	4	De-novo
853,8508	2	1705,7720	1705,812	-0,0401	-23,4841	25,1203	41,8	1	18	DSTNETSSLLLNMLNTR	Deamidation N /	4 / 14	De-novo
897,9103	2	1793,8203	1793,8273	-0,0037	-2,0194	35,303	151,255	1	17	AANDNSSILLGNMSRK	Deamidation N	14	De-novo
897,9103	2	1793,8203	1793,8273	-0,0037	-2,0194	46,4669	130,4123	1	17	AANDNSSILLGNMSRK	Deamidation N	13	De-novo

NCBI [gi|15214968|ref|NP_0 | Protein [Homo sapiens] gi|15214968|ref|NP_0 |] Total Score: 93

```
                    0        30        60        90       120
                    |         |         |         |         |
gi|15214968|ref|NP_0  1 ------------------------------------------------------------ 120
Local hits (MSMs)        ------------------------------------
```

Score = 95 (48.0 bits)
Identities = 12/14 (86%), Positives = 13/14 (92%)

```
Query:  13 LGSSPPMSSTPPW  26
           LGSSPPMSSTPPW
Sbjct:  94 LGSSPPMSSTPPW  107
```

Score = 77 (38.8 bits)
Identities = 9/10 (90%), Positives = 10/10 (100%)

```
Query:  20 PPMSSTPPWR  29
           PPMSSTPPWR
Sbjct:  101 PPMSSTPPWR  110
```

Spot 53

m/z	Charge	Peak mH	Peptide mH	Delta (Da)	Delta (ppm)	Sadder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbe	Query Scan
974.2928	2	1946.5710	1946.572	-0.0010	-0.5003	-0.8000	-94.9600	1	12	GQEAQMRNEEIR	Deamidation Q	2 / 7	De-novo
974.2928	2	1946.5710	1946.572	-0.0010	-0.4995	69.8610	185.414	1	12	EQEAQMRNEEIR	Deamidation Q /	2 / 7	De-novo
861.8928	2	1720.7710	1720.782	-0.0142	-8.2577	69.5000	201.812	1	14	AGEVIEHGIILLGMNEFE	Deamidation E	4	De-novo
861.8928	2	1720.7710	1720.782	-0.0142	-13.7125	69.5100	203.812	1	14	AGEVIEHGIILLGMNEFE	Deamidation E	4	De-novo
861.8928	2	1720.7710	1720.782	-0.0142	-13.7125	66.4687	201.982	1	14	AGEVIEHGIILLGMNEFE	Deamidation E	4	De-novo
871.5138	2	1740.8410	1740.857	-0.0153	-8.7878	69.5000	185.414	1	17	GCFETGGILLGMNEMNM	Carbamidomethylcy / /	2 / 10	De-novo
871.5138	2	1740.8410	1740.857	-0.0153	-11.5719	69.5000	185.414	1	17	GCFETGGILLGMNEMNM	Carbamidomethylcy / /	2 / 10	De-novo
871.5138	2	1740.8410	1740.857	-0.0153	-11.5719	67.4747	184.4294	1	17	GFSEACTGLLGMNEMNM	Carbamidomethylcy / /	5 / 10	De-novo
905.2796	2	1808.5442	1808.541	0.0022	1.2208	69.5000	185.414	1	15	LEVGMEFEK	Deamidation E	6	De-novo
905.2796	2	1808.5442	1808.541	0.0022	1.2208	66.1439	56.149	1	15	LEVGMEFEK	Deamidation E	6	De-novo
905.2796	2	1808.5442	1808.541	0.0022	1.2208	65.7452	56.149	1	15	LEVGMEFEK	Deamidation E	6	De-novo

MGF: [spectra/20-qtof_20_20171117-20000ng50_1ul-01_2uhpg_2ul.mgf](#) Total Scans: 53

Score = 50 (22.0 bits)
Identities = 9/12 (80%), Positives = 10/12 (83%)

Query: 46 GGGALLGGMNEFE 58
GG LLGGM EE
Sbjct: 142 GGFCLLGGMFEE 154

Score = 54 (24.3 bits)
Identities = 9/10 (90%), Positives = 10/10 (82%)

Query: 119 LLGMNEMNMGAGAFM 134
LLGMEE EG FM
Sbjct: 156 LLGMFEEGFEGFGFM 171 [Decoy]

Scter/Cyfuse [spectra/20-qtof_20_20171117-20000ng50_1ul-01_2uhpg_2ul.mgf](#) Total Scans: 1

Sp 60 EXP [spectra/20-qtof_20_20171117-20000ng50_1ul-01_2uhpg_2ul.mgf](#) Total Scans: 1

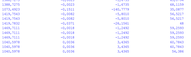
Score = 71 (28.2 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)

Query: 1 LEEGAGFGGGER 12
LEEGAGFGGGER
Sbjct: 129 LEEGAGFGGGER 139

Spot 54

m/z	Charge	Peak mH	Peptide mH	Delta (Da)	Delta (ppm)	Sadder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbe	Query Scan
474.7247	2	947.4338	947.4481	-0.0143	-15.0878	70.1111	192.602	1	8	VEEEGAER		3	De-novo
474.7247	2	947.4338	947.4481	-0.0143	-15.0878	69.5000	185.414	1	8	VEEEGAER	Deamidation E	4	De-novo
474.7247	2	947.4338	947.4481	-0.0143	-15.0878	69.5000	185.414	1	8	VEEEGAER	Deamidation E /	4	De-novo
725.8365	2	1449.6614	1449.7111	-0.0497	-15.8325	91.7656	321.248	1	14	EGLAGEMFEEAAAW		7	De-novo
725.8365	2	1449.6614	1449.7111	-0.0497	-15.8325	91.5000	321.248	1	14	EGLAGEMFEEAAAW	Deamidation E /	7	De-novo
725.8365	2	1449.6614	1449.7111	-0.0497	-15.8325	91.5000	317.4102	1	14	EGLAGEMFEEAAAW	Deamidation E /	7 / 10	De-novo
513.7808	2	1025.5502	1025.5618	-0.0108	-9.5781	59.4835	156.051	1	11	EGFAAGLGFGR			De-novo
513.7808	2	1025.5502	1025.5618	-0.0108	-9.5781	59.4835	156.051	1	11	EGFAAGLGFGR			De-novo
513.7808	2	1025.5502	1025.5618	-0.0108	-9.5781	56.5079	154.123	1	11	EGFAAGLGFGR			De-novo
713.8823	2	1424.7674	1424.7943	-0.0269	-18.8769	98.1139	276.214	1	12	FTGAGFEVEGLR		6	De-novo
713.8823	2	1424.7674	1424.7943	-0.0269	-18.8769	98.1139	276.214	1	12	FTGAGFEVEGLR	Deamidation E / Deamidation	6 / 9	De-novo
713.8823	2	1424.7674	1424.7943	-0.0269	-18.8769	98.1139	271.9558	1	12	FTGAGFEVEGLR	Deamidation E /	6 / 9	De-novo
871.4339	2	1740.8522	1740.8828	-0.3306	-17.5912	76.7675	396.597	1	17	GRLEATEMVAGLAFFLR			De-novo
871.4339	2	1740.8522	1740.8828	-0.3306	-17.5912	76.7675	396.597	1	17	GRLEATEMVAGLAFFLR			De-novo
871.4339	2	1740.8522	1740.8828	-0.3306	-17.5912	75.1126	275.4949	1	16	GRLEATEMVAGLAFFLA			De-novo
871.9307	2	1739.8558	1739.8581	-0.0233	-1.3235	55.5034	141.437	1	17	AIAGATEMVAGLAFFLR			De-novo
871.9307	2	1739.8558	1739.8581	-0.0233	-1.3235	55.5034	141.437	1	17	AIAGATEMVAGLAFFLR			De-novo
871.9307	2	1739.8558	1739.8581	-0.0233	-1.3235	55.5034	140.5054	1	17	FIAGATEMVAGLAFFLR			De-novo
452.7577	2	903.4998	903.5219	-0.0221	-24.4864	56.9006	181.393	1	8	FEFFFLIR			De-novo
452.7577	2	903.4998	903.5219	-0.0221	-24.4864	56.5000	181.393	1	8	FEFFFLIR			De-novo
452.7577	2	903.4998	903.5219	-0.0221	-24.4864	56.5000	179.4	1	8	FEFFFLIR			De-novo
495.2754	2	1986.7252	1986.7275	-0.0023	-1.1735	98.1139	115.718	1	16	LNFFGLER			De-novo
495.2754	2	1986.7252	1986.7275	-0.0023	-1.1735	98.1139	116.918	1	12	FTNFSFEGLLQR			De-novo
495.2754	2	1986.7252	1986.7275	-0.0023	-1.1735	98.1139	116.918	1	12	FTNFSFEGLLQR	Carbamidomethylcy /		De-novo
495.2754	2	1986.7252	1986.7275	-0.0023	-1.1735	98.1139	114.4859	1	12	YDNVEEGLLQR			De-novo
537.6784	2	1073.3622	1073.4063	-0.1411	-143.7719	35.0877	96.599	1	10	ERWEVLGLER			De-novo
474.2565	3	1419.7661	1419.7943	-0.0282	-19.8522	99.5000	225.522	1	12	RLFLFGEFEGLR	Deamidation E / Deamidation	1 / 8	De-novo
474.2565	3	1419.7661	1419.7943	-0.0282	-19.8522	99.5000	225.522	1	12	RLFLFGEFEGLR	Deamidation E	1	De-novo
474.2565	3	1419.7661	1419.7943	-0.0271	-19.0341	99	247.7015	1	12	ERQFLFGEFEGLR	Deamidation E	9	De-novo
474.2565	3	1419.7661	1419.7943	-0.0271	-19.0341	99.5000	247.7015	1	12	ERQFLFGEFEGLR	Deamidation E /	9	De-novo
495.9109	3	1469.7093	1469.7111	-0.0018	-1.2492	59.5000	319.518	1	14	RLLAEGEFEQGAMR	Deamidation E /	6 / 10	De-novo
495.9109	3	1469.7093	1469.7111	-0.0018	-1.2492	59.5000	316.5755	1	14	RLLAEGEFEGGAMR			De-novo
495.9109	3	1469.7093	1469.7111	-0.0018	-1.2492	59.5000	316.5755	1	14	RLLAEGEFEGGAMR			De-novo
501.3685	3	1501.4014	1501.3978	0.0036	2.4245	81.7843	76.589	1	9	RGYEQLLLR	Deamidation Q	5	De-novo
501.3685	3	1501.4014	1501.3978	0.0036	2.4245	81.7843	76.589	1	9	RGYEQLLLR			De-novo
501.3685	3	1501.4014	1501.3978	0.0036	2.4245	81.7827	76.589	1	10	GGYEQLLLR			De-novo

MGF: [spectra/20-qtof_20_20171117-20000ng50_1ul-01_2uhpg_2ul.mgf](#) Total Scans: 54



Score = 126 (45.7 bits)
Identities = 17/18 (94%), Positives = 18/18 (100%)

Query: 455 RQRLAGVFNNGVGFFGLF 472
RQRLAGVFNNGVGFFGLF
Sbjct: 49 RQRLAGVFNNGVGFFGLF 66 [Decoy]

Score = 102 (42.0 bits)
Identities = 12/17 (70%), Positives = 14/17 (94%)

Query: 46 RKLLGGVRNRRRRRRRG 62
RKLLGGVRNRRRRRRRG
Sbjct: 113 RKLLGGVRNRRRRRRRG 129 [Decoy]

Score = 98 (41.0 bits)
Identities = 12/14 (86%), Positives = 14/14 (100%)

Query: 122 QRTFGAFSFFGGGF 135
QRTFGAFSFFGGGF
Sbjct: 1 QRTFGAFSFFGGGF 15 [Decoy]

Score = 84 (36.2 bits)
Identities = 9/13 (69%), Positives = 11/13 (84%)

Query: 409 QLLRRRTCRLLAR 421
QLLr rr CLLAR
Sbjct: 47 RLLGRRVCLLLGR 59 [Decoy]

Score = 56 (25.7 bits)
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 55 GRRRRRRG 62
GRRRRRRG
Sbjct: 38 GRRRRRRG 45 [Decoy]

Score = 49 (23.4 bits)
Identities = 5/8 (63%), Positives = 6/8 (88%)

Query: 405 GLRQLLAR 413
GLrQ LAR
Sbjct: 25 GLRGLLGR 32 [Decoy]

Score = 48 (23.1 bits)
Identities = 5/6 (83%), Positives = 5/6 (83%)

Query: 201 GFRRRG 206
GF RRRG
Sbjct: 26 GFGRRR 31 [Decoy]

Sp 80 EXP [spectra/20-qtof_20_20171117-20000ng50_1ul-01_2uhpg_2ul.mgf](#) Total Scans: 80

Score = 126 (45.7 bits)
Identities = 17/18 (94%), Positives = 18/18 (100%)

Query: 455 RQRLAGVFNNGVGFFGLF 472
RQRLAGVFNNGVGFFGLF
Sbjct: 114 RQRLAGVFNNGVGFFGLF 131

Score = 102 (42.0 bits)
Identities = 12/17 (70%), Positives = 14/17 (94%)

Query: 46 RKLLGGVRNRRRRRRRG 62
RKLLGGVRNRRRRRRRG
Sbjct: 181 RKLLGGVRNRRRRRRRG 197

Score = 98 (41.0 bits)
Identities = 12/14 (86%), Positives = 14/14 (100%)

Query: 122 QRTFGAFSFFGGGF 135
QRTFGAFSFFGGGF
Sbjct: 36 QRTFGAFSFFGGGF 49

Score = 70 (27.3 bits)
Identities = 10/15 (67%), Positives = 12/15 (80%)

Query: 409 QLLRRRTCRLLAR 421
QLLr rr CLLAR
Sbjct: 77 RLLGRRVCRLLAR 89

Score = 56 (25.7 bits)
Identities = 7/8 (87%), Positives = 7/8 (87%)

Query: 55 GRRRRRRG 62
GRRRRRRG
Sbjct: 92 GRRGRRRG 99

Score = 50 (23.1 bits)
Identities = 6/8 (75%), Positives = 6/8 (75%)

Query: 248 GRGGRGGG 255
GRGGR G
Sbjct: 92 GRRGRRRG 99

Spot 55

m/z	Charge	Peak mH	Peptide mH	Delta (Da)	Delta (ppm)	Sadder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbe	Query Scan
474.9333	2	1947.8656	1947.8878	-0.0222	-11.4095	98.5000	192.602	1	13	YEQGEEEYYCGR	Carbamidomethylcy /	4	De-novo
474.9333	2	1947.8656	1947.8878	-0.0222	-11.4095	98.5000	192.602	1	13	YEQGEEEYYCGR	Carbamidomethylcy /	4	De-novo
474.9333	2	1947.8656	1947.8878	-0.0222	-11.4095	95.5000	191.2014	1	13	YEQGEEEYCGR	Carbamidomethylcy /	10	De-novo
521.7819	2	1041.5482	1041.5153	0.0329	31.6448	63.5379	146.027	1	12	EGSFEYELGR			De-novo
521.7819	2	1041.5482	1041.5153	0.0329	31.6448	63.5379	146.027	1	12	EGSFEYELGR			De-novo
521.7808	2	1041.5482	1041.5153	0.0329	31.6315	66.8857	153.756	1	9	SQEGSILK			De-novo
651.8492	2	1296.6828	1296.6857	-0.0029	-2.2448	56.6667	216.564	1	13	NFAAGGFLRLEEE			De-novo
651.8492	2	1296.6828	1296.6857	-0.0029	-2.2448	56.5000	216.564	1	13	NFAAGGFLRLEEE	Deamidation N	9	De-novo
861.3818	2	1721.7580	1721.7878	0.0304	17.6135	65.4323	175.753	1	14	TYCYQNQEGTTNR	Carbamidomethylcy /	4 / 9	De-novo
861.3818	2	1721.7580	1721.7878	0.0304	17.6135	65.4323	175.753	1	14	TYCYQNQEGTTNR	Carbamidomethylcy /	4	De-novo
861.3818	2	1721.7580	1721.7878	0.0304	17.6135	64.1979	171.141	1	14	SYCYQNQEGTTNR	Carbamidomethylcy / /	4 / 5	De-novo

MGF: [spectra/20-qtof_20_20171117-20000ng50_1ul-01_2uhpg_2ul.mgf](#) Total Scans: 55

Score = 80 (34.7 bits)
Identities = 11/11 (100%), Positives = 11/11 (100%)

Query: 1 TYQNNYCYGR 10
TYQNNYCYGR
Sbjct: 61 TYQNNYCYGR 70

Score = 74 (29.5 bits)
Identities = 9/10 (90%), Positives = 10/10 (82%)

Query: 119 LLGMNEMNMGAGAFM 134
LLGMEE EG FM
Sbjct: 156 LLGMFEEGFEGFGFM 171 [Decoy]

Sp 90 EXP [spectra/20-qtof_20_20171117-20000ng50_1ul-01_2uhpg_2ul.mgf](#) Total Scans: 90

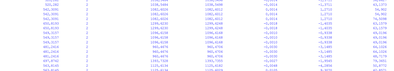
Score = 80 (37.7 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)

Query: 111 CGQNQYYNR 121
CGQNQYYNR
Sbjct: 98 CGQNQYYNR 108

Spot 56

ACA	Charge	Peak mM	Peptide mM	Delta Cmz	Delta ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbs	Query Seq.
844,8740	2	1872,726	1872,7278	0,0962	0,0513	0,0000	94,9858	1	16	VRRVRRRCLRRCTRR	Deamidation N	2	De-novo
834,8780	2	1671,748	1671,7578	0,0962	0,0573	0,0000	81,7286	1	14	YRRVRRCLRRCTRR	Deamidation N	0	De-novo
834,8780	2	1671,748	1671,7578	0,0962	0,0573	0,0000	81,7286	1	14	YRRVRRCLRRCTRR	Deamidation N	0	De-novo
818,3780	2	1634,742	1634,7322	-0,0205	-0,0205	0,0000	62,963	1	14	YRRVRRYCRRRRRR	Deamidation N / Oxidation	7 / 7	De-novo
818,3780	2	1634,742	1634,7322	-0,0205	-0,0205	0,0000	62,963	1	14	YRRVRRYCRRRRRR	Deamidation N / Oxidation	7 / 7	De-novo
818,3780	2	1634,742	1634,7322	-0,0205	-0,0205	0,0000	62,963	1	14	YRRVRRYCRRRRRR	Deamidation N / Oxidation	7 / 7	De-novo
501,282	2	1000,544	1000,5438	-0,0014	-1,4711	0,0000	56,902	1	8	YSYSFYCK	Deamidation Y	2	De-novo
501,282	2	1000,544	1000,5438	-0,0014	-1,4711	0,0000	56,9027	1	8	YSYSFYCK			De-novo
501,282	2	1000,544	1000,5438	-0,0014	-1,4711	0,0000	56,9027	1	8	YSYSFYCK			De-novo
541,3091	2	1081,6019	1081,6012	0,0014	1,2710	0,0000	162,7549	1	9	KCCCCAAAR	Deamidation N	1	De-novo
541,3091	2	1081,6019	1081,6012	0,0014	1,2710	0,0000	162,7537	1	9	KCCCCAAAR	Deamidation N	1	De-novo
541,3091	2	1081,6019	1081,6012	0,0014	1,2710	0,0000	162,7537	1	9	KCCCCAAAR	Deamidation N	1	De-novo
855,8193	2	1709,6218	1709,6236	-0,0018	-1,0535	0,0000	105,7269	1	15	RRRFQCLQLQR	Deamidation N	2	De-novo
855,8193	2	1709,6218	1709,6236	-0,0018	-1,0535	0,0000	63,1579	1	15	RRRFQCLQLQR	Deamidation N	2	De-novo
855,8193	2	1709,6218	1709,6236	-0,0018	-1,0535	0,0000	105,7269	1	15	RRRFQCLQLQR	Deamidation N	2	De-novo
549,5127	2	1096,6218	1096,6238	-0,0021	-0,9338	0,0000	69,5136	1	9	YECCLLAYY	Deamidation N	0	De-novo
549,5127	2	1096,6218	1096,6238	-0,0021	-0,9338	0,0000	69,5136	1	9	YECCLLAYY			De-novo
549,5127	2	1096,6218	1096,6238	-0,0021	-0,9338	0,0000	115,2414	1	9	YECCLLAYY			De-novo
481,2418	2	961,4676	961,4756	-0,0030	-3,1285	0,0000	56,5328	1	7	FCLFTQR	Deamidation Q	4	De-novo
481,2418	2	961,4676	961,4756	-0,0030	-3,1285	0,0000	111,0948	1	7	FCLFTQR			De-novo
481,2418	2	961,4676	961,4756	-0,0030	-3,1285	0,0000	68,7179	1	7	FCLFTQR			De-novo
563,8145	2	1125,6218	1125,6232	-0,0149	-6,2269	0,0000	56,8772	1	10	LAYGNMCCLK			De-novo
563,8145	2	1125,6218	1125,6232	-0,0149	-6,2269	0,0000	55,8772	1	10	LAYGNMCCLK			De-novo
563,8145	2	1125,6218	1125,6232	0,0155	6,5270	0,0000	62,8772	1	11	LAYGNMCCLLK	Deamidation N	9	De-novo
563,8145	2	1125,6218	1125,6232	-0,0149	-6,2269	0,0000	55,8772	1	10	LAYGNMCCLK			De-novo
504,3202	2	1003,6404	1003,6318	-0,0144	14,3618	0,0000	61,9048	1	4	KLAR			De-novo
548,2988	2	1094,5785	1094,5716	0,0255	1,8053	0,0000	60,7863	1	8	ASTEFCLR			De-novo
548,2988	2	1094,5785	1094,5716	0,0255	1,8053	0,0000	106,9557	1	8	ASTEFCLR			De-novo

NCBI gi|194399945|emb|CAM5F4 | Cryptococcus neoformans var. neoformans serotype D strain JEC21 Total Score: 110



Score = 74 (28.6 bits)
Identities = 8/10 (80%), Positives = 10/10 (100%)

Query: 142 RRRFQCLQLQ 151
RRRFQCLQLQ
Sbjct: 57 RRRFQCLQLQ 66 Ms:1394

Score = 72 (27.8 bits)
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 187 YRRVRRRCR 195
YRRVRRRCR
Sbjct: 55 YRRVRRRCR 63 Ms:1394

Score = 42 (16.2 bits)
Identities = 7/12 (58%), Positives = 10/12 (83%)

Query: 14 RRRRRRRRTRR 25
rrRRr RR RR
Sbjct: 71 rrRRRRRRRr 81 Ms:1394

Score = 32 (12.7 bits)
Identities = 6/11 (55%), Positives = 10/11 (90%)

Query: 155 QRLQFQLRR 165
QRrrFr LRr
Sbjct: 1 QRLRRQLQFr 11 Ms:1394

Score = 48 (18.5 bits)
Identities = 8/10 (80%), Positives = 8/10 (80%)

Query: 256 RRSTEFCLRR 265
RRSTEFCLRR
Sbjct: 201 RRSTEFCLRR 210 Ms:1394

Score = 46 (18.0 bits)
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 133 LCYCCCAAR 141
LCYCCCAAR
Sbjct: 57 LCYCCCAAR 65 Ms:1394

Sa NCBI none Total Score: 0

Sa RDP other Sample_Protein|Mycobacterium | Top Frame | Total Score: 110

Score = 75 (28.3 bits)
Identities = 8/10 (80%), Positives = 10/10 (100%)

Query: 256 RRSTEFCLRR 265
RRSTEFCLRR
Sbjct: 85 RRSTEFCLRR 94

Score = 74 (28.0 bits)
Identities = 8/10 (80%), Positives = 10/10 (100%)

Query: 142 RRRFQCLQLQ 151
rrRFQCLQLQ
Sbjct: 419 rrRFQCLQLQ 428

Score = 45 (16.8 bits)
Identities = 8/9 (88%), Positives = 9/9 (100%)

Query: 133 LCYCCCAAR 141
rrYCCCAAR
Sbjct: 434 rrYCCCAAR 442

Score = 41 (15.9 bits)
Identities = 4/4 (100%), Positives = 4/4 (100%)

Query: 101 LAYRR 105
LAYRR
Sbjct: 558 LAYRR 562

Score = 40 (15.4 bits)
Identities = 6/7 (86%), Positives = 6/7 (86%)

Query: 175 QLAYRRY 181
QLAYRRY
Sbjct: 436 QLAYRRY 442

Score = 40 (15.4 bits)
Identities = 6/6 (100%), Positives = 6/6 (100%)

Query: 230 RLAYRR 235
RLAYRR
Sbjct: 558 RLAYRR 563

Spot 57

ACA	Charge	Peak mM	Peptide mM	Delta Cmz	Delta ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbs	Query Seq.
501,7432	2	1000,4718	1000,4718	-0,0008	-0,8162	0,0000	52,9314	1	10	ARFDCAAYR	Deamidation N	0	De-novo
501,7432	2	1000,4718	1000,4718	-0,0008	-0,8162	0,0000	52,9314	1	10	ARFDCAAYR	Deamidation N	0	De-novo
509,787	2	1147,5784	1147,5779	0,0005	0,3875	0,0000	65,5317	1	11	QGRRYCCLAR			De-novo
509,787	2	1147,5784	1147,5779	0,0005	0,3875	0,0000	65,5317	1	11	QGRRYCCLAR			De-novo
509,787	2	1147,5784	1147,5779	0,0005	0,3875	0,0000	101,6487	1	10	QGRRYCCLAR			De-novo
744,3568	2	1486,6982	1486,694	0,0042	2,8283	0,0000	81,276	1	14	YSYSYYASRSFQR	Deamidation Y /	2 / 10	De-novo
744,3568	2	1486,6982	1486,694	0,0042	2,8283	0,0000	55,5554	1	14	YSYSYYASRSFQR	Deamidation Y /	2 / 10	De-novo
744,3568	2	1486,6982	1486,6878	0,1044	70,4483	0,0000	85,1481	1	14	YSYSYYASRSFQR	Deamidation Y /	2 / 10	De-novo
625,7918	2	1249,5880	1249,5899	-0,0019	-1,5215	0,0000	56,9223	1	10	LRMRYSCCR	Deamidation N	6	De-novo
625,7918	2	1249,5880	1249,5899	-0,0019	-1,5215	0,0000	56,9223	1	10	LRMRYSCCR			De-novo
501,2863	2	1000,5930	1000,5688	0,0232	3,0581	0,0000	56,962	1	9	YSFEFFCLR			De-novo
501,2863	2	1000,5930	1000,5688	0,0232	3,0581	0,0000	142,8875	1	9	YSFEFFCLR			De-novo
855,8215	2	1709,6274	1709,6238	0,0035	1,9821	0,0000	94,9211	1	15	RRRFQCLQLQR	Deamidation N	3	De-novo
855,8215	2	1709,6274	1709,6238	0,0035	1,9821	0,0000	126,9423	1	15	RRRFQCLQLQR	Deamidation N	3	De-novo
549,5179	2	1096,6202	1096,6148	0,0054	4,9196	0,0000	56,9894	1	9	RYCCLLAYY	Deamidation N	1	De-novo
549,5179	2	1096,6202	1096,6148	0,0054	4,9196	0,0000	56,9894	1	9	RYCCLLAYY	Deamidation N	1	De-novo
549,5179	2	1096,6202	1096,6148	0,0054	4,9196	0,0000	115,6038	1	9	RYCCLLAYY	Deamidation N	2	De-novo
481,2481	2	961,4756	961,4756	0,0000	2,0373	0,0000	76,4872	1	7	FCLFTQR	Deamidation Q	6	De-novo
481,2481	2	961,4756	961,4756	0,0000	2,0373	0,0000	76,4872	1	7	FCLFTQR			De-novo
481,2481	2	961,4756	961,4756	0,0000	2,0373	0,0000	111,7199	1	7	FCLFTQR			De-novo
549,2987	2	1094,5716	1094,576	-0,0044	-4,0225	0,0000	56,7863	1	8	ASTEFCLR	Deamidation Q	6	De-novo
549,2987	2	1094,5716	1094,576	-0,0044	-4,0225	0,0000	56,7863	1	8	ASTEFCLR			De-novo
549,2987	2	1094,5716	1094,576	-0,0044	-4,0225	0,0000	105,9513	1	8	ASTEFCLR			De-novo
481,2418	2	961,4676	961,4756	-0,0080	-8,3285	0,0000	56,5328	1	7	FCLFTQR	Deamidation Q	5	De-novo
481,2418	2	961,4676	961,4756	-0,0080	-8,3285	0,0000	111,0948	1	7	FCLFTQR			De-novo
481,2418	2	961,4676	961,4756	-0,0080	-8,3285	0,0000	68,7179	1	7	FCLFTQR			De-novo
494,7255	2	971,4430	971,4389	0,0042	4,2948	0,0000	49,7179	1	7	FRRTPRK			De-novo
494,7255	2	971,4430	971,4389	0,0042	4,2948	0,0000	81,9153	1	7	FRRTPRK			De-novo
563,8145	2	1125,6218	1125,6232	-0,0149	-6,2269	0,0000	56,8772	1	10	LAYGNMCCLK	Deamidation Q	9	De-novo
563,8145	2	1125,6218	1125,6232	-0,0149	-6,2269	0,0000	47,4779	1	10	LAYGNMCCLK			De-novo
563,8129	2	1125,6202	1125,6232	-0,0191	-7,9839	0,0000	46,7849	1	10	LAYGNMCCLK			De-novo

NCBI gi|194399945|emb|CAM5F4 | Cryptococcus neoformans var. neoformans serotype D strain JEC21 Total Score: 44

Score = 87 (32.7 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)

Query: 135 LRMRRYQLQR 146
LRMRRYQLQR
Sbjct: 413 LRMRRYQLQR 424 Ms:1394

Score = 72 (27.3 bits)
Identities = 8/9 (88%), Positives = 8/9 (100%)

Query: 188 RRRFQCRR 196
RRRFQCRR
Sbjct: 85 RRRFQCRR 93 Ms:1394

Score = 42 (15.9 bits)
Identities = 12/14 (75%), Positives = 12/14 (75%)

Query: 148 FQLQLRRRRFQLQ 159
FQL RrRRFQL
Sbjct: 413 FQRLQLRRRFQLQ 425 Ms:1394

Score = 41 (15.9 bits)
Identities = 8/10 (80%), Positives = 8/10 (80%)

Query: 242 LAYGNMCCLK 251
L AYGNMCCLK
Sbjct: 551 LCYGNMCCLK 561 Ms:1394

Score = 87 (32.7 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)

Query: 135 LRMRRYQLQR 146
LRMRRYQLQR
Sbjct: 413 LRMRRYQLQR 424 Ms:1394

Score = 44 (16.5 bits)
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 237 RRRTPRK 244
RRRTPRK
Sbjct: 113 RRRTPRK 120 Ms:1394

Score = 41 (15.9 bits)
Identities = 9/9 (100%), Positives = 9/9 (100%)

Query: 204 ASTEFCLR 212
ASTEFCLR
Sbjct: 480 ASTEFCLR 488 Ms:1394

Sa NCBI none Total Score: 0

Sa RDP Sample|Cryptococcus | Top Frame | Total Score: 110

Score = 83 (30.1 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)

Query: 42 RQRRRYCCLQR 52
RQRRRYCCLQR
Sbjct: 257 RQRRRYCCLQR 267

Spot 50

n/a	Charge	Peak mM	Peptide mM	Delta ppm	Delta ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbs	Query Text
1066.7462	2	1111.5196	1111.5181	0.0013	0.0013	0.0000	0.0000	1	4	CHGCPRCQ	Cysteine(Ethanolyl) C	1	De-novo
994.7424	2	1111.5196	1111.5181	0.0013	1.3279	50.8235	151.6969	1	4	TAELPRQE	Cysteine(Ethanolyl) C	5	De-novo
1066.7462	2	1111.5196	1111.5181	0.0013	1.3279	50.8235	151.6969	1	4	CHGCPRCQ	Cysteine(Ethanolyl) C	1	De-novo
511.2371	2	1020.4948	1020.4948	-0.0002	-0.2195	56.9627	71.6489	1	8	YAILGSTM		1	De-novo
511.2371	2	1020.4948	1020.4948	-0.0002	-0.2195	49.5136	71.232	1	8	YAILGMSM		1	De-novo
511.2371	2	1020.4948	1020.4948	-0.0002	-0.2195	56.9627	71.6489	1	8	YAILGSTM		1	De-novo
535.2105	2	1068.4514	1068.451	0.0004	0.3519	63.7601	136.9872	1	9	YTYPRQLGK	Oxidation M	1	De-novo
883.8301	2	1595.9246	1595.9967	-0.0291	-14.7359	67.9012	192.4957	1	14	YALAAKSTSTPMGF	Deamidation Q / Oxidation	7 / 12	De-novo
883.8301	2	1595.9246	1595.9967	-0.0291	-14.7359	67.9012	192.4957	1	14	YALAAKSTSTPMGF	Deamidation Q / Oxidation	7 / 12	De-novo
883.8301	2	1595.9246	1595.9967	-0.0291	-14.7359	67.9012	203.7372	1	14	YALAAKSTSTPMGF	Oxidation M	12	De-novo
875.8348	2	1595.9540	1595.9967	-0.0267	-13.4396	67.9012	191.7113	1	14	YALAAKSTSTPMGF	Deamidation N	9	De-novo
875.8348	2	1595.9540	1595.9967	-0.0267	-13.4396	67.9012	191.7113	1	14	YALAAKSTSTPMGF	Deamidation N	9	De-novo
875.8348	2	1595.9540	1595.9967	-0.0267	-13.4396	67.9012	191.7113	1	14	YALAAKSTSTPMGF	Deamidation N	9	De-novo
527.2594	2	1055.4972	1055.4961	0.0011	1.0223	66.4987	176.4372	1	9	YTYPRQLGK		1	De-novo
527.2594	2	1055.4972	1055.4961	0.0011	1.0223	66.4987	176.4372	1	9	YTYPRQLGK	Deamidation N	1	De-novo
527.2594	2	1055.4972	1055.4961	0.0011	1.0223	62.7601	155.5316	1	9	YTYPRQLGK		1	De-novo
861.5247	2	1335.8238	1335.8561	-0.0233	-16.9577	56.9627	231.852	1	13	SSAFLTPLAAGCR		1	De-novo
861.5247	2	1335.8238	1335.8561	-0.0233	-16.9577	56.9627	231.852	1	13	SSAFLTPLAAGCR		1	De-novo
621.7403	2	943.5132	943.5178	-0.0508	-16.5479	55.3334	129.6697	1	8	ATTPLLLR		1	De-novo
621.7403	2	943.5132	943.5178	-0.0508	-16.5479	55.3334	133.1303	1	8	TATPLLLR		1	De-novo
847.5103	2	1745.8032	1745.8542	-0.1460	-17.1819	46.8665	86.7	1	16	YTLNEGSLSSRVQLR		1	De-novo
847.5103	2	1745.8032	1745.8542	-0.1460	-17.1819	46.8665	86.798	1	16	YTLNEGSLSSRVQLR		1	De-novo
1996.0356	2	2176.9558	2176.9583	-0.0027	-1.2553	56.2857	212.2878	1	18	TEFSVSATTTRLLEMELA		1	De-novo
1996.0356	2	2176.9558	2176.9583	-0.0027	-1.2553	56.2857	212.2878	1	18	TEFSVSATTTRLLEMELA	Deamidation Q	10	De-novo
1996.0356	2	2176.9558	2176.9583	-0.0027	-1.2553	56.2857	211.4523	1	18	TEFSVSATTTRLLEMELA		1	De-novo
871.5875	2	1345.7134	1345.7188	0.0356	0.4298	70.4967	271.2962	1	13	SADSTPLLSLER		1	De-novo
871.5875	2	1345.7134	1345.7188	0.0356	0.4298	70.4967	271.2962	1	13	SADSTPLLSLER		1	De-novo
871.5875	2	1345.7134	1345.7188	0.0356	0.4298	70.4967	275.2568	1	13	SADSTPLLSLER		1	De-novo
708.469	2	1315.7224	1315.7166	0.0380	3.9427	88	96.4982	1	12	LQRLGTMTEEMR	Deamidation N	5	De-novo
708.469	2	1315.7224	1315.7166	0.0380	3.9427	70.4967	96.4982	1	12	LQRLGTMTEEMR	Deamidation N	5	De-novo
708.469	2	1315.7224	1315.7166	0.0380	3.8147	61.5103	91.1538	1	12	LQRLGTMQEEMR	Deamidation N	5	De-novo
873.5489	2	1344.9822	1344.7655	-0.0813	-60.4027	57.4912	115.157	1	12	TTDCCSLCSLLM	Cysteine(Ethanolyl) C	5	De-novo
873.5489	2	1344.9822	1344.7655	-0.0813	-60.4027	57.4912	115.157	1	12	TTDCCSLCSLLM		5	De-novo
873.5489	2	1344.9822	1344.7655	-0.0813	-60.4027	57.4912	111.7734	1	12	SLDLCCTMSLLM	Cysteine(Ethanolyl) C	5	De-novo

MSMS gi|15330219|gb|AAK51 [Cellulose synthase catalytic subunit [Gluconacetobacter

Total Score: 488

```
                    0        80       160       240       320
                    |         |         |         |         |
gi|15330219|gb|AAK51 ------------------------------------------------1364
Local hits (MSMs)   ||  ||  |   |   |  |   |   |   |   |   |
```

Score = 101.2(1.5 bits)
Identities = 14/14 (87%), Positives = 14/14 (100%)
Query: 104 GRLLAAMSRSTCPRGS 119
Sbjct: 1 GRLLAAMSRSTCPRGS 16
Sbjct: gi|15330219|gb|AAK51 [illegible]

Score = 88 (45.8 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)
Query: 52 LQRIGTPRTEER 63
Sbjct: 1 LQRIGTPRTEER 12
Sbjct: gi|15330219|gb|AAK51 [illegible]

Score = 81 (42.3 bits)
Identities = 12/12 (100%), Positives = 12/12 (100%)
Query: 314 SRAGSPRSRLGLAE 325
Sbjct: 1 SRAGSPRSRLGLAE 12
Sbjct: gi|15330219|gb|AAK51 [illegible]

Score = 89 (46.2 bits)
Identities = 8/10 (80%), Positives = 9/10 (90%)
Query: 147 RTPPRRGLAE 156
Sbjct: 1 RTPPRRGLAE 10
Sbjct: gi|15330219|gb|AAK51 [illegible]

Score = 46 (23.9 bits)
Identities = 8/10 (80%), Positives = 9/10 (90%)
Query: 55 TTTPRGLRRAGLAR 68
TTTPRG R G A
Sbjct: 121 TTTPRGSRRTPL 132 - Mm|0.0Kbp

Score = 38 (20.7 bits)
Identities = 7/10 (70%), Positives = 8/10 (80%)
Query: 9 RGAGLRRPGR 18
RGAGLr GR
Sbjct: 172 RGAGLRRGR 181 - Mm|0.0Kbp

Score = 52 (27.5 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 206 PPPRGLR 262
PPPRGLR
Sbjct: 4 PPPRGLR 10 - Mm|0.0Kbp

Score = 40 (21.2 bits)
Identities = 7/9 (77%), Positives = 8/9 (88%)
Query: 180 LRRLAAGR 190
LRGLA RG
Sbjct: 28 LRGLARRG 35 - Mm|0.0Kbp

Score = 46 (23.9 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 208 RRPPRGLR 214
R PPRGLR
Sbjct: 7 RRPPRGLR 13 - Mm|0.0Kbp

No HS HSP None

No HSP other [illegible] [illegible] [illegible] [illegible]

Total Score: 187

```
                    0        100       200       300       400
                    |         |         |         |         |
                    ------------------------------------------------1452
Local hits (MSMs)   ||  ||  |   |   |  |   |   |   |   |   |
```

Score = 96 (48.6 bits)
Identities = 14/15 (93%), Positives = 15/15 (100%)
Query: 314 SRAGSPRSRLGLAEP 328
SRAGSPRSRLGLAEP
Sbjct: 137 SRAGSPRSRLGLAEP 151

Score = 90 (45.6 bits)
Identities = 13/14 (93%), Positives = 13/14 (93%)
Query: 154 GRLLAAMSRSTCPR 167
GRLLAAMSRSTCPR GP
Sbjct: 38 GRLLAAMSRSTCPR 51

Score = 90 (45.6 bits)
Identities = 13/14 (93%), Positives = 13/14 (93%)
Query: 340 LQRLGTMTEEMRGR 353
LQ+GTMTE MR
Sbjct: 65 LQ+GTMTEEMRGR 77

Score = 77 (40.1 bits)
Identities = 8/10 (80%), Positives = 10/10 (100%)
Query: 147 RTPPRRGLAE 156
RTPPRRGLAE
Sbjct: 263 RTPPRRGLAE 272

Score = 72 (37.7 bits)
Identities = 8/10 (80%), Positives = 10/10 (100%)
Query: 55 TTTPRGLRRAGLAR 68
TTTPRG R G A
Sbjct: 164 TTTPRGSRRTPL 175

Score = 56 (29.8 bits)
Identities = 8/10 (80%), Positives = 9/10 (90%)
Query: 201 ATTPLLLRP 209
ATTPLLLRP
Sbjct: 270 ATTPLLLRP 281

Score = 56 (29.8 bits)
Identities = 8/10 (80%), Positives = 9/10 (90%)
Query: 497 GRATPLLLR 488
GRATPLLLR
Sbjct: 271 GRATPLLLR 280

Score = 52 (27.5 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 206 PPPRGLR 262
PPPRGLR
Sbjct: 4 PPPRGLR 10

Score = 52 (27.5 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 209 PPRGLR 262
PPRGLR
Sbjct: 174 RRAGSPRGLR 203

Spot 51

n/a	Charge	Peak mM	Peptide mM	Delta ppm	Delta ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbs	Query Text
794.3928	2	1496.8860	1496.8888	-0.0012	-0.8014	75.7778	236.3024	1	14	LGSGGNAGLFCR	Deamidation N	7	De-novo
794.3928	2	1496.8860	1496.8888	-0.0012	-0.8014	75.7778	236.3024	1	14	LGSGGNAGLFCR	Deamidation N	8 / 9	De-novo
794.3928	2	1496.8860	1496.8888	-0.0012	-0.8014	75.7778	231.1288	1	14	LGSGGNAGLFCR	Deamidation N	7	De-novo
591.2881	2	1056.5604	1056.5607	-0.0001	-0.0171	56.9627	81.6237	1	9	EGECFRLAK	Deamidation N	8	De-novo
591.2881	2	1056.5604	1056.5607	-0.0001	-0.0171	56.9627	81.6237	1	9	EGECFRLAK	Deamidation N	8	De-novo
591.2881	2	1056.5604	1056.5607	-0.0002	-0.0218	56.9627	81.6088	1	9	EGECFRLAK		8	De-novo
872.5404	2	1742.6650	1742.683	0.0029	1.6346	56.9627	86.7748	1	12	WGRNGGLFLGR	Deamidation N	2	De-novo
872.5404	2	1742.6650	1742.683	0.0029	1.6346	56.9627	86.7748	1	12	WGRNGGLFLGR		2	De-novo
872.5404	2	1742.6650	1742.683	0.0029	1.6346	56.9627	86.7748	1	12	WGRNGGLFLGR	Deamidation N	1	De-novo
965.5108	2	1132.6060	1132.6072	-0.0013	-1.1784	56.9627	94.2558	1	9	LFTPTQFLR	Deamidation Q	5	De-novo
965.5108	2	1132.6060	1132.6072	-0.0013	-1.1784	56.9627	94.2558	1	9	LFTPTQFLR		5	De-novo
965.5108	2	1132.6060	1132.6072	-0.0013	-1.1784	49.5136	91.1111	1	9	LFTPQFLR	Deamidation Q	4	De-novo

MSMS gi|15330219|gb|AAK51 [Cellulose synthase catalytic subunit [Gluconacetobacter

Total Score: 59

```
                    0        100       200       300       400
                    |         |         |         |         |
gi|15330219|gb|AAK51 ------------------------------------------------1379
Local hits (MSMs)   ||  ||  |   |   |  |   |   |   |   |   |
```

Score = 96 (48.6 bits)
Identities = 13/13 (100%), Positives = 13/13 (100%)
Query: 81 WNGRNGGLFLGRP 93
WNGRNGGLFLGRP
Sbjct: 268 WNGRNGGLFLGRP 280 - Mm|0.0Kbp

Score = 81 (47.0 bits)
Identities = 13/13 (100%), Positives = 13/13 (100%)
Query: 132 RLGGGNAGLFCRP 144
RLGG GNAGLFCRP
Sbjct: 282 RLGGGNAGLFCRP 294 - Mm|0.0Kbp

Score = 48 (26.6 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 123 LFTPTQFRR 131
LFTPTQFRR
Sbjct: 172 LFTPTQFRR 178

Score = 34 (18.7 bits)
Identities = 8/10 (80%), Positives = 8/10 (80%)
Query: 38 LFTPTQELAT 47
LFTPTQ LA
Sbjct: 224 LFTPTQELAT 233 - Mm|0.0Kbp

No HS HSP [illegible] [illegible] [illegible] [illegible]

Total Score: 59

```
                    0        100       200       300       400
                    |         |         |         |         |
                    ------------------------------------------------1452
Local hits (MSMs)   ||  ||  |   |   |  |   |   |   |   |   |
```

Score = 96 (48.6 bits)
Identities = 13/13 (100%), Positives = 13/13 (100%)
Query: 81 WNGRNGGLFLGRP 93
WNGRNGGLFLGRP
Sbjct: 215 WNGRNGGLFLGRP 227

Score = 81 (47.0 bits)
Identities = 13/13 (100%), Positives = 13/13 (100%)
Query: 132 RLGGGNAGLFCRP 144
RLGG GNAGLFCRP
Sbjct: 242 RLGGGNAGLFCRP 254

Score = 48 (26.6 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 123 LFTPTQFRR 131
LFTPTQFRR
Sbjct: 170 LFTPTQFRR 178

Score = 49 (26.6 bits)
Identities = 7/7 (100%), Positives = 7/7 (100%)
Query: 40 NELEQTE 46
NELEQTE
Sbjct: 227 NELEQTE 233

Score = 36 (19.7 bits)
Identities = 8/10 (80%), Positives = 8/10 (80%)
Query: 38 LFTPTQELAT 47
LFTPTQ LA
Sbjct: 224 LFTPTQELAT 233 - Mm|0.0Kbp

Spot 52

n/a	Charge	Peak mM	Peptide mM	Delta ppm	Delta ppm	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rdbs	Query Text
851.5192	2	1702.9980	1702.9966	0.0008	0.8215	56.9627	96.7748	1	14	YGTPGGNAGLFCR		1	De-novo
851.5192	2	1702.9980	1702.9966	0.0008	0.8215	56.9627	96.7748	1	14	YGTPGGNAGLFCR		1	De-novo
851.5192	2	1702.9980	1702.9966	0.0008	0.8215	56.9627	101.1298	1	14	YGTPGGNAGLFCR		1	De-novo
851.5192	2	1702.9980	1702.9966	0.0008	0.8215	56.9627	101.1298	1	14	YGTPGGNAGLFCR	Deamidation Q	2	De-novo
851.5192	2	1702.9980	1702.9966	0.0008	0.8215	56.9627	101.1298	1	14	YGTPGGNAGLFCR		1

Hsp# 81

n/a	Charge	Rank HM	Peptide MW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Protein(s)	Query Scan
864.2287	2	814.4278	814.4282	-0.0004	-0.4	-0.0000	-0.0000	1	8	SSGQPLLP			De-novo
871.2287	2	821.4278	821.4282	-0.0014	-1.7027	57.7778	131.1324	1	8	RAAQPLLP			De-novo
871.2287	2	821.4278	821.4282	-0.0014	-1.7027	0.0000	131.1324	1	8	QSSQPLLP			De-novo
884.7776	2	871.2336	871.1283	0.1057	0.7268	59.6400	171.2574	1	10	LLPGTPAP			De-novo
884.7776	2	871.5396	871.5383	0.0957	0.7268	58.8235	146.2324	1	9	LLPGTPGM			De-novo
894.2208	2	853.2960	853.4058	-0.1098	-132.1223	59.4118	151.1144	1	7	GPYAPGM	Deamidation Q	1	De-novo
894.2208	2	853.2960	853.4058	-0.1098	-132.1223	59.4118	151.1144	1	7	GPYAPGN	Deamidation N	1	De-novo
894.2208	2	853.2960	853.4058	-0.1098	-132.1223	51.0815	151.9919	1	7	MLYAPGN	Oxidation M	1	De-novo
894.2208	2	853.2960	853.4058	-0.1098	-132.1223	51.0815	151.9919	1	7	MLYAPGM	Oxidation M	1	De-novo
913.895	2	1455.7624	1455.7774	-0.1549	-5.3498	56.3878	206.6562	1	15	ANGRGLPAGTPAAW			De-novo
913.895	2	1455.7624	1455.7774	-0.1549	-5.3498	46.4667	228.1997	1	15	RAGRGLPAGTPAAW			De-novo
913.895	2	1455.7624	1455.7774	-0.1549	-5.3498	46.4667	228.1997	1	15	QAGRGLPAGTPAAW			De-novo
913.2206	2	855.4436	855.4467	-0.0257	-0.8824	58.9746	137.9913	1	7	LAYTQR	Deamidation Q	4	De-novo
913.2206	2	855.4436	855.4467	-0.0257	-0.8824	58.9746	138.1982	1	7	LAYTER			De-novo
913.2206	2	855.4436	855.4467	-0.0257	-0.8824	58.9746	138.1982	1	7	LAYTKR			De-novo
917.5371	2	833.4366	833.4265	-0.1023	-122.2287	66.6666	131.9494	1	8	LGLGPGR	Deamidation R	4	De-novo
917.5371	2	833.4366	833.4265	-0.1023	-122.2287	66.6666	131.9494	1	8	LGLGPGK			De-novo
917.5371	2	833.4366	833.4265	-0.1023	-122.2287	66.6666	131.9494	1	8	LGLGPGM			De-novo
923.4207	2	1845.8638	1845.8613	0.2025	1.0984	76.521	46.8138	1	14	YPYPPPYYYGLLR			De-novo
923.4207	2	1845.8638	1845.8613	0.2025	1.0984	76.521	46.1923	1	14	PYPPPYYYGGLLR			De-novo
923.4207	2	1845.8638	1845.8613	0.2025	1.0984	76.521	46.1923	1	14	YPYPPPYYGGLLR			De-novo

Hsp# 82

n/a	Charge	Rank HM	Peptide MW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Protein(s)	Query Scan
794.3784	2	1596.7622	1596.7272	0.3497	3.6052	32.7273	255.3268	1	15	GYTPYPYLGGRPR	Deamidation Q	12	De-novo
794.3784	2	1596.7622	1596.7272	0.3497	3.6052	40.9140	136.8941	1	15	WYPYPYLGGRPRR	Deamidation W	12	De-novo
794.3784	2	1596.7622	1596.7272	0.3497	3.6052	40.9140	136.8941	1	15	YWPYPYLGGRPRR	Deamidation W	12	De-novo
801.3123	2	1596.6074	1596.6039	0.0338	0.1243	49.3553	156.2268	1	11	YLNFGVRGGR	Deamidation W	7	De-novo
801.3123	2	1596.6074	1596.6039	0.0338	0.1243	51.561	153.9722	1	11	LYNFGVRGGR	Deamidation W	7	De-novo
801.3123	2	1596.6074	1596.6039	0.0338	0.1243	49.3553	156.2268	1	11	YLNFGVRGGK	Deamidation W	7	De-novo
807.8088	2	1213.4020	1213.3979	0.0041	3.3998	73.0862	215.1268	1	10	RLQTGYLGAF			De-novo
807.8088	2	1213.4020	1213.3979	0.0041	3.3998	61.9948	211.722	1	10	KLQATYRLGAF	Deamidation Q	5	De-novo
807.8088	2	1213.4020	1213.3979	0.0041	3.3998	61.9948	211.722	1	10	KLQATYKLGAF	Deamidation Q	5	De-novo
807.8088	2	1215.4040	1215.399	0.0050	3.8448	66.6667	211.2855	1	11	RPPRPRLQQF	Deamidation Q	5	De-novo
807.8088	2	1215.4040	1215.399	0.0050	3.8448	66.6667	211.4994	1	11	PPRRPRLQQF	Deamidation Q	5 - 10	De-novo
807.8088	2	1215.4040	1215.399	0.0050	3.8448	66.6667	211.4994	1	11	PPRRPRLQQF	Deamidation Q	5 - 10	De-novo
723.8787	2	1447.7418	1447.7271	0.0147	5.0377	75.1865	276.12	1	13	CYQGCGCLCGFR	Carbamidomethyl C /	1 / 7 / 10	De-novo
723.8787	2	1447.7418	1447.7271	0.0147	5.0377	81.963	276.1912	1	14	CYNGCGCLCGFGR	Carbamidomethyl C /	1	De-novo
731.7684	2	1461.5212	1461.5179	0.0338	1.3498	81.9924	224.3924	1	11	CYCYGMYPFM	Carbamidomethyl C /	1 / 4	De-novo
731.7684	2	1461.5212	1461.5179	0.0338	1.3498	81.9924	224.3924	1	11	CYCYMGYPFM	Carbamidomethyl C /	1 / 4	De-novo
731.7684	2	1461.5212	1461.5179	0.0338	1.3498	76.1865	209.2039	1	11	CYCYGMYPFM	Carbamidomethyl C /	1	De-novo
731.7684	2	1461.5212	1461.5179	0.0338	1.3498	76.1865	209.2039	1	11	CYCYMGYPFM	Carbamidomethyl C /	1 / 4	De-novo
755.3613	2	1448.7070	1448.7227	-0.0157	-10.8219	59.5217	131.9542	1	12	CRGPCYLCGMR	Carbamidomethyl C /	1 / 4	De-novo
755.3613	2	1448.7070	1448.6828	0.0242	16.8243	80.8696	131.94	1	12	CRGPPCYLCGMR	Carbamidomethyl C /	1 / 4 / 9	De-novo
576.7682	2	1071.5168	1071.5018	0.0150	14.0025	39.1129	95.8934	1	10	KYLVGWFW	Deamidation N	4	De-novo

Hsp# 83

n/a	Charge	Rank HM	Peptide MW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Protein(s)	Query Scan
873.5371	2	1745.9966	1745.9817	0.1494	8.5547	76.7574	141.193	1	14	LGYLGPGLLQLGF			De-novo
881.8971	2	1763.7780	1763.812	-0.0339	-19.2234	61.4118	141.9918	1	15	GGTGGGTGLLGGAWR	Deamidation N	5	De-novo
881.8971	2	1763.7780	1763.812	-0.0339	-19.2234	47.4118	141.1399	1	16	GGTGGGTGLLGGAWRN	Deamidation N	5	De-novo
881.8971	2	1763.7780	1763.812	-0.0339	-19.2234	61.9343	141.9918	1	17	GGTGGGTGLLGGAWRTN			De-novo
881.8971	2	1763.7780	1763.812	-0.0339	-19.2234	61.9343	141.9918	1	17	GGTGGGTGLLGGAWRTQ			De-novo
747.4300	2	1493.8628	1493.861	0.0018	1.2053	51.4567	215.4637	1	13	LYYYGPYNGFCLR	Carbamidomethyl C /	4 / 9 / 12	De-novo
747.4300	2	1493.8628	1493.861	0.0018	1.2053	51.4567	215.4637	1	13	LYYYGPYNGFCLR	Carbamidomethyl C /	7 / 9 / 12	De-novo

Hsp# 84

n/a	Charge	Rank HM	Peptide MW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Protein(s)	Query Scan
864.2287	2	814.4278	814.4282	-0.0004	-0.4	-0.0000	-0.0000	1	8	SSGQPLLP			De-novo
871.2287	2	821.4278	821.4282	-0.0014	-1.7027	57.7778	131.1324	1	8	RAAQPLLP			De-novo
871.2287	2	821.4278	821.4282	-0.0014	-1.7027	0.0000	131.1324	1	8	QSSQPLLP			De-novo
884.7776	2	871.2336	871.1283	0.1057	0.7268	59.6400	171.2574	1	10	LLPGTPAP			De-novo
884.7776	2	871.5396	871.5383	0.0957	0.7268	58.8235	146.2324	1	9	LLPGTPGM			De-novo
894.2208	2	853.2960	853.4058	-0.1098	-132.1223	59.4118	151.1144	1	7	GPYAPGM	Deamidation Q	1	De-novo
894.2208	2	853.2960	853.4058	-0.1098	-132.1223	51.0815	151.9919	1	7	MLYAPGN	Oxidation M	1	De-novo
894.2208	2	853.2960	853.4058	-0.1098	-132.1223	51.0815	151.9919	1	7	MLYAPGM	Oxidation M	1	De-novo
913.895	2	1455.7624	1455.7774	-0.1549	-5.3498	56.3878	206.6562	1	15	ANGRGLPAGTPAAW			De-novo
913.895	2	1455.7624	1455.7774	-0.1549	-5.3498	46.4667	228.1997	1	15	RAGRGLPAGTPAAW			De-novo
913.895	2	1455.7624	1455.7774	-0.1549	-5.3498	46.4667	228.1997	1	15	QAGRGLPAGTPAAW			De-novo
913.2206	2	855.4436	855.4467	-0.0257	-0.8824	58.9746	137.9913	1	7	LAYTQR	Deamidation Q	4	De-novo
913.2206	2	855.4436	855.4467	-0.0257	-0.8824	58.9746	138.1982	1	7	LAYTER			De-novo
913.2206	2	855.4436	855.4467	-0.0257	-0.8824	58.9746	138.1982	1	7	LAYTKR			De-novo
917.5371	2	833.4366	833.4265	-0.1023	-122.2287	66.6666	131.9494	1	8	LGLGPGR	Deamidation R	4	De-novo
917.5371	2	833.4366	833.4265	-0.1023	-122.2287	66.6666	131.9494	1	8	LGLGPGK			De-novo
917.5371	2	833.4366	833.4265	-0.1023	-122.2287	66.6666	131.9494	1	8	LGLGPGM			De-novo
923.4207	2	1845.8638	1845.8613	0.2025	1.0984	76.521	46.8138	1	14	YPYPPPYYYGLLR			De-novo
923.4207	2	1845.8638	1845.8613	0.2025	1.0984	76.521	46.1923	1	14	PYPPPYYYGGLLR			De-novo
923.4207	2	1845.8638	1845.8613	0.2025	1.0984	76.521	46.1923	1	14	YPYPPPYYGGLLR			De-novo

Hsp# 85

n/a	Charge	Rank HM	Peptide MW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Protein(s)	Query Scan
794.3784	2	1596.7622	1596.7272	0.3497	3.6052	32.7273	255.3268	1	15	GYTPYPYLGGRPR	Deamidation Q	12	De-novo
794.3784	2	1596.7622	1596.7272	0.3497	3.6052	40.9140	136.8941	1	15	WYPYPYLGGRPRR	Deamidation W	12	De-novo
794.3784	2	1596.7622	1596.7272	0.3497	3.6052	40.9140	136.8941	1	15	YWPYPYLGGRPRR	Deamidation W	12	De-novo
801.3123	2	1596.6074	1596.6039	0.0338	0.1243	49.3553	156.2268	1	11	YLNFGVRGGR	Deamidation W	7	De-novo
801.3123	2	1596.6074	1596.6039	0.0338	0.1243	51.561	153.9722	1	11	LYNFGVRGGR	Deamidation W	7	De-novo
801.3123	2	1596.6074	1596.6039	0.0338	0.1243	49.3553	156.2268	1	11	YLNFGVRGGK	Deamidation W	7	De-novo
807.8088	2	1213.4020	1213.3979	0.0041	3.3998	73.0862	215.1268	1	10	RLQTGYLGAF			De-novo
807.8088	2	1213.4020	1213.3979	0.0041	3.3998	61.9948	211.722	1	10	KLQATYRLGAF	Deamidation Q	5	De-novo
807.8088	2	1213.4020	1213.3979	0.0041	3.3998	61.9948	211.722	1	10	KLQATYKLGAF	Deamidation Q	5	De-novo
807.8088	2	1215.4040	1215.399	0.0050	3.8448	66.6667	211.2855	1	11	RPPRPRLQQF	Deamidation Q	5	De-novo
807.8088	2	1215.4040	1215.399	0.0050	3.8448	66.6667	211.4994	1	11	PPRRPRLQQF	Deamidation Q	5 - 10	De-novo
807.8088	2	1215.4040	1215.399	0.0050	3.8448	66.6667	211.4994	1	11	PPRRPRLQQF	Deamidation Q	5 - 10	De-novo
723.8787	2	1447.7418	1447.7271	0.0147	5.0377	75.1865	276.12	1	13	CYQGCGCLCGFR	Carbamidomethyl C /	1 / 7 / 10	De-novo
723.8787	2	1447.7418	1447.7271	0.0147	5.0377	81.963	276.1912	1	14	CYNGCGCLCGFGR	Carbamidomethyl C /	1	De-novo
731.7684	2	1461.5212	1461.5179	0.0338	1.3498	81.9924	224.3924	1	11	CYCYGMYPFM	Carbamidomethyl C /	1 / 4	De-novo
731.7684	2	1461.5212	1461.5179	0.0338	1.3498	81.9924	224.3924	1	11	CYCYMGYPFM	Carbamidomethyl C /	1 / 4	De-novo
731.7684	2	1461.5212	1461.5179	0.0338	1.3498	76.1865	209.2039	1	11	CYCYGMYPFM	Carbamidomethyl C /	1	De-novo
731.7684	2	1461.5212	1461.5179	0.0338	1.3498	76.1865	209.2039	1	11	CYCYMGYPFM	Carbamidomethyl C /	1 / 4	De-novo
755.3613	2	1448.7070	1448.7227	-0.0157	-10.8219	59.5217	131.9542	1	12	CRGPCYLCGMR	Carbamidomethyl C /	1 / 4	De-novo
755.3613	2	1448.7070	1448.6828	0.0242	16.8243	80.8696	131.94	1	12	CRGPPCYLCGMR	Carbamidomethyl C /	1 / 4 / 9	De-novo
576.7682	2	1071.5168	1071.5018	0.0150	14.0025	39.1129	95.8934	1	10	KYLVGWFW	Deamidation N	4	De-novo

Hsp# 86

n/a	Charge	Rank HM	Peptide MW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Protein(s)	Query Scan
873.5371	2	1745.9966	1745.9817	0.1494	8.5547	76.7574	141.193	1	14	LGYLGPGLLQLGF			De-novo
881.8971	2	1763.7780	1763.812	-0.0339	-19.2234	61.4118	141.9918	1	15	GGTGGGTGLLGGAWR	Deamidation N	5	De-novo
881.8971	2	1763.7780	1763.812	-0.0339	-19.2234	47.4118	141.1399	1	16	GGTGGGTGLLGGAWRN	Deamidation N	5	De-novo
881.8971	2	1763.7780	1763.812	-0.0339	-19.2234	61.9343	141.9918	1	17	GGTGGGTGLLGGAWRTN			De-novo
881.8971	2	1763.7780	1763.812	-0.0339	-19.2234	61.9343	141.9918	1	17	GGTGGGTGLLGGAWRTQ			De-novo
747.4300	2	1493.8628	1493.861	0.0018	1.2053	51.4567	215.4637	1	13	LYYYGPYNGFCLR	Carbamidomethyl C /	4 / 9 / 12	De-novo
747.4300	2	1493.8628	1493.861	0.0018	1.2053	51.4567	215.4637	1	13	LYYYGPYNGFCLR	Carbamidomethyl C /	7 / 9 / 12	De-novo

Hsp# 87

n/a	Charge	Rank HM	Peptide MW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Protein(s)	Query Scan
864.2287	2	814.4278	814.4282	-0.0004	-0.4	-0.0000	-0.0000	1	8	SSGQPLLP			De-novo
871.2287	2	821.4278	821.4282	-0.0014	-1.7027	57.7778	131.1324	1	8	RAAQPLLP			De-novo
871.2287	2	821.4278	821.4282	-0.0014	-1.7027	0.0000	131.1324	1	8	QSSQPLLP			De-novo
884.7776	2	871.2336	871.1283	0.1057	0.7268	59.6400	171.2574	1	10	LLPGTPAP			De-novo
884.7776	2	871.5396	871.5383	0.0957	0.7268	58.8235	146.2324	1	9	LLPGTPGM			De-novo
894.2208	2	853.2960	853.4058	-0.1098	-132.1223	59.4118	151.1144	1	7	GPYAPGM	Deamidation Q	1	De-novo
894.2208	2	853.2960	853.4058	-0.1098	-132.1223	51.0815	151.9919	1	7	MLYAPGN	Oxidation M	1	De-novo
894.2208	2	853.2960	853.4058	-0.1098	-132.1223	51.0815	151.9919	1	7	MLYAPGM	Oxidation M	1	De-novo
913.895	2	1455.7624	1455.7774	-0.1549	-5.3498	56.3878	206.6562	1	15	ANGRGLPAGTPAAW			De-novo
913.895	2	1455.7624	1455.7774	-0.1549	-5.3498	46.4667	228.1997	1	15	RAGRGLPAGTPAAW			De-novo
913.895	2	1455.7624	1455.7774	-0.1549	-5.3498	46.4667	228.1997	1	15	QAGRGLPAGTPAAW			De-novo
913.2206	2	855.4436	855.4467	-0.0257	-0.8824	58.9746	137.9913	1	7	LAYTQR	Deamidation Q	4	De-novo
913.2206	2	855.4436	855.4467	-0.0257	-0.8824	58.9746	138.1982	1	7	LAYTER			De-novo
913.2206	2	855.4436	855.4467	-0.0257	-0.8824	58.9746	138.1982	1	7	LAYTKR			De-novo
917.5371	2	833.4366	833.4265	-0.1023	-122.2287	66.6666	131.9494	1	8	LGLGPGR	Deamidation R	4	De-novo
917.5371	2	833.4366	833.4265	-0.1023	-122.2287	66.6666	131.9494	1	8	LGLGPGK			De-novo
917.5371	2	833.4366	833.4265	-0.1023	-122.2287	66.6666	131.9494	1	8	LGLGPGM			De-novo
923.4207	2	1845.8638	1845.8613	0.2025	1.0984	76.521	46.8138	1	14	YPYPPPYYYGLLR			De-novo
923.4207	2	1845.8638	1845.8613	0.2025	1.0984	76.521	46.1923	1	14	PYPPPYYYGGLLR			De-novo
923.4207	2	1845.8638	1845.8613	0.2025	1.0984	76.521	46.1923	1	14	YPYPPPYYGGLLR			De-novo

Hsp# 88

n/a	Charge	Rank HM	Peptide MW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Protein(s)	Query Scan
794.3784	2	1596.7622	1596.7272	0.3497	3.6052	32.7273	255.3268	1	15	GYTPYPYLGGRPR	Deamidation Q	12	De-novo
794.3784	2	1596.7622	1596.7272	0.3497	3.6052	40.9140	136.8941	1	15	WYPYPYLGGRPRR	Deamidation W	12	De-novo
794.3784	2	1596.7622	1596.7272	0.3497	3.6052	40.9140	136.8941	1	15	YWPYPYLGGRPRR	Deamidation W	12	De-novo
801.3123	2	1596.6074	1596.6039	0.0338	0.1243	49.3553	156.2268	1	11	YLNFGVRGGR	Deamidation W	7	De-novo
801.3123	2	1596.6074	1596.6039	0.0338	0.1243	51.561	153.9722	1	11	LYNFGVRGGR	Deamidation W	7	De-novo
801.3123	2	1596.6074	1596.6039	0.0338	0.1243	49.3553	156.2268	1	11	YLNFGVRGGK	Deamidation W	7	De-novo
807.8088	2	1213.4020	1213.3979	0.0041	3.3998	73.0862	215.1268	1	10	RLQTGYLGAF			De-novo
807.8088	2	1213.4020	1213.3979	0.0041	3.3998	61.9948	211.722	1	10	KLQATYRLGAF	Deamidation Q	5	De-novo
807.8088	2	1213.4020	1213.3979	0.0041	3.3998	61.9948	211.722	1	10	KLQATYKLGAF	Deamidation Q	5	De-novo
807.8088	2	1215.4040	1215.399	0.0050	3.8448	66.6667	211.2855	1	11	RPPRPRLQQF	Deamidation Q	5	De-novo
807.8088	2	1215.4040	1215.399	0.0050	3.8448	66.6667	211.4994	1	11	PPRRPRLQQF	Deamidation Q	5 - 10	De-novo
807.8088	2	1215.4040	1215.399	0.0050	3.8448	66.6667	211.4994	1	11	PPRRPRLQQF	Deamidation Q	5 - 10	De-novo
723.8787	2	1447.7418	1447.7271	0.0147	5.0377	75.1865	276.12	1	13	CYQGCGCLCGFR	Carbamidomethyl C /	1 / 7 / 10	De-novo
723.8787	2	1447.7418	1447.7271	0.0147	5.0377	81.963	276.1912	1	14	CYNGCGCLCGFGR	Carbamidomethyl C /	1	De-novo
731.7684	2	1461.5212	1461.5179	0.0338	1.3498	81.9924	224.3924	1	11	CYCYGMYPFM	Carbamidomethyl C /	1 / 4	De-novo
731.7684	2	1461.5212	1461.5179	0.0338	1.3498	81.9924	224.3924	1	11	CYCYMGYPFM	Carbamidomethyl C /	1 / 4	De-novo
731.7684	2	1461.5212	1461.5179	0.0338	1.3498	76.1865	209.2039	1	11	CYCYGMYPFM	Carbamidomethyl C /	1	De-novo
731.7684	2	1461.5212	1461.5179	0.0338	1.3498	76.1865	209.2039	1	11	CYCYMGYPFM	Carbamidomethyl C /	1 / 4	De-novo
755.3613	2	1448.7070	1448.7227	-0.0157	-10.8219	59.5217	131.9542	1	12	CRGPCYLCGMR	Carbamidomethyl C /	1 / 4	De-novo
755.3613	2	1448.7070	1448.6828	0.0242	16.8243	80.8696	131.94	1	12	CRGPPCYLCGMR	Carbamidomethyl C /	1 / 4 / 9	De-novo
576.7682	2	1071.5168	1071.5018	0.0150	14.0025	39.1129	95.8934	1	10	KYLVGWFW	Deamidation N	4	De-novo

Hsp# 89

n/a	Charge	Rank HM	Peptide MW	Delta (Da)	Delta (ppm)	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Protein(s)	Query Scan
873.5371	2	1745.9966	1745.9817	0.1494	8.5547	76.7574	141.193	1	14	LGYLGPGLLQLGF			De-novo
881.8971	2	1763.7780	1763.812	-0.0339	-19.2234	61.4118	141.9918	1	15	GGTGGGTGLLGGAWR	Deamidation N	5	De-novo
881.8971	2	1763.7780	1763.812	-0.0339	-19.2234	47.4118	141.1399	1	16	GGTGGGTGLLGGAWRN	Deamidation N	5	De-novo
881.8971	2	1763.7780	1763.812	-0.0339	-19.2234	61.9343	141.9918	1	17	GGTGGGTGLLGGAWRTN			De-novo
881.8971	2	1763.7780	1763.812	-0.0339	-19.2234	61.9343	141.9918	1	17	GGTGGGTGLLGGAWRTQ			De-novo
747.4300	2	1493.8628	1493.861	0.0018	1.2053	51.4567	215.4637	1	13	LYYYGPYNGFCLR	Carbamidomethyl C /	4 / 9 / 12	De-novo
747.4300	2	1493.8628	1493.861	0.0018	1.2053	51.4567	215.4637	1	13	LYYYGPYNGFCLR	Carbamidomethyl C /	7 / 9 / 12	De-novo

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ACS	Charge	Peak MH	Peptide MH	Delta ppm	Delta Spec	Ladder Score	Log Likelihood	Start	End	Sequence	Modifications	Rank	Query Scan
TCS_000	2	1494.731	1494.724	4.6997	4.6997	96.5928	262.1314	1	14	LEQLPPIQLQYSFDF			3e-scns
WCL_0187	2	1446.727	1446.726	0.6997	0.6997	95.1728	262.1314	1	14	LEQLPPIQLQYSFDF			3e-scns
TCS_000	2	1494.731	1494.724	4.6997	4.6997	95.1728	256.6463	1	14	EQLPPIQLQYSFDF			3e-scns
TCS_0203	2	1446.713	1446.724	-0.6130	-0.6130	93.3705	76.7752	1	14	EQLPPIQLQYSFDF			3e-scns
WCL_0187	2	1446.727	1446.726	0.6997	0.6997	92.1875	262.1947	1	14	EQLPPIQLQYSFDF			3e-scns
WCL_0187	2	1446.727	1446.726	0.6997	0.6997	92.1875	262.1947	1	14	EQLPPIQLQYSFDF			3e-scns
TCS_0203	2	1446.713	1446.724	-0.6130	-0.6130	79.5123	261.8710	1	14	LEQLPPIQLQYSFDF			3e-scns
TCS_0203	2	1446.713	1446.724	-0.6130	-0.6130	79.5123	261.8710	1	14	LEQLPPIQLQYSFDF	Deamidation Q	7	3e-scns
TCS_0178	2	1136.5636	1136.5663	-0.0337	-0.0337	90.9519	261.4299	1	11	EQLAVYIQLQF			3e-scns
TCS_0178	2	1136.5636	1136.5663	-0.0337	-0.0337	90.9519	261.4299	1	11	EQLAVYIQLQF			3e-scns
TCS_0178	2	1136.5636	1136.5663	-0.0337	-0.0337	79.7123	255.4211	1	12	EQLAVYIQLQFS			3e-scns
TCS_0623	2	1431.7090	1431.7108	-0.0914	-0.1343	92.969	172.0202	1	13	TSTSPCSEQLSQIFCF			3e-scns
TCS_0623	2	1431.7090	1431.7108	-0.0914	-0.1343	92.969	172.0202	1	13	TSTSPCSEQLSQIFCF			3e-scns
TCS_0181	2	2225.0249	2225.057	0.1475	35.5755	88.2950	276.528	1	25	KNTFSAGSSSFSPGSCFFTTCTCF	Deamidation N	18 / 25	3e-scns
TCS_0181	2	2225.0249	2225.057	0.1475	35.5755	88.2950	277.4711	1	25	KNTFSAGSSSFSPGSCFFTTCTCF	Deamidation N	18 / 25	3e-scns
TCS_0207	2	2206.0277	2205.9777	0.2983	65.8137	92.7734	325.6553	1	25	KFFPPNNPCTSSLCTPPPCTSCCF	Deamidation N	14	3e-scns
TCS_0207	2	2206.0277	2205.9777	0.2983	65.8137	92.7734	325.6553	1	25	KFFPPNNPCTSSLCTPPPCTSCCF	Deamidation N	14	3e-scns
TCS_0207	2	2206.0277	2205.9777	0.2983	65.8137	92.7734	325.6914	1	25	FFPPNNPCTSSLCTPPPCTSCCF	Deamidation N	18	3e-scns
TCS_0207	2	2206.0277	2205.9777	0.2983	65.8137	92.7734	325.6914	1	25	FFPPNNPCTSSLCTPPPCTSCCF	Deamidation N	18	3e-scns
TCS_0171	2	1491.8966	1491.8965	-0.0019	-0.0247	96.5247	126.1939	1	14	YCYFYGSSLLCFLR	Deamidation N	4	3e-scns
TCS_0171	2	1491.8966	1491.8965	-0.0019	-0.0247	96.5247	126.1939	1	14	YCYFYGSSLLCFLR	Deamidation N	4	3e-scns

MCMC [1:1:1: