Supplementary Table 1

(this table contains all original peptides data, used to calculate most statistics throughout this study)

content: **page**

descriptions:

hit	MASCOT protein hit no.
accession	database accession no.
z	peptide charge
mass	peptide calculated mass [Da]
ppm	peptide accuracy [ppm]
start	peptide start in protein sequence
end	peptide end in protein sequence
mc	no. of missed cleavages
score	peptide MS/MS ions score
id	peptide identity threshold score
-	residue before peptide sequence
sequence	peptide sequence
+	residue after peptide sequence
gravy	peptide GRAVY score
pI	peptide isoelectric point
modification	peptide modification

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
I. Corynebacterium glutamicum membrane; elastase digest, nLC-ESI MS/MS, no search specificity															
1	Cg1537	1	553.3839	1.1	307	311	0	26.4	24	S	IVIPL	L	3.1	6.02	
1	Cg1537	1	580.3584	1.0	235	240	0	28.6	18	F	PPLIAA	I	1.5	6.02	
1	Cg1537	1	595.304	1.7	455	459	0	28.5	28	V	SMFLV	L	2.4	6.02	
1	Cg1537	1	601.3873	0.3	268	272	0	27.5	16	S	LLIMI	P	3.7	6.02	
1	Cg1537	1	605.3061	1.2	204	208	0	29.0	27	L	TPEFL	A	0.2	3.3	
1	Cg1537	1	621.356	0.8	456	460	0	26.1	19	S	MFLVL	A	3.3	6.02	
1	Cg1537	1	640.416	2.0	306	311	0	31.4	23	L	SIVIPL	L	2.4	6.02	
1	Cg1537	1	642.3588	0.9	533	538	0	36.6	27	V	DIVSPL	E	1.1	3.1	
1	Cg1537	1	654.4064	-0.3	557	563	0	27.2	23	G	KLGPGIA	I	0.5	10.1	
1	Cg1537	1	656.3897	0.8	234	239	0	29.4	20	V	FPPLIA	A	1.6	6.02	
1	Cg1537	1	676.416	1.2	392	397	0	40.4	25	S	LYGVLL	R	2.3	5.92	
1	Cg1537	1	684.4211	-0.9	314	319	0	41.8	22	Y	PFLVPL	G	1.9	6.02	
1	Cg1537	1	693.4425	0.6	235	241	0	27.8	20	F	PPLIAAI	G	1.9	6.02	
1	Cg1537	1	701.3596	-0.7	528	534	0	39.8	32	A	AGEVVDI	V	1.0	3	
1	Cg1537	1	726.3225	-1.7	634	639	0	42.1	24	T	FDADFI	R	0.8	2.92	
1	Cg1537	1	727.3865	-1.0	568	575	0	37.0	28	T	GNTVVAPA	D	0.7	6.02	
1	Cg1537	1	730.4047	-2.1	328	333	0	32.7	28	A	IMIQNI	N	1.4	6.02	
1	Cg1537	1	739.3865	0.3	602	608	0	40.2	26	V	HVGLDTV	Q	0.6	4.94	
1	Cg1537	1	742.369	1.3	262	267	0	25.9	24	V	FVPFFS	L	1.7	6.02	
1	Cg1537	1	745.401	0.4	205	211	0	35.7	28	T	PEFLALG	S	1.0	3.3	
1	Cg1537	1	746.3996	1.2	328	333	0	35.0	29	A	IMIQNI	N	1.4	6.02	Oxidation (M)
1	Cg1537	1	755.3701	-0.4	546	552	0	46.0	22	L	SEVPDPI	F	-0.3	3	
1	Cg1537	1	758.4174	-0.9	291	297	0	35.5	32	I	SNLLEAI	N	0.9	3.3	
1	Cg1537	1	769.4772	-2.3	268	274	0	19.2	17	S	LLIMIPA	T	2.7	6.02	
1	Cg1537	2	782.465	1.0	555	563	0	29.8	26	A	AGKLGPGIA	I	0.6	10.1	
1	Cg1537	1	798.4316	-0.3	173	178	0	36.0	25	V	FYFLPI	M	1.8	5.92	
1	Cg1537	1	816.3766	-0.1	189	196	0	34.9	27	L	GANEWIGA	A	-0.1	3.3	
1	Cg1537	1	827.3701	0.4	633	639	0	25.9	24	I	TFDADFI	R	0.6	2.92	
1	Cg1537	1	828.3654	0.6	74	79	0	34.9	25	A	NYYQEI	L	-1.4	3.3	
1	Cg1537	1	828.4229	-0.2	533	540	0	29.4	27	V	DIVSPLEG	K	0.3	3	
1	Cg1537	1	831.4742	0.0	202	208	0	30.4	28	A	LLTPEFL	A	1.2	3.3	
1	Cg1537	1	832.4331	-2.6	205	212	0	35.8	30	T	PEFLALGS	A	0.7	3.3	
1	Cg1537	1	835.4844	-1.4	264	270	0	25.9	22	V	PFFSLLI	M	2.2	6.02	
1	Cg1537	1	838.4549	0.1	601	608	0	59.2	27	L	VHVGLDTV	Q	1.1	4.94	
1	Cg1537	1	854.4862	-0.4	53	61	0	44.1	26	S	VLGVVPQGS	T	1.1	6.02	
1	Cg1537	2	862.4953	0.0	277	284	0	34.5	27	A	FLLGPFGI	G	1.9	6.02	
1	Cg1537	1	866.5113	-2.0	643	650	0	29.7	20	K	DLPLITPV	V	1.1	3.1	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	Cg1537	2	902.5113	1.0	201	208	0	54.6	25	A	ALLTPEFL	A	1.3	3.3	
1	Cg1537	1	903.4014	-0.4	113	119	0	38.2	26	I	DYAFEFL	S	0.4	3	
1	Cg1537	1	933.5324	0.1	276	284	0	29.1	27	T	AFLLGPFGI	G	1.9	6.02	
1	Cg1537	1	941.4494	1.0	334	341	0	42.7	25	I	NTLGYDFI	Q	0.2	3.1	
1	Cg1537	1	950.4862	-1.4	242	249	0	34.1	29	I	GLYWVEKG	L	-0.3	6.86	
1	Cg1537	1	950.4862	0.0	297	304	0	33.0	29	A	INNFSPFI	L	0.7	6.02	
1	Cg1537	1	951.539	-2.3	600	608	0	43.7	23	I	LVHVGLDTV	Q	1.4	4.94	
1	Cg1537	2	960.5684	1.6	312	319	0	24.9	18	L	LYPFLVPL	G	1.7	5.92	
1	Cg1537	1	965.5546	-0.5	558	567	0	42.7	24	K	LGPGIAIQPT	G	0.6	6.02	
1	Cg1537	2	973.5484	1.5	201	209	0	26.8	25	A	ALLTPEFLA	L	1.3	3.3	
1	Cg1537	1	975.5463	-1.8	218	226	0	31.2	24	V	TVFGLPMVL	N	2.0	6.02	
1	Cg1537	1	991.5413	-1.4	218	226	0	35.1	24	V	TVFGLPMVL	N	2.0	6.02	Oxidation (M)
1	Cg1537	2	994.6063	-0.8	642	650	0	25.4	21	S	KDLPLITPV	V	0.6	6.76	
1	Cg1537	1	1000.5553	-1.1	592	600	0	33.2	29	L	RLDSGVEIL	V	0.4	4.08	
1	Cg1537	1	1000.5706	-0.3	553	563	0	38.0	28	I	FAAGKLGPGIA	I	0.9	10.1	
1	Cg1537	1	1009.6535	-1.0	250	258	0	32.8	21	G	LKKIIPEAV	Q	0.7	9.88	
1	Cg1537	2	1018.5852	0.6	277	286	0	61.6	26	A	FLLGPFGIGV	G	1.9	6.02	
1	Cg1537	1	1019.5552	-2.7	320	328	0	32.2	27	L	GLHWPLNAI	M	0.5	7.84	
1	Cg1537	1	1023.5964	-1.4	536	545	0	34.4	23	V	SPLEGKAIPL	S	0.2	6.94	
1	Cg1537	1	1034.488	-1.2	667	676	0	30.5	27	A	DQANSSTTVI	K	-0.3	3.1	
1	Cg1537	1	1034.5801	-2.3	275	284	0	37.1	26	A	TAFLLGPFGI	G	1.6	6.02	
1	Cg1537	1	1044.4916	-1.5	108	115	0	29.7	27	G	KYSWIDYA	F	-0.7	6.62	
1	Cg1537	1	1059.56	-0.3	657	666	0	47.2	30	A	KFGEIEGIPA	D	0.0	4.26	
1	Cg1537	1	1063.5702	0.8	297	305	0	39.3	28	A	INNFSPFIL	S	1.0	6.02	
1	Cg1537	1	1081.6212	-1.0	262	270	0	24.5	24	V	FVPFFSLLI	M	2.5	6.02	
1	Cg1537	1	1089.6223	-1.7	276	286	0	31.7	26	T	AFLLGPFGIGV	G	1.9	6.02	
1	Cg1537	1	1093.6495	-0.6	557	567	0	54.4	21	G	KLGPGIAIQPT	G	0.2	10.1	
1	Cg1537	1	1094.5107	-0.5	438	446	0	29.5	28	A	MDPWLGYTI	G	0.2	3.1	
1	Cg1537	1	1097.5142	-2.6	144	152	0	28.9	27	A	DTFGLQDFR	A	-0.7	3.88	
1	Cg1537	1	1097.5968	-2.4	528	538	0	39.0	27	A	AGEVVDIVSPL	E	1.2	3	
1	Cg1537	1	1099.6026	-0.5	279	290	0	40.3	28	L	LGPFGIGVGNGI	S	1.1	6.02	
1	Cg1537	1	1100.5365	0.0	259	267	0	37.2	28	V	QMVFVPFFS	L	1.4	6.02	
1	Cg1537	1	1122.6648	-2.3	535	545	0	22.8	21	I	VSPLEGKAIPL	S	0.6	6.94	
1	Cg1537	2	1150.671	-0.3	556	567	0	36.9	23	A	GKLGPGIAIQPT	G	0.2	10.1	
1	Cg1537	1	1154.5067	-2.9	337	347	0	42.4	23	L	GYDFIQGPMGA	W	0.0	3.1	
1	Cg1537	1	1170.7053	-0.9	310	319	0	25.8	25	I	PLLYPFLVPL	G	1.6	5.92	
1	Cg1537	1	1189.6496	-1.8	277	288	0	28.5	28	A	FLLGPFGIGVGN	G	1.3	6.02	
1	Cg1537	1	1190.67	0.9	275	286	0	32.0	27	A	TAFLLGPFGIGV	G	1.7	6.02	
1	Cg1537	2	1213.6567	0.2	186	196	0	43.7	28	A	RKLGANEWIGA	A	-0.5	10.08	
1	Cg1537	2	1221.7081	0.1	555	567	0	52.0	22	A	AGKLGPGIAIQPT	G	0.3	10.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	Cg1537	2	1237.7394	0.5	640	650	0	46.6	22	I	RSKDLPLITPV	V	0.0	10.08	
1	Cg1537	1	1257.6388	-0.2	55	67	0	32.8	28	L	GVVPQGSTGMQVV	M	0.6	6.02	
1	Cg1537	1	1264.5282	-3.6	153	163	0	27.0	22	R	APMDEQPDTYV	F	-1.0	2.88	
1	Cg1537	1	1264.6162	-2.5	438	448	0	38.7	29	A	MDPWLGYTIGI	A	0.5	3.1	
1	Cg1537	1	1275.6347	-1.6	205	217	0	39.6	29	T	PEFLALGSAGDTV	T	0.6	3	
1	Cg1537	2	1277.5347	-0.7	83	94	0	31.0	22	L	DGMKHFADGEAT	E	-0.9	4.3	
1	Cg1537	1	1277.7231	-4.0	541	552	0	55.0	25	G	KAIPLSEVPDPI	F	0.2	4.08	
1	Cg1537	1	1283.6609	-0.5	528	540	0	41.3	28	A	AGEVVDIVSPLEG	K	0.7	2.94	
1	Cg1537	2	1287.6306	-0.9	478	489	0	46.9	29	V	AADKQAEEDLKA	E	-1.2	4.06	
1	Cg1537	1	1322.6394	-2.0	628	639	0	54.6	28	A	GDPLITFDADFI	R	0.6	2.82	
1	Cg1537	2	1345.6361	-1.7	480	491	0	78.9	28	A	DKQAEEDLKAEA	N	-1.6	3.92	
1	Cg1537	1	1350.7758	-4.1	533	545	0	47.5	23	V	DIVSPLEGKAIPL	S	0.6	4.08	
1	Cg1537	2	1359.7551	-0.1	277	290	0	71.0	27	A	FLLGPFGIGVGNGI	S	1.4	6.02	
1	Cg1537	1	1373.6827	-1.0	657	669	0	85.9	29	A	KFGEIEGIPADQA	N	-0.4	3.82	
1	Cg1537	1	1376.6824	0.7	204	217	0	50.1	29	L	TPEFLALGSAGDTV	T	0.5	3	
1	Cg1537	1	1393.6766	-0.4	627	639	0	52.4	28	K	AGDPLITFDADFI	R	0.7	2.82	
1	Cg1537	1	1402.7092	-2.7	653	666	0	35.2	29	V	SNAAKFGEIEGIPA	D	0.0	4.26	
1	Cg1537	2	1411.7559	1.3	528	541	0	45.1	27	A	AGEVVDIVSPLEGK	A	0.4	3.82	
1	Cg1537	1	1412.7374	0.1	431	443	0	47.7	28	T	SLLTIPAMDPWLG	Y	0.8	3.1	
1	Cg1537	2	1416.6732	-1.0	479	491	0	68.9	28	A	ADKQAEEDLKAEA	N	-1.4	3.92	
1	Cg1537	2	1418.7154	-1.2	10	22	0	69.8	30	S	QHILENLGGPDNI	T	-0.5	4.06	
1	Cg1537	1	1419.7034	-0.8	227	239	0	34.5	29	L	NDYSGQVFPPLIA	A	0.1	3.1	
1	Cg1537	2	1439.8136	-0.6	553	567	0	74.1	26	I	FAAGKLGPGIAIQPT	G	0.6	10.1	
1	Cg1537	1	1444.7198	-3.0	656	669	0	55.1	29	A	AKFGEIEGIPADQA	N	-0.2	3.82	
1	Cg1537	2	1464.83	0.6	557	571	0	37.9	25	G	KLGPGIAIQPTGNTV	V	0.1	10.1	
1	Cg1537	1	1469.7912	0.1	53	67	0	40.5	28	S	VLGVVPQGSTGMQVV	M	1.0	6.02	
1	Cg1537	1	1482.6813	-1.9	334	347	0	51.4	27	I	NTLGYDFIQGPMGA	W	0.0	3.1	
1	Cg1537	2	1487.7103	0.3	478	491	0	53.6	28	V	AADKQAEEDLKAEA	N	-1.1	3.92	
1	Cg1537	2	1493.6093	-1.2	83	96	0	24.2	19	L	DGMKHFADGEATES	S	-1.1	4.06	
1	Cg1537	2	1498.6762	1.0	334	347	0	28.4	26	I	NTLGYDFIQGPMGA	W	0.0	3.1	Oxidation (M)
1	Cg1537	1	1505.7474	-2.8	9	22	0	89.8	30	T	SQHILENLGGPDNI	T	-0.5	4.06	
1	Cg1537	2	1519.7631	-1.3	10	23	0	59.0	29	S	QHILENLGGPDNIT	S	-0.5	4.06	
1	Cg1537	1	1521.7715	-2.5	626	639	0	32.3	29	V	KAGDPLITFDADFI	R	0.4	3.6	
1	Cg1537	1	1531.8399	-2.4	275	290	0	49.6	28	A	TAFLLGPFGIGVGNGI	S	1.3	6.02	
1	Cg1537	2	1557.8072	-0.4	375	391	0	68.4	29	V	SLGGMLAGLLGGISEPS	L	0.8	3.3	
1	Cg1537	1	1602.8505	-2.7	202	217	0	32.1	29	A	LLTPEFLALGSAGDTV	T	0.9	3	
1	Cg1537	2	1612.9188	-1.9	637	650	0	37.6	26	A	DFIRSKDLPLITPV	V	0.3	6.9	
1	Cg1537	1	1629.7998	-2.9	654	669	0	46.7	28	S	NAAKFGEIEGIPADQA	N	-0.3	3.82	
1	Cg1537	1	1673.8876	-2.2	201	217	0	58.6	29	A	ALLTPEFLALGSAGDTV	T	0.9	3	
1	Cg1537	1	1690.893	-2.5	291	305	0	47.6	29	I	SNLLEAINNFSPFIL	S	0.7	3.3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	Cg1537	1	1716.8318	-1.9	653	669	0	62.2	29	V	SNAAKFGEIEGIPADQA	N	-0.3	3.82	
1	Cg1537	2	1760.956	-0.1	536	552	0	50.2	27	V	SPLEGKAIPLSEVPDPI	F	0.0	3.82	
1	Cg1537	1	1786.9982	-3.0	277	294	0	45.7	27	A	FLLGPFGIGVGNGISNLL	E	1.3	6.02	
1	Cg1537	2	1803.0254	-0.6	557	575	0	30.9	25	G	KLGPGIAIQPTGNTVVAPA	D	0.4	10.1	
1	Cg1537	1	1806.0139	-2.7	528	545	0	91.4	25	A	AGEVVDIVSPLEGKAIPL	S	0.8	3.82	
1	Cg1537	2	1831.9428	-1.3	33	47	0	78.6	30	L	RFQVKDQSIVDQQEI	D	-0.9	4.3	
1	Cg1537	2	1838.8833	0.2	10	26	0	58.3	29	S	QHILENLGGPDNITSMT	H	-0.4	4.06	
1	Cg1537	1	1840.0094	-3.1	279	297	0	56.8	28	L	LGPFGIGVGNGISNLLEAI	N	1.0	3.3	
1	Cg1537	1	1859.9492	-4.2	223	239	0	60.2	30	L	PMVLNDYSGQVFPPLIA	A	0.5	3.1	
1	Cg1537	2	1860.0244	-1.5	535	552	0	42.1	27	I	VSPLEGKAIPLSEVPDPI	F	0.2	3.82	
1	Cg1537	2	1863.885	-1.6	657	674	0	37.8	29	A	KFGEIEGIPADQANSSTT	V	-0.6	3.82	
1	Cg1537	1	1874.0037	0.3	201	219	0	63.6	28	A	ALLTPEFLALGSAGDTVTV	F	1.0	3	
1	Cg1537	1	1987.0779	-1.9	277	296	0	43.3	28	A	FLLGPFGIGVGNGISNLLEA	I	1.0	3.3	
1	Cg1537	2	2072.0758	-2.3	371	391	0	44.9	30	A	MRQVSLGGMLAGLLGGISEPS	L	0.6	6.98	
1	Cg1537	2	2076.0375	-2.5	657	676	0	61.2	30	A	KFGEIEGIPADQANSSTTVI	K	-0.1	3.82	
1	Cg1537	2	2088.1354	-2.8	533	552	0	35.0	28	V	DIVSPLEGKAIPLSEVPDPI	F	0.3	3.58	
1	Cg1537	2	2100.1619	0.0	277	297	0	35.8	28	A	FLLGPFGIGVGNGISNLLEAI	N	1.2	3.3	
1	Cg1537	2	2147.0746	-3.7	656	676	0	33.6	30	A	AKFGEIEGIPADQANSSTTVI	K	0.0	3.82	
1	Cg1537	2	2332.1546	-2.8	654	676	0	69.5	30	S	NAAKFGEIEGIPADQANSSTTVI	K	-0.1	3.82	
1	Cg1537	2	2344.0318	-0.7	144	163	0	55.5	23	A	DTFGLQDFRAPMDEQPDTYV	F	-0.9	3.36	
1	Cg1537	2	2419.1867	-2.9	653	676	0	56.0	30	V	SNAAKFGEIEGIPADQANSSTTVI	K	-0.1	3.82	
1	Cg1537	2	2442.1525	-3.0	74	94	0	69.8	28	A	NYYQEILKLDGMKHFADGEAT	E	-0.7	4.54	
1	Cg1537	2	2543.3734	1.2	528	552	0	111.1	29	A	AGEVVDIVSPLEGKAIPLSEVPDPI	F	0.5	3.5	
1	Cg1537	2	2604.1843	-0.4	144	165	0	39.9	26	A	DTFGLQDFRAPMDEQPDTYVFL	H	-0.5	3.36	
1	Cg1537	2	2646.3501	-2.0	653	678	0	34.8	31	V	SNAAKFGEIEGIPADQANSSTTVIKV	N	-0.1	4.44	
1	Cg1537	2	2658.2271	-1.5	74	96	0	52.6	27	A	NYYQEILKLDGMKHFADGEATES	S	-0.9	4.28	
1	Cg1537	3	2828.2752	0.2	144	167	0	32.0	25	A	DTFGLQDFRAPMDEQPDTYVFLHS	M	-0.6	3.76	
2	P00772|ELA1	1	532.2646	0.8	157	161	0	32.2	29	T	GWGLT	R	0.3	6.02	
2	P00772|ELA1	1	532.2646	1.1	156	160	0	30.8	29	I	TGWGL	T	0.3	6.02	
2	P00772|ELA1	1	649.2894	0.5	64	68	0	31.2	28	Q	NWVMT	A	0.2	6.02	
2	P00772|ELA1	1	650.3024	0.0	223	228	0	29.3	25	V	NGQYAV	H	-0.5	5.92	
2	P00772|ELA1	1	665.3384	0.6	133	138	0	43.8	30	N	SYVQLG	V	0.3	5.92	
2	P00772|ELA1	2	668.397	-0.1	138	144	0	45.2	24	L	GVLPRAG	T	0.4	11.04	
2	P00772|ELA1	1	711.3228	-0.3	189	194	0	27.7	21	S	YWGSTV	K	0.0	5.92	
2	P00772|ELA1	1	720.3265	0.6	64	69	0	41.7	27	Q	NWVMTA	A	0.5	6.02	
2	P00772|ELA1	2	726.4388	1.5	140	146	0	30.7	25	V	LPRAGTI	L	0.4	11.04	
2	P00772|ELA1	1	731.3602	0.5	257	262	0	38.1	27	I	SWINNV	I	0.0	6.02	
2	P00772|ELA1	1	736.3214	0.0	64	69	0	32.7	26	Q	NWVMTA	A	0.5	6.02	Oxidation (M)
2	P00772|ELA1	1	748.3028	0.1	109	114	0	35.1	25	Y	WNTDDV	A	-1.3	2.92	
2	P00772|ELA1	2	772.3868	1.2	225	231	0	51.4	25	G	QYAVHGV	T	0.3	7.76	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	P00772|ELA1	1	779.3814	0.3	132	138	0	37.6	29	L	NSYVQLG	V	-0.2	5.92	
2	P00772|ELA1	1	781.481	-0.8	137	144	0	26.5	23	Q	LGVLPRAG	T	0.8	11.04	
2	P00772|ELA1	1	786.3184	0.3	187	193	0	30.6	21	S	SSYWGST	V	-0.8	5.92	
2	P00772|ELA1	2	789.4133	0.5	156	162	0	49.8	29	I	TGWGLTR	T	-0.5	11.04	
2	P00772|ELA1	1	797.4759	-0.5	141	148	0	31.9	25	L	PRAGTILA	N	0.6	11.04	
2	P00772|ELA1	1	807.3255	-1.4	198	206	0	34.3	23	S	MVCAGGDGV	R	1.1	3.1	
2	P00772|ELA1	1	819.4127	-0.2	172	178	0	34.9	31	L	QQAYLPT	V	-0.7	5.92	
2	P00772|ELA1	2	825.5072	1.5	139	146	0	38.4	24	G	VLPRAGTI	L	0.9	11.04	
2	P00772|ELA1	1	828.4494	0.2	258	264	0	29.5	24	S	WINNVIA	S	1.0	6.02	
2	P00772|ELA1	1	830.3923	-0.7	36	42	0	29.0	28	R	NSWPSQI	S	-0.9	6.02	
2	P00772|ELA1	1	834.4487	-1.0	116	123	0	33.1	28	A	AGYDIALL	R	1.3	3.1	
2	P00772|ELA1	1	843.445	-0.9	164	171	0	51.1	29	T	NGQLAQTL	Q	-0.3	6.02	
2	P00772|ELA1	1	844.4443	0.8	257	263	0	35.6	27	I	SWINNVI	A	0.6	6.02	
2	P00772|ELA1	2	882.5287	0.9	138	146	0	48.6	25	L	GVLPRAGTI	L	0.7	11.04	
2	P00772|ELA1	1	885.3869	-1.5	187	194	0	29.8	24	S	SSYWGSTV	K	-0.2	5.92	
2	P00772|ELA1	2	890.461	-0.4	156	163	0	36.4	29	I	TGWGLTRT	N	-0.6	11.04	
2	P00772|ELA1	2	909.5396	1.2	136	144	0	47.2	21	V	QLGVLPRAG	T	0.4	11.04	
2	P00772|ELA1	1	911.3661	-1.2	108	114	0	35.6	23	P	YWNTDDV	A	-1.3	2.92	
2	P00772|ELA1	2	915.4814	1.2	257	264	0	43.2	27	I	SWINNVIA	S	0.8	6.02	
2	P00772|ELA1	2	943.4512	1.0	223	231	0	49.1	26	V	NGQYAVHGV	T	-0.2	7.76	
2	P00772|ELA1	1	966.4295	0.1	92	100	0	34.4	27	N	DGTEQYVGV	Q	-0.5	3	
2	P00772|ELA1	1	993.5131	-1.9	130	138	0	56.0	27	V	TLNSYVQLG	V	0.2	5.92	
2	P00772|ELA1	2	1009.6284	1.3	139	148	0	42.0	20	G	VLPRAGTILA	N	1.3	11.04	
2	P00772|ELA1	2	1013.4818	0.9	187	195	0	34.0	27	S	SSYWGSTVK	N	-0.6	9.72	
2	P00772|ELA1	2	1014.4923	0.6	104	111	0	35.5	25	I	VVHPYWNT	D	-0.4	7.76	
2	P00772|ELA1	1	1020.4811	-1.8	62	69	0	28.2	28	I	RQNWVMTA	A	-0.7	11.04	Oxidation (M)
2	P00772|ELA1	2	1029.5203	-0.9	27	36	0	64.0	28	R	VVGGTEAQRN	S	-0.6	6.98	
2	P00772|ELA1	1	1040.4927	-1.7	189	197	0	35.7	27	S	YWGSTVKNS	M	-0.9	9.72	
2	P00772|ELA1	2	1044.4989	0.0	223	232	0	27.6	27	V	NGQYAVHGVT	S	-0.3	7.76	
2	P00772|ELA1	2	1066.6499	0.8	138	148	0	50.1	22	L	GVLPRAGTILA	N	1.1	11.04	
2	P00772|ELA1	2	1100.5938	0.4	162	171	0	44.6	29	T	RTNGQLAQTL	Q	-0.7	11.04	
2	P00772|ELA1	1	1114.5519	0.4	34	42	0	31.1	28	A	QRNSWPSQI	S	-1.6	11.04	
2	P00772|ELA1	2	1116.5564	1.9	257	266	0	37.6	28	I	SWINNVIASN	-	0.2	6.02	
2	P00772|ELA1	2	1123.6713	-0.1	136	146	0	23.8	23	V	QLGVLPRAGTI	L	0.6	11.04	
2	P00772|ELA1	2	1127.5247	0.4	187	196	0	47.0	26	S	SSYWGSTVKN	S	-0.9	9.72	
2	P00772|ELA1	2	1145.4778	-0.3	106	114	0	42.0	21	V	HPYWNTDDV	A	-1.6	3.88	
2	P00772|ELA1	1	1166.484	-1.0	89	98	0	26.5	22	L	NQNDGTEQYV	G	-1.9	3	
2	P00772|ELA1	2	1170.5993	0.3	164	174	0	62.4	27	T	NGQLAQTLQQA	Y	-0.7	6.02	
2	P00772|ELA1	2	1214.5568	0.5	187	197	0	51.0	25	S	SSYWGSTVKNS	M	-0.9	9.72	
2	P00772|ELA1	2	1240.5836	0.1	43	53	0	65.4	26	I	SLQYRSGSSWA	H	-0.7	9.84	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	P00772|ELA1	2	1244.5462	1.2	105	114	0	69.3	25	V	VHPYWNTDDV	A	-1.0	3.88	
2	P00772|ELA1	2	1258.7034	-0.2	133	144	0	66.4	27	N	SYVQLGVLPRAG	T	0.4	9.84	
2	P00772|ELA1	2	1307.7925	0.5	136	148	0	30.8	20	V	QLGVLPRAGTILA	N	1.0	11.04	
2	P00772|ELA1	2	1315.5833	0.7	105	115	0	46.5	25	V	VHPYWNTDDVA	A	-0.7	3.88	
2	P00772|ELA1	2	1343.6146	1.1	104	114	0	65.6	27	I	VVHPYWNTDDV	A	-0.5	3.88	
2	P00772|ELA1	2	1372.7463	-0.1	132	144	0	86.1	28	L	NSYVQLGVLPRAG	T	0.1	9.84	
2	P00772|ELA1	2	1386.6204	0.7	105	116	0	48.5	26	V	VHPYWNTDDVAA	G	-0.5	3.88	
2	P00772|ELA1	2	1395.6379	-1.8	82	94	0	56.2	27	V	VVGEHNLNQNDGT	E	-1.0	4.06	
2	P00772|ELA1	2	1414.6517	0.9	104	115	0	58.9	27	I	VVHPYWNTDDVA	A	-0.3	3.88	
2	P00772|ELA1	2	1417.7929	0.5	117	129	0	28.0	26	A	GYDIALLRLAQSV	T	0.7	6.7	
2	P00772|ELA1	2	1425.612	-1.5	83	95	0	74.7	23	V	VGEHNLNQNDGTE	Q	-1.6	3.82	
2	P00772|ELA1	2	1427.7481	0.5	162	174	0	45.0	29	T	RTNGQLAQTLQQA	Y	-1.0	11.04	
2	P00772|ELA1	2	1443.6419	-0.4	105	117	0	29.9	24	V	VHPYWNTDDVAAG	Y	-0.5	3.88	
2	P00772|ELA1	2	1456.6987	0.1	103	114	0	63.6	28	K	IVVHPYWNTDDV	A	-0.1	3.88	
2	P00772|ELA1	2	1458.8195	-1.2	130	142	0	37.5	27	V	TLNSYVQLGVLPR	A	0.3	9.84	
2	P00772|ELA1	2	1485.6889	0.5	104	116	0	45.7	27	I	VVHPYWNTDDVAA	G	-0.2	3.88	
2	P00772|ELA1	2	1485.8304	0.5	131	144	0	50.2	27	T	LNSYVQLGVLPRAG	T	0.4	9.84	
2	P00772|ELA1	2	1486.7165	-0.8	27	40	0	31.0	28	R	VVGGTEAQRNSWPS	Q	-0.7	6.98	
2	P00772|ELA1	2	1524.6805	-2.0	82	95	0	54.4	25	V	VVGEHNLNQNDGTE	Q	-1.2	3.82	
2	P00772|ELA1	1	1542.7103	-1.6	104	117	0	51.4	26	I	VVHPYWNTDDVAAG	Y	-0.2	3.88	
2	P00772|ELA1	2	1553.6706	-1.1	83	96	0	72.7	23	V	VGEHNLNQNDGTEQ	Y	-1.8	3.82	
2	P00772|ELA1	2	1586.878	0.3	130	144	0	75.7	27	V	TLNSYVQLGVLPRAG	T	0.3	9.84	
2	P00772|ELA1	2	1652.739	-2.2	82	96	0	86.0	25	V	VVGEHNLNQNDGTEQ	Y	-1.4	3.82	
2	P00772|ELA1	2	1659.7125	-0.5	85	98	0	63.1	23	G	EHNLNQNDGTEQYV	G	-1.8	3.82	
2	P00772|ELA1	2	1705.7737	-0.1	104	118	0	51.9	26	I	VVHPYWNTDDVAAGY	D	-0.2	3.88	
2	P00772|ELA1	2	1712.8522	-1.8	101	114	0	36.3	28	V	QKIVVHPYWNTDDV	A	-0.6	5.1	
2	P00772|ELA1	2	1716.7339	-1.1	84	98	0	35.4	22	V	GEHNLNQNDGTEQYV	G	-1.7	3.82	
2	P00772|ELA1	2	1716.7339	-1.0	83	97	0	28.7	22	V	VGEHNLNQNDGTEQY	V	-1.7	3.82	
2	P00772|ELA1	2	1727.8591	-1.6	27	42	0	42.6	29	R	VVGGTEAQRNSWPSQI	S	-0.6	6.98	
2	P00772|ELA1	2	1770.9992	0.0	132	148	0	38.9	27	L	NSYVQLGVLPRAGTILA	N	0.7	9.84	
2	P00772|ELA1	2	1806.7849	-1.3	106	121	0	32.4	23	V	HPYWNTDDVAAGYDIA	L	-0.6	3.6	
2	P00772|ELA1	2	1815.8024	-0.2	85	100	0	68.2	24	G	EHNLNQNDGTEQYVGV	Q	-1.4	3.82	
2	P00772|ELA1	1	1815.8024	-0.8	83	98	0	71.9	24	V	VGEHNLNQNDGTEQYV	G	-1.4	3.82	
2	P00772|ELA1	2	1815.8024	-0.3	82	97	0	29.9	24	V	VVGEHNLNQNDGTEQY	V	-1.4	3.82	
2	P00772|ELA1	2	1901.0371	0.0	127	144	0	110.7	28	A	QSVTLNSYVQLGVLPRAG	T	0.3	9.84	
2	P00772|ELA1	2	1905.8533	0.9	105	121	0	66.6	26	V	VHPYWNTDDVAAGYDIA	L	-0.3	3.6	
2	P00772|ELA1	2	1907.9086	-0.2	80	96	0	77.8	29	F	RVVVGEHNLNQNDGTEQ	Y	-1.2	4.42	
2	P00772|ELA1	1	1914.8708	-1.1	82	98	0	107.8	26	V	VVGEHNLNQNDGTEQYV	G	-1.0	3.82	
2	P00772|ELA1	2	1933.8847	0.0	104	120	0	35.3	27	I	VVHPYWNTDDVAAGYDI	A	-0.2	3.6	
2	P00772|ELA1	1	1971.8923	-2.4	83	100	0	77.1	26	V	VGEHNLNQNDGTEQYVGV	Q	-1.0	3.82	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	P00772|ELA1	2	2004.9218	-1.6	104	121	0	75.5	26	I	VVHPYWNTDDVAAGYDIA	L	-0.1	3.6	
2	P00772|ELA1	2	2070.9607	-0.5	82	100	0	71.1	28	V	VVGEHNLNQNDGTEQYVGV	Q	-0.7	3.82	
2	P00772|ELA1	2	2118.0058	-0.8	103	121	0	32.0	29	K	IVVHPYWNTDDVAAGYDIA	L	0.2	3.6	
2	P00772|ELA1	2	2231.0899	1.6	104	123	0	58.4	30	I	VVHPYWNTDDVAAGYDIALL	R	0.3	3.6	
3	Cg0446	1	641.3748	1.2	50	55	0	46.7	29	M	NLVSPL	N	1.0	6.02	
3	Cg0446	1	670.2962	-0.1	286	291	0	23.8	23	A	YFASPS	F	0.0	5.92	
3	Cg0446	1	753.4021	0.1	205	211	0	34.8	26	I	HLGSVEI	F	0.7	5.12	
3	Cg0446	1	796.4443	-0.5	372	380	0	43.5	25	I	NAGLGVGPL	N	0.8	6.02	
3	Cg0446	1	837.4273	1.4	661	667	0	23.0	23	L	FFESVPL	Q	1.1	3.3	
3	Cg0446	1	888.3613	-0.6	643	650	0	28.2	21	V	SAWEPGEN	G	-1.6	3.12	
3	Cg0446	2	888.4494	0.7	292	298	0	32.8	25	S	FIQFHPT	G	0.2	7.84	
3	Cg0446	1	935.4825	-0.7	171	179	0	35.8	28	T	RSFGGVQVS	R	0.1	11.04	
3	Cg0446	2	966.4559	1.1	159	167	0	37.9	25	A	PFAREYGGA	L	-0.6	6.88	
3	Cg0446	1	1029.5495	-1.2	487	496	0	34.8	30	I	PNYLGPLLGS	E	0.2	5.92	
3	Cg0446	1	1046.4305	-0.8	643	652	0	28.0	22	V	SAWEPGENGT	F	-1.4	3.12	
3	Cg0446	1	1066.5335	-2.8	661	669	0	34.2	27	L	FFESVPLQT	R	0.4	3.3	
3	Cg0446	1	1067.4845	-0.2	598	606	0	49.7	26	A	DYIDLGELM	C	0.2	2.88	
3	Cg0446	1	1083.4794	-0.6	598	606	0	43.4	24	A	DYIDLGELM	C	0.2	2.88	Oxidation (M)
3	Cg0446	1	1094.459	-0.5	415	424	0	29.0	23	A	IGEDPYSSPM	R	-0.7	3	
3	Cg0446	1	1094.5145	-0.7	157	167	0	32.6	28	I	GAPFAREYGGA	L	-0.4	6.88	
3	Cg0446	1	1095.5673	-0.5	372	383	0	51.7	27	I	NAGLGVGPLNNA	A	0.2	6.02	
3	Cg0446	2	1134.5921	-0.4	77	87	0	63.1	29	A	ALGELGYDVKA	F	0.2	4.08	
3	Cg0446	1	1166.6044	-0.7	372	384	0	40.0	28	I	NAGLGVGPLNNAA	Y	0.3	6.02	
3	Cg0446	1	1203.5594	-4.2	212	221	0	39.8	26	I	FTHNEMVDVI	V	0.3	4.06	
3	Cg0446	1	1205.5353	-2.3	644	654	0	26.6	24	S	AWEPGENGTFV	R	-0.5	3.12	
3	Cg0446	1	1205.6292	-2.7	76	87	0	28.6	28	A	AALGELGYDVKA	F	0.4	4.08	
3	Cg0446	2	1207.5986	0.3	156	167	0	56.7	28	A	IGAPFAREYGGA	L	0.0	6.88	
3	Cg0446	1	1216.6815	-3.3	489	499	0	29.6	27	N	YLGPLLGSERL	S	0.2	6.88	
3	Cg0446	2	1243.568	-0.6	497	507	0	36.3	27	S	ERLSEDAPEAQ	A	-1.5	3.68	
3	Cg0446	2	1244.5997	1.6	553	563	0	59.7	28	V	SRNVEDLQDGI	N	-1.0	3.7	
3	Cg0446	2	1254.6761	-1.8	292	302	0	60.2	27	S	FIQFHPTGLPV	N	0.6	7.84	
3	Cg0446	1	1292.5673	0.2	643	654	0	34.9	25	V	SAWEPGENGTFV	R	-0.5	3.12	
3	Cg0446	2	1330.6001	-1.2	496	507	0	64.1	26	G	SERLSEDAPEAQ	A	-1.5	3.68	
3	Cg0446	2	1363.6442	-0.2	415	426	0	38.8	28	A	IGEDPYSSPMRI	A	-0.6	4.08	
3	Cg0446	1	1372.6194	-2.5	521	532	0	47.0	26	L	MGNRPEWVGDNV	H	-1.0	4.08	
3	Cg0446	2	1379.6834	0.9	157	170	0	29.4	28	I	GAPFAREYGGALAT	R	0.1	6.88	
3	Cg0446	2	1400.6896	0.1	551	563	0	43.0	28	C	GVSRNVEDLQDGI	N	-0.5	3.7	
3	Cg0446	2	1427.7772	0.2	487	499	0	49.6	28	I	PNYLGPLLGSERL	S	-0.2	6.88	
3	Cg0446	1	1455.6188	-3.5	581	593	0	45.2	23	T	GSTDEMNQVLEYA	A	-0.7	2.94	
3	Cg0446	1	1469.6609	-3.9	256	269	0	46.4	25	A	TGGYGNVYHMSTLA	K	-0.1	7.7	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
3	Cg0446	1	1526.6559	-2.9	581	594	0	31.2	23	T	GSTDEMNQVLEYAA	R	-0.5	2.94	
3	Cg0446	1	1540.8038	-1.8	655	667	0	36.2	28	V	RHAEPLFFESVPL	Q	0.0	5.3	
3	Cg0446	1	1556.6664	-4.1	580	593	0	24.0	23	I	TGSTDEMNQVLEYA	A	-0.7	2.94	
3	Cg0446	2	1599.8216	-1.8	553	566	0	76.8	29	V	SRNVEDLQDGINKI	R	-1.0	4.3	
3	Cg0446	2	1641.8111	-0.1	182	195	0	46.5	29	T	YYTRGQTGQQLQLS	T	-1.2	9.58	
3	Cg0446	1	1669.7505	-4.1	579	593	0	43.1	26	R	ITGSTDEMNQVLEYA	A	-0.3	2.94	
3	Cg0446	1	1724.8832	-2.8	17	34	0	29.1	29	V	SVLPEVSAGTVLDAAEPA	G	0.6	2.94	
3	Cg0446	2	1756.8315	-1.4	518	532	0	47.3	27	I	DRLMGNRPEWVGDNV	H	-1.0	4.3	
3	Cg0446	2	1769.9101	-1.5	655	669	0	88.0	29	V	RHAEPLFFESVPLQT	R	-0.2	5.3	
3	Cg0446	2	1775.8049	-1.1	151	167	0	72.5	26	I	DHMNAIGAPFAREYGGA	L	-0.3	5.22	
3	Cg0446	2	1805.9676	-2.0	8	23	0	62.4	29	T	TRPEFIHPVSVLPEVS	A	0.1	5.3	
3	Cg0446	2	1835.8335	-2.1	39	52	0	57.9	26	T	KDMWEYQKDHMNLV	S	-1.4	5.28	
3	Cg0446	2	1852.8625	-0.7	581	597	0	66.3	28	T	GSTDEMNQVLEYAARVA	D	-0.3	3.82	
3	Cg0446	2	1869.9156	-0.9	517	532	0	31.2	29	R	IDRLMGNRPEWVGDNV	H	-0.7	4.3	
3	Cg0446	2	1953.9102	0.4	580	597	0	89.8	27	I	TGSTDEMNQVLEYAARVA	D	-0.4	3.82	
3	Cg0446	2	1959.9261	-2.3	151	169	0	77.4	28	I	DHMNAIGAPFAREYGGALA	T	0.0	5.22	
3	Cg0446	2	2044.0113	-0.6	489	507	0	80.6	30	N	YLGPLLGSERLSEDAPEAQ	A	-0.5	3.68	
3	Cg0446	2	2060.9738	-2.3	151	170	0	60.5	28	I	DHMNAIGAPFAREYGGALAT	R	-0.1	5.22	
3	Cg0446	2	2133.0023	-2.6	39	55	0	85.7	28	T	KDMWEYQKDHMNLVSPL	N	-1.0	5.28	
3	Cg0446	2	2144.0585	-2.4	148	167	0	84.3	30	V	RVIDHMNAIGAPFAREYGGA	L	-0.1	7.76	
3	Cg0446	2	2190.0238	-1.8	35	52	0	55.1	28	A	GVPTKDMWEYQKDHMNLV	S	-1.0	5.28	
3	Cg0446	2	2255.1069	-0.2	487	507	0	57.3	30	I	PNYLGPLLGSERLSEDAPEAQ	A	-0.7	3.68	
3	Cg0446	2	2257.1426	-1.9	148	168	0	31.2	30	V	RVIDHMNAIGAPFAREYGGAL	A	0.1	7.76	
3	Cg0446	3	2349.1866	-0.6	77	97	0	66.8	30	A	ALGELGYDVKAFTYHDAPRRA	H	-0.5	7.68	
3	Cg0446	3	2429.2274	-3.4	148	170	0	34.3	31	V	RVIDHMNAIGAPFAREYGGALAT	R	0.1	7.76	
3	Cg0446	2	2448.2285	-2.4	2	23	0	65.5	30	M	STHSETTRPEFIHPVSVLPEVS	A	-0.4	5.22	
3	Cg0446	2	2487.1926	-2.8	35	55	0	48.3	29	A	GVPTKDMWEYQKDHMNLVSPL	N	-0.8	5.28	
3	Cg0446	2	2678.3745	-1.8	475	498	0	95.0	30	A	SVDGWFTLPFTIPNYLGPLLGSER	L	0.1	4.08	
3	Cg0446	2	2728.3286	-1.3	644	667	0	31.2	30	S	AWEPGENGTFVRHAEPLFFESVPL	Q	-0.2	4.24	
3	Cg0446	2	2791.4585	-2.1	475	499	0	53.8	30	A	SVDGWFTLPFTIPNYLGPLLGSERL	S	0.3	4.08	
3	Cg0446	2	2801.46	-2.1	8	34	0	92.5	30	T	TRPEFIHPVSVLPEVSAGTVLDAAEPA	G	0.3	4.16	
3	Cg0446	2	2878.4905	-2.4	475	500	0	48.4	31	A	SVDGWFTLPFTIPNYLGPLLGSERLS	E	0.2	4.08	
3	Cg0446	2	2957.4348	-2.3	644	669	0	34.5	30	S	AWEPGENGTFVRHAEPLFFESVPLQT	R	-0.4	4.24	
3	Cg0446	2	3044.4668	-3.7	643	669	0	46.9	30	V	SAWEPGENGTFVRHAEPLFFESVPLQT	R	-0.4	4.24	
3	Cg0446	3	3443.7209	-2.8	2	34	0	51.7	31	M	STHSETTRPEFIHPVSVLPEVSAGTVLDAAEPA	G	-0.1	4.34	
3	Cg0446	2	3618.7882	-0.8	475	507	0	44.1	31	A	SVDGWFTLPFTIPNYLGPLLGSERLSEDAPEAQ	A	-0.2	3.5	
3	Cg0446	2	3689.8253	-3.1	475	508	0	32.9	31	A	SVDGWFTLPFTIPNYLGPLLGSERLSEDAPEAQA	A	-0.1	3.5	
3	Cg0446	2	3760.8624	-3.8	475	509	0	33.0	31	A	SVDGWFTLPFTIPNYLGPLLGSERLSEDAPEAQAA	I	-0.1	3.5	
4	Cg2705	1	680.317	0.6	342	346	0	29.6	26	V	DWLFT	S	0.3	3.1	
4	Cg2705	1	809.3959	0.0	360	366	0	29.0	28	G	FIAPFES	Y	0.9	3.3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
4	Cg2705	1	975.4662	-1.1	38	45	0	42.6	29	L	NFKPEQDV	A	-1.6	4.08	
4	Cg2705	1	1013.4859	0.0	340	347	0	39.5	26	D	FVDWLFTS	E	1.0	3.1	
4	Cg2705	1	1019.4712	-2.3	211	218	0	28.3	26	A	NAPIWQEY	Q	-1.0	3.3	
4	Cg2705	1	1159.6237	-2.5	418	427	0	50.5	28	A	SGKLKWEDVV	K	-0.5	6.98	
4	Cg2705	1	1169.5757	-1.5	338	346	0	44.1	27	T	KDFVDWLFT	S	0.1	3.88	
4	Cg2705	1	1184.5383	-2.7	258	268	0	45.3	26	S	KTVSDSMAEFA	Q	-0.1	4.08	
4	Cg2705	1	1222.6234	-2.7	356	366	0	39.8	27	V	KDLGFIAPFES	Y	0.2	4.08	
4	Cg2705	1	1235.6186	-2.5	36	45	0	43.5	28	Y	FLNFKPEQDV	A	-0.6	4.08	
4	Cg2705	1	1246.4635	-0.3	99	108	0	13.9	13	I	TWQDYMADMS	D	-0.9	2.92	
4	Cg2705	1	1273.6303	-3.5	126	137	0	36.6	28	T	EDGEVRGVPFAV	E	0.0	3.82	
4	Cg2705	1	1340.7188	-0.2	114	125	0	57.6	28	A	KQLTDDIPPLTT	E	-0.6	3.88	
4	Cg2705	1	1385.6867	-1.0	356	367	0	48.9	29	V	KDLGFIAPFESY	T	0.1	4.08	
4	Cg2705	1	1412.6419	-1.0	370	382	0	34.6	26	A	ENTPNDPLSEQVA	E	-1.2	2.94	
4	Cg2705	1	1445.7402	-2.3	79	91	0	31.5	30	A	EIGKDEAPTLFQV	N	-0.3	3.82	
4	Cg2705	1	1484.6797	-3.2	199	210	0	33.1	26	T	SGEDWRWQTHLA	N	-1.4	5.22	
4	Cg2705	2	1490.6929	-0.2	144	155	0	33.2	27	I	YNDEIFDKYIAT	S	-0.6	3.7	
4	Cg2705	2	1496.642	-3.3	215	226	0	30.1	23	I	WQEYQDKGVEDT	N	-2.0	3.58	
4	Cg2705	1	1552.7443	-3.4	254	268	0	53.6	28	S	LAPSKTVSDSMAEFA	Q	0.2	4.08	
4	Cg2705	1	1557.7715	-5.0	356	369	0	35.9	29	V	KDLGFIAPFESYTA	E	0.1	4.08	
4	Cg2705	1	1563.6374	-1.6	96	108	0	32.2	19	A	GFITWQDYMADMS	D	-0.1	2.92	
4	Cg2705	2	1577.7249	1.2	144	156	0	31.0	27	I	YNDEIFDKYIATS	G	-0.6	3.7	
4	Cg2705	1	1579.7518	-3.4	38	50	0	44.3	28	L	NFKPEQDVAYQEI	A	-1.1	3.82	
4	Cg2705	1	1584.7267	-2.8	368	382	0	51.7	26	Y	TAENTPNDPLSEQVA	E	-1.0	2.94	
4	Cg2705	1	1612.7216	-2.7	370	384	0	36.3	25	A	ENTPNDPLSEQVAEA	I	-1.2	2.88	
4	Cg2705	1	1650.7889	-1.6	38	51	0	38.9	28	L	NFKPEQDVAYQEIA	K	-0.9	3.82	
4	Cg2705	2	1690.809	0.6	143	156	0	33.4	29	I	IYNDEIFDKYIATS	G	-0.3	3.7	
4	Cg2705	1	1712.8046	-1.8	333	346	0	41.0	27	V	DQQATKDFVDWLFT	S	-0.6	3.6	
4	Cg2705	1	1725.8057	-3.8	370	385	0	40.9	27	A	ENTPNDPLSEQVAEAI	A	-0.8	2.88	
4	Cg2705	1	1739.84	3.0	167	181	0	49.4	29	I	TSYQKLKEVAEDMQA	K	-1.0	4.44	
4	Cg2705	1	1747.7901	-1.4	367	382	0	47.6	26	S	YTAENTPNDPLSEQVA	E	-1.0	2.94	
4	Cg2705	1	1749.7781	-3.8	274	288	0	32.7	24	A	MVQNGNWAWSQISET	S	-0.6	3.3	
4	Cg2705	1	1784.8064	-2.5	368	384	0	35.0	26	Y	TAENTPNDPLSEQVAEA	I	-1.0	2.88	
4	Cg2705	2	1785.8434	-1.2	196	210	0	51.9	28	T	SLTSGEDWRWQTHLA	N	-0.9	5.22	
4	Cg2705	2	1788.7955	-1.3	403	417	0	46.6	25	S	QQFKDDFGQDLSQYA	S	-1.3	3.6	
4	Cg2705	1	1799.8367	-3.3	333	347	0	55.3	27	V	DQQATKDFVDWLFTS	E	-0.6	3.6	
4	Cg2705	1	1820.8152	-3.5	273	288	0	42.7	25	A	AMVQNGNWAWSQISET	S	-0.5	3.3	
4	Cg2705	2	1849.921	-2.4	38	53	0	58.0	29	L	NFKPEQDVAYQEIAKA	Y	-0.9	4.44	
4	Cg2705	2	1852.8115	-0.5	215	229	0	66.8	24	I	WQEYQDKGVEDTNEI	E	-1.8	3.5	
4	Cg2705	1	1871.9781	-3.3	350	366	0	76.2	30	A	GKEHVVKDLGFIAPFES	Y	0.0	5.34	
4	Cg2705	1	1891.8588	-0.6	211	226	0	75.3	27	A	NAPIWQEYQDKGVEDT	N	-1.4	3.58	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
4	Cg2705	1	1897.8905	-3.6	368	385	0	36.1	28	Y	TAENTPNDPLSEQVAEAI	A	-0.7	2.88	
4	Cg2705	2	1936.9564	-2.5	254	272	0	92.4	29	S	LAPSKTVSDSMAEFAQGKA	A	-0.2	6.98	
4	Cg2705	1	1947.8698	-3.0	367	384	0	41.3	24	S	YTAENTPNDPLSEQVAEA	I	-1.0	2.88	
4	Cg2705	2	1973.9232	-2.0	194	210	0	60.9	27	A	STSLTSGEDWRWQTHLA	N	-0.9	5.22	
4	Cg2705	2	2003.9849	-0.7	299	315	0	61.7	30	I	KFLPMYMGLPDEEKHGI	N	-0.5	5.34	
4	Cg2705	2	2060.9538	-0.5	367	385	0	36.4	27	S	YTAENTPNDPLSEQVAEAI	A	-0.7	2.88	
4	Cg2705	2	2090.9738	-0.5	386	402	0	75.9	28	I	ANKDLTTYPWNFQYFPS	Q	-0.9	6.62	
4	Cg2705	2	2107.015	-0.2	138	155	0	36.9	29	V	EGFGIIYNDEIFDKYIAT	S	0.0	3.58	
4	Cg2705	2	2194.047	-1.8	138	156	0	54.0	29	V	EGFGIIYNDEIFDKYIATS	G	0.0	3.58	
4	Cg2705	2	2215.9546	-1.9	215	232	0	56.2	22	I	WQEYQDKGVEDTNEIEFS	Y	-1.6	3.44	
4	Cg2705	3	2217.0962	0.4	299	317	0	41.3	30	I	KFLPMYMGLPDEEKHGINV	G	-0.4	5.34	
4	Cg2705	2	2227.1009	-0.6	117	137	0	50.8	30	L	TDDIPPLTTEDGEVRGVPFAV	E	-0.2	3.42	
4	Cg2705	2	2248.0284	-2.9	211	229	0	61.1	26	A	NAPIWQEYQDKGVEDTNEI	E	-1.3	3.5	
4	Cg2705	2	2390.0712	-1.9	88	108	0	26.4	25	T	LFQVNGPAGFITWQDYMADMS	D	0.1	2.92	
4	Cg2705	2	2426.2329	-1.7	114	135	0	67.6	30	A	KQLTDDIPPLTTEDGEVRGVPF	A	-0.6	3.84	
4	Cg2705	2	2596.3385	-1.4	114	137	0	72.9	30	A	KQLTDDIPPLTTEDGEVRGVPFAV	E	-0.3	3.84	
4	Cg2705	2	2611.1714	-0.7	211	232	0	49.0	25	A	NAPIWQEYQDKGVEDTNEIEFS	Y	-1.2	3.44	
4	Cg2705	2	2716.214	-0.9	326	349	0	31.6	24	V	NSEASEVDQQATKDFVDWLFTSEA	G	-0.7	3.38	
4	Cg2705	2	2780.3902	-1.7	167	191	0	51.1	31	I	TSYQKLKEVAEDMQAKKDELGIEGA	F	-0.9	4.44	
4	Cg2705	2	2905.2939	-1.3	88	113	0	48.4	24	T	LFQVNGPAGFITWQDYMADMSDTEVA	K	0.0	2.78	
4	Cg2705	2	3152.4826	-2.6	356	384	0	50.3	29	V	KDLGFIAPFESYTAENTPNDPLSEQVAEA	I	-0.5	3.44	
4	Cg2705	2	3265.5666	-1.6	356	385	0	47.9	30	V	KDLGFIAPFESYTAENTPNDPLSEQVAEAI	A	-0.4	3.44	
4	Cg2705	3	3365.5688	-1.8	326	355	0	78.3	27	V	NSEASEVDQQATKDFVDWLFTSEAGKEHVV	K	-0.7	3.96	
4	Cg2705	3	3453.7184	-3.1	161	191	0	90.9	31	I	KSTDEITSYQKLKEVAEDMQAKKDELGIEGA	F	-1.0	4.34	
4	Cg2705	2	3499.5997	1.5	386	414	0	42.0	26	I	ANKDLTTYPWNFQYFPSQQFKDDFGQDLS	Q	-1.1	3.88	
4	Cg2705	2	3612.6838	-0.8	385	414	0	32.8	28	A	IANKDLTTYPWNFQYFPSQQFKDDFGQDLS	Q	-0.9	3.88	
4	Cg2705	2	3845.7441	-4.1	79	113	0	39.7	24	A	EIGKDEAPTLFQVNGPAGFITWQDYMADMSDTEVA	K	-0.3	3.28	
4	Cg2705	3	3861.7587	-3.0	386	417	0	57.7	25	I	ANKDLTTYPWNFQYFPSQQFKDDFGQDLSQYA	S	-1.1	3.88	
4	Cg2705	2	3974.8428	-0.2	385	417	0	42.0	27	A	IANKDLTTYPWNFQYFPSQQFKDDFGQDLSQYA	S	-0.9	3.88	
5	Cg3009	1	657.3697	0.5	24	29	0	38.0	32	A	LQSIPT	L	0.3	6.02	
5	Cg3009	1	664.3181	-0.2	16	22	0	32.0	27	T	FGGNIGT	A	0.3	6.02	
5	Cg3009	1	672.4058	1.5	30	35	0	31.8	24	T	LLDSIL	N	1.9	3.1	
5	Cg3009	2	715.448	1.7	5	10	0	28.5	25	S	LLKETL	G	0.6	6.94	
5	Cg3009	2	728.4068	1.0	23	29	0	37.7	30	T	ALQSIPT	L	0.5	6.02	
5	Cg3009	1	757.4222	0.4	28	34	0	31.4	29	I	PTLLDSI	L	0.8	3.1	
5	Cg3009	1	786.3184	-0.4	12	18	0	38.8	22	G	NYETFGG	N	-1.0	3.3	
5	Cg3009	1	843.3399	-0.7	11	18	0	33.9	21	L	GNYETFGG	N	-0.9	3.3	
5	Cg3009	1	870.5062	0.2	27	34	0	44.5	27	S	IPTLLDSI	L	1.3	3.1	
5	Cg3009	1	870.5062	-1.1	28	35	0	32.4	27	I	PTLLDSIL	N	1.2	3.1	
5	Cg3009	1	956.424	-1.4	10	18	0	29.8	25	T	LGNYETFGG	N	-0.4	3.3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
5	Cg3009	1	981.4039	-0.5	49	57	0	27.0	23	T	GENLDNFSS	-	-1.0	3	
5	Cg3009	1	1044.4553	-0.4	37	45	0	24.9	24	N	FFDNFGDLA	D	0.3	2.92	
5	Cg3009	1	1070.4669	-0.2	12	21	0	32.2	24	G	NYETFGGNIG	T	-0.6	3.3	
5	Cg3009	1	1080.5855	-1.0	30	38	0	31.1	26	T	LLDSILNFF	D	1.5	3.1	
5	Cg3009	1	1087.4611	1.0	36	44	0	37.6	23	L	NFFDNFGDL	A	-0.2	2.92	
5	Cg3009	1	1158.4982	-0.1	36	45	0	39.5	22	L	NFFDNFGDLA	D	0.0	2.92	
5	Cg3009	1	1171.5146	0.1	12	22	0	37.1	24	G	NYETFGGNIGT	A	-0.6	3.3	
5	Cg3009	1	1198.6809	-1.1	24	34	0	33.3	27	A	LQSIPTLLDSI	L	0.9	3.1	
5	Cg3009	2	1200.5452	-0.4	35	44	0	25.7	25	I	LNFFDNFGDL	A	0.2	2.92	
5	Cg3009	1	1228.536	0.1	11	22	0	30.3	23	L	GNYETFGGNIGT	A	-0.6	3.3	
5	Cg3009	1	1240.5724	0.5	10	21	0	30.1	26	T	LGNYETFGGNIG	T	-0.3	3.3	
5	Cg3009	1	1242.5517	-1.2	12	23	0	46.2	25	G	NYETFGGNIGTA	L	-0.4	3.3	
5	Cg3009	2	1271.5823	0.1	35	45	0	74.8	26	I	LNFFDNFGDLA	D	0.3	2.92	
5	Cg3009	2	1279.666	0.4	5	15	0	63.1	27	S	LLKETLGNYET	F	-0.6	4.26	
5	Cg3009	1	1298.5263	-0.2	46	57	0	30.0	20	A	DTTGENLDNFSS	-	-1.2	2.88	
5	Cg3009	1	1299.5732	-1.7	11	23	0	30.5	25	L	GNYETFGGNIGTA	L	-0.4	3.3	
5	Cg3009	1	1314.6092	-1.1	7	18	0	60.6	26	L	KETLGNYETFGG	N	-1.0	4.26	
5	Cg3009	2	1341.6201	0.5	10	22	0	75.9	27	T	LGNYETFGGNIGT	A	-0.3	3.3	
5	Cg3009	1	1361.5776	-0.4	37	48	0	35.8	23	N	FFDNFGDLADTT	G	-0.2	2.82	
5	Cg3009	2	1412.6572	0.7	10	23	0	44.9	27	T	LGNYETFGGNIGTA	L	-0.1	3.3	
5	Cg3009	1	1475.6205	-1.1	36	48	0	34.3	21	L	NFFDNFGDLADTT	G	-0.4	2.82	
5	Cg3009	2	1487.6569	0.8	35	47	0	84.4	24	I	LNFFDNFGDLADT	T	-0.1	2.82	
5	Cg3009	2	1540.7773	0.4	5	18	0	89.7	29	S	LLKETLGNYETFGG	N	-0.3	4.26	
5	Cg3009	2	1586.7253	2.0	32	45	0	42.6	26	L	DSILNFFDNFGDLA	D	0.3	2.82	
5	Cg3009	2	1588.7046	2.2	35	48	0	102.6	25	I	LNFFDNFGDLADTT	G	-0.1	2.82	
5	Cg3009	2	1598.7576	0.1	7	21	0	59.5	28	L	KETLGNYETFGGNIG	T	-0.7	4.26	
5	Cg3009	2	1627.8093	0.7	4	18	0	50.7	29	L	SLLKETLGNYETFGG	N	-0.3	4.26	
5	Cg3009	2	1699.8053	0.4	7	22	0	109.1	28	L	KETLGNYETFGGNIGT	A	-0.7	4.26	
5	Cg3009	2	1701.7886	-0.2	34	48	0	31.7	27	S	ILNFFDNFGDLADTT	G	0.2	2.82	
5	Cg3009	2	1770.8424	0.2	7	23	0	102.3	28	L	KETLGNYETFGGNIGTA	L	-0.6	4.26	
5	Cg3009	2	1802.7999	0.1	32	47	0	40.9	25	L	DSILNFFDNFGDLADT	T	0.0	2.74	
5	Cg3009	2	1812.8934	2.3	30	45	0	101.6	29	T	LLDSILNFFDNFGDLA	D	0.7	2.82	
5	Cg3009	2	1824.9258	0.4	5	21	0	56.0	29	S	LLKETLGNYETFGGNIG	T	-0.2	4.26	
5	Cg3009	2	1881.9109	0.1	12	29	0	45.0	29	G	NYETFGGNIGTALQSIPT	L	-0.2	3.3	
5	Cg3009	2	1883.9265	1.8	7	24	0	47.8	29	L	KETLGNYETFGGNIGTAL	Q	-0.3	4.26	
5	Cg3009	2	1903.8476	0.6	32	48	0	105.9	25	L	DSILNFFDNFGDLADTT	G	-0.1	2.74	
5	Cg3009	2	1925.9735	-0.1	5	22	0	102.6	29	S	LLKETLGNYETFGGNIGT	A	-0.2	4.26	
5	Cg3009	2	1938.9323	-1.1	11	29	0	38.8	29	L	GNYETFGGNIGTALQSIPT	L	-0.2	3.3	
5	Cg3009	2	1997.0106	-0.3	5	23	0	106.7	30	S	LLKETLGNYETFGGNIGTA	L	-0.1	4.26	
5	Cg3009	2	2001.8956	-2.4	35	52	0	29.7	25	I	LNFFDNFGDLADTTGENL	D	-0.3	2.78	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
5	Cg3009	2	2011.9851	-0.5	7	25	0	62.9	29	L	KETLGNYETFGGNIGTALQ	S	-0.5	4.26	
5	Cg3009	2	2013.0055	-0.1	4	22	0	85.0	29	L	SLLKETLGNYETFGGNIGT	A	-0.3	4.26	
5	Cg3009	2	2028.968	0.9	30	47	0	97.2	29	T	LLDSILNFFDNFGDLADT	T	0.4	2.74	
5	Cg3009	2	2084.0426	0.1	4	23	0	65.9	29	L	SLLKETLGNYETFGGNIGTA	L	-0.2	4.26	
5	Cg3009	2	2110.0946	0.1	5	24	0	85.2	30	S	LLKETLGNYETFGGNIGTAL	Q	0.1	4.26	
5	Cg3009	2	2130.0157	0.6	30	48	0	112.1	29	T	LLDSILNFFDNFGDLADTT	G	0.3	2.74	
5	Cg3009	2	2238.1532	0.0	5	25	0	107.9	30	S	LLKETLGNYETFGGNIGTALQ	S	-0.1	4.26	
5	Cg3009	2	2410.2016	-0.3	7	29	0	79.7	30	L	KETLGNYETFGGNIGTALQSIPT	L	-0.4	4.26	
5	Cg3009	2	2452.2526	1.2	24	45	0	40.0	30	A	LQSIPTLLDSILNFFDNFGDLA	D	0.6	2.82	
5	Cg3009	2	2552.098	0.2	35	57	0	47.7	21	I	LNFFDNFGDLADTTGENLDNFSS	-	-0.5	2.72	
5	Cg3009	2	2624.3374	-0.6	22	45	0	31.1	31	G	TALQSIPTLLDSILNFFDNFGDLA	D	0.6	2.82	
5	Cg3009	2	2636.3697	-0.9	5	29	0	62.5	30	S	LLKETLGNYETFGGNIGTALQSIPT	L	0.0	4.26	
5	Cg3009	2	2840.412	0.3	23	48	0	42.1	30	T	ALQSIPTLLDSILNFFDNFGDLADTT	G	0.4	2.74	
5	Cg3009	3	3093.4091	-0.5	30	57	0	52.7	26	T	LLDSILNFFDNFGDLADTTGENLDNFSS	-	-0.1	2.66	
6	Cg2181	1	645.3122	0.2	362	366	0	25.4	25	A	QELWA	Q	-0.5	3.3	
6	Cg2181	1	686.3275	0.9	528	532	0	24.2	22	A	YYQIT	K	-0.5	5.86	
6	Cg2181	1	746.3446	-0.7	87	93	0	30.9	30	V	NDVAESI	E	-0.1	3	
6	Cg2181	1	774.3946	-0.3	153	159	0	36.3	29	S	MEGLQVV	D	1.0	3.3	
6	Cg2181	1	872.4716	-0.5	64	72	0	38.7	29	V	GGGRIVDSI	F	0.4	6.78	
6	Cg2181	1	906.4487	2.5	184	191	0	36.6	27	A	FFPLPESA	F	0.5	3.3	
6	Cg2181	1	950.4246	-0.3	124	131	0	36.5	25	V	NAWNYNVA	N	-0.6	5.92	
6	Cg2181	1	1008.4553	0.7	372	380	0	38.7	27	I	SPWSGEFSI	S	-0.2	3.3	
6	Cg2181	2	1074.5305	-0.7	316	324	0	33.6	29	A	VNRDEITQT	I	-1.2	4.08	
6	Cg2181	1	1098.4942	-0.2	341	351	0	32.1	25	V	IDGHSDSLQGA	D	-0.5	3.88	
6	Cg2181	1	1108.5553	0.3	444	454	0	32.7	28	G	NFLGPLYGTGA	G	0.4	5.92	
6	Cg2181	2	1114.5731	0.0	277	287	0	29.0	28	L	SGRSINQPSAV	F	-0.5	11.04	
6	Cg2181	1	1115.571	-1.3	252	261	0	30.3	30	A	DLLSDNLDVL	D	0.5	2.82	
6	Cg2181	1	1123.5146	-0.1	508	518	0	26.6	26	A	VGGYSTNVDNV	E	-0.1	3.1	
6	Cg2181	2	1131.4945	1.0	380	390	0	31.7	24	S	ISYNADGGHQA	W	-0.8	4.94	
6	Cg2181	1	1177.5615	-1.3	352	361	0	29.5	29	A	DVLTYDPERA	Q	-0.9	3.7	
6	Cg2181	1	1187.6146	-1.0	316	325	0	50.3	29	A	VNRDEITQTI	F	-0.7	4.08	
6	Cg2181	1	1201.5615	-0.2	362	371	0	33.9	27	A	QELWAQADEI	S	-0.7	2.94	
6	Cg2181	2	1360.6735	-0.8	221	233	0	57.4	29	T	IVPNADYTGGRQA	Q	-0.5	6.7	
6	Cg2181	1	1365.6089	-1.5	369	380	0	31.1	26	A	DEISPWSGEFSI	S	-0.3	2.94	
6	Cg2181	1	1369.5496	-1.2	192	203	0	36.0	19	A	FDDMDAFGENPI	G	-0.5	2.78	
6	Cg2181	2	1377.6776	-0.6	105	117	0	61.7	29	T	IKDGQTFTDGTPV	T	-0.6	3.88	
6	Cg2181	2	1381.6474	0.2	338	351	0	66.2	27	T	SPVIDGHSDSLQGA	D	-0.3	3.88	
6	Cg2181	2	1429.7161	0.0	59	72	0	78.5	28	G	NTNEVGGGRIVDSI	F	-0.3	4.08	
6	Cg2181	2	1436.646	1.5	368	380	0	36.4	26	Q	ADEISPWSGEFSI	S	-0.2	2.94	
6	Cg2181	1	1443.6729	0.4	255	268	0	29.6	27	L	SDNLDVLDAIPDSA	F	-0.1	2.74	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
6	Cg2181	2	1461.7212	-0.7	220	233	0	31.8	29	A	TIVPNADYTGGRQA	Q	-0.6	6.7	
6	Cg2181	2	1472.6783	0.3	269	281	0	77.2	27	A	FSSFEDELSGRSI	N	-0.4	3.82	
6	Cg2181	2	1478.7253	-2.6	104	117	0	41.6	29	I	TIKDGQTFTDGTPV	T	-0.6	3.88	
6	Cg2181	2	1489.6222	-0.1	381	394	0	29.9	21	I	SYNADGGHQAWVDA	T	-0.8	3.88	
6	Cg2181	2	1543.7882	0.4	167	179	0	74.8	30	V	ELTQPESDFPLRL	G	-0.7	3.82	
6	Cg2181	1	1549.6896	-1.4	475	489	0	56.9	26	A	NAADVDASTPLYNEA	Q	-0.4	2.88	
6	Cg2181	2	1590.6699	-0.4	381	395	0	51.0	21	I	SYNADGGHQAWVDAT	A	-0.8	3.88	
6	Cg2181	2	1624.7733	0.1	326	340	0	51.3	29	I	FEGTRTPATDFTSPV	I	-0.5	4.08	
6	Cg2181	2	1664.7642	-0.8	271	285	0	45.7	27	S	SFEDELSGRSINQPS	A	-1.1	3.82	
6	Cg2181	2	1708.8268	0.5	338	354	0	68.1	29	T	SPVIDGHSDSLQGADVL	T	0.0	3.6	
6	Cg2181	2	1737.8574	-0.4	325	340	0	34.7	29	T	IFEGTRTPATDFTSPV	I	-0.2	4.08	
6	Cg2181	2	1741.7683	0.3	78	93	0	26.2	25	V	YYDVDGSPVNDVAESI	E	-0.3	2.78	
6	Cg2181	2	1744.7693	-0.6	503	518	0	33.8	24	T	WYSNAVGGYSTNVDNV	E	-0.4	3.1	
6	Cg2181	2	1784.7489	-0.1	455	471	0	50.6	21	A	GSNDGDYSNPDFDAKLA	E	-1.2	3.42	
6	Cg2181	1	1784.868	-2.9	252	268	0	40.0	29	A	DLLSDNLDVLDAIPDSA	F	0.2	2.68	
6	Cg2181	2	1834.8697	-1.4	271	287	0	37.7	28	S	SFEDELSGRSINQPSAV	F	-0.6	3.82	
6	Cg2181	2	1845.8381	-1.7	334	351	0	30.1	26	A	TDFTSPVIDGHSDSLQGA	D	-0.4	3.6	
6	Cg2181	2	1898.8646	-1.1	269	285	0	32.2	26	A	FSSFEDELSGRSINQPS	A	-0.8	3.82	
6	Cg2181	1	1919.8748	-4.0	475	492	0	47.9	26	A	NAADVDASTPLYNEAQEI	L	-0.5	2.84	
6	Cg2181	2	2090.0055	-1.1	249	268	0	34.5	29	S	AYADLLSDNLDVLDAIPDSA	F	0.3	2.68	
6	Cg2181	2	2098.9306	-1.0	192	210	0	62.2	25	A	FDDMDAFGENPIGNGPYKL	Q	-0.7	3.5	
6	Cg2181	2	2114.9294	-1.5	211	228	0	23.1	23	L	QEWNHNQDATIVPNADYT	G	-1.3	3.7	
6	Cg2181	2	2138.9797	0.7	288	306	0	27.7	27	V	FQSFTIPESLEHFSGEEGV	L	-0.3	3.78	
6	Cg2181	2	2173.0175	-0.3	334	354	0	35.8	28	A	TDFTSPVIDGHSDSLQGADVL	T	-0.1	3.42	
6	Cg2181	2	2192.0062	0.8	362	380	0	57.8	27	A	QELWAQADEISPWSGEFSI	S	-0.4	2.88	
6	Cg2181	2	2257.9878	-1.2	184	203	0	70.1	23	A	FFPLPESAFDDMDAFGENPI	G	-0.1	2.76	
6	Cg2181	2	2273.9827	-2.2	184	203	0	28.7	22	A	FFPLPESAFDDMDAFGENPI	G	-0.1	2.76	Oxidation (M)
6	Cg2181	2	2329.0249	-3.1	183	203	0	69.4	23	S	AFFPLPESAFDDMDAFGENPI	G	0.0	2.76	
6	Cg2181	2	2514.1286	1.0	78	100	0	146.9	25	V	YYDVDGSPVNDVAESIELEGDKT	Y	-0.7	3.28	
6	Cg2181	3	2584.1691	-0.8	211	233	0	44.0	25	L	QEWNHNQDATIVPNADYTGGRQA	Q	-1.4	4.3	
6	Cg2181	2	2633.3045	-0.1	47	72	0	44.7	31	V	NGTEPQNPLVPGNTNEVGGGRIVDSI	F	-0.6	3.82	
6	Cg2181	3	2705.2569	1.7	326	351	0	29.4	28	I	FEGTRTPATDFTSPVIDGHSDSLQGA	D	-0.5	3.96	
6	Cg2181	3	2818.341	-1.5	325	351	0	31.6	29	T	IFEGTRTPATDFTSPVIDGHSDSLQGA	D	-0.3	3.96	
6	Cg2181	2	2875.2937	-0.9	444	471	0	78.5	25	G	NFLGPLYGTGAGSNDGDYSNPDFDAKLA	E	-0.6	3.42	
6	Cg2181	2	2987.3688	2.8	184	210	0	44.9	27	A	FFPLPESAFDDMDAFGENPIGNGPYKL	Q	-0.3	3.42	
6	Cg2181	3	3032.4364	-2.2	326	354	0	47.1	29	I	FEGTRTPATDFTSPVIDGHSDSLQGADVL	T	-0.3	3.76	
7	Cg2120	1	553.3839	1.1	462	466	0	26.4	24	V	VIIPL	L	3.1	6.02	
7	Cg2120	1	640.4523	-0.9	504	509	0	28.6	25	A	ILLGII	L	3.5	6.02	
7	Cg2120	1	651.3665	0.6	476	480	0	24.1	17	V	MYLLL	G	2.4	5.92	
7	Cg2120	1	703.3541	1.1	516	522	0	30.0	30	C	FDLGGPV	N	0.7	3.1	

hit	**accession**	**z**	**mass**	**ppm**	**start**	**end**	**mc**	**score**	**id**	**-**	**sequence**	**+**	**gravy**	**pI**	**modification**
7	Cg2120	1	741.3697	1.3	526	532	0	35.1	24	A	AYLFGTA	G	1.1	5.92	
7	Cg2120	1	758.4327	1.3	581	587	0	52.4	27	S	SWLLGLA	F	1.6	6.02	
7	Cg2120	1	767.5157	0.9	462	468	0	20.0	19	V	VIIPLLT	S	2.6	6.02	
7	Cg2120	1	796.4517	1.0	552	559	0	25.1	22	A	GMVPPIAL	S	1.6	6.02	
7	Cg2120	2	835.4188	-0.6	31	38	0	45.9	29	V	IFDAGRAS	S	0.2	6.78	
7	Cg2120	2	907.5239	0.3	406	415	0	33.7	23	A	LAGRPGIAPG	F	0.3	11.04	
7	Cg2120	1	910.476	-1.1	150	158	0	33.7	24	N	PAPKTTEPA	A	-1.1	6.94	
7	Cg2120	1	911.4753	0.0	526	534	0	33.4	28	A	AYLFGTAGL	S	1.2	5.92	
7	Cg2120	1	912.4415	-0.1	316	323	0	39.3	26	V	SYMVPFVA	A	1.4	5.92	
7	Cg2120	2	939.5389	-0.6	147	155	0	33.7	26	A	VLNPAPKTT	E	-0.2	10.1	
7	Cg2120	2	984.5393	0.3	599	607	0	29.0	28	A	ADPFRVIPA	M	0.4	6.78	
7	Cg2120	1	1107.5601	-2.6	588	598	0	31.9	28	A	FVSEGAIPFAA	A	1.2	3.3	
7	Cg2120	1	1122.5016	-0.7	490	499	0	28.0	27	T	GLQDWLSSMS	G	-0.1	3.1	
7	Cg2120	2	1125.603	0.1	145	155	0	80.0	27	V	DAVLNPAPKTT	E	-0.4	6.76	
7	Cg2120	1	1131.5659	-2.8	135	144	0	31.6	29	A	TTEQEIVDVV	D	0.2	2.94	
7	Cg2120	2	1137.603	-1.0	148	158	0	56.6	27	V	LNPAPKTTEPA	A	-0.9	6.94	
7	Cg2120	1	1138.6598	-1.8	219	229	0	31.5	23	S	SAVTPVDPKII	E	0.6	6.76	
7	Cg2120	1	1198.583	-0.5	355	366	0	28.6	28	T	NLPGNTVDVDGV	A	-0.1	2.92	
7	Cg2120	1	1205.5201	-2.0	87	98	0	47.0	24	V	DFSGPDGDANLV	F	-0.4	2.82	
7	Cg2120	1	1229.5961	-2.8	263	273	0	35.8	27	A	INEPAKMIDEA	I	-0.5	3.82	
7	Cg2120	2	1236.6714	-0.2	147	158	0	46.3	26	A	VLNPAPKTTEPA	A	-0.5	6.94	
7	Cg2120	1	1336.6333	-2.7	486	497	0	28.1	28	A	SIMTGLQDWLSS	M	0.2	3.1	
7	Cg2120	2	1409.7766	1.2	219	232	0	41.9	25	S	SAVTPVDPKIIEAA	D	0.5	4.08	
7	Cg2120	2	1410.7719	1.3	216	229	0	29.5	27	T	QGSSAVTPVDPKII	E	0.2	6.76	
7	Cg2120	1	1416.6984	0.0	135	147	0	35.9	29	A	TTEQEIVDVVDAV	L	0.3	2.84	
7	Cg2120	1	1422.7354	-2.2	145	158	0	40.6	28	V	DAVLNPAPKTTEPA	A	-0.5	4.08	
7	Cg2120	2	1444.7157	0.1	39	52	0	65.1	29	S	SADALAKDALDREA	K	-0.5	3.96	
7	Cg2120	1	1484.7544	-2.4	263	276	0	29.5	28	A	INEPAKMIDEAIAA	S	0.2	3.82	
7	Cg2120	2	1489.7049	0.2	84	98	0	63.3	28	S	KGVDFSGPDGDANLV	F	-0.3	3.6	
7	Cg2120	2	1551.7417	0.5	11	24	0	103.8	29	V	RLDVDFGDSTTDVI	N	-0.1	3.42	
7	Cg2120	2	1576.7369	0.0	83	98	0	42.8	28	L	SKGVDFSGPDGDANLV	F	-0.3	3.6	
7	Cg2120	2	1694.9091	-0.5	219	235	0	40.0	28	S	SAVTPVDPKIIEAADAV	I	0.6	3.7	
7	Cg2120	2	1759.8224	-0.2	197	212	0	58.7	27	A	DSLTQNAEGRDDVELV	V	-0.8	3.42	
7	Cg2120	2	1845.9221	-1.5	81	98	0	66.1	30	A	RLSKGVDFSGPDGDANLV	F	-0.3	4.18	
7	Cg2120	2	2037.063	0.3	135	153	0	39.0	29	A	TTEQEIVDVVDAVLNPAPK	T	0.0	3.58	
7	Cg2120	2	2239.1584	-1.4	135	155	0	82.1	30	A	TTEQEIVDVVDAVLNPAPKTT	E	-0.1	3.58	
7	Cg2120	2	2355.203	-0.9	39	62	0	41.5	30	S	SADALAKDALDREAKSGTGVPGQV	A	-0.4	4.46	
7	Cg2120	2	2536.2908	-3.0	135	158	0	56.6	30	A	TTEQEIVDVVDAVLNPAPKTTEPA	A	-0.2	3.5	
7	Cg2120	2	2597.261	-1.1	14	38	0	75.7	30	D	VDFGDSTTDVINNLATVIFDAGRAS	S	0.3	3.42	
7	Cg2120	2	2680.3807	-1.7	131	155	0	82.2	31	A	LQEATTEQEIVDVVDAVLNPAPKTT	E	-0.1	3.5	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
7	Cg2120	2	2712.2879	-2.1	13	38	0	99.4	29	L	DVDFGDSTTDVINNLATVIFDAGRAS	S	0.1	3.3	
7	Cg2120	2	2977.5132	-1.8	131	158	0	64.8	31	A	LQEATTEQEIVDVVDAVLNPAPKTTEPA	A	-0.2	3.44	
7	Cg2120	2	2981.4731	-0.7	11	38	0	68.2	31	V	RLDVDFGDSTTDVINNLATVIFDAGRAS	S	0.1	3.7	
8	Cg2911	1	551.3683	2.2	9	13	0	25.9	18	L	PILPL	V	1.8	6.02	
8	Cg2911	1	765.5	-1.6	7	13	0	23.3	13	W	TLPILPL	V	1.7	6.02	
8	Cg2911	2	791.3813	0.4	259	265	0	31.3	30	L	IYNPQSA	S	-0.6	5.92	
8	Cg2911	1	858.4698	0.5	84	91	0	29.1	29	V	SEADIIIV	G	1.5	3	
8	Cg2911	1	921.4443	-0.8	164	171	0	32.2	29	V	AEEFAEKV	T	-0.5	3.96	
8	Cg2911	1	972.44	-0.4	172	180	0	26.7	24	V	TELDPEAQA	D	-1.0	2.94	
8	Cg2911	1	1076.5139	-1.1	41	50	0	34.4	29	V	TSTQVWADVA	E	0.2	3.1	
8	Cg2911	1	1088.535	-4.4	103	111	0	33.5	29	G	TLEDDDRII	H	-0.7	3.5	
8	Cg2911	1	1192.5612	-1.6	284	293	0	45.7	29	V	VEIYETPQNT	E	-1.0	3.12	
8	Cg2911	1	1236.5874	-0.6	161	171	0	40.5	29	V	SEVAEEFAEKV	T	-0.4	3.8	
8	Cg2911	1	1254.6707	-2.2	53	64	0	35.7	27	A	VAPDVDIEAIIT	G	1.1	2.88	
8	Cg2911	2	1256.531	0.0	65	76	0	43.3	23	T	GGDIDPHSFEPS	A	-1.0	3.7	
8	Cg2911	1	1259.5517	-2.6	172	183	0	37.4	24	V	TELDPEAQADAT	A	-0.9	2.84	
8	Cg2911	1	1276.5936	1.3	41	52	0	28.4	28	V	TSTQVWADVAEA	V	0.0	3	
8	Cg2911	2	1353.5871	-1.0	219	230	0	35.0	25	S	DMVESTPEGYRA	T	-1.0	3.82	
8	Cg2911	1	1397.7766	0.0	271	283	0	58.5	28	T	SLKDLAEEKGIPV	V	-0.2	4.44	
8	Cg2911	2	1454.6347	0.4	219	231	0	25.2	25	S	DMVESTPEGYRAT	T	-1.0	3.82	
8	Cg2911	1	1519.7155	-0.7	245	258	0	31.0	28	A	SFQDAINNGDLDVL	I	-0.1	2.82	
8	Cg2911	2	1678.7257	-0.8	217	231	0	46.1	23	S	HSDMVESTPEGYRAT	T	-1.1	4.42	
8	Cg2911	2	1738.9716	0.6	271	286	0	59.1	26	T	SLKDLAEEKGIPVVEI	Y	0.1	4.16	
8	Cg2911	2	1755.7985	-1.6	218	233	0	48.0	27	H	SDMVESTPEGYRATTL	S	-0.6	3.82	
8	Cg2911	2	1775.8578	1.7	55	71	0	47.7	29	A	PDVDIEAIITGGDIDPH	S	-0.1	3.36	
8	Cg2911	1	1839.8891	-2.4	294	310	0	48.9	29	T	ENFLDAFTKAVDDLTAA	T	0.1	3.5	
8	Cg2911	2	1878.8418	0.1	215	231	0	35.9	25	I	LSHSDMVESTPEGYRAT	T	-0.8	4.42	
8	Cg2911	2	1940.9367	-0.6	294	311	0	69.3	29	T	ENFLDAFTKAVDDLTAAT	N	0.1	3.5	
8	Cg2911	2	1945.9633	0.9	53	71	0	116.4	30	A	VAPDVDIEAIITGGDIDPH	S	0.2	3.36	
8	Cg2911	2	2028.0574	-2.3	188	204	0	92.0	30	T	KMDELHNQIHDLPAVRI	A	-0.6	6.02	
8	Cg2911	2	2099.0946	1.2	188	205	0	40.2	30	T	KMDELHNQIHDLPAVRIA	Q	-0.4	6.02	
8	Cg2911	2	2156.0273	-0.6	292	311	0	91.5	29	Q	NTENFLDAFTKAVDDLTAAT	N	-0.2	3.5	
8	Cg2911	2	2191.0168	0.5	161	180	0	39.6	27	V	SEVAEEFAEKVTELDPEAQA	D	-0.6	3.44	
8	Cg2911	2	2200.9913	-1.1	92	111	0	118.7	26	V	GGGGYDSWLYGTLEDDDRII	H	-0.6	3.36	
8	Cg2911	2	2282.1067	-1.1	294	314	0	89.9	30	T	ENFLDAFTKAVDDLTAATNQV	-	-0.1	3.5	
8	Cg2911	2	2329.1114	1.1	284	303	0	69.9	29	V	VEIYETPQNTENFLDAFTKA	V	-0.6	3.68	
8	Cg2911	3	2400.2583	-0.9	184	204	0	64.6	30	T	AVTTKMDELHNQIHDLPAVRI	A	-0.2	6.02	
8	Cg2911	2	2471.2955	0.3	184	205	0	40.8	30	T	AVTTKMDELHNQIHDLPAVRIA	Q	-0.1	6.02	
8	Cg2911	2	2493.1911	-1.2	53	76	0	29.3	29	A	VAPDVDIEAIITGGDIDPHSFEPS	A	0.0	3.32	
8	Cg2911	2	2497.1973	-2.6	292	314	0	93.8	29	Q	NTENFLDAFTKAVDDLTAATNQV	-	-0.3	3.5	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
8	Cg2911	2	2665.2759	-3.2	53	78	0	61.5	29	A	VAPDVDIEAIITGGDIDPHSFEPSAT	D	0.1	3.32	
8	Cg2911	2	2673.2446	0.0	287	310	0	35.8	28	I	YETPQNTENFLDAFTKAVDDLTAA	T	-0.5	3.42	
8	Cg2911	2	2770.2708	-1.8	156	180	0	38.2	26	Y	STEYVSEVAEEFAEKVTELDPEAQA	D	-0.6	3.38	
8	Cg2911	2	2853.3239	-1.0	205	230	0	83.8	27	I	AQTEPIADHILSHSDMVESTPEGYRA	T	-0.6	4.28	
8	Cg2911	2	2954.3716	-4.2	205	231	0	68.3	27	I	AQTEPIADHILSHSDMVESTPEGYRAT	T	-0.6	4.28	
8	Cg2911	2	3168.5033	-3.0	205	233	0	79.9	29	I	AQTEPIADHILSHSDMVESTPEGYRATTL	S	-0.5	4.28	
8	Cg2911	2	3456.6573	-1.0	284	314	0	61.3	30	V	VEIYETPQNTENFLDAFTKAVDDLTAATNQV	-	-0.4	3.38	
9	Cg2925	1	551.3683	2.2	116	120	0	25.9	18	V	PLIPI	L	1.9	6.02	
9	Cg2925	1	600.302	1.3	555	560	0	26.2	23	S	GHAFAV	R	1.2	7.84	
9	Cg2925	1	628.3544	-0.3	131	136	0	43.3	28	I	NNVLVA	Q	1.2	6.02	
9	Cg2925	1	641.3748	-0.5	539	544	0	39.5	29	G	QLVSPV	S	1.1	6.02	
9	Cg2925	1	642.3701	-2.6	647	652	0	37.8	29	A	NLLNVA	K	1.1	6.02	
9	Cg2925	1	702.3952	0.9	112	117	0	28.2	24	A	DIFVPL	I	1.7	3.1	
9	Cg2925	1	733.401	-1.0	221	227	0	34.5	29	S	LFGLDVA	Q	1.8	3.1	
9	Cg2925	1	764.3891	-0.1	58	64	0	29.4	25	T	GGMFQII	V	1.3	6.02	
9	Cg2925	1	803.4429	0.5	261	267	0	40.0	25	A	DFLITPV	L	1.4	3.1	
9	Cg2925	1	826.4913	-0.6	537	544	0	41.7	27	T	KGQLVSPV	S	0.3	10.1	
9	Cg2925	1	836.3916	-1.1	74	80	0	38.4	29	V	FKELDDA	T	-0.9	3.7	
9	Cg2925	1	866.4174	1.5	299	306	0	29.4	26	G	LYDFGGPV	G	0.5	3.1	
9	Cg2925	2	893.4243	0.4	65	73	0	47.8	29	I	VGPGDVDHV	F	0.0	3.88	
9	Cg2925	1	918.427	-0.3	574	581	0	50.1	29	L	MHIGFDTV	N	0.7	4.94	
9	Cg2925	1	930.5022	-1.0	89	96	0	51.5	29	S	TEQLKDVV	A	-0.4	4.08	
9	Cg2925	1	942.5572	-0.2	121	130	0	27.1	27	I	LVGGGLLMAI	N	2.3	6.02	
9	Cg2925	1	1003.4975	-0.2	137	145	0	32.7	30	A	QDLFGPQSL	V	-0.3	3.1	
9	Cg2925	1	1065.4978	-0.9	635	644	0	29.2	28	V	NTYGLGEIEA	G	-0.3	3.12	
9	Cg2925	1	1072.6321	-1.5	165	174	0	42.9	25	S	APFAFLPVLV	G	2.2	6.02	
9	Cg2925	1	1076.5754	-0.7	616	625	0	29.1	28	A	GYEVTTPIVV	S	0.9	3.3	
9	Cg2925	1	1109.4344	-0.1	211	220	0	23.0	20	T	MAAGEMPMWS	L	0.2	3.3	
9	Cg2925	1	1115.5822	0.1	89	98	0	32.6	29	S	TEQLKDVVAN	N	-0.5	4.08	
9	Cg2925	1	1159.5721	-0.4	563	573	0	39.8	29	T	KAEDGSNVDIL	M	-0.4	3.7	
9	Cg2925	1	1193.5564	-0.4	635	646	0	33.0	28	V	NTYGLGEIEAGA	N	-0.2	3.12	
9	Cg2925	1	1199.6146	0.5	11	21	0	51.0	28	I	LRDIGGEDNIV	A	-0.2	3.7	
9	Cg2925	1	1209.7373	-2.8	110	120	0	27.7	22	V	LADIFVPLIPI	L	2.1	3.1	
9	Cg2925	2	1270.6517	-0.4	11	22	0	34.1	29	I	LRDIGGEDNIVA	A	0.0	3.7	
9	Cg2925	2	1300.6623	-0.5	89	100	0	29.4	29	S	TEQLKDVVANNA	N	-0.5	4.08	
9	Cg2925	2	1376.7162	-0.1	160	172	0	48.6	28	I	NLMASAPFAFLPV	L	1.3	6.02	
9	Cg2925	2	1387.6943	-2.0	88	100	0	39.4	29	V	STEQLKDVVANNA	N	-0.5	4.08	
9	Cg2925	1	1421.8898	-2.8	110	122	0	18.3	18	V	LADIFVPLIPILV	G	2.4	3.1	
9	Cg2925	2	1429.699	1.2	293	306	0	70.8	29	L	AHGLQGLYDFGGPV	G	0.1	4.94	
9	Cg2925	2	1551.6941	0.3	44	57	0	59.0	26	Q	SLDDDPDLKGTFET	G	-1.1	3.36	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
9	Cg2925	2	1637.8148	-0.2	74	88	0	51.1	29	V	FKELDDATSKDIAVS	T	-0.3	3.96	
9	Cg2925	2	1639.8029	0.9	58	73	0	40.0	28	T	GGMFQIIVGPGDVDHV	F	0.6	3.88	
9	Cg2925	1	1712.9097	-2.0	131	146	0	35.4	29	I	NNVLVAQDLFGPQSLV	E	0.5	3.1	
9	Cg2925	2	1934.9448	-2.5	137	153	0	70.1	29	A	QDLFGPQSLVEMFPQIS	G	0.1	3	
9	Cg2925	2	1950.9397	-0.9	137	153	0	73.3	29	A	QDLFGPQSLVEMFPQIS	G	0.1	3	Oxidation (M)
9	Cg2925	2	2430.222	-2.5	321	342	0	41.6	31	I	TGLHQSFPPIELELFNQGGSFI	F	0.1	4.24	
10	Cg2409	1	557.3247	0.2	225	229	0	33.4	19	V	MVLPV	N	2.5	6.02	
10	Cg2409	1	774.3371	-2.5	44	50	0	31.2	20	R	MGWPDGI	T	-0.1	3.1	
10	Cg2409	1	777.3909	-0.5	270	275	0	32.7	30	V	FQIEEI	T	0.2	3.12	
10	Cg2409	1	930.4382	-0.9	43	50	0	39.3	27	L	RMGWPDGI	T	-0.6	6.78	
10	Cg2409	1	936.4745	-1.2	246	252	0	28.5	27	S	FWVPEFL	F	1.1	3.3	
10	Cg2409	1	974.5073	-0.2	104	111	0	32.2	30	L	QYNVPLEL	V	-0.2	3.3	
10	Cg2409	2	985.508	-1.2	137	145	0	29.9	28	T	ALDKNPEVT	V	-0.8	4.08	
10	Cg2409	1	1073.5757	0.5	104	112	0	34.8	30	L	QYNVPLELV	L	0.3	3.3	
10	Cg2409	1	1085.5142	0.3	328	337	0	40.6	26	L	EHIGQAPYAT	S	-0.6	5.12	
10	Cg2409	2	1086.5557	0.1	136	145	0	52.2	29	V	TALDKNPEVT	V	-0.8	4.08	
10	Cg2409	2	1095.5197	0.2	338	347	0	68.7	27	T	STSPFVSDRT	A	-0.6	6.78	
10	Cg2409	1	1101.4801	-2.7	44	53	0	38.5	24	R	MGWPDGITPE	A	-0.6	3	
10	Cg2409	1	1108.4785	-0.5	313	322	0	24.6	24	I	SFRDSNPDAT	N	-1.4	3.88	
10	Cg2409	2	1137.5675	1.1	295	303	0	42.1	28	A	MMNFELRVV	D	0.8	6.98	
10	Cg2409	1	1140.5452	0.5	45	55	0	29.4	28	M	GWPDGITPEAV	A	-0.2	3	
10	Cg2409	1	1160.5655	-2.0	244	252	0	30.5	29	A	HSFWVPEFL	F	0.4	5.12	
10	Cg2409	1	1193.5452	-0.6	270	279	0	56.6	28	V	FQIEEITEEG	A	-0.7	2.96	
10	Cg2409	1	1257.5812	-0.6	43	53	0	41.4	25	L	RMGWPDGITPE	A	-1.0	4.08	
10	Cg2409	1	1271.5856	-2.9	44	55	0	31.7	26	R	MGWPDGITPEAV	A	0.0	3	
10	Cg2409	2	1296.6714	1.2	207	216	0	35.5	28	S	YLEFNRIETL	G	-0.2	4.26	
10	Cg2409	2	1383.7034	1.7	206	216	0	54.8	29	V	SYLEFNRIETL	G	-0.3	4.26	
10	Cg2409	1	1397.6939	-1.9	325	337	0	52.1	28	A	QALEHIGQAPYAT	S	-0.3	5.12	
10	Cg2409	1	1427.6867	-2.9	43	55	0	45.8	27	L	RMGWPDGITPEAV	A	-0.4	4.08	
10	Cg2409	2	1449.612	-1.5	170	182	0	68.7	23	G	GQDYQGSDPERQA	A	-2.2	3.7	
10	Cg2409	1	1500.7672	-3.6	136	149	0	43.6	30	V	TALDKNPEVTVDVT	A	-0.2	3.7	
10	Cg2409	1	1582.7739	-3.2	323	337	0	64.6	28	T	NAQALEHIGQAPYAT	S	-0.4	5.12	
10	Cg2409	2	1597.7988	0.6	204	216	0	34.1	29	S	DVSYLEFNRIETL	G	-0.2	3.82	
10	Cg2409	1	1632.7606	-0.1	40	53	0	42.2	28	G	DFLRMGWPDGITPE	A	-0.5	3.7	
10	Cg2409	2	1690.778	0.2	150	162	0	42.2	27	T	AYQWNWKFGYSEI	D	-0.8	6.8	
10	Cg2409	2	1716.7703	-0.5	166	181	0	45.6	25	S	LAPGGQDYQGSDPERQ	A	-1.7	3.7	
10	Cg2409	2	1787.8074	-1.2	166	182	0	87.2	25	S	LAPGGQDYQGSDPERQA	A	-1.4	3.7	
10	Cg2409	2	1802.8662	-2.1	40	55	0	45.2	29	G	DFLRMGWPDGITPEAV	A	-0.1	3.7	
10	Cg2409	1	1832.9156	-3.4	209	224	0	36.1	30	L	EFNRIETLGTTDEIPV	M	-0.4	3.68	
10	Cg2409	2	1874.8395	-0.2	165	182	0	36.7	25	G	SLAPGGQDYQGSDPERQA	A	-1.4	3.7	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
10	Cg2409	2	1972.9717	-0.4	38	55	0	43.4	29	V	LGDFLRMGWPDGITPEAV	A	0.1	3.7	
10	Cg2409	2	2046.8879	-1.1	163	182	0	83.3	22	I	DGSLAPGGQDYQGSDPERQA	A	-1.5	3.5	
10	Cg2409	2	2196.095	0.2	206	224	0	34.1	30	V	SYLEFNRIETLGTTDEIPV	M	-0.2	3.68	
10	Cg2409	2	2539.1099	-0.1	159	182	0	40.4	23	G	YSEIDGSLAPGGQDYQGSDPERQA	A	-1.3	3.42	
10	Cg2409	2	2673.2419	-2.2	313	337	0	86.4	28	I	SFRDSNPDATNAQALEHIGQAPYAT	S	-0.8	4.3	
11	Cg0447	1	599.3894	1.5	33	37	0	30.2	19	S	ILELL	D	2.5	3.3	
11	Cg0447	1	645.297	0.2	22	27	0	35.7	31	T	VQVDDA	V	0.0	2.92	
11	Cg0447	1	686.4214	0.7	32	37	0	33.7	26	M	SILELL	D	1.9	3.3	
11	Cg0447	1	701.3232	0.1	137	143	0	28.2	27	T	APDADTL	H	-0.3	2.92	
11	Cg0447	1	715.3653	0.0	174	180	0	35.4	25	A	AHLFTGA	K	0.8	7.84	
11	Cg0447	1	767.3813	-0.9	151	157	0	37.1	26	A	ELALDHA	A	0.1	4.06	
11	Cg0447	1	791.4905	0.4	184	190	0	31.2	18	V	HLSLLPL	G	1.4	7.84	
11	Cg0447	1	846.4884	0.5	1	7	0	52.9	27	-	MKLTLEI	W	0.8	6.94	
11	Cg0447	1	879.4338	-0.6	15	22	0	39.1	29	T	AEGKFETV	Q	-0.4	4.26	
11	Cg0447	1	890.5589	-1.1	183	190	0	18.6	15	L	VHLSLLPL	G	1.7	7.84	
11	Cg0447	1	927.5277	-1.4	95	102	0	35.9	27	G	DTLKIEPL	R	-0.1	4.08	
11	Cg0447	1	975.4332	-0.4	23	31	0	40.4	26	V	QVDDAVAQM	S	0.0	2.92	
11	Cg0447	1	991.4281	-0.5	23	31	0	46.6	26	V	QVDDAVAQM	S	0.0	2.92	Oxidation (M)
11	Cg0447	1	996.4586	0.4	124	132	0	28.6	27	V	MEQGGYVTI	N	0.1	3.3	
11	Cg0447	2	1010.492	0.1	89	97	0	30.0	26	L	VSYKEGDTL	K	-0.7	4.08	
11	Cg0447	1	1037.5757	-1.2	32	40	0	40.6	24	M	SILELLDHV	N	1.0	4.06	
11	Cg0447	1	1044.4724	-0.6	133	143	0	25.4	25	I	NAGTAPDADTL	H	-0.4	2.92	
11	Cg0447	2	1061.5539	-1.9	110	118	0	36.8	29	V	IKDMVVDRS	A	-0.2	6.9	
11	Cg0447	2	1071.5097	-1.4	8	17	0	48.9	27	I	WRQAGPTAEG	K	-1.2	6.98	
11	Cg0447	2	1077.5488	-0.9	110	118	0	39.8	30	V	IKDMVVDRS	A	-0.2	6.9	Oxidation (M)
11	Cg0447	1	1270.667	-2.5	4	14	0	41.4	28	L	TLEIWRQAGPT	A	-0.5	6.98	
11	Cg0447	1	1310.7558	-2.7	186	197	0	28.1	25	L	SLLPLGKEERGL	R	-0.3	7.1	
11	Cg0447	1	1320.6562	0.0	18	29	0	32.9	29	G	KFETVQVDDAVA	Q	0.0	3.7	
11	Cg0447	2	1491.7755	0.3	106	118	0	64.3	29	A	AYPVIKDMVVDRS	A	0.1	6.82	
11	Cg0447	2	1491.782	-2.9	90	102	0	57.1	29	V	SYKEGDTLKIEPL	R	-0.8	4.44	
11	Cg0447	2	1521.7463	-0.3	41	53	0	55.4	29	V	NNKFIEEGKEPFA	F	-1.2	4.56	
11	Cg0447	1	1550.7763	-3.2	119	132	0	57.5	29	S	ALDRVMEQGGYVTI	N	0.2	4.08	
11	Cg0447	2	1562.8127	-1.7	105	118	0	83.8	29	S	AAYPVIKDMVVDRS	A	0.3	6.82	
11	Cg0447	1	1579.7552	-2.0	18	31	0	65.2	28	G	KFETVQVDDAVAQM	S	-0.1	3.7	
11	Cg0447	2	1659.9672	-1.4	183	197	0	30.7	24	L	VHLSLLPLGKEERGL	R	0.1	7.82	
11	Cg0447	1	1739.8519	-3.9	41	55	0	32.7	29	V	NNKFIEEGKEPFAFA	S	-0.7	4.56	
11	Cg0447	2	1836.8564	-1.0	15	31	0	46.1	27	T	AEGKFETVQVDDAVAQM	S	-0.2	3.58	
11	Cg0447	2	1969.0156	-2.2	32	48	0	52.8	30	M	SILELLDHVNNKFIEEG	K	-0.1	4.16	
11	Cg0447	2	2238.1137	-2.5	113	132	0	41.7	30	D	MVVDRSALDRVMEQGGYVTI	N	0.2	4.3	
11	Cg0447	3	2541.3115	-1.1	32	53	0	65.5	31	M	SILELLDHVNNKFIEEGKEPFA	F	-0.3	4.36	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
11	Cg0447	2	2582.1997	-2.6	133	157	0	79.4	27	I	NAGTAPDADTLHVNHETAELALDHA	A	-0.5	4.18	
11	Cg0447	2	2759.417	-2.2	32	55	0	54.7	31	M	SILELLDHVNNKFIEEGKEPFAFA	S	-0.1	4.36	
11	Cg0447	2	3024.5413	-2.6	106	132	0	58.0	31	A	AYPVIKDMVVDRSALDRVMEQGGYVTI	N	0.2	4.46	
11	Cg0447	3	3095.5784	-0.3	105	132	0	49.4	31	S	AAYPVIKDMVVDRSALDRVMEQGGYVTI	N	0.2	4.46	
11	Cg0447	3	3489.7126	-0.3	25	55	0	39.6	31	V	DDAVAQMSILELLDHVNNKFIEEGKEPFAFA	S	-0.1	3.96	
11	Cg0447	3	3498.7341	-1.1	23	53	0	40.7	31	V	QVDDAVAQMSILELLDHVNNKFIEEGKEPFA	F	-0.2	3.96	
12	Cg2708	1	641.2809	-0.2	83	87	0	20.9	19	V	FQNYA	L	-0.7	5.92	
12	Cg2708	1	647.3279	0.6	234	240	0	38.5	31	A	GFIGSPA	M	0.8	6.02	
12	Cg2708	1	656.3745	1.2	297	302	0	33.6	26	T	DLSIPI	K	1.2	3.1	
12	Cg2708	1	750.3436	1.6	305	310	0	40.0	24	L	DFVEEL	G	0.1	2.94	
12	Cg2708	1	823.3534	-0.1	94	101	0	32.5	25	T	VGENMGFA	L	0.4	3.3	
12	Cg2708	1	827.4389	3.4	334	341	0	33.4	28	V	PESGQIVV	R	0.4	3.3	
12	Cg2708	1	837.3691	0.5	95	102	0	41.8	26	V	GENMGFAL	K	0.3	3.3	
12	Cg2708	1	945.4403	-0.3	52	61	0	32.5	28	L	AGLENVTDGA	I	0.0	3	
12	Cg2708	1	991.5226	-0.2	303	310	0	44.0	28	I	KLDFVEEL	G	0.0	3.82	
12	Cg2708	1	1039.4822	-1.3	245	254	0	36.2	25	G	TFSVKDGDAT	S	-0.5	3.88	
12	Cg2708	2	1086.5094	-1.7	359	368	0	29.1	26	R	IVEGGQHNFS	A	-0.4	5.12	
12	Cg2708	1	1175.5459	-1.6	191	200	0	38.4	28	V	YVTHDQTEAL	T	-0.7	4.06	
12	Cg2708	2	1232.6765	1.2	207	217	0	47.2	28	I	AVLKDGYLQQV	G	0.2	6.68	
12	Cg2708	2	1243.6309	-0.2	218	228	0	36.4	29	V	GAPRELYDRPA	N	-1.2	6.96	
12	Cg2708	2	1245.6023	-0.1	270	280	0	59.9	28	A	MTPEDNGRITI	G	-0.7	4.08	
12	Cg2708	1	1383.6281	-2.2	83	93	0	37.3	26	V	FQNYALYPHMT	V	-0.4	7.7	
12	Cg2708	2	1454.6712	0.5	241	254	0	70.7	27	A	MNLGTFSVKDGDAT	S	-0.2	3.88	
12	Cg2708	2	1482.6966	-1.6	83	94	0	54.6	28	V	FQNYALYPHMTV	G	-0.1	7.7	
12	Cg2708	2	1604.812	-0.7	157	170	0	39.4	29	V	FLMDEPLSNLDAKL	R	0.1	3.7	
12	Cg2708	1	1743.8679	-3.0	281	296	0	75.5	30	I	GFRPEALEIIPEGEST	D	-0.4	3.8	
12	Cg2708	2	1806.8207	-3.9	241	258	0	77.1	26	A	MNLGTFSVKDGDATSGHA	R	-0.3	5.1	
12	Cg2708	2	1848.8676	-4.0	191	206	0	81.5	28	V	YVTHDQTEALTMGDRI	A	-0.6	4.3	
12	Cg2708	2	1905.9982	-3.0	201	217	0	44.0	29	L	TMGDRIAVLKDGYLQQV	G	-0.1	6.82	
12	Cg2708	2	2019.0823	-3.4	200	217	0	30.1	28	A	LTMGDRIAVLKDGYLQQV	G	0.2	6.82	
12	Cg2708	2	2623.4108	-2.4	281	304	0	35.7	29	I	GFRPEALEIIPEGESTDLSIPIKL	D	0.0	4	
12	Cg2708	2	3063.5335	-0.9	191	217	0	61.1	31	V	YVTHDQTEALTMGDRIAVLKDGYLQQV	G	-0.3	4.44	
13	Cg3138	1	890.3869	-0.1	217	224	0	29.9	24	V	SEELADEV	A	-0.6	2.88	
13	Cg3138	1	898.5276	-0.4	159	166	0	45.8	28	A	AIIVWQVA	D	2.1	6.02	
13	Cg3138	1	905.3879	-0.4	148	155	0	25.3	24	V	NDYNGNPI	N	-1.6	3.1	
13	Cg3138	1	970.5335	0.9	229	238	0	28.3	28	A	AVAGLEIVEA	R	1.5	3.12	
13	Cg3138	1	988.4978	1.4	27	34	0	28.6	28	I	NEKNVWSL	G	-1.0	6.94	
13	Cg3138	1	1115.6227	-2.3	120	130	0	39.4	28	T	GLSFVPPLSVT	K	1.2	6.02	
13	Cg3138	2	1158.5881	-1.0	2	12	0	74.0	30	M	STIEERTPGAV	A	-0.5	4.26	
13	Cg3138	1	1185.6394	3.0	159	169	0	68.7	28	A	AIIVWQVADTA	Q	1.3	3.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
13	Cg3138	1	1188.6139	-2.3	25	34	0	50.0	29	V	SINEKNVWSL	G	-0.4	6.94	
13	Cg3138	2	1285.5575	0.1	194	205	0	43.6	23	V	ATQHPYDSPVDG	R	-1.2	3.88	
13	Cg3138	1	1305.6928	-1.7	239	250	0	42.5	28	A	RISSLSYAPEIA	Q	0.3	6.88	
13	Cg3138	1	1312.6987	-2.4	280	290	0	39.6	27	T	ALDQLEQREIV	D	-0.4	3.82	
13	Cg3138	1	1391.5994	-1.0	176	186	0	48.4	23	V	EDFEEFLHQQA	E	-1.2	3.68	
13	Cg3138	1	1541.7838	-3.8	25	39	0	71.2	29	V	SINEKNVWSLGAGPA	A	-0.2	6.94	
13	Cg3138	2	1612.7046	2.2	172	184	0	56.6	25	A	SFSVEDFEEFLHQ	Q	-0.5	3.68	
13	Cg3138	2	1653.7311	-0.8	173	185	0	63.1	25	S	FSVEDFEEFLHQQ	A	-0.7	3.68	
13	Cg3138	1	1676.8006	-2.7	310	325	0	58.4	28	C	SDTNAQPIVNAGSLYQ	-	-0.4	3.1	
13	Cg3138	2	1740.7631	-0.7	172	185	0	69.8	24	A	SFSVEDFEEFLHQQ	A	-0.7	3.68	
13	Cg3138	2	1811.8002	-2.0	172	186	0	77.5	25	A	SFSVEDFEEFLHQQA	E	-0.5	3.68	
13	Cg3138	2	1818.8483	-2.0	208	224	0	102.9	28	V	SLRGATDEVSEELADEV	A	-0.5	3.44	
13	Cg3138	2	2027.8749	1.1	172	188	0	39.9	23	A	SFSVEDFEEFLHQQAES	A	-0.7	3.58	
13	Cg3138	2	2098.912	-0.5	172	189	0	29.5	23	A	SFSVEDFEEFLHQQAESA	L	-0.6	3.58	
13	Cg3138	2	2245.0822	-2.6	208	228	0	108.8	29	V	SLRGATDEVSEELADEVAQRA	A	-0.6	3.82	
13	Cg3138	3	2265.1713	-1.1	280	298	0	43.0	30	T	ALDQLEQREIVDLDPERRA	A	-1.0	4.06	
13	Cg3138	2	2486.2248	-3.0	208	231	0	85.5	30	V	SLRGATDEVSEELADEVAQRAAVA	G	-0.2	3.82	
13	Cg3138	3	3041.5703	-0.1	264	290	0	32.0	31	V	DAREKIVEGAVTMVETALDQLEQREIV	D	-0.2	4.02	
13	Cg3138	3	3324.7599	-1.8	261	290	0	39.7	31	S	AIVDAREKIVEGAVTMVETALDQLEQREIV	D	0.2	4.02	
13	Cg3138	3	3411.7919	-1.0	260	290	0	37.6	31	A	SAIVDAREKIVEGAVTMVETALDQLEQREIV	D	0.1	4.02	
14	Cg1366	1	597.3486	1.3	59	65	0	41.0	27	F	PGGVIGV	A	1.4	6.02	
14	Cg1366	1	655.3217	2.0	300	304	0	22.8	22	G	DVFYL	H	1.2	3.1	
14	Cg1366	1	755.4429	0.9	326	332	0	37.4	25	T	ALPIIET	K	1.3	3.3	
14	Cg1366	1	808.3603	-0.4	409	416	0	30.5	30	T	FASDLDAA	S	0.5	2.92	
14	Cg1366	1	820.4079	-0.6	399	405	0	30.3	29	A	AFRDLEA	F	-0.2	4.08	
14	Cg1366	1	914.5185	-1.4	390	398	0	30.3	29	V	AGSLRLDLA	A	0.6	6.78	
14	Cg1366	2	952.4502	-0.5	271	278	0	34.2	27	I	YDDLTKQA	E	-1.4	3.88	
14	Cg1366	2	1014.5094	0.1	66	74	0	53.3	28	V	AQNLEADRV	G	-0.8	4.08	
14	Cg1366	1	1038.5134	0.4	399	407	0	31.8	27	A	AFRDLEAFA	T	0.4	4.08	
14	Cg1366	1	1055.5499	-0.5	95	105	0	39.6	27	T	GDVLSIPVGEA	F	0.8	3	
14	Cg1366	1	1065.5342	-0.8	270	278	0	32.2	28	V	IYDDLTKQA	E	-0.7	3.88	
14	Cg1366	1	1139.5611	-2.9	399	408	0	37.6	27	A	AFRDLEAFAT	F	0.3	4.08	
14	Cg1366	1	1151.5346	-0.9	223	232	0	31.9	28	T	LEEQGALEYT	T	-0.7	3.02	
14	Cg1366	1	1159.6084	-2.5	313	324	0	34.5	29	A	AKLSDELGAGSI	T	0.2	4.08	
14	Cg1366	2	1163.6128	0.9	244	254	0	39.9	28	A	GFKWLAPFAGA	A	0.7	10.1	
14	Cg1366	2	1307.7085	0.0	139	149	0	41.4	27	T	VLERQPVEEPL	A	-0.5	3.96	
14	Cg1366	2	1387.7307	-0.7	529	541	0	38.2	30	L	DAGQVKKDQLTVS	R	-0.7	6.88	
14	Cg1366	2	1388.6419	0.3	119	131	0	45.6	27	I	DGLGEIASEEDRV	L	-0.7	3.5	
14	Cg1366	1	1413.7504	-1.6	52	65	0	36.9	29	M	ANELLEFPGGVIGV	A	0.8	3.12	
14	Cg1366	2	1422.8347	2.0	106	118	0	50.9	24	A	FLGRVINPLGQPI	D	0.6	11.04	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
14	Cg1366	2	1476.746	0.1	79	91	0	55.2	30	V	LGNYELLKEGDQV	R	-0.6	3.82	
14	Cg1366	2	1479.7933	-1.6	139	151	0	45.3	27	T	VLERQPVEEPLAT	G	-0.4	3.96	
14	Cg1366	1	1484.7875	-1.3	52	66	0	43.4	29	M	ANELLEFPGGVIGVA	Q	0.9	3.12	
14	Cg1366	1	1507.746	-4.1	240	254	0	33.9	29	A	SDAAGFKWLAPFAGA	A	0.5	6.76	
14	Cg1366	1	1743.8526	-2.6	119	134	0	69.2	29	I	DGLGEIASEEDRVLEL	Q	-0.3	3.44	
14	Cg1366	2	3081.5805	-2.1	45	74	0	55.8	31	V	SGLPSVMANELLEFPGGVIGVAQNLEADRV	G	0.4	3.68	
14	Cg1366	2	3430.7467	-2.9	119	149	0	53.3	31	I	DGLGEIASEEDRVLELQAPTVLERQPVEEPL	A	-0.5	3.62	
14	Cg1366	3	3581.8801	-3.3	409	441	0	37.1	31	T	FASDLDAASKSQLERGQRLVQLLIQSENAPQAV	E	-0.3	4.56	
14	Cg1366	2	3602.8315	-1.3	119	151	0	32.7	32	I	DGLGEIASEEDRVLELQAPTVLERQPVEEPLAT	G	-0.4	3.62	
15	Cg2780	1	717.4061	1.8	105	110	0	42.6	29	A	NYVLPL	Q	0.9	5.92	
15	Cg2780	1	753.4061	0.7	370	376	0	25.5	25	T	FLFGGLT	G	1.7	6.02	
15	Cg2780	1	808.3028	-1.1	509	515	0	18.9	16	V	DDPWGYG	N	-1.7	2.92	
15	Cg2780	1	898.5892	-0.6	223	230	0	26.7	20	L	LIFPLLLA	A	2.8	6.02	
15	Cg2780	1	921.4708	-2.2	500	506	0	29.4	26	S	WRYGELV	T	-0.4	6.88	
15	Cg2780	1	923.5117	-1.7	370	378	0	31.9	26	T	FLFGGLTGI	M	1.8	6.02	
15	Cg2780	1	949.5273	-0.8	272	280	0	29.0	28	L	ALPFFGIVS	E	1.9	6.02	
15	Cg2780	1	958.5488	-2.4	105	112	0	57.1	28	A	NYVLPLQI	G	0.8	5.92	
15	Cg2780	1	995.5076	-2.0	382	390	0	32.3	26	A	SPPLDFHLA	D	0.2	4.94	
15	Cg2780	1	1020.5348	-1.6	189	197	0	31.6	28	I	NMLTTILCL	R	1.7	5.32	
15	Cg2780	1	1082.7103	-1.8	222	231	0	23.1	18	A	LLIFPLLLAA	A	2.8	6.02	
15	Cg2780	1	1122.4618	-2.9	509	518	0	35.1	20	V	DDPWGYGNSL	E	-1.2	2.92	
15	Cg2780	1	1144.4924	-0.7	464	473	0	38.3	24	A	DYLDSDGFTI	Y	-0.3	2.82	
15	Cg2780	2	1185.5641	-0.4	544	552	0	29.0	26	A	FELHYPHMI	E	0.0	6.02	
15	Cg2780	2	1225.5662	-1.6	522	532	0	34.2	26	A	TSCPPPRHNFA	S	-0.9	9.02	
15	Cg2780	1	1322.5779	-1.4	507	518	0	36.0	25	V	TVDDPWGYGNSL	E	-0.7	2.92	
15	Cg2780	1	1395.646	-1.9	140	153	0	35.3	27	T	GFLTPGGAADFGWT	M	0.3	3.1	
15	Cg2780	2	1401.7001	-2.0	8	20	0	41.6	30	R	VDGHVAPQRPEPT	G	-1.1	5.22	
15	Cg2780	1	1429.8221	-1.6	273	285	0	31.8	26	A	LPFFGIVSEIIPV	F	1.8	3.3	
15	Cg2780	1	1437.5837	-2.2	509	520	0	33.9	19	V	DDPWGYGNSLEW	A	-1.4	2.88	
15	Cg2780	1	1508.6208	-2.6	509	521	0	42.8	20	V	DDPWGYGNSLEWA	T	-1.1	2.88	
15	Cg2780	1	1601.7072	-3.1	149	162	0	42.2	24	A	DFGWTMYSPLSDAI	H	0.1	2.92	
15	Cg2780	1	1601.7483	-1.5	544	555	0	41.0	27	A	FELHYPHMIERM	R	-0.5	6.02	
15	Cg2780	2	1607.6892	0.1	508	521	0	50.8	23	T	VDDPWGYGNSLEWA	T	-0.8	2.88	
15	Cg2780	1	1708.7369	-1.2	507	521	0	32.1	23	V	TVDDPWGYGNSLEWA	T	-0.7	2.88	
15	Cg2780	1	1809.7846	-1.9	507	522	0	41.4	23	V	TVDDPWGYGNSLEWAT	S	-0.7	2.88	
15	Cg2780	1	1986.9186	-3.7	140	158	0	46.8	27	T	GFLTPGGAADFGWTMYSPL	S	0.3	3.1	
16	Cg2404	1	543.3057	-0.9	265	269	0	38.4	17	V	FPLPA	E	1.0	6.02	
16	Cg2404	1	642.3741	-0.9	264	269	0	21.1	17	T	VFPLPA	E	1.6	6.02	
16	Cg2404	1	676.3948	0.0	58	62	0	25.6	19	T	FWLVL	G	2.7	6.02	
16	Cg2404	1	679.4268	-1.2	376	381	0	22.6	21	A	LPQLPI	T	0.9	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
16	Cg2404	1	879.543	-1.1	376	383	0	46.5	18	A	LPQLPITV	D	1.1	6.02	
16	Cg2404	1	906.5651	-1.1	374	381	0	26.8	18	A	RALPQLPI	T	0.3	11.04	
16	Cg2404	2	915.4848	-2.5	164	174	0	30.1	27	I	MGLAGGGAVLA	G	1.6	6.02	
16	Cg2404	1	956.4967	-2.2	394	402	0	52.2	28	G	NFIEPLGPA	F	0.3	3.3	
16	Cg2404	1	975.4662	-1.6	147	154	0	29.1	27	A	LLNDSWQT	S	-0.7	3.1	
16	Cg2404	1	977.6022	-1.8	373	381	0	24.8	17	A	ARALPQLPI	T	0.5	11.04	
16	Cg2404	1	1084.5553	-2.0	392	402	0	37.3	27	A	AGNFIEPLGPA	F	0.3	3.3	
16	Cg2404	1	1090.5369	-3.0	260	269	0	33.0	29	A	SMETVFPLPA	E	0.6	3.3	
16	Cg2404	1	1106.5318	-2.6	260	269	0	31.0	29	A	SMETVFPLPA	E	0.6	3.3	Oxidation (M)
16	Cg2404	1	1230.6456	-2.6	24	34	0	55.3	29	A	RLGTELDDVTI	A	0.0	3.7	
16	Cg2404	1	1284.5087	-1.1	321	330	0	50.5	17	S	FHYGDYYAYS	K	-0.9	4.94	
16	Cg2404	1	1301.6827	-2.1	24	35	0	57.1	29	A	RLGTELDDVTIA	Y	0.1	3.7	
16	Cg2404	1	1303.5914	-2.0	73	81	0	27.0	26	A	TYIFWPWEY	K	-0.3	3.3	
16	Cg2404	1	1309.5132	-2.6	270	281	0	29.1	18	A	EMVNDGAEYDPA	K	-0.9	2.84	
16	Cg2404	1	1349.7819	-4.1	369	381	0	34.3	23	V	FGPAARALPQLPI	T	0.5	11.04	
16	Cg2404	2	1502.7234	0.1	73	83	0	29.4	29	A	TYIFWPWEYKA	H	-0.5	6.8	
16	Cg2404	2	1510.7238	-0.9	187	199	0	39.8	28	I	KNPWNPKEGPMDV	Q	-1.7	6.98	
16	Cg2404	2	1553.6958	-0.8	2	14	0	50.1	26	M	SNNNDKQYTTQEL	N	-2.2	4.08	
16	Cg2404	1	1698.908	-4.7	376	390	0	32.0	28	A	LPQLPITVDEEGYLI	A	0.3	2.94	
16	Cg2404	1	1769.9451	-2.2	376	391	0	39.7	29	A	LPQLPITVDEEGYLIA	A	0.4	2.94	
16	Cg2404	2	1789.9151	-0.8	394	408	0	63.4	30	G	NFIEPLGPAFWERKS	-	-0.6	7.1	
16	Cg2404	2	1868.8913	-1.2	183	199	0	55.0	28	M	GGMIKNPWNPKEGPMDV	Q	-1.0	6.98	
16	Cg2404	2	1917.9737	-2.4	392	408	0	43.2	30	A	AGNFIEPLGPAFWERKS	-	-0.4	7.1	
16	Cg2404	2	2440.3002	-0.4	369	391	0	51.3	30	V	FGPAARALPQLPITVDEEGYLIA	A	0.4	3.82	
16	Cg2404	2	2665.343	-0.2	175	199	0	58.4	31	A	GLTIIAPMGGMIKNPWNPKEGPMDV	Q	-0.1	6.98	
16	Cg2404	3	3751.7181	-2.5	270	302	0	45.6	26	A	EMVNDGAEYDPAKDVYEHQMHSVHGPRNAVMLI	R	-0.6	4.72	
17	Cg2875	1	648.3231	0.0	23	29	0	34.6	25	I	FAGAQGV	F	0.9	6.02	
17	Cg2875	1	680.3381	0.7	30	35	0	30.9	28	V	FDSIVT	A	1.1	3.1	
17	Cg2875	1	751.3752	-2.0	30	36	0	32.5	29	V	FDSIVTA	S	1.2	3.1	
17	Cg2875	1	820.4331	0.2	4	10	0	35.2	30	S	VFDIIQS	I	1.2	3.1	
17	Cg2875	1	850.4436	-0.4	29	36	0	32.8	28	G	VFDSIVTA	S	1.6	3.1	
17	Cg2875	1	907.4651	0.0	28	36	0	32.2	29	Q	GVFDSIVTA	S	1.3	3.1	
17	Cg2875	1	907.4651	1.4	3	10	0	38.6	29	T	SVFDIIQS	I	0.9	3.1	
17	Cg2875	2	986.4822	1.5	12	21	0	34.5	26	I	FDGVHGLVGS	I	0.6	4.94	
17	Cg2875	1	1012.5342	0.6	11	20	0	31.6	27	S	IFDGVHGLVG	S	1.2	4.94	
17	Cg2875	1	1071.5349	0.6	9	18	0	32.8	27	I	QSIFDGVHGL	V	0.4	4.94	
17	Cg2875	1	1092.5452	0.0	25	35	0	31.5	29	A	GAQGVFDSIVT	A	0.7	3.1	
17	Cg2875	2	1099.5662	-1.2	11	21	0	61.2	28	S	IFDGVHGLVGS	I	1.0	4.94	
17	Cg2875	1	1163.5823	-0.5	25	36	0	41.6	29	A	GAQGVFDSIVTA	S	0.8	3.1	
17	Cg2875	2	1212.6503	0.2	11	22	0	81.4	28	S	IFDGVHGLVGSI	F	1.3	4.94	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
17	Cg2875	2	1314.6568	1.3	9	21	0	61.1	29	I	QSIFDGVHGLVGS	I	0.5	4.94	
17	Cg2875	2	1381.6878	2.6	23	36	0	66.1	28	I	FAGAQGVFDSIVTA	S	1.0	3.1	
17	Cg2875	2	1427.7409	0.9	9	22	0	70.4	29	I	QSIFDGVHGLVGSI	F	0.8	4.94	
17	Cg2875	1	1494.7719	-2.5	22	36	0	33.6	28	S	IFAGAQGVFDSIVTA	S	1.3	3.1	
17	Cg2875	2	1581.8039	0.5	21	36	0	46.5	29	G	SIFAGAQGVFDSIVTA	S	1.1	3.1	
17	Cg2875	2	1658.8668	-0.1	4	18	0	33.4	30	S	VFDIIQSIFDGVHGL	V	1.1	3.88	
17	Cg2875	1	1745.8989	-2.4	3	18	0	40.1	29	T	SVFDIIQSIFDGVHGL	V	1.0	3.88	
17	Cg2875	2	2015.0728	-1.0	4	22	0	33.7	30	S	VFDIIQSIFDGVHGLVGSI	F	1.2	3.88	
17	Cg2875	2	2102.1048	-0.7	3	22	0	38.2	30	T	SVFDIIQSIFDGVHGLVGSI	F	1.1	3.88	
17	Cg2875	2	2645.3854	0.8	4	29	0	43.7	30	S	VFDIIQSIFDGVHGLVGSIFAGAQGV	F	1.1	3.88	
17	Cg2875	2	2732.4174	0.6	3	29	0	35.0	31	T	SVFDIIQSIFDGVHGLVGSIFAGAQGV	F	1.1	3.88	
18	Cg3182	1	539.3683	-0.2	172	176	0	26.5	23	A	IVVLP	V	3.0	6.02	
18	Cg3182	1	709.4738	1.4	171	177	0	42.6	21	N	AIVVLPV	G	3.0	6.02	
18	Cg3182	2	748.3868	0.9	359	365	0	41.3	29	A	SFRPSGV	H	-0.2	11.04	
18	Cg3182	1	752.3493	0.5	591	596	0	36.4	26	G	NIYWSA	S	0.0	5.92	
18	Cg3182	1	789.3657	-0.9	483	489	0	34.5	28	V	TFEHGSI	Y	-0.2	5.12	
18	Cg3182	1	896.4127	0.0	62	69	0	28.8	26	V	TDGLTDYL	K	-0.3	2.92	
18	Cg3182	1	1039.5914	-2.0	171	181	0	45.0	25	N	AIVVLPVGGES	S	1.5	3.3	
18	Cg3182	1	1087.4723	-0.6	605	614	0	25.8	23	L	HGDIFDAWGA	K	-0.1	3.88	
18	Cg3182	2	1133.5465	1.1	451	461	0	44.2	28	I	NARYSELGGPA	S	-0.8	6.88	
18	Cg3182	1	1153.504	-0.8	507	516	0	39.9	25	A	AWGTQDYEKG	S	-1.6	4.08	
18	Cg3182	2	1176.5887	0.2	640	649	0	42.0	28	I	DFQNGTIRQV	N	-0.8	6.78	
18	Cg3182	1	1182.5305	-0.3	580	590	0	25.5	25	I	NGGAFQEFEKG	N	-1.1	4.26	
18	Cg3182	1	1184.5536	-2.6	496	506	0	27.0	26	T	GPWEIPGDMLA	A	0.0	3	
18	Cg3182	1	1200.5564	0.7	604	614	0	48.8	27	I	LHGDIFDAWGA	K	0.3	3.88	
18	Cg3182	2	1239.5004	-1.5	308	320	0	28.3	19	V	SSGNGADDFGKEG	S	-1.3	3.7	
18	Cg3182	2	1256.5673	-0.2	161	170	0	63.5	26	T	NIEQYYADKN	A	-1.8	4.08	
18	Cg3182	1	1386.649	0.5	494	506	0	34.2	27	A	TTGPWEIPGDMLA	A	-0.1	3	
18	Cg3182	2	1486.6576	-0.8	159	170	0	34.2	25	I	ETNIEQYYADKN	A	-1.8	3.82	
18	Cg3182	2	1496.6379	-0.3	308	323	0	23.2	23	V	SSGNGADDFGKEGSVA	I	-0.7	3.7	
18	Cg3182	2	1828.7904	0.3	615	630	0	43.2	23	A	KGWEQGEYGFPTSDQT	A	-1.6	3.82	
18	Cg3182	2	2233.9341	-1.1	183	200	0	35.1	20	S	FYSDWEGPNNGKNYQWET	F	-1.9	3.82	
18	Cg3182	2	2320.9661	-0.1	182	200	0	20.7	18	S	SFYSDWEGPNNGKNYQWET	F	-1.8	3.82	
19	Cg2403	1	640.4523	-0.9	211	216	0	28.6	25	A	ILLGLI	A	3.3	6.02	
19	Cg2403	1	667.3945	-0.7	376	380	0	23.2	15	V	FYILL	T	2.7	5.92	
19	Cg2403	1	704.3857	-0.3	25	30	0	41.2	27	I	NKVFPT	H	-0.5	10.1	
19	Cg2403	1	751.5207	0.9	207	213	0	20.0	17	L	IIPAILL	G	3.0	6.02	
19	Cg2403	1	779.3854	0.1	311	316	0	34.5	26	A	WELYLG	N	0.3	3.3	
19	Cg2403	1	845.3953	-1.3	73	80	0	37.2	27	L	PLNGVEMS	R	0.0	3.3	
19	Cg2403	1	938.4749	-2.0	56	63	0	29.5	26	T	LFFDPSIT	K	0.9	3.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
19	Cg2403	1	1027.5484	-1.3	441	450	0	44.9	26	T	GIIKQMPNGA	F	-0.1	10.1	
19	Cg2403	1	1078.5157	0.1	308	316	0	30.4	29	V	MPAWELYLG	N	0.4	3.3	
19	Cg2403	2	1137.5414	-1.0	6	15	0	32.0	27	T	VGNNLDSRYT	M	-1.0	6.7	
19	Cg2403	1	1147.7944	-1.3	206	216	0	25.0	13	V	LIIPAILLGLI	A	3.0	6.02	
19	Cg2403	1	1236.6754	-2.7	64	74	0	35.9	26	T	KVIYDGGYLPL	N	0.4	6.62	
19	Cg2403	2	1238.5891	0.1	5	15	0	57.4	27	A	TVGNNLDSRYT	M	-1.0	6.7	
19	Cg2403	2	1305.599	0.5	492	503	0	46.1	27	T	RGGFFGPDPEDI	R	-0.8	3.7	
19	Cg2403	1	1333.6853	-3.5	306	316	0	36.8	28	A	RVMPAWELYLG	N	0.3	6.88	
19	Cg2403	1	1344.6462	-1.7	275	286	0	31.0	28	I	NAIWNLGPYNPS	Q	-0.6	5.92	
19	Cg2403	1	1481.6497	-2.4	292	304	0	35.4	25	G	SQPDVYMLWTDGA	A	-0.3	2.92	
19	Cg2403	1	1538.6712	-2.3	291	304	0	40.4	25	A	GSQPDVYMLWTDGA	A	-0.4	2.92	
19	Cg2403	1	1571.7732	-2.2	275	288	0	41.3	29	I	NAIWNLGPYNPSQV	S	-0.5	5.92	
19	Cg2403	1	1626.7599	-3.1	66	80	0	42.8	27	V	IYDGGYLPLNGVEMS	R	0.1	3	
19	Cg2403	1	1696.7403	-2.4	289	304	0	46.3	24	V	SAGSQPDVYMLWTDGA	A	-0.2	2.92	
19	Cg2403	1	1767.7774	-1.6	289	305	0	33.4	24	V	SAGSQPDVYMLWTDGAA	R	-0.1	2.92	
19	Cg2403	1	1853.9233	-4.5	64	80	0	55.9	30	T	KVIYDGGYLPLNGVEMS	R	0.1	4.08	
19	Cg2403	2	2410.1077	-1.4	482	503	0	93.2	27	M	NQLGYAEVETRGGFFGPDPEDI	R	-0.7	3.5	
19	Cg2403	2	2476.254	-3.1	451	472	0	51.2	30	A	FIEVHQPLGPVDDHGHPIPLPY	A	-0.3	5.02	
19	Cg2403	2	2604.3125	-3.0	451	474	0	45.2	31	A	FIEVHQPLGPVDDHGHPIPLPYAG	A	-0.2	5.02	
19	Cg2403	2	2675.3496	-3.0	451	475	0	49.6	30	A	FIEVHQPLGPVDDHGHPIPLPYAGA	A	-0.1	5.02	
20	Cg0953	1	613.2748	2.6	88	92	0	30.0	26	G	YDGFL	Y	0.3	3.1	
20	Cg0953	1	640.416	2.0	506	511	0	26.8	23	G	LVSIPL	A	2.3	6.02	
20	Cg0953	1	735.3803	1.1	265	270	0	42.3	30	T	TQLDFI	S	0.6	3.1	
20	Cg0953	2	754.4337	1.5	327	333	0	31.0	27	A	LVGPDRV	I	0.3	6.78	
20	Cg0953	1	827.4752	0.0	442	449	0	30.2	29	A	SANLPTIL	Y	0.9	6.02	
20	Cg0953	1	931.4803	-0.6	494	501	0	30.3	29	G	ADWAIFPL	K	1.1	3.1	
20	Cg0953	1	1096.6645	-1.3	498	507	0	27.5	24	A	IFPLKNPGLV	S	0.8	10.1	
20	Cg0953	1	1170.6033	-2.9	382	392	0	38.0	27	A	AVGHDIYNAVI	R	0.8	4.94	
20	Cg0953	1	1187.6186	-0.9	251	261	0	30.7	30	T	QILEPGLQYGA	T	0.0	3.3	
20	Cg0953	1	1386.6966	-4.3	516	528	0	36.9	28	A	GWIGTLVGKPDNM	D	-0.1	6.76	
20	Cg0953	2	1429.7161	-1.7	391	403	0	65.2	29	A	VIRNGQSTEAEQV	R	-0.7	4.26	
20	Cg0953	1	1800.8716	-2.9	516	532	0	72.0	29	A	GWIGTLVGKPDNMDDLA	A	-0.1	3.6	
20	Cg0953	1	1871.9088	-4.9	516	533	0	43.7	29	A	GWIGTLVGKPDNMDDLAA	E	0.0	3.6	
20	Cg0953	1	1945.9244	-2.2	483	501	0	43.1	28	A	VSGNDSAMVPGADWAIFPL	K	0.5	2.92	
20	Cg0953	1	1978.9888	-1.7	247	264	0	53.3	29	G	YDPTQILEPGLQYGATLT	T	-0.3	3	
20	Cg0953	2	2360.1028	-0.6	516	537	0	44.9	28	A	GWIGTLVGKPDNMDDLAAEMEV	R	-0.1	3.42	
20	Cg0953	2	2528.2255	-1.5	380	403	0	68.7	30	A	SAAVGHDIYNAVIRNGQSTEAEQV	R	-0.3	4.42	
20	Cg0953	2	3366.7686	-1.5	483	515	0	42.0	31	A	VSGNDSAMVPGADWAIFPLKNPGLVSIPLAFIA	G	0.8	3.88	
21	Cg1332	1	475.2101	-4.6	220	224	0	33.4	27	S	AMAPS	L	0.6	6.02	
21	Cg1332	1	913.4181	-1.4	112	118	0	34.4	25	M	YQNYDLV	A	-0.7	3.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
21	Cg1332	1	926.4709	-0.4	360	368	0	27.8	27	S	GQTPIPDVT	D	-0.4	3.1	
21	Cg1332	1	949.4757	-0.7	499	506	0	44.9	29	I	NDIVVDYL	R	0.6	2.92	
21	Cg1332	1	956.4491	-0.5	416	423	0	45.2	25	G	DVFDIYSV	K	0.8	2.92	
21	Cg1332	1	1013.4706	0.5	415	423	0	31.6	26	T	GDVFDIYSV	K	0.7	2.92	
21	Cg1332	1	1036.4106	-0.9	299	308	0	24.6	20	A	WAGQAGADMM	T	0.1	3.1	
21	Cg1332	1	1062.5597	-0.1	498	506	0	39.2	28	A	INDIVVDYL	R	1.0	2.92	
21	Cg1332	2	1176.639	0.8	184	194	0	32.0	27	A	LGDDKISIFGL	S	0.6	3.88	
21	Cg1332	1	1208.4954	0.3	299	310	0	47.5	20	A	WAGQAGADMMTA	T	0.1	3.1	
21	Cg1332	1	1213.5979	-1.6	514	524	0	36.5	28	A	TWVEGNTPTPI	T	-0.4	3.3	
21	Cg1332	2	1215.5844	-2.2	438	449	0	44.0	27	T	SGRQPTDGSQLA	V	-1.2	6.78	
21	Cg1332	2	1319.5742	-0.3	170	180	0	36.0	23	T	TDNTANDWERV	R	-1.7	3.7	
21	Cg1332	2	1451.7045	0.1	266	277	0	65.0	28	V	YQNWSNKIVAET	G	-0.9	6.86	
21	Cg1332	2	1506.7175	-0.5	483	498	0	46.8	28	V	NGPGHGQSIGGTNQAI	N	-0.7	7.84	
21	Cg1332	2	1533.7059	0.2	168	180	0	76.9	27	S	LTTDNTANDWERV	R	-1.2	3.7	
21	Cg1332	2	1593.7496	-0.9	481	497	0	49.7	27	V	TVNGPGHGQSIGGTNQA	I	-0.7	7.84	
21	Cg1332	2	1620.738	-0.7	167	180	0	44.8	26	S	SLTTDNTANDWERV	R	-1.1	3.7	
21	Cg1332	2	1694.79	0.5	509	524	0	36.9	27	T	GHTDATWVEGNTPTPI	T	-0.7	4.06	
21	Cg1332	2	1707.77	-0.6	166	180	0	86.8	26	T	SSLTTDNTANDWERV	R	-1.1	3.7	
21	Cg1332	2	2132.9803	0.3	233	250	0	35.7	27	A	SQEQGYKNSLNDFFTWVA	E	-0.8	4.08	
21	Cg1332	2	2438.1826	0.0	483	506	0	64.6	30	V	NGPGHGQSIGGTNQAINDIVVDYL	R	-0.3	3.88	
21	Cg1332	2	2487.1376	0.0	454	475	0	35.3	27	L	LLQGTSDPQTPYWTHNELADAM	N	-0.7	3.7	
22	Cg1656	1	759.3915	1.3	414	420	0	34.2	28	I	SWGLNAL	S	0.5	6.02	
22	Cg1656	1	907.4287	-0.7	338	345	0	36.0	30	S	GEYVAEQI	E	-0.2	3.12	
22	Cg1656	1	960.4665	0.1	323	331	0	45.7	28	M	NYNNLPGVA	Q	-0.4	5.92	
22	Cg1656	1	970.4648	-0.2	108	115	0	64.2	25	V	FEYDSLVV	G	0.7	3	
22	Cg1656	1	1031.4957	-1.0	182	191	0	39.1	29	V	ELAGQLAEMA	H	0.4	3.12	
22	Cg1656	2	1141.6343	1.1	281	291	0	38.9	28	A	SPLGKLVAEQT	G	-0.1	6.94	
22	Cg1656	2	1156.5149	-2.3	196	205	0	54.7	24	L	AGEYKNFNTN	S	-1.6	6.86	
22	Cg1656	2	1179.4907	0.9	360	369	0	35.0	23	A	FDYFDKGSMA	T	-0.4	3.88	
22	Cg1656	2	1269.5989	-0.7	195	205	0	28.5	27	T	LAGEYKNFNTN	S	-1.1	6.86	
22	Cg1656	2	1274.6103	-2.4	287	298	0	55.5	27	L	VAEQTGVETDRA	G	-0.7	3.82	
22	Cg1656	1	1306.6405	-1.7	334	345	0	34.3	29	V	AIQSGEYVAEQI	E	0.0	3.12	
22	Cg1656	2	1314.584	-0.5	196	207	0	25.6	25	L	AGEYKNFNTNSA	K	-1.2	6.86	
22	Cg1656	2	1470.6204	0.3	123	135	0	30.7	22	S	YFGNDHFAEFAPG	M	-0.4	4.06	
22	Cg1656	2	1532.7141	0.2	302	315	0	84.7	28	V	MVNDDLSVGDQKNV	F	-0.6	3.6	
22	Cg1656	2	1569.8475	-0.8	70	83	0	60.8	28	S	TRQILGSQENVNVI	K	-0.2	6.98	
22	Cg1656	2	2312.0487	-1.2	302	322	0	72.5	25	V	MVNDDLSVGDQKNVFVVGDMM	N	0.2	3.42	
23	Cg1363	1	584.3897	1.5	71	76	0	31.7	31	A	LIGLVA	G	3.0	6.02	
23	Cg1363	1	625.3799	-1.0	28	34	0	27.6	27	T	IGPGLGI	G	1.4	6.02	
23	Cg1363	1	795.4854	0.5	28	36	0	33.4	24	T	IGPGLGIGI	L	1.6	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
23	Cg1363	1	797.4647	0.0	24	32	0	29.9	27	Y	GIATIGPGL	G	1.2	6.02	
23	Cg1363	1	818.4538	0.6	62	69	0	34.1	29	L	GIAFVEAL	A	1.9	3.3	
23	Cg1363	2	967.5702	2.3	26	36	0	35.0	25	I	ATIGPGLGIGI	L	1.4	6.02	
23	Cg1363	1	1165.7071	0.1	27	39	0	21.0	21	A	TIGPGLGIGILVG	K	1.6	6.02	
23	Cg1363	1	1191.6499	0.1	14	26	0	29.4	27	S	TITGLGAVGYGIA	T	1.3	5.92	
23	Cg1363	2	1231.5689	-0.3	42	52	0	38.0	26	A	LEGMARQPEMA	G	-0.5	4.26	
23	Cg1363	2	1247.5638	-0.4	42	52	0	52.5	26	A	LEGMARQPEMA	G	-0.5	4.26	Oxidation (M)
23	Cg1363	2	1364.8391	0.5	27	41	0	51.2	20	A	TIGPGLGIGILVGKA	L	1.3	10.1	
23	Cg1363	2	1435.8763	0.8	26	41	0	45.7	19	I	ATIGPGLGIGILVGKA	L	1.3	10.1	
23	Cg1363	1	1487.7224	-3.0	39	52	0	44.2	28	V	GKALEGMARQPEMA	G	-0.6	7.1	
23	Cg1363	2	1663.9873	-1.0	27	44	0	44.0	21	A	TIGPGLGIGILVGKALEG	M	1.0	6.94	
23	Cg1363	2	1699.8749	-0.5	37	52	0	33.3	29	I	LVGKALEGMARQPEMA	G	0.0	7.1	
23	Cg1363	2	1866.0649	-1.2	27	46	0	77.7	25	A	TIGPGLGIGILVGKALEGMA	R	1.1	6.94	
23	Cg1363	2	1869.9804	-1.6	35	52	0	65.3	30	I	GILVGKALEGMARQPEMA	G	0.2	7.1	
23	Cg1363	2	1937.102	-1.9	26	46	0	39.2	26	I	ATIGPGLGIGILVGKALEGMA	R	1.2	6.94	
23	Cg1363	2	2040.086	-0.2	33	52	0	39.7	29	L	GIGILVGKALEGMARQPEMA	G	0.4	7.1	
23	Cg1363	2	2364.2657	-1.9	29	52	0	73.3	29	I	GPGLGIGILVGKALEGMARQPEMA	G	0.4	7.1	
23	Cg1363	2	2578.3975	-2.5	27	52	0	86.1	29	A	TIGPGLGIGILVGKALEGMARQPEMA	G	0.5	7.1	
23	Cg1363	2	2649.4346	-2.6	26	52	0	57.2	29	I	ATIGPGLGIGILVGKALEGMARQPEMA	G	0.6	7.1	
24	Cg0683	1	526.3115	0.8	8	12	0	32.0	30	A	NPLIA	L	1.0	6.02	
24	Cg0683	1	551.3683	0.9	373	377	0	34.3	18	A	IPIPL	P	1.9	6.02	
24	Cg0683	1	648.421	-0.3	373	378	0	14.7	14	A	IPIPLP	G	1.3	6.02	
24	Cg0683	1	651.3666	0.6	92	96	0	24.1	17	I	FMLLL	L	3.2	6.02	Oxidation (M)
24	Cg0683	1	679.4268	-1.5	371	377	0	23.0	21	L	GAIPIPL	P	1.6	6.02	
24	Cg0683	1	982.5158	-2.4	374	383	0	28.5	25	I	PIPLPGGTTM	S	0.3	6.02	
24	Cg0683	1	1155.6023	-2.9	137	147	0	49.1	28	V	ELIEGIDPSLA	S	0.5	2.94	
24	Cg0683	1	1172.7533	-0.6	368	379	0	32.1	14	G	LLLGAIPIPLPG	G	1.7	6.02	
24	Cg0683	1	1238.5779	-2.8	496	507	0	27.1	26	I	SYLNGQTGTDLA	N	-0.5	3.1	
24	Cg0683	1	1275.8166	-0.9	365	377	0	30.7	14	L	SLGLLLGAIPIPL	P	1.9	6.02	
24	Cg0683	2	1288.7867	-1.6	395	407	0	22.3	20	A	GLILGALKHTGPL	T	0.8	10.1	
24	Cg0683	1	1320.8017	-0.5	352	364	0	22.0	20	S	LADVNLLPLAIGL	S	1.7	3.1	
24	Cg0683	1	1429.8908	-1.6	365	379	0	41.2	14	L	SLGLLLGAIPIPLPG	G	1.5	6.02	
24	Cg0683	1	1587.96	-2.0	365	381	0	37.1	19	L	SLGLLLGAIPIPLPGGT	T	1.3	6.02	
24	Cg0683	1	1599.9964	-2.6	363	379	0	48.2	15	I	GLSLGLLLGAIPIPLPG	G	1.6	6.02	
24	Cg0683	1	1758.0655	-0.6	363	381	0	60.8	18	I	GLSLGLLLGAIPIPLPGGT	T	1.3	6.02	
24	Cg0683	1	1820.0481	-2.1	365	383	0	39.2	25	L	SLGLLLGAIPIPLPGGTTM	S	1.2	6.02	
24	Cg0683	1	1990.1537	-3.9	363	383	0	73.3	24	I	GLSLGLLLGAIPIPLPGGTTM	S	1.3	6.02	
24	Cg0683	3	2980.5063	0.5	235	262	0	63.0	31	L	ADPDLPITEGMELLINGTEEAVDRAIKA	L	-0.1	3.68	
25	Cg1603	1	640.3544	0.5	298	304	0	26.2	26	I	VNVGGPV	T	1.0	6.02	
25	Cg1603	1	854.4862	-1.4	298	306	0	31.4	26	I	VNVGGPVTL	D	1.1	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
25	Cg1603	1	1000.4436	-1.7	290	297	0	46.0	23	A	DFHNPQMI	V	-0.8	4.94	
25	Cg1603	1	1158.5768	1.0	212	223	0	29.2	28	I	GVDGAADTLVEL	G	0.6	2.88	
25	Cg1603	2	1449.6008	0.1	307	319	0	35.8	20	L	DGVFENREDSDPA	A	-1.5	3.42	
25	Cg1603	2	1663.7326	0.5	305	319	0	34.5	25	V	TLDGVFENREDSDPA	A	-1.1	3.42	
25	Cg1603	2	1710.8901	0.1	167	183	0	32.7	29	I	DGLGIPDTGNAIEGRKV	L	-0.4	4.3	
25	Cg1603	2	2070.968	-1.3	138	155	0	65.6	28	A	DAQQSLLDRMEAYFGNTI	Q	-0.5	3.7	
25	Cg1603	2	2289.0736	-0.8	136	155	0	91.8	28	A	FADAQQSLLDRMEAYFGNTI	Q	-0.2	3.7	
25	Cg1603	2	2446.2679	-1.6	67	89	0	80.2	31	S	RFTTGSVPNFGPQMLIDGGIQLV	E	0.3	6.78	
25	Cg1603	2	2539.3394	-3.3	247	271	0	66.3	30	A	NVILPADPDGHAVGLERIQDLGIGA	M	0.2	3.96	
25	Cg1603	3	2571.3656	-1.9	159	183	0	43.3	30	I	HSEAPLLIDGLGIPDTGNAIEGRKV	L	-0.1	4.54	
25	Cg1603	2	2589.254	-1.8	376	397	0	59.9	30	G	SFTDNLIDTWNSFALTVQGWFK	-	0.0	3.88	
25	Cg1603	2	2667.398	-0.9	245	271	0	70.0	30	S	GANVILPADPDGHAVGLERIQDLGIGA	M	0.2	3.96	
25	Cg1603	2	2677.2846	-1.3	136	158	0	49.1	29	A	FADAQQSLLDRMEAYFGNTIQFI	H	0.0	3.7	
26	Cg3186	1	810.3759	-0.2	256	262	0	39.6	27	A	NTDVYIS	A	-0.2	3.1	
26	Cg3186	1	861.4344	-0.5	293	299	0	33.2	29	T	STRIWEA	K	-0.6	6.98	
26	Cg3186	1	885.4994	0.5	118	125	0	40.5	29	N	NITLVMPV	G	1.6	6.02	
26	Cg3186	1	888.4341	0.8	104	111	0	38.3	28	A	WLVDTNAA	R	0.4	3.1	
26	Cg3186	1	897.5032	-0.7	302	309	0	30.9	24	A	RLQGLNPT	A	-0.8	11.04	
26	Cg3186	2	916.48	1.4	331	338	0	26.0	26	T	QGRVLDVM	N	0.3	6.78	
26	Cg3186	1	928.4	0.2	310	317	0	24.1	24	T	ADYPMYGI	H	0.0	3.1	
26	Cg3186	1	1073.5142	-0.4	102	111	0	67.9	28	S	NAWLVDTNAA	R	0.1	3.1	
26	Cg3186	1	1100.4563	-0.7	131	139	0	43.4	21	S	FYADWNSQA	S	-0.8	3.1	
26	Cg3186	2	1121.5465	-0.5	322	330	0	40.0	28	A	QFNSQLERT	Q	-1.5	6.98	
26	Cg3186	2	1134.6509	-0.1	72	81	0	33.0	23	G	RNIPVQIQPA	G	-0.3	11.04	
26	Cg3186	1	1159.5146	-2.5	265	275	0	27.8	24	A	SGLWSPQDDGV	R	-0.7	2.92	
26	Cg3186	1	1218.5631	-0.7	148	156	0	34.8	27	V	IYMWETFLT	Q	0.7	3.3	Oxidation (M)
26	Cg3186	2	1414.6841	0.6	265	277	0	52.0	28	A	SGLWSPQDDGVRV	D	-0.6	3.88	
26	Cg3186	2	1485.7212	0.2	264	277	0	39.9	28	A	ASGLWSPQDDGVRV	D	-0.4	3.88	
27	Cg0413	1	585.2435	0.2	205	209	0	23.4	23	G	FYDAA	A	0.3	3.1	
27	Cg0413	1	777.348	0.3	116	121	0	38.8	26	A	NWVMQT	D	-0.4	6.02	
27	Cg0413	1	900.4454	-1.0	332	338	0	30.0	27	A	DWNLRPT	G	-1.6	6.78	
27	Cg0413	1	926.4458	-1.4	93	101	0	26.3	24	A	DESAGPRPV	I	-1.1	4.08	
27	Cg0413	1	974.4193	-0.5	46	55	0	31.7	24	T	ISDSAPADEA	S	-0.4	2.88	
27	Cg0413	1	1000.4138	0.4	248	255	0	26.9	23	G	EYNIYNDA	L	-1.3	3	
27	Cg0413	2	1019.5328	0.4	220	227	0	35.7	29	S	SLLPWEYL	K	0.4	3.3	
27	Cg0413	1	1033.4716	-1.1	273	282	0	33.9	28	A	SGLAGEWESV	D	-0.1	3.12	
27	Cg0413	1	1075.4669	-1.2	45	55	0	35.2	25	S	TISDSAPADEA	S	-0.4	2.88	
27	Cg0413	2	1098.5305	-1.5	91	101	0	80.9	25	I	TADESAGPRPV	I	-0.8	4.08	
27	Cg0413	1	1135.5332	0.9	154	163	0	29.7	29	A	SLGGKQMWET	F	-0.8	6.94	
27	Cg0413	2	1141.592	0.5	195	204	0	35.6	28	T	SLLFPQHFPG	F	0.2	7.84	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
27	Cg0413	2	1154.6482	0.4	81	90	0	36.6	25	S	MDRNVPLVVI	T	1.0	6.78	
27	Cg0413	2	1211.6146	0.0	90	101	0	30.3	27	V	ITADESAGPRPV	I	-0.4	4.08	
27	Cg0413	2	1251.7074	0.6	167	177	0	52.1	24	V	KELPGPLEEKL	N	-1.0	4.56	
27	Cg0413	1	1288.5248	-0.2	144	153	0	32.4	20	S	YYTDWVEENA	S	-1.2	2.94	
27	Cg0413	2	1347.6089	-1.3	230	241	0	31.4	26	L	TLDRGNATPEQM	W	-1.2	4.08	Oxidation (M)
27	Cg0413	2	1353.6816	0.5	122	132	0	68.3	28	T	DVLDFYLEKNV	N	0.0	3.7	
27	Cg0413	2	1549.695	1.1	345	356	0	51.7	26	G	WWQDDLRGSWTT	F	-1.4	3.88	
27	Cg0413	2	1610.9283	-0.1	164	177	0	56.7	25	T	FLVKELPGPLEEKL	N	0.0	4.56	
27	Cg0413	2	1650.7202	-0.3	141	153	0	32.8	24	G	KFSYYTDWVEENA	S	-1.1	3.82	
27	Cg0413	2	1708.825	0.1	195	209	0	29.3	28	T	SLLFPQHFPGFYDAA	A	0.2	4.94	
28	Cg3365	1	583.4309	-0.2	447	451	0	24.1	18	L	ILLLI	I	4.1	6.02	
28	Cg3365	1	651.3665	0.6	240	244	0	24.1	17	I	MYIIL	A	2.7	5.92	
28	Cg3365	1	674.4367	1.5	20	25	0	25.0	24	A	FLIGII	T	3.3	6.02	
28	Cg3365	1	707.4582	2.0	363	369	0	20.9	16	L	ILPGLVP	H	1.8	6.02	
28	Cg3365	1	775.4844	0.9	20	26	0	35.6	23	A	FLIGIIT	A	2.7	6.02	
28	Cg3365	1	794.5266	0.0	361	368	0	21.5	21	V	ALILPGLV	P	2.5	6.02	
28	Cg3365	1	835.3613	-0.2	471	477	0	23.9	23	G	HWDPAPN	R	-1.8	4.94	
28	Cg3365	1	943.5379	-1.3	7	14	0	50.7	29	I	PLFLVNEI	L	1.3	3.3	
28	Cg3365	1	948.5281	0.5	339	348	0	34.6	28	S	SFVGGLVGLT	V	1.6	6.02	
28	Cg3365	2	1009.6536	0.6	151	161	0	27.0	21	I	VVGVGALLLGI	L	2.6	6.02	
28	Cg3365	1	1423.8228	-2.9	361	373	0	40.8	24	V	ALILPGLVPHFFT	G	1.5	7.84	
28	Cg3365	1	1425.7405	1.2	365	379	0	43.1	28	L	PGLVPHFFTGGAAGV	Y	0.8	7.84	
28	Cg3365	1	1477.6979	-2.8	64	78	0	42.0	28	A	SLEPLGAMIMGATGM	R	0.9	3.3	
28	Cg3365	1	1742.9607	-2.0	319	334	0	42.8	28	A	LDAPIVFPYAQNAVLI	G	1.1	3.1	
28	Cg3365	1	1836.0298	-4.0	361	379	0	66.1	27	V	ALILPGLVPHFFTGGAAGV	Y	1.4	7.84	
29	Cg1081	1	773.4171	2.3	9	15	0	35.5	28	A	IDVTDLV	R	1.3	2.92	
29	Cg1081	2	909.5647	0.8	78	85	0	43.9	22	A	ILRPELGI	M	0.8	6.98	
29	Cg1081	1	959.5175	0.2	49	57	0	40.1	29	T	STLEVIEGL	S	0.8	3.12	
29	Cg1081	1	1099.6125	0.0	116	125	0	43.5	28	I	KDVLADVDLL	H	0.7	3.6	
29	Cg1081	1	1399.7824	-3.8	230	242	0	60.4	28	I	SFVLRGGQVELPV	L	0.6	6.98	
29	Cg1081	2	1485.8402	-0.9	217	229	0	45.2	27	G	TLDELVAREKSII	S	0.2	4.44	
29	Cg1081	2	1671.9043	-2.3	215	229	0	33.9	29	V	EGTLDELVAREKSII	S	-0.1	4.16	
29	Cg1081	2	1779.9917	-1.0	78	94	0	39.8	27	A	ILRPELGIMLQSGGLPS	Q	0.5	6.98	
29	Cg1081	1	1799.8942	-2.3	9	24	0	35.8	29	A	IDVTDLVRTYGDYTAV	K	0.2	3.6	
29	Cg1081	2	1842.0098	-1.8	213	229	0	38.7	28	I	AVEGTLDELVAREKSII	S	0.3	4.16	
29	Cg1081	2	2021.1343	-2.8	78	96	0	33.5	27	A	ILRPELGIMLQSGGLPSQL	T	0.5	6.98	
29	Cg1081	2	2169.0511	-0.5	289	308	0	64.9	29	A	TLESVFMDIASLENTSLQTA	-	0.3	2.94	
29	Cg1081	2	3181.6659	-2.4	259	288	0	78.4	31	A	TTTLQQHTLEILTWAAETGIALEGFAAKPA	T	0.2	4.54	
30	Cg0737	1	656.3745	0.9	117	122	0	26.5	26	S	SEIVPL	A	1.1	3.3	
30	Cg0737	1	795.3399	-1.0	102	109	0	28.1	24	A	EYNVGSGA	D	-0.5	3.3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
30	Cg0737	1	894.4236	-0.1	258	264	0	34.1	27	L	WHDPEVL	A	-0.7	4.06	
30	Cg0737	2	935.4461	-0.2	207	214	0	38.3	27	I	NNSFLDRA	G	-0.9	6.78	
30	Cg0737	1	982.388	-1.4	75	83	0	26.0	21	F	SDYSTPNEA	L	-1.5	3	
30	Cg0737	2	1078.6387	-0.3	165	175	0	38.4	23	L	KTPGLVTPAPV	D	0.3	10.1	
30	Cg0737	2	1098.5305	-1.5	278	287	0	32.0	25	P	VDRPGADLQE	I	-1.1	3.7	
30	Cg0737	2	1167.5632	-1.9	143	153	0	52.2	28	I	PNDPSNQGRAI	N	-1.5	6.78	
30	Cg0737	1	1226.5091	-0.3	73	83	0	29.8	23	V	PFSDYSTPNEA	L	-1.2	3	
30	Cg0737	2	1280.6473	-0.2	142	153	0	41.9	28	A	IPNDPSNQGRAI	N	-1.0	6.78	
30	Cg0737	2	1351.6844	-0.1	141	153	0	48.8	28	V	AIPNDPSNQGRAI	N	-0.8	6.78	
30	Cg0737	2	1504.8038	-1.4	253	264	0	42.3	28	A	RLVELWHDPEVL	A	-0.1	4.42	
30	Cg0737	2	1621.8563	0.3	165	180	0	39.0	28	L	KTPGLVTPAPVDIDEA	A	0.0	3.7	
30	Cg0737	2	1652.8522	0.5	84	97	0	67.2	28	A	LAQDQLDVNLFQHL	K	0.0	3.88	
30	Cg0737	2	1980.8476	-0.5	222	238	0	26.4	22	A	VFEDDPESEEAEPYINV	F	-0.9	2.74	
30	Cg0737	2	2328.0322	0.0	222	241	0	29.7	24	A	VFEDDPESEEAEPYINVFVT	K	-0.5	2.74	
30	Cg0737	3	2367.1302	0.4	279	299	0	43.7	29	V	DRPGADLQEILDRLEADQENA	-	-1.2	3.62	
30	Cg0737	2	2857.3181	0.2	58	83	0	53.8	27	V	FEDKAAEEGITLDIVPFSDYSTPNEA	L	-0.5	3.32	
31	Cg1368	1	963.3822	-1.0	322	330	0	25.7	22	A	DDYTDPAPA	T	-1.3	2.82	
31	Cg1368	1	993.5019	-1.4	437	445	0	32.6	27	G	SYVPLTDTV	D	0.4	3.1	
31	Cg1368	1	1157.5863	-2.0	73	84	0	28.8	28	I	AMAPTDGLVRGA	A	0.4	6.78	
31	Cg1368	2	1173.5812	0.5	73	84	0	36.1	28	I	AMAPTDGLVRGA	A	0.4	6.78	Oxidation (M)
31	Cg1368	1	1228.6088	-3.3	28	38	0	39.4	27	V	DVEFPRGELPA	L	-0.5	3.82	
31	Cg1368	2	1256.5997	-0.2	335	345	0	59.4	27	A	HLDATTELDRS	I	-1.0	4.3	
31	Cg1368	1	1264.5493	-4.6	399	409	0	36.6	24	L	GMDELSEEDKI	T	-1.1	3.5	
31	Cg1368	1	1326.6721	-3.5	418	428	0	31.3	28	I	ERFLGQNFFVA	E	0.3	6.98	
31	Cg1368	2	1372.702	0.8	292	303	0	34.3	30	T	LADEMGVLQERI	T	0.1	3.82	
31	Cg1368	1	1377.6333	-1.5	398	409	0	49.2	27	I	LGMDELSEEDKI	T	-0.7	3.5	
31	Cg1368	2	1426.7456	0.9	26	38	0	63.7	29	A	VVDVEFPRGELPA	L	0.2	3.82	
31	Cg1368	2	1440.7209	0.6	335	347	0	39.2	29	A	HLDATTELDRSIA	S	-0.4	4.3	
31	Cg1368	2	1473.7497	-0.3	292	304	0	42.0	29	T	LADEMGVLQERIT	S	0.0	3.82	
31	Cg1368	2	1561.7545	-0.4	396	409	0	59.5	28	I	AILGMDELSEEDKI	T	-0.2	3.5	
31	Cg1368	2	1648.7865	-0.4	398	412	0	45.2	28	I	LGMDELSEEDKITVA	R	-0.2	3.5	
31	Cg1368	2	2095.095	-0.9	464	483	0	37.7	29	A	FNGLGGLDDVEAAYKKLTGK	-	-0.4	6.96	
31	Cg1368	2	2157.1066	-2.4	335	354	0	46.8	30	A	HLDATTELDRSIASKGIYPA	V	-0.3	5.28	
32	Cg0957	1	532.2646	1.1	1801	1805	0	30.8	29	T	GTWGL	P	0.3	6.02	
32	Cg0957	1	599.3894	1.5	1569	1573	0	30.2	19	L	LIELL	S	2.5	3.3	
33	Cg2843	1	641.3384	0.2	23	28	0	40.7	29	V	NLEVPA	R	0.2	3.3	
33	Cg2843	1	829.3858	0.5	218	224	0	23.1	22	A	FYSLEAT	G	0.3	3.3	
33	Cg2843	1	1109.6444	-2.1	160	169	0	34.5	24	A	RAIAVEPEIL	L	0.8	4.26	
33	Cg2843	1	1197.5455	-3.5	10	19	0	36.1	25	V	NIYYGDFHAV	Q	0.0	4.94	
33	Cg2843	1	1331.5881	-3.4	213	224	0	35.8	25	V	SDQTAFYSLEAT	G	-0.4	3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
33	Cg2843	1	1353.769	-4.1	160	171	0	47.9	26	A	RAIAVEPEILLM	D	1.1	4.26	
33	Cg2843	2	1626.7049	-1.3	240	252	0	73.0	24	I	FENPDQKETEDYI	S	-1.9	3.5	
33	Cg2843	2	1770.7584	-1.7	240	254	0	86.7	22	I	FENPDQKETEDYISG	R	-1.7	3.5	
33	Cg2843	2	1873.9673	-0.1	64	80	0	43.1	29	G	EILLDGENIYGSKIDPV	A	0.0	3.58	
33	Cg2843	2	2059.0837	-2.9	62	80	0	46.2	30	V	KGEILLDGENIYGSKIDPV	A	-0.3	4.06	
33	Cg2843	2	2130.9494	-1.9	240	257	0	103.8	24	I	FENPDQKETEDYISGRFG	-	-1.6	3.92	
33	Cg2843	2	2392.2526	-1.3	59	80	0	47.4	30	G	AYVKGEILLDGENIYGSKIDPV	A	0.0	4.06	
34	Cg0924	1	995.5651	-2.9	258	267	0	26.1	24	I	AAANPDLILV	M	1.3	3.1	
34	Cg0924	2	1150.5289	-0.7	266	276	0	63.5	28	I	LVMDRDGGTST	R	-0.4	3.88	
34	Cg0924	2	1206.588	0.6	182	192	0	58.7	28	I	VADFESALERA	K	0.0	3.82	
34	Cg0924	1	1255.7176	-1.8	83	94	0	36.7	28	V	AAPLQLVPFTVT	G	1.2	6.02	
34	Cg0924	1	1361.7231	-1.8	225	237	0	39.2	28	T	YGPIFDLVGLTPA	L	0.9	3.1	
34	Cg0924	1	1508.6518	-2.7	166	179	0	43.0	24	A	ETLGEIFGEEEDAA	K	-0.6	2.8	
34	Cg0924	2	1935.9789	0.5	146	162	0	36.9	29	T	VVELDPRDGEPLDQELI	R	-0.5	3.38	
34	Cg0924	2	2517.1767	-2.0	315	336	0	28.0	28	Y	TNENIITYTEILNGMADMFEKA	A	-0.2	3.68	
34	Cg0924	2	2896.3146	-0.6	312	336	0	108.6	26	A	DTYTNENIITYTEILNGMADMFEKA	A	-0.4	3.5	
34	Cg0924	2	3095.4103	-1.3	312	338	0	66.6	25	A	DTYTNENIITYTEILNGMADMFEKAAQ	-	-0.4	3.5	
34	Cg0924	3	3583.6801	-1.3	148	179	0	62.8	28	V	ELDPRDGEPLDQELIRQAETLGEIFGEEEDAA	K	-1.0	3.42	
34	Cg0924	3	3781.817	-2.1	146	179	0	53.5	30	T	VVELDPRDGEPLDQELIRQAETLGEIFGEEEDAA	K	-0.7	3.42	
35	Cg1314	1	690.3952	1.0	323	328	0	39.6	26	S	IFLDLA	R	2.2	3.1	
35	Cg1314	1	715.3653	0.6	251	257	0	32.1	25	G	NLGWGLG	Y	0.3	6.02	
35	Cg1314	1	800.4796	-0.2	466	473	0	34.3	30	E	IIPGFALA	T	2.2	6.02	
35	Cg1314	1	953.4454	-0.8	316	323	0	26.2	25	T	DTRAYESI	F	-1.0	4.08	
35	Cg1314	1	1079.4746	-3.0	211	219	0	32.1	24	A	NPMDIWSFA	N	0.1	3.1	
35	Cg1314	2	1127.6802	-0.4	362	371	0	34.1	24	S	SLIEDLLKVV	K	1.3	4.08	
35	Cg1314	1	1146.4903	-2.7	30	38	0	25.0	23	T	EKYDDYMLA	G	-1.1	3.7	
35	Cg1314	1	1214.7122	-2.4	361	371	0	26.4	25	A	SSLIEDLLKVV	K	1.1	4.08	
35	Cg1314	1	1263.5958	-2.5	209	219	0	32.6	28	A	LANPMDIWSFA	N	0.6	3.1	
35	Cg1314	1	1265.5412	-1.0	503	514	0	31.0	24	A	AAVESNEDVDFA	D	-0.1	2.84	
35	Cg1314	1	1328.701	-0.2	399	411	0	33.5	28	A	MAINPSDSILGLV	G	1.1	3.1	
35	Cg1314	2	1657.6969	-0.7	220	235	0	66.3	21	A	NSNDYGPHTDGIGNPT	Y	-1.5	3.88	
35	Cg1314	2	1735.8152	-0.3	484	498	0	32.0	28	L	TKEPSEEILNEFETA	K	-1.1	3.68	
35	Cg1314	2	2049.0153	-1.6	481	498	0	44.7	30	V	SLLTKEPSEEILNEFETA	K	-0.5	3.68	
36	Cg2810	1	584.3897	1.5	36	41	0	31.7	31	L	ILGLVA	R	3.0	6.02	
36	Cg2810	1	640.4523	0.3	32	37	0	30.8	25	L	ILGLIL	G	3.3	6.02	
36	Cg2810	1	640.4523	-0.9	31	36	0	28.6	25	G	LILGLI	L	3.3	6.02	
36	Cg2810	1	1246.6558	-1.9	54	66	0	38.6	29	A	SWLTGLLSGVGSA	Y	0.9	6.02	
36	Cg2810	2	1317.63	-1.4	452	463	0	34.3	29	A	TVSEKETEPAEV	R	-1.0	3.8	
36	Cg2810	1	1547.7468	-1.7	50	65	0	31.0	29	A	DGEASWLTGLLSGVGS	A	0.3	3	
36	Cg2810	1	1614.8002	-3.1	427	440	0	52.5	29	V	AKREGILDQDVWDA	A	-0.8	3.96	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
36	Cg2810	1	1618.7839	-3.5	50	66	0	33.5	28	A	DGEASWLTGLLSGVGSA	Y	0.4	3	
36	Cg2810	2	2015.0476	-1.5	139	157	0	33.5	30	A	ADPSRVGSWLGFIQSVIPS	N	0.3	6.78	
36	Cg2810	2	2200.1277	-4.0	137	157	0	33.8	30	S	NAADPSRVGSWLGFIQSVIPS	N	0.2	6.78	
37	Cg0756	1	545.3213	-0.2	580	584	0	29.7	26	F	PLFGI	A	1.8	6.02	
37	Cg0756	1	601.3873	0.8	200	204	0	22.9	16	S	IMIII	I	4.0	6.02	
37	Cg0756	1	635.3683	0.5	358	362	0	24.1	19	F	PFLFI	T	2.5	6.02	
37	Cg0756	1	816.4382	0.0	618	624	0	34.4	32	L	AWDLIVT	M	1.3	3.1	
37	Cg0756	2	900.5029	0.4	668	675	0	36.5	30	A	IDAVIRNT	M	0.4	6.78	
37	Cg0756	1	1245.7122	-1.8	573	584	0	31.3	26	L	GGINVLFPLFGI	A	1.7	6.02	
37	Cg0756	1	1273.6489	-3.1	329	339	0	43.2	28	I	LFARPEVQMPS	V	-0.1	6.98	
37	Cg0756	1	1376.6183	-2.8	743	754	0	46.1	26	A	MWDERYPGGAPV	S	-0.8	4.08	
37	Cg0756	1	1575.7106	-2.2	633	646	0	54.1	25	I	FHSDPAIGYWAQNA	N	-0.4	4.94	
37	Cg0756	1	1598.6624	-3.9	716	729	0	24.3	20	T	TEEPDTESEFFAPT	G	-1.2	2.84	
37	Cg0756	2	1771.8637	1.0	481	498	0	30.1	29	A	FGMSEILSGFIGGAGMKA	F	0.8	6.94	
37	Cg0756	1	1986.8735	-3.3	716	733	0	42.2	23	T	TEEPDTESEFFAPTGFLA	S	-0.5	2.84	
38	Cg3008	1	630.3489	-0.3	32	37	0	30.3	22	S	KWAGAV	A	0.4	10.1	
38	Cg3008	1	642.3952	1.2	39	44	0	43.8	27	A	DLIGLL	G	2.0	3.1	
38	Cg3008	1	668.317	1.5	24	29	0	30.8	28	V	FDFLGA	S	1.2	3.1	
38	Cg3008	1	699.4167	1.1	39	45	0	41.6	30	A	DLIGLLG	-	1.7	3.1	
38	Cg3008	1	701.386	-0.7	32	38	0	28.0	26	S	KWAGAVA	D	0.6	10.1	
38	Cg3008	1	770.4538	0.5	38	45	0	46.6	29	V	ADLIGLLG	-	1.7	3.1	
38	Cg3008	1	802.3902	0.1	22	27	0	35.2	28	G	YVFDFL	G	1.5	3.1	
38	Cg3008	1	804.413	-1.2	30	37	0	38.9	26	A	SSKWAGAV	A	0.1	10.1	
38	Cg3008	1	859.4116	0.6	21	27	0	35.4	26	I	GYVFDFL	G	1.2	3.1	
38	Cg3008	1	869.5222	-0.3	37	45	0	51.9	27	A	VADLIGLLG	-	2.0	3.1	
38	Cg3008	2	875.4501	1.0	30	38	0	44.8	28	A	SSKWAGAVA	D	0.3	10.1	
38	Cg3008	1	930.4487	-0.8	22	29	0	44.9	28	G	YVFDFLGA	S	1.3	3.1	
38	Cg3008	1	987.4702	-1.8	21	29	0	41.5	27	I	GYVFDFLGA	S	1.1	3.1	
38	Cg3008	2	1229.6332	1.2	17	27	0	55.4	30	G	SGLIGYVFDFL	G	1.4	3.1	
38	Cg3008	2	1270.6598	-1.3	18	29	0	45.0	28	S	GLIGYVFDFLGA	S	1.5	3.1	
38	Cg3008	1	1357.6918	-2.6	17	29	0	29.2	29	G	SGLIGYVFDFLGA	S	1.3	3.1	
39	Cg0834	1	716.3493	1.3	176	181	0	40.9	28	A	NWADLV	E	0.3	3.1	
39	Cg0834	1	859.4803	-0.7	293	299	0	33.3	31	G	KFEVQPL	V	-0.2	6.94	
39	Cg0834	1	880.4331	0.2	384	391	0	47.0	29	V	SPFYPAIS	K	0.4	5.92	
39	Cg0834	1	918.4811	0.0	151	158	0	37.0	30	T	LYALPQNT	N	-0.2	5.92	
39	Cg0834	2	965.5294	1.2	375	383	0	27.1	25	S	LENAAPRPV	S	-0.3	6.98	
39	Cg0834	1	987.5389	-0.4	291	299	0	44.6	30	T	AGKFEVQPL	V	0.0	6.94	
39	Cg0834	2	1063.5298	-1.0	392	401	0	31.2	29	S	KAIQDNAYAA	L	-0.4	6.68	
39	Cg0834	1	1163.5492	-0.8	412	422	0	43.3	29	A	TTDMKAAIENA	S	-0.4	4.08	
39	Cg0834	2	1179.5441	-1.9	412	422	0	35.7	27	A	TTDMKAAIENA	S	-0.4	4.08	Oxidation (M)

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
39	Cg0834	2	1422.783	0.5	371	383	0	79.6	26	A	LKESLENAAPRPV	S	-0.6	7.1	
39	Cg0834	2	1850.8758	-0.3	308	325	0	97.0	28	V	STLGGYNNGINVNSENKA	T	-0.9	6.86	
39	Cg0834	2	1856.8792	-1.5	119	135	0	40.0	28	A	ANQWLAPLEGDLEVDTS	G	-0.4	2.84	
39	Cg0834	2	1938.9323	-1.2	326	341	0	52.4	29	A	TARDFIEFIINEENQT	W	-0.6	3.68	
39	Cg0834	2	2000.9255	-0.6	354	370	0	47.2	27	A	SIYDDESLVEQYPYLPA	L	-0.5	2.84	
40	Cg2743	1	641.3748	1.2	1891	1897	0	37.5	29	R	GVAVSLP	S	1.6	6.02	
40	Cg2743	1	656.3745	-1.2	1529	1534	0	27.1	27	H	LDSLIP	A	1.0	3.1	
40	Cg2743	1	854.4143	3.6	2518	2524	0	31.5	28	R	MAMTRFV	G	1.1	11.04	
40	Cg2743	1	861.4596	4.1	1765	1773	0	32.8	30	L	GVEFGLGAI	D	1.4	3.3	
41	Cg1082	1	582.3741	0.7	252	257	0	28.1	27	I	PLGILA	A	2.0	6.02	
41	Cg1082	1	640.416	1.6	129	134	0	29.5	23	F	TVVIIP	L	2.5	6.02	
41	Cg1082	1	640.4523	0.3	155	160	0	30.8	25	V	LIGLLL	C	3.2	6.02	
41	Cg1082	1	1108.7294	-1.3	130	139	0	23.1	14	T	VVIIPLLMVL	G	3.3	6.02	
41	Cg1082	1	1315.721	-2.1	244	255	0	32.8	28	A	GIFQDMLIPLGI	L	1.4	3.1	
41	Cg1082	1	1424.8391	-2.7	51	65	0	41.8	24	V	GIPLLLFLIGNGGAA	E	1.6	6.02	
41	Cg1082	1	1427.8792	0.8	46	58	0	27.4	21	A	TVFPVGIPLLLFL	I	2.3	6.02	
41	Cg1082	2	1640.9137	-0.9	51	67	0	30.2	26	V	GIPLLLFLIGNGGAAES	A	1.2	3.3	
41	Cg1082	1	1831.9906	-2.3	241	257	0	35.5	29	A	NFAGIFQDMLIPLGILA	A	1.4	3.1	
41	Cg1082	1	1848.9873	-4.9	207	223	0	29.6	29	A	DILAYTPFAAISDLVQI	G	1.1	2.92	
41	Cg1082	1	1903.0277	-0.7	241	258	0	51.3	28	A	NFAGIFQDMLIPLGILAA	W	1.4	3.1	
41	Cg1082	1	1968.1448	-0.4	46	65	0	53.8	24	A	TVFPVGIPLLLFLIGNGGAA	E	1.6	6.02	
42	Cg2845	1	526.3115	0.8	114	118	0	32.0	30	I	PNLLA	A	0.9	6.02	
42	Cg2845	1	755.4615	-1.7	223	229	0	20.6	19	V	MILPVIA	A	2.7	6.02	
42	Cg2845	1	815.3524	0.4	107	113	0	24.9	24	I	DAMYFGI	P	0.8	3.1	
42	Cg2845	1	925.567	-3.3	222	230	0	25.3	25	A	VMILPVIAA	T	2.8	6.02	
42	Cg2845	1	1116.5961	-1.6	275	285	0	36.6	29	A	MLGLGRALGET	M	0.5	6.98	
42	Cg2845	1	1318.6737	-4.3	275	287	0	31.3	29	A	MLGLGRALGETMA	L	0.7	6.98	
42	Cg2845	1	1394.6904	-2.6	107	119	0	36.2	28	I	DAMYFGIPNLLAA	T	0.9	3.1	
42	Cg2845	1	1464.7357	1.5	155	168	0	32.2	28	L	GYMVDMLAAVPSIV	Y	1.5	3.1	
42	Cg2845	2	1647.8064	-1.9	2	16	0	44.5	30	M	ATNESVSEKQRLDAT	R	-1.2	4.44	
43	Cg2195	2	835.4804	0.5	108	115	0	39.6	23	L	VYTGVIKG	-	0.8	9.72	
43	Cg2195	1	1014.6114	-0.1	94	103	0	38.0	27	A	SLLGVIVFPA	Y	2.2	6.02	
43	Cg2195	1	1130.4516	-1.4	50	59	0	29.5	19	V	GEDWDADQPV	T	-1.4	2.78	
43	Cg2195	1	1229.5201	-1.1	49	59	0	35.0	22	A	VGEDWDADQPV	T	-0.9	2.78	
43	Cg2195	1	1300.5572	0.5	48	59	0	31.6	22	A	AVGEDWDADQPV	T	-0.7	2.78	
43	Cg2195	2	2158.9039	-1.7	60	78	0	65.4	19	V	TGEDIFGEEHERDNENTPA	W	-1.8	3.74	
43	Cg2195	3	3271.345	-1.0	50	78	0	90.7	15	V	GEDWDADQPVTGEDIFGEEHERDNENTPA	W	-1.7	3.42	
43	Cg2195	3	3370.4134	-1.2	49	78	0	73.8	17	A	VGEDWDADQPVTGEDIFGEEHERDNENTPA	W	-1.5	3.42	
43	Cg2195	3	3441.4505	-1.6	48	78	0	101.2	17	A	AVGEDWDADQPVTGEDIFGEEHERDNENTPA	W	-1.4	3.42	
43	Cg2195	3	3512.4876	-1.3	47	78	0	73.7	17	A	AAVGEDWDADQPVTGEDIFGEEHERDNENTPA	W	-1.3	3.42	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
44	Cg1556	1	526.3115	0.8	92	96	0	32.0	30	I	PNILA	R	1.0	6.02	
44	Cg1556	1	761.4072	0.7	260	266	0	54.8	28	A	NFALQVA	E	1.1	6.02	
44	Cg1556	1	853.5273	-0.6	89	96	0	29.1	24	I	LTIPNILA	R	1.6	6.02	
44	Cg1556	1	895.3712	0.2	100	106	0	44.0	25	A	FWETQDA	D	-1.1	3	
44	Cg1556	1	903.543	1.2	121	129	0	32.7	25	I	ALLGGLFIT	S	2.1	6.02	
44	Cg1556	1	938.4822	-1.3	27	35	0	46.3	26	S	AHVEGTQVV	L	0.3	5.12	
44	Cg1556	1	966.6113	0.6	88	96	0	24.6	22	A	ILTIPNILA	R	1.9	6.02	
44	Cg1556	1	1109.5241	-1.5	12	22	0	36.5	28	A	SVYVADGAETV	L	0.5	3	
44	Cg1556	1	1120.54	-1.6	260	269	0	37.3	29	A	NFALQVAEET	S	0.0	3.12	
44	Cg1556	1	1251.7802	-1.7	85	96	0	21.7	20	A	TLAILTIPNILA	R	1.8	6.02	
44	Cg1556	2	1683.7264	0.3	223	237	0	24.2	23	A	TSYLEENSGDWLEAA	Q	-0.7	2.88	
44	Cg1556	1	1776.7479	-1.9	172	186	0	42.4	21	A	SDWFNDTSDKVTEYA	Y	-1.2	3.5	
44	Cg1556	2	2014.9272	-0.3	187	203	0	50.8	27	A	YTAQDFVGENKDDWIKS	A	-1.2	3.96	
45	Cg1228	1	853.4294	-1.4	225	233	0	28.3	26	V	GQLPGAQPS	T	-0.7	6.02	
45	Cg1228	1	1029.4767	-0.4	425	433	0	28.5	26	V	SVTHDPDFI	A	-0.2	3.88	
45	Cg1228	2	1048.5553	1.1	125	134	0	38.6	28	V	GLDLPLSHPT	K	0.0	4.94	
45	Cg1228	2	1080.5928	-0.6	223	233	0	26.4	26	I	KVGQLPGAQPS	T	-0.5	10.1	
45	Cg1228	2	1187.6146	-1.3	261	273	0	67.9	30	A	STVITGPNGAGKS	T	-0.2	10.1	
45	Cg1228	2	1288.6623	-1.7	261	274	0	31.3	29	A	STVITGPNGAGKST	L	-0.2	10.1	
45	Cg1228	2	1560.8181	0.1	411	424	0	47.8	30	V	TMLRELTDNGISIV	S	0.4	4.08	
45	Cg1228	2	2276.1464	-1.4	391	410	0	39.1	30	K	LLILDEPTFGQDPETFTELV	T	0.1	2.8	
46	Cg1345	1	675.3956	0.7	183	189	0	39.7	28	M	GFGLLGI	G	2.0	6.02	
46	Cg1345	1	689.4112	1.5	268	273	0	34.7	27	A	QFGLII	N	2.0	6.02	
46	Cg1345	1	977.5182	-0.5	131	141	0	31.6	28	A	ALTGIGGGVFS	G	1.3	6.02	
46	Cg1345	1	998.6165	-3.3	300	309	0	25.4	25	A	FLGPLIGALV	R	2.2	6.02	
46	Cg1345	1	1150.6097	-1.8	85	94	0	39.2	28	I	YMFLPPILGT	R	1.1	5.92	
46	Cg1345	1	1216.722	-1.4	298	309	0	24.9	24	T	FAFLGPLIGALV	R	2.2	6.02	
47	Cg0587	1	698.3275	1.0	47	52	0	34.3	26	A	FAFDSI	D	1.3	3.1	
47	Cg0587	1	930.5208	0.9	187	194	0	40.0	29	W	GKQILELM	Q	0.3	6.94	
47	Cg0587	1	1050.4505	-0.5	38	46	0	27.1	25	A	DTYPELNEA	F	-1.3	2.94	
47	Cg0587	1	1142.6812	-2.2	126	135	0	32.0	25	A	RQVGVPYILV	A	1.0	9.84	
47	Cg0587	1	1234.5717	-1.1	36	46	0	31.1	28	V	LADTYPELNEA	F	-0.6	2.94	
47	Cg0587	2	1237.5251	-1.1	300	310	0	37.2	23	G	AYTPHTEFEGS	V	-1.0	4.24	
47	Cg0587	1	1391.6092	-1.2	160	171	0	37.1	25	L	LAEQDYDEEAPI	V	-1.0	2.8	
47	Cg0587	2	1461.7351	0.8	34	46	0	42.0	29	T	KVLADTYPELNEA	F	-0.5	3.82	
48	Cg2184	1	773.4171	1.3	287	293	0	43.8	30	G	IESAELL	S	0.9	3.12	
48	Cg2184	1	867.5065	0.7	474	481	0	26.4	25	A	LALNPEVI	V	1.2	3.3	
48	Cg2184	1	1044.5638	-2.6	438	446	0	32.2	30	A	RVAELLDMV	S	0.9	4.08	
48	Cg2184	1	1146.5153	-3.1	280	290	0	29.2	25	I	QSAQEQGIESA	E	-1.0	3.12	
48	Cg2184	2	1190.6143	-1.7	350	362	0	71.4	27	A	LVGESGSGKSTVA	N	0.2	6.94	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
48	Cg2184	2	1261.6514	-0.4	349	362	0	53.6	30	T	ALVGESGSGKSTVA	N	0.3	6.94	
48	Cg2184	1	1267.5543	-1.0	402	412	0	33.6	25	V	FQNPYGSLDPM	Y	-0.7	3.1	
48	Cg2184	2	1949.0193	-0.6	106	122	0	48.6	29	I	GLVPQDPMTNLNPVWRI	G	-0.2	6.78	
49	Cg3395	1	582.3741	0.7	219	224	0	28.1	27	I	PLGIIA	V	2.1	6.02	
49	Cg3395	1	670.3149	1.5	75	80	0	39.8	23	V	MFGFAV	S	2.2	6.02	
49	Cg3395	1	796.5058	0.5	117	124	0	35.7	23	T	ALIGLLPT	A	1.9	6.02	
49	Cg3395	1	844.5058	-1.4	320	327	0	26.5	26	M	SLLLPFVG	M	2.0	6.02	
49	Cg3395	2	1123.6601	2.1	88	99	0	35.6	24	L	GGLVLGPLGDKV	G	0.8	6.76	
49	Cg3395	2	1258.6193	-0.1	296	306	0	52.7	28	V	YLEEQIGLHSA	S	-0.2	4.24	
49	Cg3395	2	1726.7621	-0.4	488	502	0	93.3	25	S	HMPFPDEENVGAEKQ	N	-1.4	4.16	
49	Cg3395	2	2039.9548	-1.8	230	247	0	37.7	28	T	RIPETPAFENNQDEPNAV	V	-1.3	3.68	
50	Cg1995	2	668.3969	1.0	388	393	0	44.1	24	M	RLPNIG	Q	-0.3	11.04	
50	Cg1995	1	755.3701	0.1	727	733	0	26.7	22	T	VEPDPVT	G	-0.4	3	
51	Cg0780	1	1019.4899	-1.0	132	140	0	32.2	28	A	LWSGLGWMA	N	0.9	6.02	
51	Cg0780	1	1087.6277	-0.6	248	258	0	38.2	27	A	ALLGAIGFEVV	K	2.1	3.3	
51	Cg0780	1	1205.6656	-2.7	189	199	0	55.0	26	A	SGLTKNLLDFV	G	0.5	6.76	
51	Cg0780	2	1742.0342	-0.5	249	265	0	44.4	22	A	LLGAIGFEVVKQVGSLL	A	1.4	6.94	
51	Cg0780	2	1813.0713	-0.2	248	265	0	36.2	23	A	ALLGAIGFEVVKQVGSLL	A	1.4	6.94	
51	Cg0780	2	2029.1096	0.0	189	208	0	38.2	28	A	SGLTKNLLDFVGLGEIPGIS	Y	0.6	4.08	
52	Cg2262	1	656.3381	-1.2	175	180	0	29.0	27	A	IVEEPA	V	0.3	3.12	
52	Cg2262	2	891.416	0.7	371	378	0	37.7	27	A	MPYEGKPA	V	-1.1	6.86	
52	Cg2262	1	1038.5233	-0.8	206	215	0	26.1	26	V	VEEPAVAEVP	E	0.3	3.02	
52	Cg2262	1	1238.603	-1.5	199	210	0	36.0	28	A	VAEEPAVVEEPA	V	0.1	2.96	
52	Cg2262	1	1252.6187	-1.0	175	186	0	37.1	29	A	IVEEPAVAEEPA	V	0.1	2.96	
52	Cg2262	1	1591.7617	-3.0	249	263	0	33.8	28	A	ALEETPVPDVEPEPA	A	-0.6	2.84	
52	Cg2262	2	1728.8934	0.6	551	567	0	35.0	30	V	KLVGLGEGADDLAPFEV	E	0.3	3.58	
52	Cg2262	1	1848.8992	-4.1	171	188	0	50.0	30	A	EEPAIVEEPAVAEEPAVA	E	0.0	2.86	
52	Cg2262	2	2021.9681	-0.8	150	168	0	47.1	29	V	VAVEPEVETEEPAVVEEPA	V	-0.2	2.82	
52	Cg2262	2	2630.348	-1.2	551	576	0	39.0	31	V	KLVGLGEGADDLAPFEVEGFVDALLG	-	0.5	3.38	
52	Cg2262	3	2709.2756	-1.2	126	149	0	52.5	29	A	TPEPETSDDVVEEPEVKEPEVKEV	V	-1.3	3.56	
53	Cg3368	1	621.356	0.8	87	91	0	22.5	19	M	MVLLF	S	3.3	6.02	
53	Cg3368	1	656.3745	-1.2	313	318	0	27.1	27	L	IDSLLP	S	1.0	3.1	
53	Cg3368	1	672.4058	1.5	312	317	0	31.8	24	P	LIDSLL	P	1.9	3.1	
53	Cg3368	1	709.4738	1.4	357	363	0	42.6	21	S	IAVVLPV	I	3.0	6.02	
53	Cg3368	1	1032.612	-2.5	459	467	0	25.0	22	I	HLAWLPIIA	A	1.6	7.84	
53	Cg3368	1	1060.6169	-1.2	472	481	0	32.5	25	V	TLLGPLFSLT	E	1.4	6.02	
53	Cg3368	1	1345.7857	-2.7	469	481	0	24.7	23	A	SVVTLLGPLFSLT	E	1.6	6.02	
53	Cg3368	1	1416.8228	-0.8	468	481	0	34.2	24	A	ASVVTLLGPLFSLT	E	1.7	6.02	
53	Cg3368	2	2732.352	-1.0	472	495	0	82.3	30	V	TLLGPLFSLTEQQMEFSPLTHSWA	N	0.1	4.24	
53	Cg3368	2	2831.4415	-1.1	468	493	0	62.9	31	A	ASVVTLLGPLFSLTEQQMEFSPLTHS	W	0.4	4.24	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
54	Cg2912	1	794.3923	-0.6	175	181	0	53.0	27	V	THDVNPL	M	-0.6	4.94	
54	Cg2912	2	926.5185	-1.0	29	38	0	26.4	26	A	VLGPNGVGKS	T	0.1	10.1	
54	Cg2912	2	962.5437	0.0	158	166	0	31.4	27	T	VSLFGELKA	E	0.9	6.94	
54	Cg2912	2	1097.5869	2.1	189	198	0	30.6	26	I	LYLAPNGHTI	G	0.3	7.76	
54	Cg2912	2	1403.766	0.9	158	171	0	57.9	27	T	VSLFGELKAEGVGV	V	0.9	4.26	
54	Cg2912	1	1463.8347	-1.4	136	148	0	40.0	23	T	RPQLLLADEPLLS	L	0.1	4.08	
54	Cg2912	2	1578.8188	-2.9	175	188	0	47.9	29	V	THDVNPLMGLVDRI	L	0.1	5.1	
54	Cg2912	2	1700.9713	0.5	158	174	0	47.3	25	T	VSLFGELKAEGVGVVVV	T	1.4	4.26	
54	Cg2912	2	1971.9724	0.6	189	207	0	38.1	30	I	LYLAPNGHTIGTVGDVMQS	E	0.2	4.94	
54	Cg2912	2	3415.7334	-3.0	189	220	0	41.9	31	I	LYLAPNGHTIGTVGDVMQSEKLSELYNAPVTV	A	0.1	4.42	
55	Cg1791	1	1013.4454	-1.1	98	107	0	25.4	24	S	TGFFTDANAA	K	0.2	3.1	
55	Cg1791	2	1390.694	-0.6	32	44	0	48.8	29	V	AVNDLTDNKTLST	L	-0.6	3.88	
55	Cg1791	2	1450.7126	0.8	165	177	0	53.8	29	V	LNDKFGIENGLMT	T	-0.2	4.08	
55	Cg1791	2	1551.7603	-1.0	165	178	0	58.5	29	V	LNDKFGIENGLMTT	V	-0.2	4.08	
55	Cg1791	2	1566.7526	0.1	60	73	0	67.9	29	V	EYDDDSITVGGKRI	A	-0.9	3.96	
55	Cg1791	2	1650.8287	0.1	165	179	0	47.6	29	V	LNDKFGIENGLMTTV	H	0.1	4.08	
55	Cg1791	3	2907.5012	-1.7	34	59	0	55.3	31	V	NDLTDNKTLSTLLKFDSIMGRLGQEV	E	-0.3	4.46	
55	Cg1791	3	3077.6067	0.2	32	59	0	58.1	31	V	AVNDLTDNKTLSTLLKFDSIMGRLGQEV	E	-0.1	4.46	
56	Cg2844	1	640.416	2.0	102	107	0	26.8	23	S	VISIPI	G	2.6	6.02	
56	Cg2844	1	695.4581	-0.7	43	49	0	27.3	24	M	LIAAVPL	V	2.6	6.02	
56	Cg2844	1	815.4753	-2.1	214	222	0	29.2	29	T	ALSGIVTGV	M	1.8	6.02	
56	Cg2844	1	1086.4883	-1.2	247	256	0	42.7	25	I	NWNPFGGPQA	S	-1.1	6.02	
56	Cg2844	1	1130.6369	-1.8	214	225	0	43.3	28	T	ALSGIVTGVMLA	V	2.0	6.02	
56	Cg2844	1	1871.9062	-2.6	247	263	0	53.5	28	I	NWNPFGGPQASLPLMML	D	0.1	6.02	
56	Cg2844	2	2480.1691	-0.6	247	268	0	68.3	28	I	NWNPFGGPQASLPLMMLDMYKA	G	-0.1	6.68	
56	Cg2844	2	2877.3652	-4.0	247	273	0	58.8	28	I	NWNPFGGPQASLPLMMLDMYKAGTAPA	T	-0.1	6.68	
57	Cg2984	1	621.356	0.8	125	129	0	22.5	19	P	MVIIF	G	3.6	6.02	
57	Cg2984	1	1275.8206	-4.2	16	26	0	15.1	14	V	ILIVLFLVSLF	S	3.4	6.02	
57	Cg2984	2	1491.7821	1.1	555	567	0	52.5	28	A	TIDTEVQFLLDKA	H	0.1	3.7	
57	Cg2984	2	1562.8192	-0.4	554	567	0	36.8	29	A	ATIDTEVQFLLDKA	H	0.2	3.7	
58	Cg1169	1	1059.4873	-2.2	507	517	0	29.0	26	T	LVDGPPGSDFG	V	-0.1	2.92	
58	Cg1169	1	1104.6219	-0.8	68	77	0	33.3	26	A	GIPLLFLDFA	I	1.8	3.1	
58	Cg1169	1	1175.659	-1.5	67	77	0	27.0	27	T	AGIPLLFLDFA	I	1.8	3.1	
58	Cg1169	1	1304.535	-0.9	134	144	0	33.2	20	A	WGADPDTYFFS	D	-0.5	2.92	
58	Cg1169	2	1445.7741	-0.5	494	506	0	33.0	28	A	AFLLPMVSWPKGT	L	0.6	10.1	
58	Cg1169	1	1679.7144	-3.6	134	147	0	25.8	21	A	WGADPDTYFFSDFL	N	-0.2	2.82	
58	Cg1169	3	2030.0473	-0.2	507	525	0	52.0	29	T	LVDGPPGSDFGVLPEFKRT	L	-0.3	4.3	
58	Cg1169	2	2249.0237	-0.2	534	554	0	64.0	26	A	SNDPISPFDANEDASRFPTVA	I	-0.7	3.5	
59	Cg1001	1	771.3915	-1.8	52	58	0	27.7	27	V	EGLGFHI	R	0.5	5.12	
59	Cg1001	1	773.4171	1.3	115	121	0	30.0	30	A	SIEAELL	T	0.9	3.12	

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59	Cg1001	1	866.4538	0.6	66	73	0	29.1	26	T	FVDFGAVI	T	2.1	3.1	
59	Cg1001	1	945.3927	-1.0	106	114	0	24.4	21	K	GVEEDETPA	S	-1.2	2.88	
59	Cg1001	1	1068.5492	0.5	65	74	0	33.2	28	A	TFVDFGAVIT	A	1.5	3.1	
59	Cg1001	1	1273.6918	-2.2	33	44	0	37.8	28	T	AFSESIINPLIA	S	1.1	3.3	
59	Cg1001	3	2324.2699	-1.9	117	135	0	33.0	28	I	EAELLTEIRDLLQEQKRLQ	-	-0.9	4.36	
59	Cg1001	3	2524.386	1.1	115	135	0	92.4	28	A	SIEAELLTEIRDLLQEQKRLQ	-	-0.6	4.36	
60	Cg2032	1	553.3839	1.3	353	357	0	24.5	24	W	LIVIP	V	3.1	6.02	
61	Cg2361	2	1015.5047	-0.5	121	129	0	31.3	28	K	SAQDQLQRA	Q	-1.3	6.78	
61	Cg2361	2	1056.4658	-0.4	177	186	0	38.4	23	A	ANVDTHMQAA	K	-0.3	4.94	
61	Cg2361	2	1113.4873	-0.9	175	185	0	32.2	24	T	GAANVDTHMQA	A	-0.3	4.94	
61	Cg2361	2	1184.5244	-0.5	175	186	0	25.9	24	T	GAANVDTHMQAA	K	-0.1	4.94	
61	Cg2361	2	1229.6	0.2	248	258	0	38.5	28	A	QNRADTLVNEA	D	-1.0	4.08	
61	Cg2361	2	1229.6252	-1.5	312	322	0	58.3	29	A	AVKEQQNALET	R	-1.0	4.26	
61	Cg2361	2	1300.6623	-1.6	311	322	0	37.2	29	M	AAVKEQQNALET	R	-0.7	4.26	
61	Cg2361	2	1527.7892	-0.3	341	354	0	70.4	29	S	LLEGQLEELNARGS	S	-0.5	3.96	
61	Cg2361	2	1571.7652	-1.3	116	129	0	42.6	29	A	QNDAKSAQDQLQRA	Q	-1.8	6.9	
61	Cg2361	2	1603.7875	-1.2	189	203	0	30.3	29	V	LGLAQEMADRLTSEA	R	-0.1	3.82	
61	Cg2361	2	1831.8621	-2.0	210	225	0	39.3	28	S	MLDEAREAAEKQIEEA	N	-1.0	3.88	
62	Cg2703	1	545.3247	2.0	274	278	0	29.9	28	A	MLVLA	I	3.1	6.02	
62	Cg2703	1	620.2992	0.0	144	148	0	28.8	27	I	PFQMV	M	0.8	6.02	
62	Cg2703	1	850.5892	-0.1	277	284	0	30.4	16	V	LAIIPIVI	F	3.3	6.02	
62	Cg2703	1	1193.7821	0.0	274	284	0	15.1	13	A	MLVLAIIPIVI	F	3.3	6.02	
62	Cg2703	2	1402.7344	1.0	185	197	0	41.2	29	A	GFVKSIPLDVEEA	A	0.3	3.82	
62	Cg2703	2	1595.8096	0.6	285	297	0	31.4	29	I	FYFSTQRHIIEGV	A	0.1	7.76	
63	Cg2704	2	994.5851	0.9	4	11	0	24.7	23	A	TLKKYFPV	F	-0.1	10.18	
63	Cg2704	1	1059.4655	-1.0	224	234	0	38.7	24	T	NGAPGGQTEMV	A	-0.6	3.3	
63	Cg2704	1	1092.5604	-1.8	46	54	0	45.2	29	A	KWVGIDNYV	K	-0.1	6.68	
63	Cg2704	1	1295.651	-3.2	211	221	0	52.4	28	S	NSFKLFDQNLA	L	-0.3	6.76	
63	Cg2704	2	1319.7312	-0.1	106	117	0	36.8	25	V	FFMPNLIGGIVL	G	1.9	6.02	
63	Cg2704	2	1648.7991	1.3	240	254	0	44.4	29	I	NTLFNRMNVEGVGQA	K	-0.3	6.98	
63	Cg2704	1	1917.0142	-3.2	235	251	0	33.7	29	V	ALNIINTLFNRMNVEGV	G	0.5	6.98	
63	Cg2704	3	2958.4691	-1.0	224	251	0	47.3	31	T	NGAPGGQTEMVALNIINTLFNRMNVEGV	G	0.1	4.26	
63	Cg2704	2	3214.5863	-2.3	224	254	0	49.2	31	T	NGAPGGQTEMVALNIINTLFNRMNVEGVGQA	K	0.0	4.26	
64	Cg0359	1	545.3247	2.0	134	138	0	29.9	28	F	MLVIA	A	3.2	6.02	
64	Cg0359	1	621.356	0.8	133	137	0	26.1	19	L	FMLVI	A	3.4	6.02	
64	Cg0359	1	814.3974	-1.4	190	197	0	32.5	25	A	SFHSPGAI	T	0.3	7.84	
64	Cg0359	1	981.5607	-0.3	163	171	0	38.4	25	V	NQLKNLVPG	Q	-0.5	10.1	
64	Cg0359	2	1013.5506	-1.3	153	162	0	40.5	28	M	GAPKNTIQSV	N	-0.4	10.1	
64	Cg0359	1	1065.4462	-1.3	43	53	0	33.9	23	L	SDVDTSVSGEA	S	-0.3	2.88	
64	Cg0359	1	1133.608	-2.0	68	77	0	37.6	28	S	SLFRAEVELA	K	0.6	4.26	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
64	Cg0359	2	1224.5524	0.1	190	201	0	39.6	26	A	SFHSPGAITGDH	-	-0.5	6	
64	Cg0359	1	1559.7831	-0.7	28	42	0	39.0	29	T	DGNSTFAPKVDSIPL	S	-0.2	3.88	
64	Cg0359	2	1689.8461	-0.8	33	48	0	43.3	29	T	FAPKVDSIPLSDVDTS	V	0.0	3.6	
64	Cg0359	2	2133.0478	-0.1	33	53	0	57.1	30	T	FAPKVDSIPLSDVDTSVSGEA	S	0.1	3.5	
64	Cg0359	3	3469.6373	-1.3	20	53	0	62.4	29	V	SNKDGLFTDGNSTFAPKVDSIPLSDVDTSVSGEA	S	-0.4	3.64	
65	Cg0647	1	632.3897	-1.3	74	79	0	29.3	27	S	IFAIGI	M	3.0	6.02	
65	Cg0647	1	821.4357	-1.7	278	284	0	32.6	23	S	SLIYMPV	L	1.5	5.92	
65	Cg0647	1	1488.8626	-0.7	278	290	0	27.5	23	S	SLIYMPVLITQIV	N	1.8	5.92	
65	Cg0647	1	1575.8946	-0.7	277	290	0	58.1	25	A	SSLIYMPVLITQIV	N	1.6	5.92	
66	Cg3187	1	509.3213	0.4	272	276	0	21.3	21	A	LPLPA	A	1.2	6.02	
66	Cg3187	1	580.3584	1.0	272	277	0	27.6	18	A	LPLPAA	Y	1.3	6.02	
66	Cg3187	1	798.4388	0.0	237	242	0	22.3	22	S	WLVRPE	L	-0.4	6.98	
67	Cg2137	1	866.4022	0.9	288	295	0	33.0	28	G	DLSFLDAS	-	0.5	2.92	
67	Cg2137	1	1641.8879	-3.3	128	142	0	55.6	28	V	NFGGPYLLTHQALLV	R	0.6	7.76	
67	Cg2137	2	1715.8512	-0.2	99	113	0	90.9	30	S	AQRETLIQNGEVDMI	A	-0.4	3.82	
67	Cg2137	2	2325.1489	-1.2	261	281	0	37.1	30	M	YADGTFQRLLTENLGEDSVVV	E	-0.1	3.58	
67	Cg2137	2	2661.2704	-3.2	49	73	0	53.2	29	G	TKYDQPGLGLRNPDNSMSGLDVDVA	E	-0.7	3.88	
67	Cg2137	3	3601.7319	-1.2	39	73	0	63.0	30	A	AIENGSVNVGTKYDQPGLGLRNPDNSMSGLDVDVA	E	-0.4	3.76	
68	Cg0753	1	693.381	-1.2	180	186	0	29.6	27	A	HLGLSPA	E	0.5	7.84	
68	Cg0753	1	818.3923	-1.0	99	105	0	38.7	26	L	TWANQVT	A	-0.5	6.02	
68	Cg0753	1	834.3971	-0.5	190	197	0	45.6	26	V	SVTEALDT	S	0.1	3	
68	Cg0753	1	1200.6602	-0.2	87	98	0	31.9	28	A	ALLGEGLDISTL	T	1.0	3	
68	Cg0753	1	1233.603	0.8	113	122	0	35.5	29	S	LFNEHAYELV	S	0.1	4.24	
68	Cg0753	2	1453.6725	-1.3	167	179	0	39.3	27	V	TFDPDGQITFKDA	H	-0.7	3.6	
68	Cg0753	2	1454.6678	1.8	75	86	0	62.3	27	L	GFLDYLDEEQRA	A	-1.0	3.58	
68	Cg0753	2	1562.7616	0.4	110	122	0	45.9	29	V	LESLFNEHAYELV	S	0.1	3.96	
68	Cg0753	2	1638.7889	1.0	73	86	0	96.2	28	T	ALGFLDYLDEEQRA	A	-0.4	3.58	
69	Cg0129	1	770.4538	0.5	149	156	0	29.4	29	N	LLGEAVLG	R	1.6	3.3	
70	Cg2211	2	1131.5884	1.0	117	126	0	45.2	29	G	NLTDSQLRSV	N	-0.6	6.78	
70	Cg2211	1	1222.5142	-2.5	100	109	0	29.0	22	H	VEPDWTYDQA	T	-1.3	2.88	
70	Cg2211	2	1416.5946	-0.1	98	109	0	48.4	22	V	GHVEPDWTYDQA	T	-1.3	3.7	
70	Cg2211	2	1475.7369	-0.5	114	126	0	67.1	29	G	TWGNLTDSQLRSV	N	-0.6	6.78	
70	Cg2211	2	1532.7583	-1.3	113	126	0	69.6	29	T	GTWGNLTDSQLRSV	N	-0.6	6.78	
70	Cg2211	2	1614.8002	-0.9	2	16	0	68.3	29	M	AGSSHTIEPEIYRGV	S	-0.4	5.3	
70	Cg2211	2	1633.806	-0.1	112	126	0	41.1	30	L	TGTWGNLTDSQLRSV	N	-0.6	6.78	
70	Cg2211	2	1847.9378	0.6	110	126	0	104.6	29	A	TLTGTWGNLTDSQLRSV	N	-0.3	6.78	
70	Cg2211	2	2486.1925	-1.8	2	25	0	59.8	29	M	AGSSHTIEPEIYRGVSTLDEPSAA	W	-0.4	4.16	
71	Cg0944	1	642.3588	-0.8	268	273	0	33.6	27	I	PDLSIV	G	1.1	3.1	
71	Cg0944	1	674.4367	1.5	219	224	0	25.0	24	G	LFIGIL	G	3.2	6.02	
71	Cg0944	1	901.364	3.2	301	308	0	27.3	21	A	NFFDAMGT	M	0.2	3.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
71	Cg0944	2	915.35	0.8	404	411	0	25.1	18	G	AMMMGQVT	E	0.9	6.02	3 Oxidation (M)
71	Cg0944	1	1681.8927	-1.4	257	273	0	41.8	28	A	VPGLPDSFGGIPDLSIV	G	0.8	2.92	
72	Cg3024	1	621.356	0.8	674	678	0	26.1	19	V	FMLVL	R	3.3	6.02	
72	Cg3024	1	680.4836	0.6	273	278	0	36.2	15	Y	LIIIPL	G	3.3	6.02	
72	Cg3024	1	789.4306	-3.4	667	673	0	29.2	26	V	ETIVMVV	F	2.1	3.3	
72	Cg3024	1	850.5892	-0.1	589	596	0	22.2	16	T	IVPLIALI	T	3.2	6.02	
73	Cg0545	1	583.4309	-0.2	5	9	0	24.1	18	L	IILLI	V	4.2	6.02	
73	Cg0545	1	678.3775	-1.5	206	211	0	27.0	23	T	MGVIFL	S	2.8	6.02	
73	Cg0545	1	712.4734	-0.6	3	8	0	39.9	22	T	ELIILL	I	2.8	3.3	
73	Cg0545	1	1041.5607	-1.7	115	125	0	50.6	27	S	SHALFGGLIGA	A	1.2	7.84	
73	Cg0545	2	1302.6051	-2.3	415	425	0	78.3	26	V	QDLNNENEVTK	-	-1.9	3.82	
73	Cg0545	1	1334.6718	-3.7	68	79	0	59.1	29	A	KGVVDLDQFDLS	N	0.0	3.6	
74	Cg0668	1	621.356	0.8	85	89	0	22.5	19	P	MVLIF	P	3.4	6.02	
74	Cg0668	1	686.4214	0.6	379	384	0	39.8	26	G	ELLSLL	G	1.8	3.3	
75	Cg0968	1	557.3425	2.0	173	177	0	28.2	28	V	DVVII	D	2.8	3.1	
75	Cg0968	2	782.465	0.0	356	363	0	25.1	25	A	GKAPQVIA	R	0.4	10.1	
76	Cg0326	1	751.5207	0.9	605	611	0	20.0	17	D	LIPLAII	A	3.0	6.02	
76	Cg0326	1	1207.7904	1.7	412	424	0	20.5	18	V	VLLLVGAAIGAVL	T	2.8	6.02	
76	Cg0326	1	1222.7359	-1.5	459	470	0	27.3	24	A	ALPGLMSLPLVL	V	1.9	6.02	
76	Cg0326	1	1434.8884	-1.8	459	472	0	29.2	19	A	ALPGLMSLPLVLVL	S	2.2	6.02	
77	Cg0577	1	872.4677	3.9	743	750	0	30.2	29	A	MSDVLVLP	N	1.5	3.1	
77	Cg0577	1	933.5284	4.4	850	857	0	29.4	27	S	FREGLTVL	E	0.7	6.98	
77	Cg0577	1	961.5596	3.7	113	120	0	29.9	25	S	RLGYLLDL	A	0.7	6.7	
78	Cg1362	1	509.3213	-0.2	220	224	0	30.4	21	N	IPPAL	H	1.4	6.02	
78	Cg1362	1	539.3683	-0.2	227	231	0	26.5	23	V	LVVPI	E	3.0	6.02	
78	Cg1362	1	855.4014	-1.4	129	135	0	32.4	25	A	EYALDFV	R	0.6	3	
78	Cg1362	1	957.4266	-2.0	79	86	0	38.1	24	V	NMLFTDFA	N	0.7	3.1	
78	Cg1362	1	1153.7223	-1.1	221	231	0	34.9	21	I	PPALHVLVVPI	E	1.7	7.84	
78	Cg1362	2	1315.6085	1.2	125	135	0	34.2	27	V	QNFAEYALDFV	R	0.2	3	
78	Cg1362	1	1354.7285	-2.4	232	242	0	37.8	28	I	EFFSTFILRPV	T	0.9	6.98	
78	Cg1362	1	1471.6983	-1.0	123	135	0	43.7	27	H	GVQNFAEYALDFV	R	0.4	3	
78	Cg1362	1	1477.9021	-2.6	218	231	0	32.4	18	I	PNIPPALHVLVVPI	E	1.3	7.84	
78	Cg1362	1	1647.7569	-2.2	56	69	0	43.4	27	G	EFHAPDLDKEFFPG	H	-0.8	4.06	
78	Cg1362	2	1876.155	0.1	214	231	0	35.6	18	S	SVVIPNIPPALHVLVVPI	E	1.7	7.84	
78	Cg1362	2	2571.1918	-3.2	56	78	0	45.5	27	G	EFHAPDLDKEFFPGHVTDSGEVV	N	-0.4	4.06	
78	Cg1362	3	2887.3487	-3.0	53	78	0	51.7	27	S	MKGEFHAPDLDKEFFPGHVTDSGEVV	N	-0.5	4.36	
79	Cg2405	2	1349.6472	-3.5	223	234	0	31.2	29	A	MLTGPQNMPKFS	D	-0.5	10.1	
79	Cg2405	1	1653.7304	-3.1	161	174	0	55.2	24	A	MEELRGENYDGQIT	S	-1.3	3.68	
79	Cg2405	2	1860.9945	-1.6	235	250	0	85.6	29	S	DRQLSADEKKDIIAFI	K	-0.4	4.46	
79	Cg2405	1	1936.9166	-2.1	206	222	0	55.8	28	G	KYAPNLDAANEQEIYQA	M	-1.0	3.82	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
79	Cg2405	1	1993.9381	-2.7	205	222	0	72.0	28	S	GKYAPNLDAANEQEIYQA	M	-1.0	3.82	
79	Cg2405	2	2080.9701	-2.3	204	222	0	50.8	28	S	SGKYAPNLDAANEQEIYQA	M	-1.0	3.82	
79	Cg2405	2	2095.0949	-2.1	233	250	0	35.1	30	K	FSDRQLSADEKKDIIAFI	K	-0.3	4.46	
79	Cg2405	2	2517.0965	-0.6	153	174	0	61.4	23	V	YNEDGTLAMEELRGENYDGQIT	S	-1.2	3.44	
80	Cg0455	1	545.3247	2.0	378	382	0	29.9	28	L	IMVLA	L	3.2	6.02	
80	Cg0455	1	582.3741	0.7	210	215	0	28.1	27	V	PIGIIA	L	2.2	6.02	
81	Cg1624	1	695.4006	0.3	61	66	0	23.5	14	I	PPLLWA	L	0.9	6.02	
81	Cg1624	1	700.3829	-0.6	53	58	0	21.4	19	A	DLMLPI	F	1.5	3.1	
81	Cg1624	1	1331.7125	-1.4	37	49	0	40.0	29	A	AGGALLPFLPEFT	I	1.0	3.3	
81	Cg1624	1	1637.9255	-1.0	53	66	0	38.1	25	A	DLMLPIFIPPLLWA	L	1.5	3.1	
81	Cg1624	1	1653.9204	-2.2	53	66	0	37.2	28	A	DLMLPIFIPPLLWA	L	1.5	3.1	Oxidation (M)
81	Cg1624	1	1678.86	-2.1	499	512	0	46.9	29	A	YVDEVLTNIDRMLV	A	0.4	3.7	
82	Cg0133	1	678.3775	-4.1	341	346	0	35.0	23	D	MIGFLV	L	2.8	6.02	
82	Cg0133	1	911.548	1.2	127	135	0	25.6	21	A	FVVVPPLAA	M	2.2	6.02	
83	Cg1281	1	711.4894	-1.3	94	100	0	30.7	25	I	ALIVLLA	L	3.4	6.02	
83	Cg1281	1	767.5157	0.9	843	849	0	20.2	19	V	PIIIVLT	L	2.7	6.02	
84	Cg0456	1	640.4523	0.3	263	268	0	30.8	25	I	IIGLII	T	3.6	6.02	
84	Cg0456	1	640.4523	-0.9	262	267	0	28.6	25	P	IIIGLI	I	3.6	6.02	
84	Cg0456	1	850.5892	-0.1	261	268	0	18.8	16	D	PIIIGLII	T	3.0	6.02	
84	Cg0456	1	1147.7944	-1.3	521	531	0	13.6	13	M	PLIGIALLLLL	F	2.9	6.02	
85	Cg0445	1	664.3584	2.1	195	199	0	25.1	24	I	WYIIA	N	1.7	5.92	
85	Cg0445	2	803.345	-0.6	173	179	0	30.6	26	T	SFEHGEV	Y	-0.6	4.24	
85	Cg0445	1	944.5331	-0.4	243	251	0	30.6	30	I	GNITIPFAI	A	1.3	6.02	
85	Cg0445	1	1037.4454	-1.0	173	181	0	34.4	24	T	SFEHGEVYA	N	-0.4	4.24	
85	Cg0445	2	1072.4825	0.1	170	179	0	26.9	26	A	APTSFEHGEV	Y	-0.5	4.24	
85	Cg0445	1	1170.7012	-2.2	241	251	0	28.6	24	V	LIGNITIPFAI	A	1.8	6.02	
85	Cg0445	1	1239.6135	-1.3	75	84	0	46.9	28	V	DVYGEFLREI	G	-0.1	3.82	
85	Cg0445	1	1382.8537	-1.2	239	251	0	27.0	22	A	LVLIGNITIPFAI	A	2.2	6.02	
85	Cg0445	1	1452.6344	-4.6	173	185	0	59.4	24	T	SFEHGEVYANMVA	S	0.0	4.24	
85	Cg0445	2	1466.7405	0.3	73	84	0	46.9	29	A	QVDVYGEFLREI	G	-0.1	3.82	
86	Cg1604	1	1893.9068	-3.0	145	163	0	34.2	28	A	QLSETQLDPGTHAGEALGA	A	-0.5	3.82	
86	Cg1604	2	2475.3221	-1.2	66	88	0	89.0	29	A	DSIIDHIVEDVVAGTLTDRPVLV	M	0.6	3.76	
86	Cg1604	2	2789.4447	-0.5	63	88	0	96.9	31	A	DQADSIIDHIVEDVVAGTLTDRPVLV	M	0.4	3.62	
86	Cg1604	2	2988.5404	-2.0	61	88	0	75.3	31	V	QADQADSIIDHIVEDVVAGTLTDRPVLV	M	0.3	3.62	
86	Cg1604	2	3272.6889	-2.9	58	88	0	105.7	31	V	NAVQADQADSIIDHIVEDVVAGTLTDRPVLV	M	0.3	3.62	
87	Cg0284	1	617.4152	-0.5	603	607	0	25.8	21	I	FLLIL	V	3.7	6.02	
87	Cg0284	1	730.4993	0.0	602	607	0	22.2	16	A	IFLLIL	V	3.9	6.02	
87	Cg0284	2	936.4917	1.6	572	580	0	33.5	27	G	TTGFTAVQL	D	0.7	6.02	
88	Cg1429	1	802.4953	0.6	245	252	0	32.1	24	E	LAAGVFLL	L	2.7	6.02	
88	Cg1429	1	878.4134	-2.4	106	113	0	28.1	27	T	SYVQAQPS	Q	-0.7	5.92	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
88	Cg1429	2	1362.7004	-1.8	53	66	0	38.5	29	T	GRAAPQNIPPASNA	A	-0.7	11.04	
88	Cg1429	2	1457.7263	-1.4	71	83	0	47.8	29	T	AFERPDNQSAKPV	A	-1.2	7.02	
88	Cg1429	2	1471.6579	-1.0	134	146	0	26.3	25	I	SRPEEPGYQPEPS	Y	-2.2	3.96	
88	Cg1429	1	1589.6522	-3.0	147	161	0	19.3	18	S	YSEPYTDSDFAPAGA	A	-0.7	2.88	
88	Cg1429	2	1764.8754	-2.3	53	70	0	57.0	29	T	GRAAPQNIPPASNAAETT	A	-0.7	6.98	
89	Cg0738	1	640.416	2.0	807	812	0	26.8	23	G	VSILPI	T	2.4	6.02	
89	Cg0738	1	910.5851	3.2	673	681	0	26.7	24	S	LGKTLGIPL	F	1.0	10.1	
90	Cg3178	1	656.3745	1.2	141	146	0	27.1	26	G	ISDLPI	G	1.2	3.1	
91	Cg3356	1	640.4523	-0.9	18	23	0	28.6	25	A	IILGII	C	3.6	6.02	
91	Cg3356	1	915.4662	-0.4	371	380	0	38.7	29	A	NVTGDGAIAV	I	0.8	3.1	
91	Cg3356	1	1435.6983	-2.0	114	126	0	41.4	29	I	DLDAGALQPYFNI	E	0.1	2.92	
91	Cg3356	2	1706.8475	-0.6	260	274	0	37.1	29	V	TYQQTLKNDVDVNVA	G	-0.6	3.88	
92	Cg2590	1	539.3683	-0.2	53	57	0	26.2	23	A	VIVPL	L	3.0	6.02	
92	Cg2590	1	651.3666	0.6	351	355	0	24.1	17	G	FMIIL	G	3.5	6.02	Oxidation (M)
92	Cg2590	1	757.4772	-3.8	352	358	0	24.2	23	F	MIILGVL	P	3.2	6.02	
93	Cg1701	1	557.3425	2.0	1009	1013	0	28.2	28	D	DVVIL	E	2.6	3.1	
94	Cg0275	1	1098.7053	-1.5	302	311	0	27.0	19	V	VLALFIPLLT	G	2.6	6.02	
94	Cg0275	2	1439.6205	1.7	74	85	0	37.8	24	L	DYFADLDPDDRV	S	-1.0	3.3	
95	Cg2811	1	730.4047	-1.2	652	658	0	39.1	28	D	AIGNMII	S	1.9	6.02	
95	Cg2811	1	1333.6765	0.4	693	704	0	41.0	29	T	NLEDAVADYIVI	S	0.8	2.88	
97	Cg2111	1	553.3839	1.1	881	885	0	26.4	24	T	VLIPI	P	3.1	6.02	
97	Cg2111	1	1066.5699	-2.4	199	207	0	27.6	27	L	NIDFILGYL	R	1.2	3.1	
98	Cg0229	1	509.3213	-0.2	630	634	0	30.4	21	A	PIPAL	L	1.4	6.02	
98	Cg0229	1	526.3115	0.8	1351	1355	0	32.0	30	N	PNIIA	G	1.1	6.02	
98	Cg0229	1	557.3425	2.0	1039	1043	0	28.2	28	A	DVVLI	S	2.6	3.1	
98	Cg0229	1	656.3745	-1.2	1203	1208	0	34.5	27	H	LDLSPI	F	1.0	3.1	
98	Cg0229	2	1166.6408	-3.0	1026	1038	0	28.9	26	G	VGTVAAGVSKAHA	D	0.8	10.1	
99	Cg2496	2	1859.8497	-0.6	463	481	0	69.7	26	I	SDEINEAGQLKQSAGADGA	R	-0.8	3.58	
99	Cg2496	2	2484.2343	-1.0	454	476	0	59.1	30	A	NVADLIQEISDEINEAGQLKQSA	G	-0.4	3.5	
99	Cg2496	2	2855.3784	-3.1	454	481	0	99.1	30	A	NVADLIQEISDEINEAGQLKQSAGADGA	R	-0.4	3.38	
100	Cg2052	1	667.3694	0.1	204	209	0	30.1	16	I	PWVGPI	S	0.7	6.02	
100	Cg2052	1	996.4917	0.2	190	198	0	29.8	29	A	AFYGDVNLV	A	0.9	3.1	
100	Cg2052	1	1138.6175	-0.4	200	209	0	39.3	25	A	FPNIPWVGPI	S	0.6	6.02	
100	Cg2052	2	1197.6102	0.3	178	190	0	41.4	27	T	SNPRGGIEGGLAA	F	-0.3	6.98	
100	Cg2052	1	1209.6546	-1.7	199	209	0	33.4	26	V	AFPNIPWVGPI	S	0.7	6.02	
100	Cg2052	2	1399.7056	-0.8	176	190	0	30.8	29	V	TTSNPRGGIEGGLAA	F	-0.3	6.98	
100	Cg2052	2	2165.0277	-1.1	40	59	0	69.4	29	A	FAEFERTTAEDVANGVPEAI	A	-0.2	3.58	
101	Cg2157	1	642.3952	1.2	251	256	0	27.2	27	F	LLDGLL	D	1.9	3.1	
101	Cg2157	1	655.3217	2.0	136	140	0	22.8	22	S	DVFYI	F	1.3	3.1	
101	Cg2157	1	864.4085	0.0	208	215	0	33.5	27	V	SIGMVDLM	F	1.5	3.1	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
101	Cg2157	1	1267.67	-2.4	224	234	0	28.9	27	A	IYGITTEPYIV	F	0.7	3.3	
101	Cg2157	1	1665.8111	-0.7	282	296	0	64.7	29	A	LHENNLPFINGGENV	S	-0.5	4.24	
101	Cg2157	2	1839.7435	-0.1	342	357	0	52.9	17	A	KYEGDNWETGEEPETG	S	-2.2	3.5	
101	Cg2157	2	2044.0126	-1.0	278	296	0	32.4	30	L	GLHALHENNLPFINGGENV	S	-0.3	5.12	
101	Cg2157	2	2305.0573	-0.3	153	171	0	31.5	27	L	LWDEVRDTPETDPNDMFII	K	-0.7	3.32	
102	Cg0507	1	584.3897	1.5	532	537	0	31.7	31	A	IIGIVA	L	3.2	6.02	
103	Cg3100	2	1576.7621	1.8	261	274	0	45.4	29	V	DADKNPLFLDETLS	R	-0.6	3.5	
104	Cg1367	1	1101.5917	-2.9	100	109	0	30.3	29	A	AELEKLLAES	G	0.0	3.96	
104	Cg1367	2	1548.7559	-0.3	215	227	0	77.7	29	V	IEDEIFEKGEDLL	S	-0.5	3.44	
104	Cg1367	2	1630.8526	-1.0	281	295	0	75.5	30	S	ATDNATELVKDLSRV	A	-0.3	4.3	
104	Cg1367	2	1701.8897	-2.0	281	296	0	63.6	30	S	ATDNATELVKDLSRVA	N	-0.2	4.3	
104	Cg1367	2	2015.0283	-4.3	281	299	0	79.5	30	S	ATDNATELVKDLSRVANQA	R	-0.4	4.3	
105	Cg0583	1	812.4028	-1.5	478	485	0	28.3	26	A	NIGDPQVA	Y	-0.3	3.1	
105	Cg0583	1	819.3473	1.5	405	411	0	25.6	22	S	MDFPDPV	I	-0.2	2.92	
105	Cg0583	1	1376.646	-1.2	169	181	0	38.8	28	I	GAEDNFDGVIDLL	E	0.2	2.78	
105	Cg0583	1	1656.8069	-3.3	397	411	0	30.5	28	A	NAPIILESMDFPDPV	I	0.3	2.88	
106	Cg3255	1	980.4927	-2.7	87	96	0	28.3	27	I	GHTIAEGSPI	D	0.0	5.12	
106	Cg3255	2	1146.5517	-1.1	10	21	0	30.2	29	V	AVDGSDASKQAV	R	-0.2	3.88	
106	Cg3255	2	1202.6547	-0.2	226	236	0	47.0	28	L	APLVEKYPSVT	V	0.1	6.86	
106	Cg3255	1	1221.5257	0.7	97	107	0	24.1	23	I	DMLLEMSPDAT	M	0.0	2.88	
106	Cg3255	2	2185.0976	-1.7	52	70	0	55.0	30	G	MVPPQELFDDLQAEALEKI	N	-0.2	3.5	
106	Cg3255	2	3659.7415	-4.1	39	70	0	31.9	29	A	SSYTMPQFLYAEGMVPPQELFDDLQAEALEKI	N	-0.2	3.44	
107	Cg3019	1	656.3745	-1.4	548	553	0	27.3	27	V	TVDIPI	T	1.2	3.1	
107	Cg3019	1	793.5677	0.0	664	670	0	25.6	13	L	LIPLLIL	Y	3.2	6.02	
107	Cg3019	1	1893.9837	-0.4	560	578	0	40.7	29	V	WIAPGTQLSGVLPDGVDGI	A	0.5	2.92	
109	Cg0040	2	1391.6429	-0.1	269	281	0	27.4	27	V	QAPDSYGRIGNQS	G	-1.3	6.7	
109	Cg0040	2	1430.7042	-0.5	141	153	0	38.8	29	T	DITYSTDKPGHVV	N	-0.5	5.1	
109	Cg0040	2	1471.6943	-0.2	389	401	0	71.8	27	A	YVSDPSNNELHVV	D	-0.4	4.06	
109	Cg0040	2	1595.7832	0.6	161	175	0	31.1	29	V	LFGDGDGKIQIFDTA	S	0.0	3.6	
109	Cg0040	2	1694.8516	0.6	160	175	0	51.4	29	T	VLFGDGDGKIQIFDTA	S	0.3	3.6	
109	Cg0040	2	2032.945	-1.6	269	288	0	27.4	27	V	QAPDSYGRIGNQSGSDVSPV	V	-0.8	3.88	
110	Cg2425	1	595.304	1.7	1	5	0	28.5	28	-	MSFLV	E	2.4	6.02	
110	Cg2425	1	759.4565	-4.1	369	375	0	26.4	26	G	LMIGVLV	G	3.1	6.02	Oxidation (M)
110	Cg2425	2	973.4465	-0.9	255	263	0	24.2	24	V	GADEELNRA	E	-1.3	3.82	
110	Cg2425	2	1335.7285	-0.7	210	221	0	39.1	27	A	DLPALENIPELL	N	0.4	2.94	
110	Cg2425	1	1505.8341	-1.6	208	221	0	27.9	26	T	VADLPALENIPELL	N	0.7	2.94	
111	Cg0015	1	1401.6776	4.1	268	279	0	29.3	29	I	TELPYQVNPDNL	I	-0.9	3	
112	Cg2677	1	1031.5652	0.4	240	250	0	29.2	29	A	GILFGELVGGA	V	1.4	3.3	
112	Cg2677	1	1560.7784	-2.1	39	52	0	75.5	30	A	RYSSPDLGLSPEQI	A	-0.7	4.08	
112	Cg2677	2	1848.072	-0.8	187	203	0	72.7	23	I	PITAPLAQVLIRSIEEV	K	0.8	4.26	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
112	Cg2677	2	2375.4039	1.2	182	203	0	54.5	20	T	ITLSIPITAPLAQVLIRSIEEV	K	1.1	4.26	
113	Cg1730	2	1034.5145	-1.5	242	250	0	57.8	28	A	RYLQAQGEA	R	-1.0	6.88	
113	Cg1730	2	1200.6098	-1.3	220	230	0	37.4	29	A	SILNAEAERQA	M	-0.5	4.26	
113	Cg1730	2	1570.9083	0.0	43	57	0	35.3	25	T	VSGGLTLLVPFVDRV	R	1.3	6.78	
113	Cg1730	1	1852.7639	-2.5	334	349	0	58.8	18	A	DNVEDWFSTESDPEIA	A	-1.0	2.72	
114	Cg2338	1	509.3213	-0.2	485	489	0	30.4	21	E	LPPAI	M	1.4	6.02	
115	Cg3161	1	551.3683	0.9	357	361	0	34.3	18	T	IPLPL	Q	1.8	6.02	
115	Cg3161	1	686.4214	0.6	546	551	0	39.8	26	G	EILSLL	D	1.9	3.3	
115	Cg3161	1	853.5021	2.8	446	453	0	35.1	25	W	AVRDAIPL	V	0.8	6.78	
116	Cg2323	1	543.3057	-0.9	175	179	0	27.7	17	L	FPIAP	G	1.2	6.02	
117	Cg0486	1	577.3475	2.3	738	742	0	28.1	28	I	IYGLL	A	2.1	5.92	
117	Cg0486	1	786.4851	-0.6	414	421	0	34.3	27	T	LGISLTIA	G	2.1	6.02	
117	Cg0486	1	980.5001	2.0	17	26	0	28.5	27	L	GTAFLCGSLL	L	1.6	5.32	
118	Cg3398	1	707.4582	2.0	613	619	0	20.9	16	I	ILPVAVP	P	2.2	6.02	
119	Cg2546	1	635.3716	-4.9	160	164	0	20.5	19	T	MFIIL	A	3.5	6.02	
119	Cg2546	1	651.3666	0.6	160	164	0	24.1	17	T	MFIIL	A	3.5	6.02	Oxidation (M)
119	Cg2546	1	674.4367	1.5	229	234	0	25.0	24	L	IFLGIL	I	3.2	6.02	
119	Cg2546	1	767.5157	0.9	234	240	0	21.4	19	I	LIPVILT	I	2.6	6.02	
120	Cg1664	1	622.4054	-0.6	189	194	0	17.6	17	V	IPAPLI	V	1.9	6.02	
120	Cg1664	1	632.3897	-1.3	171	176	0	29.3	27	P	LFALGI	G	2.7	6.02	
120	Cg1664	1	854.5113	0.9	47	54	0	30.0	23	A	LALIPESI	A	1.6	3.3	
121	Cg0835	1	1093.6019	-2.3	2	11	0	39.8	25	M	ATVTFDKVTI	R	0.8	6.76	
121	Cg0835	2	1685.7857	-1.7	65	80	0	57.7	28	I	DGKDVTGQEPADRDIA	M	-1.3	3.76	
122	Cg1054	1	757.4772	-3.8	649	655	0	23.9	23	P	IMLIGLV	F	3.2	6.02	
123	Cg1238	1	583.4309	-0.2	76	80	0	24.1	18	K	IIIIL	P	4.4	6.02	
123	Cg1238	1	680.4836	0.6	77	82	0	36.2	15	I	IIILPI	A	3.4	6.02	
123	Cg1238	1	751.5207	0.9	79	85	0	20.0	17	I	ILPIALL	L	2.9	6.02	
123	Cg1238	1	864.6048	-0.9	78	85	0	20.8	13	I	IILPIALL	L	3.1	6.02	
123	Cg1238	1	1085.591	-1.5	88	97	0	29.1	28	S	AFAPWALTPI	L	1.2	6.02	
123	Cg1238	1	1177.8049	-1.7	77	87	0	22.7	13	I	IIILPIALLLS	A	3.0	6.02	
123	Cg1238	1	1268.6976	-1.2	2	15	0	34.5	27	M	AGGLAALLDDVAAI	T	1.5	2.92	
123	Cg1238	1	1369.7453	-2.3	2	16	0	33.4	28	M	AGGLAALLDDVAAIT	R	1.4	2.92	
123	Cg1238	2	2042.0685	-2.5	39	58	0	53.7	30	A	GVVVDDTAVTPQYVQGVKPA	R	0.2	3.88	
126	Cg3125	1	950.4817	2.4	1	8	0	36.9	28	-	MDILSLLM	E	1.9	3.1	Oxidation (M)
127	Cg1661	1	539.3683	-0.2	275	279	0	26.5	23	S	LVVLP	L	2.9	6.02	
127	Cg1661	1	680.4836	0.6	172	177	0	36.2	15	L	LILIPL	V	3.1	6.02	
127	Cg1661	1	686.4214	1.6	299	304	0	22.8	21	Q	TLVELI	G	2.0	3.3	
127	Cg1661	1	730.4993	0.0	170	175	0	22.2	16	F	FLLILI	P	3.9	6.02	
127	Cg1661	1	902.4605	0.2	201	208	0	32.7	29	A	EAIMVPLM	M	1.6	3.3	
128	Cg0732	1	630.3775	-4.8	427	432	0	27.2	27	L	VCALLI	A	3.4	5.32	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
128	Cg0732	1	667.3945	-0.7	242	246	0	23.2	15	R	YFLLL	A	2.6	5.92	
128	Cg0732	1	711.4894	-1.3	473	479	0	30.7	25	A	LIAVILA	G	3.5	6.02	
129	Cg3174	1	557.3425	2.0	69	73	0	28.2	28	G	DVVLL	F	2.5	3.1	
130	Cg0845	1	826.48	-1.7	266	273	0	28.7	25	A	PTAEALIL	A	1.2	3.3	
131	Cg0414	1	640.4523	-0.9	179	184	0	28.6	25	N	ILLGLL	V	3.2	6.02	
131	Cg0414	1	787.3963	-1.7	88	94	0	32.2	28	V	DELGLEL	T	0.1	2.94	
131	Cg0414	2	1198.583	-2.5	457	467	0	42.3	26	I	NAPKPDNTELT	T	-1.5	4.08	
131	Cg0414	2	1632.9086	-1.2	221	235	0	55.6	26	G	GIIADSEVEKHPLII	K	0.5	4.42	
132	Cg1579	1	1038.5233	-0.8	62	71	0	57.3	26	A	VEEPAVEAPV	E	0.3	3.02	
132	Cg1579	1	1857.9472	0.4	81	98	0	46.6	30	V	EQAPVVEQAPVEQAPAPV	Q	-0.2	3.02	
132	Cg1579	2	2254.1481	-1.6	77	98	0	71.4	30	V	EAPVEQAPVVEQAPVEQAPAPV	Q	-0.1	2.96	
132	Cg1579	2	2652.2568	-3.0	106	134	0	79.6	28	V	EQAPAPVQEAPAADAPPALPGGGGGHAGY	-	-0.4	3.82	
132	Cg1579	2	3344.6062	-3.1	99	134	0	81.6	30	V	QEAPAPVEQAPAPVQEAPAADAPPALPGGGGGHAGY	-	-0.4	3.68	
133	Cg3419	1	786.4851	-0.8	285	292	0	29.7	27	I	GVTLLTAI	M	2.0	6.02	
134	Cg3026	1	722.4003	1.1	384	389	0	23.2	23	I	LYFIPA	I	1.7	5.92	
134	Cg3026	1	1251.7301	-3.6	10	20	0	34.2	23	V	PLIPYMVPLPI	I	1.4	5.92	
134	Cg3026	1	1970.1202	-1.2	4	20	0	48.8	26	S	LYETLVPLIPYMVPLPI	I	1.3	3.3	
135	Cg0468	1	773.4283	-1.3	310	318	0	30.2	30	L	GGAALISVS	D	1.5	6.02	
135	Cg0468	2	2126.1987	-0.8	316	335	0	35.3	26	I	SVSDILARTLIPYADLPIGI	F	0.9	3.88	
136	Cg1790	1	585.3737	1.5	114	118	0	27.8	25	G	DILLL	E	2.5	3.1	
137	Cg2949	1	900.4076	-1.9	98	105	0	26.6	24	V	ELDDAEPI	E	-0.7	2.84	
137	Cg2949	2	1202.5528	-1.2	173	184	0	42.0	27	S	GVENREVGGDTA	E	-0.9	3.82	
137	Cg2949	1	1504.7562	-3.5	136	150	0	41.9	29	T	SLENPGFAYGGVVPV	E	0.5	3.3	
137	Cg2949	2	1531.7114	0.5	170	184	0	29.0	28	V	LESGVENREVGGDTA	E	-0.7	3.68	
137	Cg2949	2	1885.9017	-0.8	166	184	0	62.9	28	V	SAPVLESGVENREVGGDTA	E	-0.4	3.68	
137	Cg2949	2	2272.0819	-2.8	162	184	0	32.1	29	I	DATVSAPVLESGVENREVGGDTA	E	-0.2	3.5	
137	Cg2949	2	3465.6788	-0.1	151	184	0	42.0	31	V	EFVFDTGAITIDATVSAPVLESGVENREVGGDTA	E	0.2	3.32	
141	Cg1359	1	630.3775	-4.8	358	363	0	27.2	27	S	ICGILI	A	3.2	5.32	
141	Cg1359	1	758.436	-3.0	359	366	0	35.0	27	I	CGILIAVA	V	2.8	5.32	
141	Cg1359	1	782.5266	1.3	244	251	0	32.7	25	M	LIGLLLAA	A	2.9	6.02	
142	Cg1744	1	601.3873	0.8	838	842	0	22.9	16	A	LMLIL	Q	3.6	6.02	
143	Cg0235	1	823.5392	4.6	478	484	0	16.4	16	Y	RRLPLIG	A	0.2	12.4	
143	Cg0235	1	1365.63	-2.5	207	219	0	29.6	27	T	GVYTELVDDPSTA	S	-0.2	2.88	
144	Cg1111	2	1756.957	-1.1	213	228	0	44.1	28	G	STREALDLIVEAIEKA	G	0.1	4.16	
144	Cg1111	2	2414.1085	-0.5	71	92	0	45.6	27	V	NEEIGDELAGLEADDQRLIDEA	M	-0.8	3.2	
144	Cg1111	2	2855.3308	-2.5	67	92	0	80.8	28	A	VENVNEEIGDELAGLEADDQRLIDEA	M	-0.6	3.16	
146	Cg2684	1	1369.6952	-2.6	14	25	0	28.6	28	A	LGPSWLDPMELL	S	0.4	3	
146	Cg2684	1	1369.703	-1.0	68	79	0	33.3	28	A	NQADPFAPLWLV	L	0.3	3.1	
146	Cg2684	1	1401.7908	-0.9	44	56	0	37.2	27	V	FIESGLLFPLLPG	D	1.3	3.3	
146	Cg2684	1	1456.7272	-3.2	14	26	0	30.9	29	A	LGPSWLDPMELLS	G	0.3	3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
146	Cg2684	1	1901.9233	-2.8	14	31	0	33.4	29	A	LGPSWLDPMELLSGSGPF	G	0.2	3	
146	Cg2684	2	2045.9768	-0.7	14	33	0	45.6	29	A	LGPSWLDPMELLSGSGPFGS	F	0.1	3	
148	Cg0336	1	972.44	-1.2	321	329	0	36.3	24	L	TLDPDVQDA	A	-0.7	2.82	
148	Cg0336	1	1227.6095	-2.9	453	464	0	31.2	27	T	LQDALAQSPNTA	F	-0.3	3.1	
148	Cg0336	1	1355.7813	-2.1	16	30	0	30.0	26	V	AAGVLGALALVPFAS	L	1.9	6.02	
148	Cg0336	2	1400.6896	0.5	46	59	0	53.3	29	T	NLSDLTDGRGPGVT	T	-0.6	3.88	
149	Cg2641	1	553.3839	1.1	301	305	0	26.4	24	D	LVLPI	D	2.9	6.02	
149	Cg2641	1	949.5233	3.5	839	846	0	30.0	28	E	YEIARLVS	S	0.5	6.88	
150	Cg0236	1	1810.9406	-0.9	201	216	0	33.9	29	A	NLLGLPGWEAFQPWAI	V	0.4	3.3	
150	Cg0236	1	1910.009	-2.4	201	217	0	40.8	29	A	NLLGLPGWEAFQPWAIV	S	0.6	3.3	
151	Cg2846	1	815.3524	0.4	70	76	0	24.9	24	S	AMDYFGI	R	0.8	3.1	
151	Cg2846	1	1061.5393	0.2	145	154	0	35.8	30	V	AYNLPGVDTL	N	0.3	3.1	
151	Cg2846	1	1146.5557	-0.4	266	276	0	41.6	29	A	NIDFGSGPVEL	N	0.1	3	
151	Cg2846	3	3759.9359	-0.1	145	178	0	56.0	32	V	AYNLPGVDTLNLDTNIIAQIFKGEITKWNDEAIA	S	0.0	3.84	
152	Cg1312	1	731.3887	2.3	109	115	0	34.0	28	M	MGALDLL	E	1.6	3.1	
152	Cg1312	1	836.5735	-0.5	60	67	0	26.7	18	S	LLVPLLGI	A	2.7	6.02	
152	Cg1312	1	1107.7267	-1.4	59	69	0	19.2	18	L	SLLVPLLGIAI	M	2.5	6.02	
152	Cg1312	2	1166.5244	-1.8	125	133	0	37.0	27	T	YEIENWDKA	K	-1.5	3.82	
152	Cg1312	1	1418.6235	-2.5	109	121	0	64.2	24	M	MGALDLLEDDEQA	A	-0.3	2.76	
152	Cg1312	1	1489.6606	-1.3	109	122	0	63.3	24	M	MGALDLLEDDEQAA	K	-0.2	2.76	
152	Cg1312	1	1549.664	-1.9	108	121	0	42.1	22	K	MMGALDLLEDDEQA	A	-0.2	2.76	
153	Cg2196	1	672.4211	0.6	103	108	0	29.6	23	G	LVVFPV	V	2.9	6.02	
153	Cg2196	1	780.329	0.3	61	67	0	41.9	28	G	DQEGYGI	D	-1.2	3	
153	Cg2196	2	1028.627	-1.0	99	108	0	29.9	25	T	SVLGLVVFPV	V	2.4	6.02	
153	Cg2196	1	1032.6008	1.7	104	112	0	31.5	22	L	VVFPVVNFL	K	2.3	6.02	
153	Cg2196	1	1202.7064	-0.8	102	112	0	28.4	24	L	GLVVFPVVNFL	K	2.2	6.02	
153	Cg2196	3	2318.3766	-0.7	99	119	0	39.2	20	T	SVLGLVVFPVVNFLKYNGLIK	-	1.3	10.18	
154	Cg2568	1	617.4152	-0.5	329	333	0	25.8	21	M	FILLL	I	3.7	6.02	
154	Cg2568	1	635.3716	-4.9	328	332	0	20.5	19	M	MFILL	L	3.4	6.02	
154	Cg2568	1	651.3666	0.6	328	332	0	24.1	17	M	MFILL	L	3.4	6.02	Oxidation (M)
154	Cg2568	1	730.4993	0.0	329	334	0	22.2	16	M	FILLLI	G	3.9	6.02	
156	Cg2095	1	551.3683	0.9	347	351	0	34.3	18	H	LPLPI	K	1.8	6.02	
156	Cg2095	1	678.3741	4.9	280	284	0	23.3	23	A	TWIFI	A	2.0	6.02	
157	Cg2990	1	782.5266	1.3	208	215	0	31.6	25	V	VALLLAIA	A	3.2	6.02	
158	Cg3060	1	583.4309	-0.2	135	139	0	24.1	18	E	ILLIL	V	4.1	6.02	
158	Cg3060	1	640.416	2.0	370	375	0	26.8	23	V	VISLPL	K	2.3	6.02	
158	Cg3060	1	712.4734	-0.6	134	139	0	39.9	22	T	EILLIL	V	2.8	3.3	
158	Cg3060	1	1335.7147	2.2	254	266	0	29.5	27	V	NSAIQLLVDAGHV	V	0.7	4.94	
159	Cg3346	1	557.3425	2.0	350	354	0	28.2	28	L	VDVLL	E	2.5	3.1	
159	Cg3346	2	900.4415	2.4	335	342	0	28.0	26	T	LFGATYMV	L	1.5	5.92	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
160	Cg0161	1	1111.6601	-3.3	269	278	0	35.2	25	A	RLLTDATLPL	A	0.6	6.78	
160	Cg0161	2	2648.4425	-1.6	51	76	0	39.3	28	A	KELPLAFDVPAGTVPQSLSGTLQIPA	E	0.3	4.08	
161	Cg0286	1	782.4367	-1.2	76	81	0	34.8	20	A	FFLFPI	S	2.5	6.02	
161	Cg0286	1	1039.6351	0.9	223	231	0	43.7	23	T	LLEVILMPI	T	2.4	3.3	
161	Cg0286	2	1317.7292	-0.3	148	160	0	29.3	27	A	SLAGYIVGQLLNA	K	1.1	5.92	
161	Cg0286	1	1734.9233	-1.5	66	81	0	32.5	29	V	EIGPLVTDGAFFLFPI	S	1.2	3	
162	Cg0206	1	1068.6947	-1.1	435	444	0	35.9	19	A	LFLIPLIGAL	S	2.7	6.02	
162	Cg0206	1	1139.7318	-1.4	434	444	0	24.2	19	A	ALFLIPLIGAL	S	2.6	6.02	
163	Cg0992	1	793.5677	0.0	171	177	0	25.6	13	A	ILPLLII	I	3.3	6.02	
163	Cg0992	1	1177.805	-1.8	170	180	0	22.2	13	D	AILPLLIIIVT	A	3.0	6.02	
164	Cg2958	1	980.4087	0.1	67	75	0	36.1	25	A	NFDSAIDEA	A	-0.4	2.88	
164	Cg2958	2	1407.7722	-0.1	220	233	0	40.5	26	A	LGRPSVPEDVAGLV	S	0.4	4.08	
164	Cg2958	2	1421.6674	-0.1	67	79	0	45.4	28	A	NFDSAIDEAAEKL	G	-0.4	3.58	
164	Cg2958	2	2408.1496	-1.1	67	89	0	63.1	29	A	NFDSAIDEAAEKLGGFDVLVNNA	G	0.0	3.42	
164	Cg2958	2	2649.2922	-2.2	67	92	0	95.6	30	A	NFDSAIDEAAEKLGGFDVLVNNAGIA	Q	0.2	3.42	
165	Cg1658	1	571.3403	0.5	321	325	0	23.2	21	A	IMIPV	S	2.7	6.02	
165	Cg1658	1	640.4523	-0.9	119	124	0	28.6	25	T	ILIGLL	P	3.3	6.02	
165	Cg1658	1	651.3666	0.6	190	194	0	24.1	17	G	FMLIL	V	3.4	6.02	Oxidation (M)
165	Cg1658	1	759.4565	-4.1	191	197	0	34.1	26	F	MLILVGV	L	3.1	6.02	Oxidation (M)
166	Cg3245	1	553.3839	1.1	35	39	0	26.4	24	T	LVIPI	I	3.1	6.02	
166	Cg3245	1	1026.6511	-3.5	211	220	0	36.2	23	G	LAMGLIALLL	A	2.9	6.02	
168	Cg1227	1	704.4109	2.1	82	87	0	23.5	23	A	IFVEVV	A	2.7	3.3	
168	Cg1227	1	1035.5601	-0.7	95	104	0	31.8	26	A	LASQFGISTI	Y	1.1	6.02	
168	Cg1227	1	1265.7132	-0.8	49	61	0	26.3	24	A	FHALTPGLGGIAI	G	1.3	7.84	
169	Cg0324	1	553.3839	1.1	5	9	0	26.4	24	D	VLLPI	F	2.9	6.02	
169	Cg0324	1	700.3829	-0.6	136	141	0	31.2	19	I	EVMLLP	S	1.4	3.3	
169	Cg0324	1	854.5266	-0.8	8	15	0	36.7	25	L	PIFVAVPL	A	2.3	6.02	
169	Cg0324	1	996.6008	-0.8	8	17	0	27.0	25	L	PIFVAVPLAA	S	2.2	6.02	
170	Cg2388	1	1039.4934	-1.8	295	304	0	25.6	25	A	NAQVPDAQPT	D	-1.0	3.1	
170	Cg2388	1	1711.9244	-2.9	234	250	0	35.7	29	S	SLIDGVPSLIDELVATA	T	1.0	2.88	
171	Cg3216	1	557.3247	-0.7	131	135	0	27.7	19	V	VMLPV	I	2.5	6.02	
171	Cg3216	2	1412.5804	-1.3	221	234	0	40.1	21	L	SGGAQEDDQPQNPA	N	-1.8	2.88	
172	Cg1399	1	642.3588	-0.8	221	226	0	33.6	27	L	DPLSIV	L	1.1	3.1	
172	Cg1399	1	651.3666	0.6	45	49	0	24.1	17	F	FMILL	D	3.4	6.02	Oxidation (M)
173	Cg1231	1	630.3775	-4.8	112	117	0	27.2	27	V	GLCLLI	G	3.0	5.32	
173	Cg1231	1	698.4578	1.0	76	81	0	23.2	22	I	IEVILI	C	3.0	3.3	
173	Cg1231	1	878.5841	-1.8	23	30	0	31.0	13	F	IIPLITLP	S	2.2	6.02	
174	Cg0885	1	758.4174	-0.7	394	400	0	39.9	32	E	SLNAIEL	E	0.9	3.3	
175	Cg2243	1	709.4738	1.8	199	205	0	23.3	21	L	VALIVVP	W	3.0	6.02	
176	Cg2263	1	915.5025	3.5	967	974	0	31.5	31	E	TQQKALLD	M	-0.7	6.76	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
177	Cg1795	2	1258.6193	-0.1	684	695	0	28.3	28	K	LAEAVYEGLHAS	K	0.4	4.24	
179	Cg2739	1	553.3839	1.1	315	319	0	26.4	24	G	LVLLP	G	2.8	6.02	
179	Cg2739	1	557.3247	0.2	180	184	0	23.0	19	V	MVPLV	F	2.5	6.02	
179	Cg2739	1	820.4364	0.2	347	354	0	33.6	30	G	GMSLVVIS	L	2.1	6.02	Oxidation (M)
180	Cg0417	1	553.3839	1.1	123	127	0	26.4	24	L	LVIPL	A	2.9	6.02	
180	Cg0417	1	684.4244	-4.4	121	126	0	24.8	18	V	MLLVIP	L	2.8	6.02	
180	Cg0417	1	690.3952	0.7	23	28	0	26.1	26	L	FLIDAL	A	2.2	3.1	
181	Cg2279	1	698.4327	-1.0	224	230	0	37.9	28	R	QGLIVGI	R	1.8	6.02	
181	Cg2279	1	1014.6114	0.0	29	38	0	37.3	27	L	LTAALIVFPA	W	2.2	6.02	
182	Cg0082	1	545.3213	-0.2	374	378	0	29.7	26	A	PLFGL	I	1.7	6.02	
182	Cg0082	1	664.3618	-3.0	314	319	0	25.1	24	T	AMFLLA	F	2.7	6.02	
182	Cg0082	2	1039.5008	-3.1	362	372	0	31.4	28	L	GAAAFLSTTMA	A	1.2	6.02	
183	Cg3079	2	981.4767	-0.8	2	10	0	36.9	27	M	SSFNPTTKT	N	-1.1	10.1	
183	Cg3079	2	1083.5309	-1.7	22	32	0	60.7	27	A	SSAGNPDIRPA	H	-0.8	6.78	
184	Cg1103	1	869.5222	-0.3	113	121	0	29.7	27	I	TSIPLGIGI	A	1.5	6.02	
185	Cg0868	1	685.401	1.0	149	155	0	39.4	30	L	GLEVGVI	L	1.8	3.3	
185	Cg0868	1	801.4492	-3.4	768	774	0	33.5	28	R	MVLMPVI	D	2.7	6.02	
186	Cg2393	1	640.4523	0.3	619	624	0	30.8	25	W	ILGILL	N	3.3	6.02	
186	Cg2393	1	850.5892	-0.8	715	722	0	18.6	16	L	LPLIAVLL	R	3.0	6.02	
186	Cg2393	1	963.6732	-0.6	711	719	0	18.6	13	H	LVLLLPLIA	V	3.1	6.02	
187	Cg0238	2	1383.7497	1.4	41	53	0	30.3	28	V	LTTPDLDIIVDAV	R	1.0	2.82	
187	Cg0238	2	1865.0564	0.8	125	141	0	34.2	26	A	ALPYGLWVPVLPGTRQV	T	0.5	9.84	
188	Cg0998	1	1432.7086	-1.7	208	221	0	37.4	29	A	DFIAGDPSTDIAVI	K	0.7	2.82	
188	Cg0998	2	2535.3544	-1.0	385	408	0	33.9	29	A	GLQPGDIVTKLNDRVIDSPDSLIA	A	0.0	3.88	
190	Cg3252	2	1749.8938	-1.3	142	157	0	52.3	29	I	GFLTPEEVESFLAGRV	S	0.3	3.96	
190	Cg3252	2	2225.1368	-2.1	138	157	0	64.9	30	V	FQSIGFLTPEEVESFLAGRV	S	0.4	3.96	
191	Cg0314	1	539.3683	-0.2	220	224	0	26.5	23	A	LVVIP	G	3.0	6.02	
191	Cg0314	1	674.4367	1.5	234	239	0	25.0	24	L	IFLGLL	T	3.1	6.02	
191	Cg0314	1	775.4844	0.9	235	241	0	23.3	23	I	FLGLLTI	R	2.5	6.02	
191	Cg0314	1	775.4844	0.0	234	240	0	24.2	23	L	IFLGLLT	I	2.5	6.02	
191	Cg0314	1	1026.6437	3.7	202	210	0	32.7	23	R	TKKQIPSLL	L	-0.3	10.6	
192	Cg2812	1	896.3916	-0.1	163	169	0	27.1	26	S	WFDEITS	R	-0.3	3	
192	Cg2812	1	1317.6452	-0.8	263	273	0	37.2	29	V	NQLFDPTIEEI	L	-0.4	2.94	
192	Cg2812	1	1495.6943	-1.1	160	171	0	62.8	27	I	DQSWFDEITSRL	G	-0.9	3.7	
192	Cg2812	2	2277.0761	0.5	206	226	0	30.8	29	I	FGDEPTGNLDSNSSREVLDIL	R	-0.6	3.42	
192	Cg2812	2	2986.4957	-2.0	258	284	0	41.8	31	A	DGRIVNQLFDPTIEEILATMNGIEDIA	-	0.1	3.38	
194	Cg2675	1	862.4986	-4.6	205	212	0	30.4	27	E	LGMGILFI	T	2.6	6.02	
194	Cg2675	1	1169.6478	-1.5	442	451	0	31.0	29	A	RAMILEPELV	V	0.7	4.26	
194	Cg2675	2	1943.9013	-1.7	141	156	0	39.1	27	V	GIDNPEVRYDQYPHEL	S	-1.4	4.06	
195	Cg3301	1	1008.6583	-1.8	390	399	0	23.9	20	R	IASIIAPLIV	P	2.7	6.02	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
195	Cg3301	1	1150.675	-1.5	400	411	0	36.9	22	V	PPVIAFGGPIAL	F	1.5	6.02	
195	Cg3301	1	1773.0804	-4.5	392	409	0	33.7	17	A	SIIAPLIVPPVIAFGGPI	A	1.8	6.02	
195	Cg3301	1	1957.2016	-2.6	392	411	0	51.9	16	A	SIIAPLIVPPVIAFGGPIAL	F	1.9	6.02	
197	Cg0896	1	553.3839	1.1	117	121	0	26.4	24	M	VIIPI	F	3.2	6.02	
197	Cg0896	1	945.5688	-3.5	21	28	0	27.0	23	T	WIFAIIAL	V	2.9	6.02	
198	Cg2678	1	1428.7646	-4.8	415	427	0	31.8	29	T	MVQEQLGDLGIKV	N	0.3	4.08	
199	Cg0972	1	584.3897	1.5	173	178	0	31.7	31	A	LLGLVA	A	2.8	6.02	
201	Cg3015	1	632.3897	-1.3	517	522	0	28.4	27	Q	IFAGII	A	3.0	6.02	
202	Cg0736	1	642.3952	1.2	56	61	0	43.8	27	G	EVIGII	G	2.3	3.3	
202	Cg0736	1	699.4167	1.1	56	62	0	41.6	30	G	EVIGIIG	Y	1.9	3.3	
202	Cg0736	1	1340.7187	-4.5	179	191	0	34.4	28	A	LATNPTLLLADEA	T	0.5	3	
202	Cg0736	3	2549.2948	-2.4	144	165	0	32.3	31	A	RVQEMLEFVGLGDKGKNYPEQL	S	-0.7	4.64	
203	Cg3335	1	633.3486	-0.6	135	140	0	28.9	28	S	FGAINL	E	1.5	6.02	
203	Cg3335	1	735.3803	1.0	260	266	0	31.5	30	F	TGADLFI	G	1.2	3.1	
203	Cg3335	1	1059.5634	-4.6	273	282	0	35.5	30	N	IGEDALKLMA	P	0.6	4.08	
206	Cg3281	1	580.3584	1.0	686	691	0	23.4	18	V	LLPPAA	A	1.3	6.02	
207	Cg0508	1	645.3122	0.2	113	118	0	27.3	25	V	LWAADA	A	0.8	3.1	
207	Cg0508	1	1372.6796	-2.0	332	343	0	38.4	29	A	DIELMTPDLEVV	T	0.5	2.84	
207	Cg0508	1	1858.9234	-3.9	332	348	0	46.9	29	A	DIELMTPDLEVVTADKA	A	0.1	3.42	
208	Cg2893	1	601.3873	0.8	242	246	0	22.9	16	V	IMLII	G	3.8	6.02	
208	Cg2893	1	672.4058	2.8	262	267	0	28.8	24	P	LLDLSL	F	1.8	3.1	
208	Cg2893	1	715.4302	1.0	243	249	0	34.6	27	I	MLIIGAV	L	2.9	6.02	
208	Cg2893	1	879.4524	-2.6	115	123	0	26.8	26	A	FLGIGAATM	M	1.7	6.02	
208	Cg2893	1	1014.6114	-2.2	186	195	0	32.1	26	I	ALIATLFVAP	A	2.2	6.02	
209	Cg1364	1	617.4152	-0.5	37	41	0	25.8	21	P	FLIIL	I	3.9	6.02	
209	Cg1364	1	730.4993	0.0	37	42	0	22.2	16	P	FLIILI	V	4.0	6.02	
209	Cg1364	1	1119.5924	-1.2	80	89	0	34.1	29	A	ALEKYNAQLA	E	-0.3	6.86	
209	Cg1364	2	1434.7355	0.9	171	183	0	37.4	28	S	GTIDRFLADLDTV	A	0.3	3.6	
209	Cg1364	2	1901.9847	-2.9	171	188	0	70.5	30	S	GTIDRFLADLDTVAPNGK	-	-0.2	4.18	
210	Cg0165	1	551.3683	2.2	332	336	0	25.9	18	E	PIIPL	A	1.9	6.02	
210	Cg0165	1	751.5207	0.9	333	339	0	20.0	17	P	IIPLALI	G	3.0	6.02	
210	Cg0165	1	831.4776	-2.9	244	250	0	23.5	23	A	LVDMLLL	V	2.5	3.1	Oxidation (M)
212	Cg3179	1	713.4323	2.0	329	335	0	34.3	27	A	LDAIIIG	S	2.2	3.1	
212	Cg3179	2	800.4644	1.6	329	336	0	45.9	29	A	LDAIIIGS	E	1.8	3.1	
213	Cg1016	1	709.4738	1.8	399	405	0	21.3	21	I	LGVLLVP	A	2.5	6.02	
213	Cg1016	1	800.483	-4.5	310	317	0	33.9	30	N	MVLAALLA	I	2.9	6.02	
214	Cg2521	2	1429.8003	3.7	508	521	0	27.1	26	A	MVVGDGKPFVGLLV	T	1.4	6.76	
215	Cg1506	1	553.3839	1.3	134	138	0	24.5	24	S	ILVPL	G	2.9	6.02	
215	Cg1506	1	640.416	2.0	133	138	0	26.7	23	V	SILVPL	G	2.3	6.02	
217	Cg0561	1	789.4273	0.9	56	62	0	28.6	26	I	SFLPEVV	G	1.3	3.3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
217	Cg0561	2	1059.5197	-1.7	44	55	0	58.9	28	S	SGSDSKPGGGVI	S	-0.4	6.76	
217	Cg0561	1	1160.6441	-2.3	98	108	0	53.8	27	V	DFLAGLGVEKI	L	0.8	4.08	
217	Cg0561	2	1403.766	0.9	95	108	0	35.8	27	V	SGVDFLAGLGVEKI	L	0.9	4.08	
217	Cg0561	1	1830.9364	-3.8	44	62	0	49.1	30	S	SGSDSKPGGGVISFLPEVV	G	0.3	4.08	
218	Cg3046	2	754.4337	1.5	269	275	0	36.1	27	Q	PDGVLRV	D	0.3	6.78	
219	Cg1456	1	707.4582	2.0	48	54	0	20.9	16	E	IIPIGVP	N	2.0	6.02	
219	Cg1456	1	726.3225	-1.7	559	564	0	25.3	24	L	DAFDFL	A	0.7	2.92	
220	Cg1247	1	824.3857	0.8	106	111	0	34.9	24	A	QFFWPT	R	-0.2	6.02	
220	Cg1247	1	1109.5506	-0.2	66	74	0	34.9	27	V	NQPWVPQEI	K	-1.0	3.3	
220	Cg1247	1	1271.5994	-1.1	184	196	0	52.2	27	L	SNTGINPDGPSTI	S	-0.7	3.1	
220	Cg1247	2	2431.1326	0.0	82	105	0	102.8	28	A	MGFITGDGSEGGDIEIPDNAPRIA	Q	-0.2	3.42	
221	Cg0722	1	601.3873	0.8	565	569	0	22.9	16	I	LMLLL	R	3.4	6.02	
221	Cg0722	1	993.7202	-4.4	556	564	0	14.0	13	P	IVLLVILVI	L	4.2	6.02	
222	Cg2939	1	601.3873	0.8	262	266	0	22.9	16	G	LMILL	T	3.6	6.02	
222	Cg2939	1	688.4523	0.1	36	41	0	24.4	21	L	LIFLLA	I	3.4	6.02	
224	Cg2971	1	527.3319	0.0	136	140	0	28.1	27	T	LTVVP	A	2.0	6.02	
224	Cg2971	1	876.5069	4.0	450	458	0	28.9	25	A	AGTKVAFIA	G	1.3	10.1	
225	Cg1883	1	752.4432	-0.5	155	161	0	25.2	22	V	KLDPIPA	R	-0.1	6.76	
225	Cg1883	2	2567.2854	-3.4	137	161	0	64.0	31	I	EAGDEVTVTLELADGSEVKLDPIPA	R	0.0	3.32	
225	Cg1883	2	2962.5023	-4.9	133	161	0	66.9	31	L	ANPIEAGDEVTVTLELADGSEVKLDPIPA	R	0.0	3.32	
227	Cg0766	1	654.4064	-0.5	88	93	0	24.2	23	S	VPQLKA	A	0.1	10.1	
228	Cg0489	2	1493.7249	-0.1	74	87	0	31.7	29	V	EAPKPEPAEEVEVA	S	-0.9	3.68	
228	Cg0489	2	1939.9123	-1.9	88	105	0	75.9	28	A	SVEGDVDKQETPERPAPS	N	-1.5	3.92	
228	Cg0489	2	2756.2811	-2.0	88	112	0	41.1	27	A	SVEGDVDKQETPERPAPSNEETMVL	R	-1.1	3.74	
229	Cg2699	1	624.3272	1.6	559	563	0	24.4	22	M	NFVFV	I	2.1	6.02	
231	Cg0864	1	685.4374	0.9	173	179	0	40.2	30	L	SAALLIV	V	2.7	6.02	
231	Cg0864	1	715.4302	1.0	13	19	0	34.6	27	V	MILLGLG	M	2.4	6.02	
232	Cg3418	1	551.3683	0.9	36	40	0	34.3	18	A	LPIPL	D	1.8	6.02	
235	Cg0047	2	943.5702	1.3	2	10	0	30.9	25	M	STIGNLKLV	V	0.8	10.1	
235	Cg0047	1	1061.4149	-1.8	237	246	0	27.0	19	A	DAEQEAAEEA	E	-1.4	2.84	
235	Cg0047	2	1133.5353	-2.1	40	50	0	47.8	28	A	AGEYAPKAEQA	V	-1.0	4.26	
235	Cg0047	1	1285.7242	-3.0	2	14	0	46.2	28	M	STIGNLKLVVDGA	R	0.7	6.76	
235	Cg0047	1	1306.5412	-1.2	211	222	0	32.4	21	A	TETPAETTEEEA	K	-1.5	2.9	
235	Cg0047	4	3159.4592	-1.6	236	264	0	56.0	27	E	ADAEQEAAEEAEAEAIQAEFDKKNAPQRT	Q	-1.3	3.86	
236	Cg1280	1	680.4836	2.2	1038	1043	0	23.9	15	K	LILLLP	H	3.0	6.02	
236	Cg1280	1	704.4109	1.4	771	776	0	23.5	23	D	VFIDLV	C	2.7	3.1	
237	Cg1424	1	1305.7122	-2.4	187	198	0	44.5	28	A	SLIWFPLVGFGA	A	1.6	6.02	
237	Cg1424	1	1376.7493	-2.8	187	199	0	45.6	27	A	SLIWFPLVGFGAA	A	1.6	6.02	
238	Cg2201	1	676.3948	0.0	49	53	0	25.6	19	A	WFLVL	S	2.7	6.02	
238	Cg2201	1	775.4844	0.9	76	82	0	24.8	23	F	FLAVLIT	T	2.9	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
240	Cg2539	1	583.4309	-0.2	247	251	0	24.1	18	L	IILII	T	4.4	6.02	
240	Cg2539	1	942.5538	2.4	404	412	0	25.1	24	D	VPAALFNVL	Q	1.9	6.02	
240	Cg2539	1	1485.6843	-0.9	505	518	0	26.3	26	M	MFSLLKGMSEDAAA	V	0.5	4.08	Oxidation (M)
241	Cg1864	1	624.3847	0.3	491	496	0	23.7	18	E	VPSIPL	A	1.4	6.02	
241	Cg1864	1	645.3122	0.2	485	489	0	25.4	25	E	EQLWA	E	-0.5	3.3	
241	Cg1864	1	836.3916	-0.2	159	165	0	40.8	30	V	FKEDLGE	R	-1.2	3.82	
242	Cg0202	1	642.3701	-2.6	330	335	0	37.8	29	F	ININVA	S	1.3	6.02	
243	Cg2183	1	851.5117	0.5	284	292	0	25.7	22	L	GIGLPPSIV	S	1.4	6.02	
243	Cg2183	1	1217.5776	-0.9	44	56	0	31.6	28	A	ATDETGLGAVDAV	A	0.4	2.88	
243	Cg2183	1	1412.8279	-2.5	279	292	0	52.2	25	A	TLSFLGIGLPPSIV	S	1.5	6.02	
244	Cg2212	1	573.3196	1.6	369	373	0	22.6	21	R	TLLMP	R	1.4	6.02	
244	Cg2212	1	632.3897	-1.3	44	49	0	29.0	27	I	FLALGL	G	2.6	6.02	
246	Cg2173	1	601.3873	0.3	149	153	0	27.5	16	P	LILMI	M	3.7	6.02	
246	Cg2173	1	679.4268	-1.2	179	185	0	25.0	21	I	PGAILIP	I	1.6	6.02	
246	Cg2173	1	715.4302	1.0	359	365	0	39.8	27	A	MIILGGI	V	2.6	6.02	
247	Cg1498	1	599.3894	1.5	379	383	0	30.2	19	A	LLEII	S	2.6	3.3	
248	Cg2563	1	532.2645	1.1	182	186	0	30.8	29	L	SAWGL	Y	0.7	6.02	
248	Cg2563	1	617.4152	-0.5	395	399	0	25.8	21	S	FILIL	A	3.9	6.02	
248	Cg2563	1	688.4523	0.1	395	400	0	28.6	21	S	FILILA	F	3.5	6.02	
252	Cg1867	2	1009.6535	0.6	465	475	0	23.7	21	D	LAGIAGLIIGI	G	2.5	6.02	
252	Cg1867	2	2454.9742	-2.8	615	637	0	32.2	13	A	STDNSSTDNSEAPGTDTNQEEEK	-	-2.1	3.32	
252	Cg1867	2	2707.3453	-0.9	359	383	0	54.2	30	T	SITGDFTQTEAQDLANNLRYGALPL	S	-0.3	3.7	
252	Cg1867	2	2879.4301	-1.9	357	383	0	44.8	31	S	ATSITGDFTQTEAQDLANNLRYGALPL	S	-0.2	3.7	
256	Cg0934	1	729.3909	-1.1	64	70	0	33.1	31	L	ELGVLEA	V	0.9	3.12	
257	Cg3244	1	765.5	-1.6	97	103	0	23.3	13	L	TPLLLPI	I	1.7	6.02	
257	Cg3244	1	878.5841	-0.6	96	103	0	25.2	13	V	LTPLLLPI	I	2.0	6.02	
257	Cg3244	1	977.6525	-1.4	95	103	0	15.4	13	R	VLTPLLLPI	I	2.2	6.02	
257	Cg3244	1	1133.7536	-1.6	94	103	0	13.8	13	A	RVLTPLLLPI	I	1.6	11.04	
257	Cg3244	2	1485.7212	0.5	124	138	0	34.4	28	A	GVTAEQLSQFAGHAA	A	0.1	5.12	
257	Cg3244	2	1845.9221	-0.5	159	174	0	30.7	30	A	GFVRDVEERLNELEAA	A	-0.5	4	
257	Cg3244	3	2142.1029	0.4	194	211	0	52.9	30	I	SRDLNQVSDQIQDRLLDK	-	-1.2	4.34	
259	Cg2408	1	601.3873	0.8	122	126	0	22.9	16	G	LMLLI	F	3.6	6.02	
259	Cg2408	1	874.3345	-2.1	71	77	0	29.2	18	L	PEDWEEA	E	-2.1	2.88	
259	Cg2408	1	1456.6834	-1.1	66	77	0	39.6	27	V	RVDVLPEDWEEA	E	-0.9	3.5	
260	Cg2735	1	645.297	0.2	34	39	0	35.7	31	S	NLVDDA	K	-0.1	2.92	
260	Cg2735	2	1240.7139	-1.5	79	88	0	30.0	26	A	NDLKEIQRLL	S	-0.7	7.02	
260	Cg2735	1	1258.6153	-0.8	34	45	0	63.7	29	S	NLVDDAKNQATA	K	-0.7	3.88	
260	Cg2735	2	1417.7049	-0.9	21	33	0	73.2	29	A	STLDELADRSKPS	N	-1.1	4.3	
260	Cg2735	2	1612.8896	-2.3	79	91	0	37.7	29	A	NDLKEIQRLLSER	-	-1.2	7.14	
261	Cg0752	1	757.397	-0.8	308	314	0	32.3	29	A	QAQVEIA	E	0.3	3.3	

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261	Cg0752	1	797.4283	-0.1	191	198	0	35.6	27	S	LGAPEIQA	K	0.4	3.3	
261	Cg0752	2	1485.7423	-0.5	218	230	0	70.9	29	S	RIANQEADLVEQT	Q	-0.8	3.82	
262	Cg0790	1	539.3683	-0.2	379	383	0	26.2	23	R	VIVLP	L	3.0	6.02	
262	Cg0790	1	553.3839	1.1	380	384	0	26.4	24	V	IVLPL	A	2.9	6.02	
263	Cg2077	1	601.3873	0.3	161	165	0	27.5	16	I	LLLML	A	3.4	6.02	
263	Cg2077	1	640.4523	-0.9	210	215	0	28.6	25	S	LILGIL	T	3.3	6.02	
264	Cg3371	1	680.4836	0.6	292	297	0	36.2	15	G	LLILPL	M	3.0	6.02	
264	Cg3371	1	690.3952	0.7	167	172	0	26.1	26	V	FLDIAI	Q	2.3	3.1	
264	Cg3371	1	1076.627	-1.6	78	87	0	26.7	25	I	TFGIFPLIGI	G	2.0	6.02	
265	Cg2406	1	645.2832	-1.5	46	50	0	25.8	24	A	MYFVS	R	1.4	5.92	
265	Cg2406	1	738.3701	-1.5	87	93	0	28.6	27	C	QFGVFAA	E	1.4	6.02	
265	Cg2406	2	842.4432	-0.6	19	25	0	33.9	23	A	LNRPNMV	S	-0.5	11.04	
265	Cg2406	2	984.5175	0.4	17	25	0	35.0	23	V	AALNRPNMV	S	0.0	11.04	
265	Cg2406	2	1100.5397	-0.9	6	16	0	43.9	27	V	GNTGMAAPQRV	A	-0.4	11.04	
265	Cg2406	2	1116.5346	-2.5	6	16	0	35.2	28	V	GNTGMAAPQRV	A	-0.4	11.04	Oxidation (M)
266	Cg2884	1	553.3839	1.1	375	379	0	26.4	24	L	LVLIP	F	2.9	6.02	
266	Cg2884	1	723.4895	-0.3	373	379	0	35.3	21	S	GLLVLIP	F	2.6	6.02	
266	Cg2884	1	725.4687	-0.4	340	346	0	24.3	23	I	LALSIPI	S	2.3	6.02	
267	Cg2840	1	1410.6667	-2.9	241	253	0	46.3	27	I	AGNFLDFLESEVA	A	0.4	2.94	
268	Cg2642	1	1022.6124	3.2	387	398	0	22.2	21	R	LGGIVGPAIGGL	I	1.6	6.02	
269	Cg1545	1	656.3931	-4.7	16	21	0	31.0	20	V	IPLMIA	L	2.5	6.02	
269	Cg1545	1	704.4473	0.6	105	110	0	22.7	22	N	VTILFL	G	3.1	6.02	
270	Cg1212	1	617.4152	-0.5	219	223	0	25.8	21	I	FILLI	C	3.9	6.02	
270	Cg1212	1	730.4993	0.0	218	223	0	22.2	16	G	IFILLI	C	4.0	6.02	
272	Cg1225	1	680.4836	0.6	182	187	0	36.2	15	G	LILLPL	L	3.0	6.02	
272	Cg1225	2	726.4276	2.5	382	389	0	28.4	28	R	LGAISGPL	L	1.3	6.02	
272	Cg1225	1	793.5677	0.0	182	188	0	16.1	13	G	LILLPLL	Y	3.1	6.02	
273	Cg0831	1	785.4721	0.0	186	192	0	30.6	29	R	MILLPLA	A	2.6	6.02	Oxidation (M)
273	Cg0831	1	879.543	-0.2	118	126	0	21.1	19	F	PGIALVTPL	F	1.5	6.02	
273	Cg0831	1	1173.6468	-3.2	116	126	0	31.8	27	S	MFPGIALVTPL	F	1.7	6.02	Oxidation (M)
274	Cg2339	1	836.5735	-0.5	173	180	0	27.9	18	T	LVLLPIAV	I	3.1	6.02	
276	Cg3165	1	585.3737	1.5	359	363	0	27.8	25	R	DILII	G	2.8	3.1	
276	Cg3165	1	836.5735	-0.5	128	135	0	28.0	18	W	LLPLVVAL	R	3.0	6.02	
277	Cg1299	1	598.4418	1.7	319	323	0	28.1	17	E	ILKLL	S	2.4	10.1	
277	Cg1299	1	878.5841	-1.8	173	180	0	25.9	13	A	IITLPLIP	V	2.2	6.02	
280	Cg2537	1	632.3897	-1.3	223	228	0	28.1	27	A	FIAGIL	L	2.8	6.02	
281	Cg1709	1	624.3483	-0.2	7	12	0	24.2	24	T	PEVPAL	A	0.5	3.3	
282	Cg3096	1	1138.6234	-1.1	203	213	0	30.5	26	I	NIIGDLIPEGV	L	0.8	3	
283	Cg3387	1	761.4072	0.3	340	347	0	34.1	27	A	NIAFGAVA	V	1.6	6.02	
284	Cg1412	1	674.4367	1.5	110	115	0	25.0	24	G	LFIGLL	A	3.1	6.02	

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284	Cg1412	1	758.436	-4.9	305	312	0	39.1	32	V	IGCVIALA	V	2.8	5.32	
286	Cg2466	2	1197.5738	-0.8	805	816	0	61.9	27	A	QLRNPGADAGEA	F	-1.0	4.08	
286	Cg2466	2	2090.9579	-4.4	251	269	0	46.2	26	A	FLGDGEMDEPESRGLIQQA	A	-0.7	3.5	
287	Cg2158	1	793.5677	0.0	280	286	0	15.0	13	V	PILLLLL	F	3.1	6.02	
287	Cg2158	1	850.5892	-0.1	278	285	0	18.8	16	L	AVPILLLL	L	3.0	6.02	
288	Cg2192	1	820.4331	0.6	249	256	0	31.5	30	A	GGYALDLL	R	1.0	3.1	
288	Cg2192	1	1034.4557	-0.7	180	188	0	33.9	26	I	SWIDEGTDI	N	-0.5	2.88	
290	Cg2372	1	726.3225	-1.7	99	104	0	25.3	24	G	FADDFI	K	0.8	2.92	
290	Cg2372	1	1863.9407	-3.8	130	146	0	48.5	30	I	FGFLVLQFPDENGLTPA	S	0.4	3	
291	Cg3132	1	617.4152	-0.5	407	411	0	25.8	21	V	FIILL	F	3.9	6.02	
291	Cg3132	2	2580.2173	-2.8	319	340	0	31.9	28	T	EWLQDFVEKYPGKYDNPEGAPV	G	-1.1	3.92	
292	Cg1419	1	656.3931	-4.4	89	94	0	25.4	20	V	IMPLIA	L	2.5	6.02	
295	Cg1787	1	526.3115	0.8	863	867	0	32.0	30	D	NPLLA	R	0.9	6.02	
297	Cg2125	1	577.3475	2.3	349	353	0	28.1	28	V	LYGLI	G	2.1	5.92	
298	Cg0061	1	532.2646	0.2	304	308	0	35.2	29	S	WGGIT	G	0.4	6.02	
298	Cg0061	1	571.3403	0.5	71	75	0	23.2	21	Q	IMLPV	V	2.6	6.02	
298	Cg0061	1	630.3741	0.6	251	255	0	27.2	27	G	SWLLI	G	2.1	6.02	
298	Cg0061	1	758.4327	1.3	251	257	0	36.4	27	G	SWLLIGA	V	1.7	6.02	
299	Cg1234	1	695.4218	1.9	330	336	0	22.6	21	A	PSVAPLL	T	1.4	6.02	
301	Cg2359	1	596.3534	0.0	849	854	0	26.6	22	L	PLPGLT	V	0.6	6.02	
303	Cg1219	1	553.3839	1.1	98	102	0	26.4	24	T	VILPI	S	3.1	6.02	
304	Cg0158	2	844.3095	4.6	334	341	0	18.5	17	G	GMADMFSS	A	0.4	3.1	
305	Cg3367	2	1762.889	-1.6	282	296	0	40.0	29	A	ASLEEIFLRHYGETV	S	0.0	4.54	
305	Cg3367	1	1971.9863	-0.4	157	174	0	55.7	30	L	IVDEPTAGLDPIMEQVFV	T	0.6	2.84	
305	Cg3367	2	2222.1794	-2.0	258	278	0	41.3	29	C	DASEVPDILRIIIDAGGQDII	S	0.5	3.36	
307	Cg2258	1	585.3737	1.5	48	52	0	27.8	25	L	DLILI	H	2.6	3.1	
307	Cg2258	1	698.4578	1.0	47	52	0	28.2	22	D	LDLILI	H	2.8	3.1	
308	Cg1784	1	945.5171	0.6	205	212	0	36.1	30	W	ALEKFPEI	E	0.0	4.26	
309	Cg3382	1	1009.6535	-2.9	485	495	0	23.1	21	V	AAIVLGAIVIA	A	3.0	6.02	
310	Cg0057	1	1009.5233	0.8	635	642	0	34.0	27	V	RLFEFDLA	A	0.4	4.08	
310	Cg0057	2	1100.59	3.6	136	145	0	32.5	29	R	DVKPANIMIT	N	0.4	6.76	
311	Cg1435	1	656.3381	-1.2	545	550	0	29.1	27	A	EEVLPA	I	0.2	3.12	
312	Cg2110	1	553.3839	1.3	336	340	0	24.5	24	L	IIVLP	V	3.1	6.02	
312	Cg2110	1	723.4895	-0.3	334	340	0	21.2	21	F	GLIIVLP	V	2.7	6.02	
313	Cg0980	1	684.3806	0.3	139	145	0	36.2	28	A	NAIGTPI	L	0.7	6.02	
313	Cg0980	1	1109.5506	-0.2	220	231	0	31.4	27	A	GGGAVDPAPWLA	E	0.4	3.1	
313	Cg0980	2	1226.6255	1.2	102	113	0	51.6	28	I	QADLDARGPSVV	R	-0.2	3.88	
313	Cg0980	2	1778.9315	-2.0	220	237	0	43.7	29	A	GGGAVDPAPWLAERGITL	-	0.2	4.08	
314	Cg3334	1	577.3475	2.3	231	235	0	28.1	28	T	YLGLI	I	2.1	5.92	
314	Cg3334	1	688.4523	0.1	216	221	0	28.6	21	V	IFLLLA	V	3.4	6.02	

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317	Cg2356	1	640.416	2.0	188	193	0	26.8	23	S	VLSLPL	A	2.2	6.02	
319	Cg1832	1	571.3403	0.5	305	309	0	23.2	21	R	LMLPV	S	2.4	6.02	
320	Cg1768	1	782.5266	1.3	60	67	0	31.6	25	P	LVALIALA	N	3.2	6.02	
322	Cg2643	1	539.3683	-0.2	239	243	0	26.5	23	E	LVVPL	A	2.9	6.02	
322	Cg2643	1	981.5933	-4.3	168	176	0	25.1	24	D	PLIALPMVI	V	2.4	6.02	Oxidation (M)
323	Cg3101	1	1076.4848	-0.4	180	188	0	35.7	26	V	GIEDLMDWV	Q	0.3	2.88	
325	Cg2552	1	598.4418	1.7	292	296	0	28.1	17	T	LLKLI	A	2.4	10.1	
325	Cg2552	1	642.3588	0.9	115	120	0	29.9	27	L	IDVSLP	E	1.1	3.1	
326	Cg1395	1	1334.6718	-3.7	55	66	0	32.3	29	M	GKTVLLNEFEDA	A	-0.2	3.82	
328	Cg1195	1	1885.0237	-3.7	232	248	0	36.0	28	S	IPSIGDLEIWSLLPYAV	G	1.0	3	
333	Cg1142	1	704.4473	0.6	346	351	0	22.7	22	W	VTIIFI	L	3.3	6.02	
333	Cg1142	1	861.4596	4.1	55	63	0	30.4	30	A	TSAIGPGFL	T	1.0	6.02	
334	Cg2680	1	726.3225	-1.7	9	14	0	25.3	24	N	FDGEFI	E	0.5	3	
334	Cg2680	1	729.3909	-2.3	436	442	0	33.4	31	A	LLDAVEA	A	1.2	3	
337	Cg2571	2	1205.6656	1.5	250	260	0	27.2	27	T	HELLEIGIVSP	T	0.7	4.24	
338	Cg2419	1	1263.6711	-2.2	503	513	0	37.7	28	T	FVQVLKDLSES	-	0.3	4.08	
340	Cg2799	1	804.3865	-0.7	181	188	0	32.5	29	A	DSSVVDAI	R	0.8	2.92	
340	Cg2799	2	1565.8665	-0.4	104	117	0	35.4	26	T	QIEDGNLVVEIKPL	N	0.1	3.82	
340	Cg2799	2	2359.1907	-1.9	220	241	0	51.1	30	R	VLQDGKDVEGNISDWITTVLAS	-	0.1	3.5	
340	Cg2799	2	2772.393	-1.0	213	238	0	34.3	31	T	GSLSSPRVLQDGKDVEGNISDWITTV	L	-0.3	3.96	
341	Cg0331	1	583.4309	-0.2	184	188	0	24.1	18	Q	ILILI	G	4.2	6.02	
341	Cg0331	2	1009.6535	0.6	181	189	0	26.3	21	G	QIQILILIG	T	2.0	6.02	
342	Cg0886	1	882.5062	-1.2	469	476	0	29.6	24	D	IPEIADLI	S	1.3	3	
347	Cg0568	1	509.3213	0.6	328	332	0	31.2	21	V	LPPLA	I	1.2	6.02	
347	Cg0568	1	666.468	0.3	359	364	0	19.9	19	I	IPVLLL	R	3.1	6.02	
347	Cg0568	1	955.6106	-1.5	385	392	0	30.4	22	H	PIFQILLI	V	2.4	6.02	
348	Cg2424	1	657.3196	0.6	86	90	0	24.1	20	A	MFIFT	R	2.3	6.02	
348	Cg2424	1	674.4367	1.5	61	66	0	25.0	24	L	FLIGLI	W	3.2	6.02	
348	Cg2424	1	793.5677	0.0	45	51	0	25.6	13	A	LIPLLLL	A	3.1	6.02	
348	Cg2424	1	864.6048	-0.9	47	54	0	20.8	13	I	PLLLLAIL	G	3.0	6.02	
348	Cg2424	2	1976.0149	-1.3	221	241	0	34.4	30	A	MDNVGNAPGGSLPKGPLPKGA	S	-0.5	9.88	
349	Cg1289	1	571.3403	0.5	301	305	0	23.2	21	G	LMLVP	M	2.4	6.02	
349	Cg1289	1	793.5677	0.0	357	363	0	25.6	13	W	LLIPIIL	F	3.3	6.02	
351	Cg2916	1	726.3258	-2.8	371	376	0	25.1	25	D	YVDAML	K	1.2	3.1	Oxidation (M)
353	Cg0522	1	674.4367	1.5	23	28	0	25.0	24	P	LFLGIL	A	3.1	6.02	
354	Cg3169	1	598.4418	1.7	253	257	0	28.1	17	L	ILKLI	N	2.5	10.1	
355	Cg0470	1	642.3952	1.2	287	292	0	43.8	27	G	DILGIL	G	2.1	3.1	
355	Cg0470	1	699.4167	1.1	287	293	0	41.6	30	G	DILGILG	I	1.8	3.1	
355	Cg0470	1	782.5266	1.3	291	298	0	31.2	25	G	ILGILAAL	G	3.0	6.02	
357	Cg2370	1	632.3897	-1.3	324	329	0	28.4	27	A	LFAGLL	Y	2.6	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
357	Cg2370	1	973.5444	3.8	382	392	0	32.9	29	S	AGGTSAIITLA	S	1.4	6.02	
357	Cg2370	1	1403.6866	-2.0	490	503	0	30.0	29	T	GSVKGRSSGQDNGR	S	-1.7	11.32	
358	Cg3068	1	1391.6973	-2.4	238	250	0	47.8	29	K	LGLADDALPFDFV	F	0.9	2.82	
358	Cg3068	2	1717.8345	1.0	2	16	0	67.3	29	M	PIATPEVYNEMLDRA	K	-0.4	3.82	
358	Cg3068	2	2622.2788	-4.0	2	25	0	33.9	30	M	PIATPEVYNEMLDRAKEGGFAFPA	I	-0.3	4.16	
359	Cg1577	1	790.4225	1.3	141	147	0	34.6	31	T	DIFVQLG	K	1.1	3.1	
359	Cg1577	2	1252.4997	0.6	116	126	0	31.4	20	I	NSDGFHFSDEV	R	-0.9	3.7	
361	Cg1365	1	1314.7031	-3.7	79	90	0	55.1	30	S	VLEVLKDAAEQT	W	0.1	3.82	
361	Cg1365	2	2372.2336	-2.3	31	52	0	30.9	30	A	QAGTELFDVVDILDGDRALRVA	V	0.2	3.76	
362	Cg1121	2	3439.6181	-1.9	24	54	0	48.9	28	S	SLKETQRPQGQNPYGGYDNFGGVYQQNVAPQ	K	-1.4	6.84	
363	Cg2618	1	674.4367	1.5	21	26	0	24.6	24	V	FIAVLL	N	3.5	6.02	
363	Cg2618	1	984.4957	-2.1	190	197	0	32.1	25	T	FFFLPESV	D	1.3	3.3	
364	Cg1479	1	598.4418	1.7	573	577	0	28.1	17	A	IIKLI	N	2.7	10.1	
364	Cg1479	1	656.3745	1.2	589	594	0	26.2	26	P	EVSPLL	K	1.0	3.3	
364	Cg1479	1	755.3701	-0.4	587	593	0	30.6	22	N	DPEVSPL	L	-0.4	3	
369	Cg2371	1	818.4386	0.4	84	91	0	30.7	27	P	TSTLLVDA	H	1.0	3.1	
371	Cg1483	1	640.4523	0.3	10	15	0	30.8	25	L	IIGLLL	G	3.3	6.02	
371	Cg1483	1	640.4523	-0.9	9	14	0	28.6	25	G	LIIGLL	L	3.3	6.02	
371	Cg1483	2	915.4848	-2.5	16	26	0	33.8	27	L	GMLGGGGAILA	I	1.4	6.02	
374	Cg3248	1	557.3247	0.2	146	150	0	23.0	19	F	MVPIV	P	2.6	6.02	
375	Cg1726	1	991.4287	-1.8	385	393	0	28.6	25	A	GGSYFVESF	T	0.3	3.3	
377	Cg1673	1	684.4422	0.7	493	498	0	39.6	25	Y	VELLLV	I	2.7	3.3	
377	Cg1673	2	715.448	1.7	204	210	0	29.4	25	A	IITASVI	A	2.6	6.02	
378	Cg2147	1	621.356	0.8	132	136	0	26.1	19	G	MFIVL	G	3.4	6.02	
380	Cg3157	1	1430.7253	-2.7	205	218	0	63.9	29	A	AISQDTIDKLAEGA	G	-0.1	3.7	
381	Cg1654	2	1085.5465	1.0	723	732	0	38.9	27	A	LENAGAEQRV	D	-0.7	4.26	
382	Cg1086	1	635.3716	-4.9	171	175	0	24.1	19	A	MLLFL	N	3.2	6.02	
382	Cg1086	1	704.4473	0.6	81	86	0	22.7	22	S	VITIFL	A	3.2	6.02	
386	Cg1880	2	1135.5258	-1.8	201	210	0	28.6	26	T	AYDNVNPRTS	E	-1.3	6.7	
386	Cg1880	2	1270.671	-0.2	565	575	0	38.7	29	A	LFGSIERFFGV	L	1.0	6.98	
387	Cg0915	2	2827.5232	-0.7	129	153	0	46.9	30	A	AFHVRLEDPLAVEILDPVRDLPQVS	N	0.2	4.2	
388	Cg1090	2	1354.5637	-0.5	157	169	0	39.2	22	A	NSAEDLSHDPEAA	A	-1.1	3.58	
394	Cg2267	1	699.4167	0.3	150	156	0	31.8	30	E	GEIVLLG	H	1.7	3.3	
395	Cg3413	1	617.4152	-0.5	214	218	0	25.8	21	Y	FLILL	L	3.7	6.02	
395	Cg3413	1	667.3945	-0.7	213	217	0	23.2	15	T	YFLIL	L	2.7	5.92	
395	Cg3413	1	730.4993	0.0	214	219	0	22.2	16	Y	FLILLL	R	3.8	6.02	
396	Cg1526	1	850.5892	-0.1	346	353	0	26.3	16	I	ALILPIVL	V	3.1	6.02	
398	Cg1665	1	968.4815	-0.2	165	174	0	43.4	25	A	VGLPTGPEEA	T	-0.2	3.12	
398	Cg1665	1	1039.5186	-0.6	164	174	0	36.5	25	A	AVGLPTGPEEA	T	0.0	3.12	
398	Cg1665	1	1833.8269	-4.5	112	129	0	57.5	25	A	GFSTPESVEEGPNGESLV	T	-0.6	2.96	

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399	Cg1690	1	642.3952	1.2	348	353	0	43.8	27	G	EVLGLL	E	2.0	3.3	
400	Cg0437	1	690.3952	0.7	278	283	0	26.1	26	E	FIDLAL	T	2.2	3.1	
403	Cg0565	1	758.4174	-0.9	150	157	0	34.2	32	A	ISGGIEAL	C	1.2	3.3	
404	Cg3242	1	782.5266	1.3	421	428	0	32.7	25	S	VLALILAA	F	3.2	6.02	
406	Cg1959	1	551.3683	0.9	557	561	0	34.3	18	G	LPLPL	K	1.6	6.02	
407	Cg2695	2	926.5185	-1.0	352	361	0	26.4	26	G	VIGPNGVGKS	T	0.2	10.1	
407	Cg2695	2	2240.9817	-1.0	113	132	0	26.8	23	T	NYTDELMEEMGVLQEALDAA	D	-0.3	2.76	
408	Cg0552	1	686.4214	0.7	35	40	0	33.7	26	P	LSLELL	A	1.8	3.3	
409	Cg2008	1	579.338	2.6	72	76	0	22.2	21	M	LLPTH	D	0.4	7.84	
410	Cg1229	1	1241.6252	-2.3	118	129	0	28.4	27	A	RIDPTDLGDGLA	Q	-0.4	3.6	
410	Cg1229	2	1595.8519	0.2	118	132	0	36.6	28	A	RIDPTDLGDGLAQLL	K	0.0	3.6	
410	Cg1229	2	2124.1943	-2.6	123	142	0	32.8	27	T	DLGDGLAQLLKLPERFVIGA	V	0.4	4.3	
410	Cg1229	3	2706.5068	-1.4	118	142	0	31.9	27	A	RIDPTDLGDGLAQLLKLPERFVIGA	V	0.1	4.46	
413	Cg2833	1	830.4538	1.2	227	233	0	31.5	27	A	NFIPEVL	D	1.0	3.3	
416	Cg0781	1	1524.6741	-3.5	144	157	0	28.4	25	A	SMYAQPFANTPAPM	Y	-0.2	5.92	
416	Cg0781	2	2625.2558	-3.7	2	25	0	41.1	29	M	NTNLPNLYTAFDLDRSESSEALGV	S	-0.4	3.58	
418	Cg2301	1	584.3897	1.5	369	374	0	31.7	31	F	LLGIVA	A	3.0	6.02	
418	Cg2301	1	678.3775	-0.1	149	154	0	23.2	23	G	MLGVFI	G	2.8	6.02	
419	Cg1305	1	711.4894	-1.3	253	259	0	30.7	25	G	AILVILA	L	3.5	6.02	
419	Cg1305	2	1009.6536	1.6	345	354	0	23.8	21	V	LIVGVILNAV	L	2.7	6.02	
420	Cg1672	1	553.3839	1.1	11	15	0	26.4	24	T	LVIIP	T	3.1	6.02	
420	Cg1672	2	1444.643	-2.4	41	54	0	83.8	24	L	IVDDNSPDGTGERA	D	-1.1	3.5	
421	Cg2166	1	654.4064	-0.5	506	512	0	23.1	23	N	AGVPLKA	P	0.8	10.1	
421	Cg2166	1	704.4109	1.4	196	201	0	24.8	23	S	VFEIVV	A	2.7	3.3	
421	Cg2166	2	715.448	1.5	403	409	0	28.5	25	Q	ILGVTTL	D	2.1	6.02	
422	Cg1546	1	553.3839	1.3	111	115	0	24.5	24	T	IIVIP	G	3.2	6.02	
422	Cg1546	1	686.4214	1.6	208	213	0	22.8	21	S	LVTELL	E	1.9	3.3	
423	Cg0396	1	640.416	2.0	237	242	0	31.4	23	L	LSVLPL	P	2.2	6.02	
423	Cg0396	1	1054.679	-1.8	245	253	0	21.7	21	L	LFVLIPQIL	G	2.5	6.02	
424	Cg0808	1	758.4327	1.3	342	348	0	31.1	27	P	SIWLGIA	V	1.8	6.02	
425	Cg0375	1	826.4953	0.0	422	429	0	35.9	27	A	IFGAPLPL	S	1.6	6.02	
426	Cg0887	2	715.448	1.5	111	117	0	28.5	25	I	LLVGTTL	S	2.0	6.02	
427	Cg2109	1	698.4578	1.0	196	201	0	28.2	22	D	LDLLLL	D	2.6	3.1	
428	Cg0318	1	639.3302	-4.5	342	346	0	25.2	23	L	VYVML	W	2.6	5.92	Oxidation (M)
430	Cg2470	1	843.361	-3.4	286	293	0	25.9	23	I	LQDGEDPA	T	-1.3	2.88	
430	Cg2470	2	2172.0698	-1.0	305	323	0	57.5	30	T	YVINEDAAERQGVEIPQEI	L	-0.5	3.58	
431	Cg2891	1	585.3737	1.5	267	271	0	27.8	25	A	DLLIL	L	2.5	3.1	
431	Cg2891	1	698.4578	1.0	267	272	0	28.2	22	A	DLLILL	G	2.7	3.1	
432	Cg0469	1	642.3952	1.2	30	35	0	43.8	27	G	EVLGLI	G	2.1	3.3	
432	Cg0469	1	699.4167	1.1	30	36	0	41.6	30	G	EVLGLIG	P	1.7	3.3	

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435	Cg2557	1	836.5735	-0.5	173	180	0	26.5	18	V	LLPVIIGL	V	2.8	6.02	
437	Cg2777	1	545.3247	2.0	146	150	0	29.9	28	L	MIVLA	F	3.2	6.02	
437	Cg2777	1	582.3741	0.7	207	212	0	28.1	27	L	IPGIIA	A	2.2	6.02	
437	Cg2777	1	680.4836	2.2	203	208	0	23.9	15	M	ILLLIP	G	3.1	6.02	
438	Cg0327	1	779.552	-0.3	18	24	0	16.1	13	A	LLLLVPL	I	3.1	6.02	
438	Cg0327	1	963.6732	-1.1	18	26	0	16.8	13	A	LLLLVPLIA	G	3.1	6.02	
438	Cg0327	2	1277.5735	-3.1	292	303	0	45.5	25	A	GTIEGTADEERT	S	-1.3	3.68	
439	Cg0088	1	489.2587	0.2	262	266	0	31.3	29	K	GFPGL	G	0.8	6.02	
439	Cg0088	1	850.5892	-0.1	479	486	0	33.4	16	P	LVPAILLL	V	3.0	6.02	
441	Cg1341	1	640.4523	0.3	106	111	0	30.8	25	G	LIGLII	R	3.5	6.02	
442	Cg3322	1	527.3319	0.0	69	73	0	28.1	27	S	LTVPV	A	2.0	6.02	
445	Cg1774	2	1626.8617	-0.1	391	406	0	47.5	29	A	LGKTLPELWGGSADLA	G	0.2	4.08	
447	Cg0623	1	836.4102	-3.7	326	332	0	27.4	27	G	SMITTWV	P	1.1	6.02	
449	Cg1737	1	545.3247	2.0	597	601	0	29.9	28	P	IMVIA	Y	3.4	6.02	
451	Cg3027	1	775.4844	0.0	13	19	0	25.1	23	V	FIIGLTL	M	2.6	6.02	
451	Cg3027	1	981.6263	-1.9	43	51	0	31.8	22	A	IVLFLPLPA	M	2.4	6.02	
452	Cg3227	1	746.3884	1.9	11	16	0	35.8	28	A	ELLELM	K	1.1	3.12	
452	Cg3227	1	1451.7079	-2.6	109	121	0	29.9	28	T	GFTRLMQTEGEIA	G	-0.2	4.26	
452	Cg3227	2	1593.796	0.7	252	265	0	42.0	29	S	AMDPTISYEDLKVI	R	0.1	3.7	
456	Cg1411	1	678.3775	-0.1	203	208	0	23.2	23	G	VAMVFI	S	3.2	6.02	
457	Cg2154	1	601.3873	0.3	71	75	0	27.5	16	F	ILLMI	T	3.7	6.02	
457	Cg2154	1	675.3956	0.7	113	118	0	39.7	28	C	FNIIGI	L	2.1	6.02	
457	Cg2154	1	1344.7289	-2.1	88	100	0	44.7	28	R	GLVTDFGKIADPI	A	0.6	3.88	
457	Cg2154	1	1500.83	-2.6	87	100	0	29.9	28	A	RGLVTDFGKIADPI	A	0.2	6.9	
462	Cg1451	1	990.5022	-2.1	306	315	0	43.1	29	A	LAGEFVADAV	N	1.3	3	
463	Cg1020	1	757.4222	0.4	25	31	0	31.4	29	L	TPILDSL	P	0.8	3.1	
463	Cg1020	1	870.5062	0.2	24	31	0	44.5	27	S	LTPILDSL	P	1.2	3.1	
464	Cg1245	1	577.3475	2.3	330	334	0	28.1	28	G	YIGLL	L	2.1	5.92	
464	Cg1245	1	617.4152	-0.5	229	233	0	25.8	21	G	FLIII	S	4.0	6.02	
465	Cg3153	1	793.5677	0.0	350	356	0	15.2	13	A	LPLLLLL	S	3.0	6.02	
466	Cg2673	1	751.5207	0.9	80	86	0	20.0	17	T	LPLALLL	L	2.7	6.02	
467	Cg0755	2	1350.7871	3.0	198	210	0	22.6	22	A	ALVRPLELGADVV	V	1.1	4.08	
468	Cg0997	1	583.4309	-0.2	172	176	0	24.1	18	V	ILLII	G	4.2	6.02	
469	Cg0018	1	640.4523	0.3	55	60	0	30.8	25	I	ILGIIL	T	3.5	6.02	
469	Cg0018	1	850.5892	-0.1	49	56	0	22.2	16	S	PLIVAIIL	G	3.2	6.02	
469	Cg0018	1	876.4779	-0.3	98	105	0	29.5	28	D	ILSLGFPM	L	1.8	6.02	
470	Cg2314	1	713.4323	2.0	119	125	0	34.3	27	C	EAVILLG	S	2.0	3.3	
471	Cg2139	1	666.468	0.3	118	123	0	19.9	19	A	IPVLIL	M	3.2	6.02	
471	Cg2139	2	1339.662	0.4	282	293	0	36.0	27	A	KVPEQPDQGLET	K	-1.5	3.82	
476	Cg0926	1	553.3839	1.3	150	154	0	24.5	24	S	LIVPI	I	3.1	6.02	

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476	Cg0926	1	836.5735	-0.5	150	157	0	26.7	18	S	LIVPIIGI	M	3.0	6.02	
478	Cg2610	1	622.4054	-0.6	488	493	0	27.8	17	D	LPAIPL	W	1.8	6.02	
481	Cg2206	1	869.5222	-0.3	11	19	0	29.7	27	N	LSTPIGLGL	P	1.3	6.02	
482	Cg0480	1	509.3213	0.4	168	172	0	21.3	21	R	LPIPA	L	1.4	6.02	
482	Cg0480	2	1898.0109	0.4	134	150	0	29.1	29	A	SPTVEQLRGQTQLETIV	S	-0.4	4.26	
483	Cg0370	1	656.3931	-4.4	695	700	0	25.4	20	G	MLPLLA	T	2.3	6.02	
487	Cg2001	1	997.5808	0.5	326	334	0	33.1	26	T	DVLIPSKNL	A	0.3	6.76	
491	Cg2151	1	1028.5866	-2.0	153	161	0	28.5	28	T	KLLSQLEQA	K	-0.2	6.94	
491	Cg2151	2	1142.5567	-1.1	245	255	0	28.6	27	A	GNKQESIEAPA	A	-1.1	4.26	
491	Cg2151	2	1213.5938	-2.3	244	255	0	30.7	26	T	AGNKQESIEAPA	A	-0.9	4.26	
491	Cg2151	2	1505.678	-1.6	207	220	0	50.0	26	A	SNSVEGRMAEVEQA	G	-0.7	3.96	
491	Cg2151	2	2066.9869	-1.0	113	130	0	41.1	29	A	EQSVEDTKQLHDQALQQA	D	-1.4	4.06	
493	Cg0195	2	1422.7467	0.6	302	314	0	41.5	28	V	GAEVPESRIPQQI	E	-0.6	4.26	
495	Cg0893	1	656.3745	0.9	98	103	0	26.5	26	D	DTIVPI	E	1.2	3.1	
495	Cg0893	1	936.4699	4.6	75	83	0	30.9	27	N	MTTVSVRSG	M	0.3	11.04	
497	Cg2291	2	1425.6049	4.1	80	92	0	23.8	23	R	FTDGATVWENGET	I	-0.7	2.94	
497	Cg2291	1	1659.8138	-3.1	19	34	0	42.4	29	A	SADGILRLVEDGMDVA	R	0.4	3.5	
500	Cg0735	1	617.4152	-0.5	76	80	0	25.8	21	P	FIILI	A	4.0	6.02	
500	Cg0735	1	688.4523	0.1	76	81	0	28.6	21	P	FIILIA	A	3.7	6.02	
500	Cg0735	1	1082.7103	-1.8	74	83	0	22.1	18	P	IPFIILIAAI	K	3.1	6.02	
502	Cg1064	1	553.3839	1.1	335	339	0	26.4	24	V	IVLLP	G	2.9	6.02	
502	Cg1064	1	670.3149	1.5	186	191	0	39.8	23	S	FMGFAV	Y	2.2	6.02	
506	Cg0688	1	699.4167	0.6	83	89	0	42.6	30	H	VDALLLG	N	1.9	3.1	
507	Cg2412	1	705.352	-1.1	173	178	0	40.3	30	S	NFVMPV	A	1.3	6.02	
507	Cg2412	1	747.4167	-0.8	209	215	0	35.4	28	L	GFLIEGI	T	1.6	3.3	
507	Cg2412	1	794.5266	-1.1	177	184	0	32.9	21	M	PVAIALLV	V	2.8	6.02	
508	Cg0952	1	633.3486	-0.6	68	73	0	28.9	28	V	FGAINI	G	1.6	6.02	
508	Cg0952	1	698.3098	-1.1	36	41	0	33.9	24	R	SFAFPM	T	1.2	6.02	
508	Cg0952	2	1020.4876	0.7	24	32	0	43.7	29	A	SPEFGELRS	K	-0.9	4.26	
508	Cg0952	2	2093.9589	-1.3	11	28	0	59.4	27	R	RQPTAQEFRDMQASPEFG	E	-1.3	4.44	
512	Cg0340	1	601.3873	0.3	132	136	0	27.5	16	V	ILIML	R	3.7	6.02	
513	Cg1350	1	698.4578	1.0	29	34	0	23.2	22	T	LLDILL	S	2.7	3.1	
513	Cg1350	1	715.4302	1.0	1	6	0	39.8	27	-	MNIIIL	A	2.6	6.02	
513	Cg1350	1	924.4076	0.3	168	175	0	29.2	26	K	DYDTVAEL	E	-0.3	2.88	
517	Cg2558	1	675.3956	0.7	55	61	0	39.7	28	W	FGGLLGL	D	1.9	6.02	
517	Cg2558	1	1425.7656	-2.4	51	64	0	34.1	28	I	IAPWFGGLLGLDPA	H	1.0	3.1	
518	Cg1115	1	642.3952	1.2	305	310	0	27.2	27	D	ILDGLI	L	2.1	3.1	
518	Cg1115	1	699.4167	0.6	306	312	0	42.6	30	I	LDGLILG	L	1.7	3.1	
519	Cg2598	1	898.5528	-0.8	49	56	0	39.6	27	A	SILIPFPI	S	2.0	6.02	
522	Cg0083	1	635.3716	-4.9	80	84	0	19.7	19	Q	IMFII	V	3.6	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
524	Cg2292	1	957.5324	0.0	14	21	0	31.1	28	V	WYLGPIPI	R	0.9	5.92	
525	Cg3017	2	1481.6787	-0.5	252	264	0	37.2	27	A	QYAENPDTFAQKA	A	-1.3	4.08	
531	Cg1578	1	635.3683	0.5	170	174	0	24.1	19	T	FPLFI	P	2.5	6.02	
532	Cg1657	1	516.1816	2.5	53	57	0	16.8	16	L	GNDPD	L	-2.5	2.92	
532	Cg1657	1	615.338	1.3	73	78	0	28.0	27	S	GWLGLA	E	1.3	6.02	
533	Cg0769	1	553.3839	1.1	212	216	0	26.4	24	V	VLIPL	L	2.9	6.02	
533	Cg0769	1	640.416	1.6	210	215	0	29.5	23	T	TVVLIP	L	2.4	6.02	
533	Cg0769	1	1137.7373	1.3	209	219	0	22.6	17	V	TTVVLIPLLVA	N	2.5	6.02	
535	Cg2369	1	791.4582	-1.4	120	126	0	25.9	25	S	LGLPFFV	H	2.2	6.02	
536	Cg0249	1	738.3952	0.1	217	222	0	27.5	24	L	FYVTPI	V	1.3	5.92	
536	Cg0249	1	1501.7816	-3.3	244	255	0	39.9	29	A	ELNPLYHYLEIV	R	0.2	4.24	
537	Cg1855	1	1028.4233	-1.5	366	374	0	27.0	20	T	DMSYGDRGL	K	-1.0	3.88	Oxidation (M)
539	Cg0262	1	656.3931	-4.4	192	197	0	25.4	20	K	MIIPLA	M	2.5	6.02	
539	Cg0262	1	1026.6477	-0.2	35	43	0	23.6	23	G	PIFALLLQI	P	2.2	6.02	
541	Cg0390	1	622.4054	-0.6	89	94	0	17.6	17	M	LPAPLI	A	1.8	6.02	
541	Cg0390	1	684.4422	0.7	57	62	0	39.6	25	F	IDLLLV	F	2.8	3.1	
542	Cg2913	1	665.4112	0.3	244	250	0	22.8	20	S	LAPGLPV	S	1.4	6.02	
542	Cg2913	1	937.4757	-1.2	9	16	0	30.1	27	S	DTQYLISV	D	0.3	3.1	
542	Cg2913	1	1475.9691	-2.0	28	42	0	14.9	13	A	LLGLLSGVIAPLIVV	R	2.6	6.02	
542	Cg2913	1	1634.0382	-1.7	26	42	0	38.1	15	A	SALLGLLSGVIAPLIVV	R	2.4	6.02	
543	Cg2559	1	882.5062	0.0	242	249	0	29.1	24	F	LDPEAILL	E	1.1	3	
544	Cg2289	1	906.5651	-1.3	20	27	0	19.2	18	P	LVKLAHNL	R	0.9	10.1	
552	Cg2390	1	642.3952	1.2	33	38	0	43.8	27	K	DLLGLL	S	1.9	3.1	
553	Cg1569	1	553.3839	1.3	144	148	0	24.5	24	G	IIVPL	A	3.1	6.02	
557	Cg1109	2	1476.7208	0.9	60	72	0	29.7	29	A	GVLEEGQYNRELA	E	-0.8	3.96	
557	Cg1109	2	1617.7059	0.4	86	99	0	24.8	24	T	QFPQIGDWNEDQAA	A	-1.2	2.88	
557	Cg1109	1	1860.9217	-3.5	59	75	0	34.5	30	A	AGVLEEGQYNRELAEAI	A	-0.3	3.8	
557	Cg1109	2	2524.1295	-1.3	78	99	0	37.2	24	A	KGEGFWTTQFPQIGDWNEDQAA	A	-1.1	3.58	
560	Cg2487	1	582.3741	0.7	569	574	0	28.1	27	S	PLGLLA	E	1.9	6.02	
560	Cg2487	1	773.4171	0.3	127	133	0	30.4	29	E	VDVESIL	R	1.3	3	
561	Cg1353	2	800.4643	1.6	128	134	0	31.8	29	Q	LGEILKE	T	0.1	4.26	
563	Cg1474	1	553.3839	1.1	266	270	0	26.4	24	D	VLLPL	A	2.8	6.02	
563	Cg1474	1	713.4323	2.0	292	298	0	34.3	27	N	LADILLG	N	2.0	3.1	
565	Cg0824	1	836.3916	-1.1	189	195	0	33.2	29	I	YQILDDA	T	-0.2	2.92	
569	Cg0701	1	632.3897	-1.3	43	48	0	28.1	27	L	FIAGLI	M	2.8	6.02	
570	Cg1643	1	642.3741	-0.8	434	439	0	29.5	17	L	PIPVFA	S	1.7	6.02	
570	Cg1643	1	773.4171	0.3	399	405	0	30.4	29	N	AELESLL	L	0.8	3.12	
572	Cg0025	1	690.3952	0.7	250	255	0	26.1	26	P	LFDIAL	I	2.2	3.1	
573	Cg1101	1	666.468	0.3	165	170	0	19.9	19	S	IPVLII	V	3.3	6.02	
574	Cg3135	1	689.4112	0.7	22	28	0	27.5	27	V	AFGGLLI	A	2.3	6.02	

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574	Cg3135	1	802.4986	-3.6	230	236	0	32.1	24	D	KAIVMLI	V	2.4	10.1	Oxidation (M)
575	Cg3237	1	766.2922	0.0	186	191	0	29.3	20	V	FNWDDA	A	-1.1	2.92	
575	Cg3237	1	1264.5513	-1.3	182	191	0	56.9	24	A	VWNVFNWDDA	A	-0.3	2.92	
575	Cg3237	1	1281.6129	-1.3	2	12	0	31.3	27	M	AVYELPELDYA	Y	0.1	2.94	
575	Cg3237	1	1406.6255	-1.5	182	193	0	36.7	25	A	VWNVFNWDDAAA	R	0.1	2.92	
575	Cg3237	2	2168.0709	-2.7	41	60	0	41.1	29	A	NAALEALEKAREEGTNPDQI	R	-1.0	4	
577	Cg2577	1	598.4418	1.7	404	408	0	28.1	17	P	LLKII	E	2.5	10.1	
577	Cg2577	1	656.3745	-0.5	351	356	0	27.6	27	A	DLVTIP	I	1.1	3.1	
578	Cg1274	1	698.4578	1.0	220	225	0	28.2	22	D	LDILLL	D	2.7	3.1	
579	Cg0444	1	1230.6819	1.1	19	31	0	31.5	27	D	LSQASLAATLGLS	A	1.0	6.02	
580	Cg0948	1	735.3803	1.1	362	368	0	41.0	30	L	TGAIDFI	L	1.3	3.1	
581	Cg1609	1	917.4858	0.7	473	480	0	29.1	28	L	VSALTEWL	D	1.0	3.3	
583	Cg0776	1	640.416	2.0	77	82	0	31.4	23	A	SLVLPI	T	2.3	6.02	
584	Cg0042	1	577.3475	2.3	241	245	0	28.1	28	I	YLGLL	I	1.9	5.92	
585	Cg1203	1	1015.5073	-4.1	250	258	0	29.4	27	L	ELDDEVAII	R	0.5	2.84	
585	Cg1203	2	1213.6554	-0.2	331	342	0	47.9	28	L	EAAVEVLGGKIE	F	0.4	3.96	
586	Cg2524	1	577.3475	2.3	18	22	0	28.1	28	Y	YLGII	V	2.2	5.92	
588	Cg0935	2	849.3769	0.5	24	30	0	27.1	23	A	WPEHNPA	D	-1.8	5.12	
588	Cg0935	2	1362.6092	0.1	46	57	0	44.9	26	A	SSPWGDDKEFPV	S	-1.1	3.7	
588	Cg0935	2	1561.7049	-0.2	43	57	0	52.3	26	V	AGASSPWGDDKEFPV	S	-0.7	3.7	
588	Cg0935	1	1879.8112	-3.3	46	62	0	46.9	22	A	SSPWGDDKEFPVSAEET	G	-1.2	3.5	
589	Cg2878	1	509.3213	0.4	204	208	0	21.3	21	V	PLLPA	Q	1.2	6.02	
591	Cg0397	1	645.3122	0.2	368	373	0	25.4	25	A	EAGLWA	V	0.4	3.3	
592	Cg2362	1	535.337	-0.4	64	68	0	23.4	22	I	PPLPL	G	0.6	6.02	
592	Cg2362	1	648.421	-0.3	63	68	0	23.2	14	V	IPPLPL	G	1.2	6.02	
592	Cg2362	1	747.4895	-1.1	62	68	0	33.1	13	R	VIPPLPL	G	1.6	6.02	
592	Cg2362	2	1258.6995	-1.3	49	59	0	37.2	29	V	FMVTDPPVKLL	R	0.9	6.76	
593	Cg0648	1	1057.5655	0.5	94	103	0	32.0	29	A	DILANLLSEA	G	0.8	3	
595	Cg3226	1	573.3196	1.6	180	184	0	22.6	21	L	LTLMP	E	1.4	6.02	
595	Cg3226	1	728.3646	0.4	403	407	0	21.3	20	G	QWWPI	A	-0.5	6.02	
596	Cg1669	1	605.3061	1.2	225	229	0	29.0	27	E	TPEFI	A	0.3	3.3	
597	Cg1505	1	730.4993	0.0	7	12	0	22.2	16	T	IFIILL	F	4.0	6.02	
597	Cg1505	2	2333.1539	-0.9	162	181	0	59.3	30	V	VFQKQLQQADPNAEYDLDVL	A	-0.6	3.5	
598	Cg1292	1	585.3737	1.5	204	208	0	27.8	25	K	DILLI	G	2.6	3.1	
599	Cg2447	1	699.4167	0.0	407	413	0	42.8	30	E	LVADILG	E	2.0	3.1	
600	Cg0334	1	927.5277	-1.4	37	44	0	37.8	27	F	ELKTVELP	I	-0.2	4.26	
600	Cg0334	2	1798.8949	-4.0	90	106	0	41.6	29	V	INTGDNLSDEKAVPDVL	R	-0.4	3.5	
604	Cg2731	2	668.3969	-0.1	510	515	0	25.1	24	V	RIIPNG	K	-0.2	11.04	
608	Cg1802	2	1170.5921	-4.1	200	208	0	28.8	28	K	EPEQWLKEL	E	-1.4	3.96	
611	Cg0363	1	701.3596	-0.7	273	279	0	39.8	32	R	GAEVVDL	L	0.9	3	

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613	Cg2511	1	861.463	0.1	403	410	0	33.9	30	T	VETCGLKL	T	0.7	6.28	
614	Cg2421	1	686.4214	1.6	174	179	0	22.8	21	G	TIVEIL	A	2.1	3.3	
615	Cg1164	2	902.5113	1.0	160	167	0	25.3	25	G	IATLPEFL	N	1.4	3.3	
617	Cg1307	2	1243.5932	-1.0	270	280	0	36.2	27	I	LEDTPDEKQVA	L	-1.3	3.58	
619	Cg2657	1	698.4578	1.0	18	23	0	28.2	22	V	EVLLLI	A	2.8	3.3	
619	Cg2657	2	2145.0127	-2.5	165	185	0	49.2	28	V	ATDETPNYYPGGNVAGRPVPA	G	-0.8	4.08	
620	Cg0982	1	535.337	-0.4	255	259	0	23.4	22	L	PPLPI	L	0.7	6.02	
620	Cg0982	1	648.421	-0.3	254	259	0	23.2	14	P	LPPLPI	L	1.2	6.02	
620	Cg0982	1	723.4895	-0.3	272	278	0	21.2	21	A	VALLVIP	A	3.0	6.02	
620	Cg0982	1	900.4051	0.7	111	118	0	27.9	24	A	AFMLFDAS	S	1.3	3.1	
623	Cg2611	1	527.3319	0.0	271	275	0	28.1	27	D	ITVPV	N	2.1	6.02	
626	Cg0554	1	656.3745	1.2	74	79	0	33.6	26	L	IDSLPI	G	1.2	3.1	
627	Cg1650	1	599.3894	1.5	246	250	0	30.2	19	I	ILEIL	I	2.6	3.3	
627	Cg1650	1	712.4734	-0.6	246	251	0	22.9	22	I	ILEILI	V	2.9	3.3	
628	Cg1904	2	715.448	1.7	51	57	0	29.2	25	F	IIGLSTL	V	2.1	6.02	
629	Cg3042	2	2380.205	-1.6	142	163	0	39.4	30	A	LLGDPEYLILDEPVNGLDPEGI	H	0.0	2.72	
631	Cg2970	1	751.3938	0.1	129	135	0	27.5	26	E	FGMILTA	E	2.0	6.02	
635	Cg3362	1	601.3873	0.3	140	144	0	27.5	16	A	ILLML	S	3.6	6.02	
637	Cg1798	1	656.3745	-0.5	219	224	0	27.6	27	Q	VETVLP	T	1.1	3.3	
639	Cg2397	1	645.2832	-1.5	68	72	0	25.8	24	L	FFMVS	G	2.2	6.02	Oxidation (M)
641	Cg2796	1	853.5749	0.0	47	54	0	18.5	18	P	IVAIRGLL	E	2.2	11.04	
644	Cg0308	1	635.3716	-4.9	71	75	0	24.1	19	V	LMLFL	K	3.2	6.02	
646	Cg3114	1	686.4214	0.7	215	220	0	33.7	26	P	TVLEIL	E	2.0	3.3	
647	Cg0004	1	551.3683	2.2	112	116	0	25.9	18	L	PLIPL	D	1.8	6.02	
647	Cg0004	3	1474.7263	-3.0	209	222	0	29.6	29	A	RSLDSGLNDSIDIA	V	-0.2	3.6	
648	Cg0794	2	694.3208	3.2	129	134	0	29.2	22	P	IDTMVT	L	1.0	3.1	Oxidation (M)
658	Cg2304	1	656.3745	1.2	6	11	0	27.1	26	T	LSDLPL	R	0.9	3.1	
660	Cg1868	1	730.4993	0.0	5	10	0	22.2	16	V	FLIILL	A	3.9	6.02	
660	Cg1868	2	2064.8661	-0.5	97	114	0	82.1	20	T	LFDQPEDDQPNDGFDGRT	D	-1.7	3.26	
661	Cg2719	1	557.3425	2.0	281	285	0	28.2	28	Q	VDVLI	D	2.6	3.1	
661	Cg2719	1	624.3847	1.3	253	258	0	17.3	17	G	LLPPVS	L	1.3	6.02	
663	Cg0559	1	664.3618	-3.0	78	83	0	25.1	24	P	MFALLA	S	2.7	6.02	
664	Cg1527	1	730.4047	-1.9	279	284	0	30.8	28	A	MNLQLL	A	1.1	6.02	
665	Cg1354	1	700.3829	-0.6	493	498	0	31.2	19	I	DLIMPI	G	1.6	3.1	
665	Cg1354	2	1253.6364	-0.8	71	82	0	30.9	28	T	RATQPSAPVEQA	Q	-0.8	6.98	
671	Cg2776	1	532.2645	1.1	397	401	0	30.8	29	A	ASWGL	P	0.7	6.02	
676	Cg1163	1	557.3425	2.0	206	210	0	28.2	28	R	VDVII	I	2.8	3.1	
677	Cg2194	1	585.3737	1.5	12	16	0	27.8	25	Y	DLIII	G	2.8	3.1	
681	Cg0400	1	726.3225	-1.7	237	242	0	25.3	24	A	GEFDFI	L	0.5	3	
682	Cg1697	2	1212.6462	3.5	352	363	0	32.8	28	L	LSSGPRAGLNEI	N	-0.1	6.98	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
685	Cg1089	2	728.4068	1.0	387	394	0	30.3	30	I	AAGLLSPT	S	1.0	6.02	
686	Cg1466	1	938.4022	0.1	46	52	0	26.6	26	V	WDFIEET	N	-0.7	2.94	
688	Cg1434	1	941.507	0.5	235	243	0	28.9	27	A	TEVTPPTVV	G	0.4	3.3	
696	Cg0783	2	1004.5291	-0.1	97	105	0	42.4	29	A	LLADRPSYA	N	-0.1	6.7	
697	Cg0041	2	1799.7791	1.3	136	151	0	23.7	23	I	DYSPGVPDPHFWTDPA	R	-1.0	3.6	
700	Cg1647	1	630.3775	-4.8	178	183	0	27.2	27	L	LCGLLI	P	3.0	5.32	
700	Cg1647	1	878.5841	-1.8	167	174	0	23.7	13	Q	TLPLLILP	Q	2.0	6.02	
703	Cg1282	1	545.3213	-0.2	204	208	0	29.7	26	I	LPFGI	G	1.8	6.02	
703	Cg1282	1	1069.6899	-3.4	199	208	0	27.5	18	A	LIGKILPFGI	G	1.8	10.1	
704	Cg2856	1	787.3963	1.3	168	174	0	32.4	29	V	VEADELL	G	0.4	2.94	
707	Cg1582	1	599.3894	1.5	279	283	0	30.2	19	V	LLELL	T	2.3	3.3	
709	Cg2550	1	632.3897	-1.3	141	146	0	28.1	27	S	FLAGIL	L	2.7	6.02	
713	Cg2208	2	728.4068	1.0	20	26	0	30.6	30	T	QALDVIA	D	1.3	3.1	
716	Cg2325	2	981.4742	1.2	24	31	0	28.2	26	A	DFFRPMGI	N	0.3	6.78	
716	Cg2325	1	1086.5499	-0.9	13	21	0	41.7	28	A	DFLHVWGLT	V	0.7	4.94	
716	Cg2325	1	1132.5189	1.2	32	41	0	29.2	28	I	NFPPADWSLS	S	-0.4	3.1	
716	Cg2325	1	1256.6554	-1.0	13	23	0	49.6	28	A	DFLHVWGLTVA	D	1.1	4.94	
717	Cg2504	1	795.449	-0.9	42	48	0	29.3	24	L	IALEHTI	N	1.0	5.12	
719	Cg2809	1	674.4367	1.5	147	152	0	25.0	24	G	FIIGLI	G	3.3	6.02	
719	Cg2809	1	675.3956	0.7	145	151	0	39.7	28	P	GGFIIGL	I	2.1	6.02	
721	Cg2535	1	1395.6882	-1.0	123	136	0	60.1	29	L	SGDDNIPLDLPLGA	G	-0.1	2.82	
721	Cg2535	1	1965.9895	-2.3	118	136	0	60.7	30	T	NIETLSGDDNIPLDLPLGA	G	0.0	2.78	
723	Cg0221	1	539.3683	-0.2	275	279	0	26.5	23	Q	IVVPL	S	3.0	6.02	
726	Cg2659	1	715.4302	1.0	150	156	0	39.8	27	L	MLIGGLI	V	2.5	6.02	
727	Cg0362	1	539.3683	-0.2	273	277	0	26.2	23	L	VLVIP	A	3.0	6.02	
727	Cg0362	1	699.4167	0.6	174	180	0	42.6	30	G	GIDLLLG	I	1.7	3.1	
728	Cg1753	1	598.4418	1.7	377	381	0	28.1	17	T	LLKLL	A	2.3	10.1	
729	Cg0524	1	545.3213	-0.2	251	255	0	29.7	26	V	PIFGL	G	1.8	6.02	
730	Cg2485	1	635.3716	-4.9	176	180	0	24.1	19	E	MLIFL	G	3.4	6.02	
733	Cg0873	1	862.4913	3.6	227	234	0	33.6	27	W	VVHPGEIL	G	1.0	5.12	
734	Cg1794	1	599.3894	1.5	61	65	0	30.2	19	I	ILELI	D	2.6	3.3	
735	Cg0062	2	1826.8421	-0.5	290	306	0	37.3	27	S	DAGTEDIPTIEEPPEKS	S	-1.3	3.44	
737	Cg0123	1	551.3683	0.9	194	198	0	34.3	18	Y	LPIPI	V	1.9	6.02	
740	Cg1503	1	1463.7694	-2.4	143	155	0	34.7	29	I	DLQSLLSNMFLLA	V	1.0	3.1	
741	Cg1623	1	577.3475	2.3	250	254	0	28.1	28	A	IYGLI	A	2.2	5.92	
741	Cg1623	1	704.4473	0.6	263	268	0	22.7	22	I	SLLLFI	-	3.0	6.02	
743	Cg0475	1	930.5426	1.0	55	62	0	22.6	22	A	TLFEVLPL	E	1.6	3.3	
743	Cg0475	1	1566.8909	-2.8	56	69	0	37.1	25	T	LFEVLPLEVLPEAV	R	1.3	3.02	
746	Cg3197	1	656.3745	-1.4	577	582	0	27.3	27	I	TDVIPI	V	1.2	3.1	
750	Cg1776	1	698.3309	-3.7	76	81	0	28.1	26	A	VYAMSI	D	1.7	5.92	Oxidation (M)

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
752	Cg0914	1	601.3873	0.8	177	181	0	22.9	16	E	IMILL	N	3.7	6.02	
752	Cg0914	1	715.4302	1.0	177	182	0	29.5	27	E	IMILLN	R	2.5	6.02	
752	Cg0914	3	3310.6715	-0.8	163	192	0	36.4	31	A	DEPTGNLDPDTSDEIMILLNRINRLGTTVV	M	-0.3	3.68	
754	Cg1685	2	1898.8547	-1.2	68	83	0	47.3	25	I	EAPQPNFEQHYQGQQV	Q	-1.7	4.24	
754	Cg1685	2	2263.0465	-2.5	46	65	0	36.1	27	M	NKDGDTPEQQQQPQQQIAPN	Q	-2.3	3.7	
754	Cg1685	3	2484.1187	-3.3	41	61	0	36.3	25	S	EVKEMNKDGDTPEQQQQPQQQ	I	-2.5	3.92	
755	Cg0007	1	1075.4669	-1.2	44	53	0	26.3	25	W	EVVDNSVDEA	M	-0.4	2.84	
756	Cg1452	1	557.3425	2.0	195	199	0	28.2	28	P	VDVIL	D	2.6	3.1	
760	Cg1836	2	2375.1969	-0.7	215	236	0	58.2	31	G	QYVVDPSNDAQGILTDLITRSA	N	-0.1	3.6	
761	Cg0064	1	829.4334	0.6	273	279	0	34.6	27	P	VDNWLLA	D	0.8	3.1	
761	Cg0064	2	1368.6746	-1.9	184	196	0	38.9	29	Q	GVPQSQVDANRQA	A	-1.0	6.78	
762	Cg0198	1	884.4756	-2.1	44	51	0	32.9	27	K	LFIVAADH	P	1.5	4.94	
763	Cg3312	1	630.3775	-4.8	342	347	0	27.2	27	S	CVAILI	L	3.6	5.32	
763	Cg3312	1	739.4632	1.6	382	387	0	21.8	15	S	LWLVPL	A	2.2	6.02	
765	Cg2334	1	787.36	-3.0	376	382	0	25.3	25	G	PDDDITL	F	-0.6	2.82	
765	Cg2334	1	1093.6496	-1.6	200	212	0	21.9	21	M	VPVGGGGLLAGVV	S	1.7	6.02	
767	Cg1648	1	712.4734	-0.6	264	269	0	22.9	22	Q	LIELLI	T	2.8	3.3	
769	Cg1806	1	509.3213	0.6	150	154	0	31.2	21	M	PLPIA	L	1.4	6.02	
769	Cg1806	2	800.4643	1.6	32	38	0	45.9	29	I	LDALLEK	D	0.3	4.08	
774	Cg2418	1	641.2809	-0.2	215	220	0	20.9	19	K	FAGNYA	A	0.2	5.92	
777	Cg2215	1	1054.4931	-1.0	4	13	0	30.5	26	A	NTPAVQEEPA	Y	-1.0	3.12	
777	Cg2215	1	1125.5302	-1.3	3	13	0	28.9	27	T	ANTPAVQEEPA	Y	-0.8	3.12	
781	Cg1727	1	667.3945	-0.7	95	99	0	23.2	15	A	FYILI	T	2.9	5.92	
782	Cg0510	1	770.4538	0.9	151	157	0	41.4	29	P	AQIVELV	Q	1.6	3.3	
784	Cg1713	1	1276.6915	-1.6	177	188	0	35.4	27	A	SLLGDLADYLVV	N	1.3	2.92	
791	Cg3134	1	930.5208	0.9	115	123	0	34.0	29	Y	IVGSALQMI	P	1.8	6.02	
792	Cg2767	1	834.3759	-1.3	222	229	0	54.2	27	A	FIASDDPA	A	0.2	2.92	
798	Cg2313	1	678.3741	4.9	167	171	0	23.3	23	Q	WTIFL	E	1.9	6.02	
802	Cg0531	1	640.4523	-0.9	125	130	0	28.6	25	L	ILIGIL	C	3.5	6.02	
804	Cg1761	2	1055.536	-0.2	336	346	0	33.1	27	I	AGPLTAEQRGG	A	-0.7	6.98	
805	Cg2896	1	751.3752	-0.7	144	150	0	29.1	29	E	FDLSVTA	T	1.1	3.1	
806	Cg2701	1	794.5266	0.0	156	163	0	21.5	21	L	LAILPGIV	L	2.6	6.02	
806	Cg2701	1	1008.6583	-1.8	154	163	0	31.0	20	R	TLLAILPGIV	L	2.4	6.02	
816	Cg3190	1	624.3847	1.8	121	126	0	26.4	17	K	SPVPLL	G	1.3	6.02	
817	Cg0045	1	763.3864	-1.0	302	308	0	33.5	27	T	NQGIVYA	G	0.3	5.92	
822	Cg1540	1	704.4473	0.6	10	15	0	22.7	22	L	LSLIFL	F	3.0	6.02	
822	Cg1540	1	800.4644	-0.7	194	201	0	36.7	29	N	DLAIISLG	G	1.7	3.1	
825	Cg3047	1	622.4054	-0.6	118	123	0	27.8	17	L	IPLAPL	H	1.8	6.02	
830	Cg0412	1	712.4734	-0.6	143	148	0	22.9	22	R	ILEILL	G	2.8	3.3	
831	Cg0193	1	834.3971	-0.5	504	511	0	28.5	26	V	LTSEGIDT	D	-0.2	3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
832	Cg0265	2	974.4168	3.8	153	160	0	25.3	25	Y	LFDEPMAH	L	-0.2	4.06	Oxidation (M)
834	Cg0759	1	509.3213	0.4	266	270	0	21.3	21	T	IPLPA	E	1.4	6.02	
834	Cg0759	1	580.3584	1.0	125	130	0	28.6	18	I	PPILAA	A	1.5	6.02	
840	Cg2836	1	767.3813	-0.9	87	93	0	36.4	26	I	IEAIDAH	I	0.3	4.06	
841	Cg0296	1	599.3894	1.5	352	356	0	30.2	19	L	LLEIL	C	2.5	3.3	
846	Cg2498	1	815.5157	0.2	179	185	0	18.8	17	T	PIIIFLT	F	2.5	6.02	
847	Cg2255	1	509.3213	0.6	198	202	0	31.2	21	Y	IPPIA	L	1.5	6.02	
848	Cg3106	1	686.4214	0.6	18	23	0	39.8	26	S	LELSLL	R	1.8	3.3	
854	Cg0778	1	836.5735	-0.5	201	208	0	25.0	18	A	IIPIIVGL	I	3.0	6.02	
856	Cg1343	1	676.416	1.2	269	274	0	40.4	25	R	YLGVLL	Y	2.3	5.92	
856	Cg1343	1	832.5171	-3.2	267	273	0	28.9	20	R	LRYLGVL	L	1.3	9.84	
857	Cg0124	1	509.3213	-0.2	335	339	0	30.4	21	N	PIPAI	P	1.5	6.02	
857	Cg0124	1	699.4167	0.6	310	316	0	42.6	30	R	IGDLILG	N	1.8	3.1	
859	Cg1696	1	667.333	1.5	245	250	0	23.2	22	T	FLNGFA	Q	1.2	6.02	
864	Cg0928	2	1929.0605	0.0	42	59	0	51.1	28	S	TLLTMIGRLLGIDEGNIT	V	0.7	4.08	
865	Cg3403	1	651.3665	0.6	231	235	0	24.1	17	V	YMIII	A	2.8	5.92	
866	Cg0368	1	758.436	-4.9	33	40	0	32.4	32	I	VCGLIIAA	M	2.8	5.32	
867	Cg1528	1	585.3737	1.5	100	104	0	27.8	25	L	DILIL	H	2.6	3.1	
867	Cg1528	1	698.4578	1.0	99	104	0	28.2	22	T	LDILIL	H	2.8	3.1	
868	Cg0143	1	567.3057	0.4	214	218	0	25.6	19	F	FLAFA	H	2.6	6.02	
869	Cg2135	1	680.3381	0.1	457	462	0	34.7	28	G	DFVTVT	V	1.1	3.1	
872	Cg2784	1	802.4225	-2.2	205	211	0	32.0	31	M	FQDIPLA	V	0.6	3.1	
876	Cg0514	1	657.3196	2.0	47	51	0	24.6	23	A	FMIFT	G	2.3	6.02	
876	Cg0514	1	711.4894	-1.3	136	142	0	30.7	25	A	IIAVLLA	L	3.5	6.02	
876	Cg0514	1	832.3789	0.0	2	9	0	34.9	29	M	PSMFPSPA	T	0.0	6.02	
881	Cg3119	1	599.3894	1.5	402	406	0	30.2	19	A	IIELL	D	2.6	3.3	
881	Cg3119	1	823.5392	4.6	71	77	0	16.4	16	K	PRLRLLG	N	0.1	12.4	
883	Cg3396	1	526.3115	0.8	221	225	0	32.0	30	Q	NPILA	K	1.0	6.02	
884	Cg0448	1	751.3938	0.1	43	49	0	27.5	26	G	MGFLLTA	L	1.9	6.02	
884	Cg0448	2	1390.6477	-1.2	26	38	0	49.1	28	V	AYSSPHSSLERSA	T	-0.8	7.76	
885	Cg0167	1	711.4894	-1.3	6	12	0	30.7	25	T	IAIVLLA	S	3.5	6.02	
887	Cg0216	1	730.4993	0.0	97	102	0	22.2	16	V	FIILII	L	4.1	6.02	
887	Cg0216	1	802.4953	0.6	93	99	0	32.1	24	L	AQIVFII	L	2.7	6.02	
889	Cg0945	1	866.4022	0.9	68	75	0	31.0	28	S	FLDSIDAS	L	0.5	2.92	
892	Cg0727	1	630.3489	-0.3	381	386	0	25.6	22	E	WAGKAV	Y	0.4	10.1	
892	Cg0727	2	668.397	-0.1	430	436	0	25.1	24	D	RLIGGPG	L	0.1	11.04	
893	Cg1166	1	802.4953	0.6	73	80	0	32.1	24	F	VAAAVFIL	W	3.1	6.02	
901	Cg2096	1	885.3505	-1.1	48	55	0	35.0	22	S	GYQDPYGS	G	-1.6	3.1	
901	Cg2096	2	1765.8271	-0.3	56	72	0	36.4	28	S	GYTGGFENSPLNAPKNT	A	-1.0	6.86	
901	Cg2096	2	2313.9774	-0.9	25	47	0	31.0	19	A	NQGEPYGAPYGESFGPSSGAQQS	G	-1.2	3.12	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
903	Cg2762	1	545.3247	2.0	86	90	0	29.9	28	K	MIVIA	C	3.4	6.02	
903	Cg2762	1	840.4957	-0.8	107	114	0	34.2	24	Y	SVPVVEVI	L	1.9	3.3	
907	Cg2374	1	642.3952	1.2	11	16	0	27.2	27	K	LIDGIL	K	2.1	3.1	
910	Cg1387	1	656.3745	-1.1	215	220	0	27.4	27	R	SIVEPL	A	1.1	3.3	
910	Cg1387	1	686.4214	0.7	18	23	0	33.7	26	P	VTLELI	T	2.0	3.3	
910	Cg1387	1	1400.7188	-2.8	295	308	0	41.7	29	A	DLGVVGDLFDIAPA	L	1.0	2.82	
914	Cg0016	1	584.3897	1.5	25	30	0	31.7	31	S	IIGLVA	W	3.1	6.02	
914	Cg0016	1	861.4596	4.1	100	107	0	33.9	30	V	DLFGGLQI	Q	0.9	3.1	
914	Cg0016	1	1403.6834	0.3	46	58	0	42.5	29	A	GVWQNFNDVIGGV	G	0.3	3.1	
916	Cg1128	1	829.397	-0.4	29	37	0	33.2	28	Q	GGPLGPEFG	K	-0.2	3.3	
916	Cg1128	1	1174.5506	-1.7	78	88	0	28.1	28	R	NGLDPFDIEGV	R	-0.1	2.88	
919	Cg1298	1	580.3584	1.0	166	171	0	28.6	18	I	PPLLAA	R	1.3	6.02	
929	Cg0422	1	1548.8035	-3.6	189	202	0	31.2	29	D	TKIANAYITPEITD	L	-0.2	4.08	
932	Cg1458	1	654.4064	-0.5	187	192	0	24.2	23	D	NLPIKA	R	0.2	10.1	
934	Cg0263	2	2422.1805	0.8	247	268	0	67.5	30	A	FAEFLSSDRAKEILASYGFGTN	-	-0.1	4.44	
935	Cg0405	1	1956.9892	-4.1	297	315	0	69.5	30	V	GIGVLGANEILDDLEETLS	-	0.3	2.8	
940	Cg3177	1	829.4949	0.0	240	246	0	30.2	29	D	LLDFLPL	T	1.8	3.1	
942	Cg0624	1	716.3705	-0.1	157	163	0	32.1	32	K	SQAELGL	D	0.2	3.3	
947	Cg3426	1	752.3705	-2.3	90	97	0	38.7	26	P	EPAAPAPT	Q	-0.5	3.3	
949	Cg3133	1	757.3858	-0.8	155	161	0	29.6	26	L	EELSLPA	R	0.0	3.12	
953	Cg1277	1	957.5383	-2.4	48	56	0	30.8	28	T	ELTIVGVDL	I	1.4	3	
953	Cg1277	1	1531.777	-3.3	36	49	0	39.1	30	A	VDLLSDNAFPVTEL	T	0.5	2.88	
957	Cg3336	1	624.3847	1.3	286	291	0	17.3	17	V	ILPSVP	E	1.4	6.02	
958	Cg2908	1	850.5892	-0.1	11	18	0	34.9	16	G	VLPLALLL	A	2.9	6.02	
962	Cg1890	2	754.4337	1.5	187	193	0	36.1	27	G	DPGVLRV	H	0.3	6.78	
964	Cg1165	1	688.4523	0.1	55	60	0	24.4	21	Q	LIFIIA	T	3.7	6.02	
964	Cg1165	1	752.3705	-2.3	247	254	0	29.7	26	S	APEAPAPT	D	-0.5	3.3	
965	Cg2549	1	686.4214	0.6	489	494	0	39.8	26	A	LELSLI	G	1.9	3.3	
968	Cg1369	2	1733.8472	-1.8	26	41	0	38.8	30	A	QTTEGEIGVLPDHEPL	L	-0.6	3.68	
969	Cg1482	1	749.3959	1.1	72	78	0	40.3	29	A	TGAEIFL	S	1.2	3.3	
970	Cg1865	1	704.4473	0.6	52	57	0	22.7	22	V	ISILFI	A	3.2	6.02	
970	Cg1865	1	725.4687	-0.4	276	282	0	24.3	23	T	IISALPI	I	2.4	6.02	
971	Cg2294	1	1417.7089	-3.1	119	131	0	34.3	29	A	NSGTLLSDWAEII	N	0.3	3	
971	Cg2294	2	1827.7873	2.2	195	209	0	46.9	23	V	MWDALDEDIDFTEKT	Q	-0.8	3.32	
981	Cg3389	1	770.4538	1.7	139	146	0	33.6	28	E	LLDAGLIG	E	1.7	3.1	
985	Cg0534	1	583.4309	-0.2	66	70	0	24.1	18	G	ILIIL	G	4.2	6.02	
985	Cg0534	2	1009.6535	0.6	111	121	0	36.9	21	A	IGAGALLLIAV	G	2.7	6.02	
994	Cg1035	1	984.5426	-3.4	157	165	0	32.6	28	D	LMRVLADAP	P	0.9	6.78	
997	Cg0862	1	585.3737	1.5	48	52	0	27.8	25	P	DLILL	D	2.5	3.1	
997	Cg0862	1	700.3829	-0.6	52	57	0	21.5	19	L	LDLMLP	G	1.4	3.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1001	Cg3407	1	715.4302	1.0	1	7	0	34.6	27	-	MIIIGAV	F	3.0	6.02	
1005	Cg1649	1	711.4894	-1.3	33	39	0	30.7	25	A	ALIVLIA	T	3.5	6.02	
1010	Cg0091	1	630.3774	-4.6	91	96	0	27.2	27	A	AMALLL	G	2.8	6.02	
1011	Cg0932	1	630.3775	-4.8	32	37	0	27.2	27	L	CLGLIL	G	3.0	5.32	
1018	Cg1104	1	863.4753	-3.0	21	29	0	31.0	28	S	VAVFTSAVA	L	2.1	6.02	
1019	Cg2900	2	668.397	0.4	158	163	0	34.5	24	R	RIPGVQ	K	-0.2	11.04	
1021	Cg0244	2	1009.6536	0.3	81	90	0	30.0	21	L	LVGNLVLLAV	D	2.6	6.02	
1025	Cg3170	1	577.3475	2.3	240	244	0	28.1	28	I	IYGII	M	2.4	5.92	
1028	Cg0010	2	800.4644	1.6	97	104	0	45.9	29	A	LDAILSVA	D	2.0	3.1	
1029	Cg2938	1	599.3894	1.5	263	267	0	30.2	19	V	IIEII	F	2.9	3.3	
1033	Cg1122	1	887.46	-0.6	30	37	0	31.8	30	I	DSELKVPT	A	-0.8	4.08	
1038	Cg2160	1	585.3737	1.5	471	475	0	27.8	25	G	DLIIL	S	2.6	3.1	
1039	Cg0742	1	816.4382	0.0	146	152	0	34.4	32	N	ADWLLVT	G	1.2	3.1	
1040	Cg0291	1	642.3588	0.9	283	288	0	36.2	27	A	SIDVPI	D	1.2	3.1	
1042	Cg0389	1	669.4425	-0.4	11	16	0	31.6	28	G	QVILVV	G	2.9	6.02	
1042	Cg0389	1	844.429	1.8	76	84	0	40.1	30	V	SSAPAAQTL	S	0.2	6.02	
1047	Cg0092	2	1118.5026	-1.3	99	108	0	48.1	25	A	MTQDDGIRPS	Q	-1.2	3.88	
1047	Cg0092	2	1363.6983	0.4	109	121	0	30.0	29	S	QDGTGLSKDLFLA	A	-0.1	3.88	
1051	Cg0472	2	3576.7795	-2.9	132	165	0	38.9	31	T	GGNSTSQGFAEQLIQELIKVTDITSDAANQTIEV	E	-0.2	3.5	
1055	Cg2955	1	532.2645	1.1	29	33	0	30.8	29	T	SAWGI	L	0.8	6.02	
1060	Cg2994	1	825.3141	-0.1	45	52	0	21.3	21	A	DGSDTFNA	R	-1.0	2.92	
1061	Cg2894	1	712.4734	-0.6	96	101	0	39.9	22	P	ELLLLI	D	2.7	3.3	
1062	Cg2342	1	787.3824	4.8	71	78	0	33.9	30	Y	AREGADVA	I	-0.3	4.08	
1064	Cg1522	2	1224.6714	1.1	113	123	0	31.8	26	S	IEKVDSHTALL	T	0.2	5.22	
1065	Cg3163	1	796.4555	-3.9	72	79	0	27.0	22	R	RAGQPVGL	Y	-0.1	11.04	
1068	Cg0923	1	640.4523	0.3	25	30	0	30.8	25	G	IIGLIL	S	3.5	6.02	
1068	Cg0923	1	715.4302	1.0	20	26	0	29.5	27	V	LMIGGII	G	2.6	6.02	
1068	Cg0923	1	1295.7238	-1.9	69	81	0	30.1	26	A	NAFGIPNPLIGIA	G	1.0	6.02	
1076	Cg0879	1	715.4302	1.0	92	97	0	39.8	27	V	MLNIIL	L	2.5	6.02	
1077	Cg3116	1	725.4687	-0.4	121	127	0	24.3	23	K	LVTALPI	L	2.3	6.02	
1080	Cg3316	1	713.4323	2.0	120	126	0	34.3	27	E	ADLILLG	S	2.0	3.1	
1087	Cg0230	1	869.5222	-0.3	411	419	0	34.2	27	E	ADLVLVALG	F	2.2	3.1	
1090	Cg3264	3	1759.7748	-1.6	275	291	0	40.7	24	A	SPEADAPEASADESEKK	-	-1.6	3.82	
1101	Cg1226	1	787.4076	4.7	76	82	0	38.5	31	A	IDISINN	E	0.3	3.1	
1104	Cg0001	2	1503.7827	-0.4	493	504	0	29.7	29	Y	ADRKIRQEMTEK	R	-1.9	9.88	
1107	Cg1002	1	624.3847	0.3	136	141	0	23.7	18	E	PSVIPL	L	1.4	6.02	
1112	Cg2127	2	1099.6125	0.7	88	97	0	33.5	28	I	NDVLSLVDII	D	1.4	2.92	
1117	Cg2049	1	532.2646	0.8	11	15	0	32.2	29	H	GWGIT	Q	0.4	6.02	
1122	Cg1741	1	1100.539	-1.1	18	26	0	38.6	28	A	DWLDLPTEL	R	-0.3	2.88	
1122	Cg1741	2	1421.7191	0.8	15	26	0	34.5	29	S	LHADWLDLPTEL	R	0.0	3.7	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1122	Cg1741	1	1783.9509	-1.7	18	32	0	45.3	29	A	DWLDLPTELRFPVIA	V	0.3	3.7	
1123	Cg3399	1	933.4596	0.9	3	10	0	38.4	27	A	VFDFPNPV	N	0.5	3.1	
1123	Cg3399	1	1004.4968	0.6	2	10	0	37.9	29	M	AVFDFPNPV	N	0.6	3.1	
1129	Cg3025	1	688.4523	0.1	5	10	0	28.6	21	N	LFLLLA	A	3.3	6.02	
1134	Cg0970	1	678.3775	-0.1	27	32	0	23.3	23	I	IACIFI	V	3.4	5.32	
1137	Cg0432	1	553.3839	1.3	104	108	0	24.5	24	T	ILVLP	D	2.9	6.02	
1141	Cg0523	1	837.5324	0.7	31	39	0	22.6	22	A	IAAIPGALL	P	2.2	6.02	
1145	Cg2510	1	598.4418	1.7	300	304	0	28.1	17	D	IIKIL	G	2.7	10.1	
1147	Cg1799	1	656.3745	1.2	156	161	0	27.1	26	F	EVSLIP	T	1.1	3.3	
1151	Cg2114	1	956.4927	2.8	54	62	0	34.2	29	P	PSIREIGDA	A	-0.4	4.08	
1156	Cg2410	1	624.3847	1.8	349	354	0	18.6	17	D	PSLVPL	Y	1.3	6.02	
1159	Cg2650	1	785.4687	4.3	94	99	0	35.7	29	A	WILLEI	I	2.0	3.3	
1166	Cg1051	1	799.415	-0.1	1	7	0	28.8	27	-	MEIPLPT	S	0.4	3.3	
1167	Cg0401	1	689.4146	-3.5	1	6	0	34.7	27	-	MKGIIL	A	1.7	10.1	Oxidation (M)
1172	Cg2936	1	672.4058	2.8	112	117	0	28.8	24	E	ILDLSL	G	1.9	3.1	
1176	Cg1129	1	700.3756	0.4	202	208	0	32.9	31	I	QVAVDAV	Q	1.3	3.1	
1180	Cg2402	1	1150.5506	-0.7	155	165	0	47.6	29	V	AYSDLQAGDIV	A	0.3	2.92	
1185	Cg2554	1	539.3683	-0.2	107	111	0	26.5	23	N	IVVIP	G	3.2	6.02	
1186	Cg2286	1	1082.7103	-1.8	3	12	0	22.1	18	N	ILFIPILAAL	I	3.0	6.02	
1187	Cg2482	1	846.4884	0.5	108	114	0	34.8	27	R	MKITLIE	P	0.9	6.94	
1194	Cg2973	1	650.3024	0.0	274	279	0	29.3	25	L	NQGYAV	L	-0.5	5.92	
1194	Cg2973	1	690.3952	0.7	138	143	0	26.1	26	T	FLDIAL	D	2.2	3.1	
1199	Cg2664	1	717.4095	-2.9	189	194	0	29.6	29	D	VEIVKM	L	1.2	6.94	
1202	Cg2457	2	882.5287	1.5	120	128	0	26.1	25	L	VGITAGRPI	A	0.8	11.04	
1202	Cg2457	2	1066.6499	0.8	119	129	0	25.2	22	E	LVGITAGRPIA	T	1.2	11.04	
1203	Cg2429	2	723.3803	2.4	118	124	0	26.9	26	Q	YLASTGI	A	1.0	5.92	
1205	Cg1355	1	718.3571	-1.1	106	111	0	27.8	25	E	DIVMEI	K	1.4	3	
1211	Cg2022	1	829.4294	4.9	303	310	0	33.4	31	R	GDRIEGLA	S	-0.3	4.08	
1215	Cg2318	1	1979.9364	-1.5	111	128	0	61.5	28	L	SGFTPNVESILDYDPDLV	V	-0.1	2.78	
1219	Cg2271	1	688.4523	0.1	173	178	0	28.6	21	C	FIILLA	L	3.5	6.02	
1221	Cg0352	1	567.3057	0.4	18	22	0	25.6	19	M	LFAFA	M	2.6	6.02	
1223	Cg0310	2	1556.8311	0.5	40	54	0	43.8	29	T	AGPQGPNVLNDIHLI	E	0.1	4.94	
1225	Cg1881	1	642.3701	-1.9	59	64	0	35.1	29	A	NLNLVA	F	1.1	6.02	
1234	Cg2348	2	1268.6725	0.1	60	71	0	28.5	27	V	VVDPGTGDLQRL	Q	-0.2	3.88	
1236	Cg1568	1	730.4993	0.0	289	294	0	22.2	16	L	FLLLLI	I	3.8	6.02	
1247	Cg1494	2	3952.9194	-1.6	101	136	0	46.3	31	A	NTVDVDGTTWLPVSDMTPGSSLETWYSVNRFPVVAI	T	0.1	3.5	
1251	Cg1733	1	955.5338	2.4	73	82	0	29.4	27	I	LTLALSGPGQ	V	0.6	6.02	
1259	Cg0649	2	2055.067	-1.9	15	35	0	29.9	29	T	AAELDAMQAAGEIVGKALQAV	R	0.6	3.82	
1260	Cg1190	1	680.4836	2.2	94	99	0	23.9	15	D	LIILLP	D	3.1	6.02	
1260	Cg1190	1	698.4578	1.0	93	98	0	28.2	22	G	DLIILL	P	2.8	3.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1262	Cg2000	1	794.5266	0.0	121	128	0	21.5	21	Y	ALLIPGLV	Y	2.5	6.02	
1263	Cg1158	2	2301.1124	-2.8	169	189	0	29.9	29	A	ATDEEFNDLLRAVANSEPLPT	N	-0.5	3.5	
1267	Cg2128	1	601.3873	0.8	26	30	0	22.9	16	C	IMLIL	W	3.7	6.02	
1267	Cg2128	1	836.5735	-0.5	16	23	0	34.5	18	K	LPLIVIGL	C	2.8	6.02	
1269	Cg1859	2	1763.8577	-1.3	79	95	0	47.1	29	V	KVIAGEAESFTSDNLPS	G	-0.2	3.82	
1270	Cg3099	2	1246.5425	-1.5	23	34	0	27.5	25	T	SADRAEQAAEEA	A	-1.2	3.68	
1275	Cg3366	2	771.449	0.0	141	147	0	35.4	30	I	QAILEKA	A	0.1	6.94	
1275	Cg3366	1	1025.587	-0.4	239	248	0	37.0	26	A	RTLGDVGIPV	H	0.6	6.78	
1275	Cg3366	1	1119.5812	-1.8	50	59	0	29.4	29	A	SVEEKGPYIV	V	-0.2	4.26	
1280	Cg2186	1	553.3839	1.3	2	6	0	24.5	24	M	LIVLP	P	2.9	6.02	
1280	Cg2186	1	684.4244	-4.4	1	6	0	24.8	18	-	MLIVLP	P	2.8	6.02	
1288	Cg2226	1	688.4523	0.1	368	373	0	28.6	21	T	IFLLIA	L	3.5	6.02	
1290	Cg0786	1	553.3839	1.3	71	75	0	24.5	24	P	IIVPI	I	3.2	6.02	
1301	Cg0353	1	671.3854	0.6	115	121	0	39.2	31	L	IGLGEAL	I	1.4	3.3	
1303	Cg1300	1	782.5266	1.3	228	235	0	32.7	25	I	LAVLIIAA	V	3.3	6.02	
1313	Cg0899	1	867.5065	0.0	61	68	0	27.8	24	V	VEPLANLI	R	1.2	3.3	
1317	Cg0237	2	1585.726	-0.2	63	77	0	86.4	27	V	AVVDFDALDTESHPA	A	0.0	3.5	
1318	Cg3172	2	726.4276	2.5	170	176	0	29.3	28	R	IIQSGPL	N	0.9	6.02	
1322	Cg2517	1	980.6019	4.1	323	331	0	25.6	22	R	LKQGVPLNL	F	0.3	10.1	
1327	Cg1738	1	773.4171	-2.1	174	180	0	40.5	29	L	SEVLDLV	E	1.2	3	
1332	Cg0596	2	1101.603	0.5	2	11	0	31.6	28	M	TNLKLDVQTA	D	-0.2	6.76	
1337	Cg2428	2	1813.8271	-2.2	17	32	0	28.4	26	A	DFDDPDAPGRWPGEKL	G	-1.5	3.76	
1340	Cg0721	1	642.3952	1.2	151	156	0	43.8	27	A	EVIGLL	C	2.1	3.3	
1341	Cg0355	1	820.3351	-1.1	236	241	0	31.3	19	T	EWDTDR	I	-2.8	3.7	
1341	Cg0355	1	858.4083	4.7	25	32	0	33.2	28	P	GQNTELTP	A	-1.3	3.3	
1343	Cg2977	1	1097.4877	-1.2	199	209	0	29.9	26	V	AVEAEEEPAPG	R	-0.7	2.96	
1345	Cg0046	1	598.4418	1.7	46	50	0	28.1	17	T	LIKIL	S	2.5	10.1	
1346	Cg1811	1	1009.6172	-1.0	59	68	0	24.3	23	S	ALLEALPKVG	K	1.0	6.94	
1350	Cg0548	1	642.3701	-1.9	233	239	0	33.4	29	M	GAVNIVA	D	1.8	6.02	
1354	Cg1180	1	715.4302	1.0	21	27	0	39.8	27	A	GMGILLL	W	2.4	6.02	
1370	Cg0330	1	767.5157	0.9	74	80	0	20.2	19	T	LPIIVLT	A	2.6	6.02	
1371	Cg3338	1	667.333	1.5	81	86	0	23.2	22	E	LFNGFA	D	1.2	6.02	
1371	Cg3338	1	1938.9575	0.1	149	167	0	45.8	29	I	GYSDVDDLLFNTIGGLIGA	S	0.6	2.82	
1372	Cg3317	2	1706.7384	-0.6	10	24	0	32.6	24	M	NTQPEHPENDLVDEA	D	-1.7	3.5	
1375	Cg0562	1	704.4109	2.1	154	159	0	40.5	23	D	IFEVVV	P	2.7	3.3	
1378	Cg0128	1	943.4862	-0.8	97	104	0	28.3	28	G	QEVLELDV	T	0.3	2.94	
1381	Cg0696	1	1627.8053	-3.9	2	16	0	54.8	29	M	ADTERELADLVPQAT	A	-0.5	3.58	
1397	Cg1056	1	725.4687	-0.4	161	167	0	24.3	23	T	LALSLPI	I	2.2	6.02	
1398	Cg2099	1	704.4473	0.6	80	85	0	22.7	22	L	SIIIFI	I	3.3	6.02	
1402	Cg3214	1	648.3483	1.2	96	101	0	42.8	31	K	DLAFAL	N	1.8	3.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1407	Cg0684	1	885.5324	-1.1	390	397	0	31.2	29	H	LPGVQLFI	T	1.7	6.02	
1414	Cg1405	1	855.4015	-1.5	97	103	0	28.6	25	G	TFDIDFV	A	0.9	2.92	
1418	Cg1242	1	617.4152	-0.5	109	113	0	25.8	21	F	FLILI	G	3.9	6.02	
1419	Cg2010	1	630.3775	-4.8	103	108	0	27.2	27	I	GLCILI	V	3.1	5.32	
1419	Cg2010	1	678.3775	-1.5	97	102	0	27.0	23	L	MVGLFI	G	2.8	6.02	
1421	Cg1260	1	656.3745	-0.5	78	83	0	27.8	27	H	IDTVPI	A	1.2	3.1	
1429	Cg0602	2	1693.9515	-1.1	67	81	0	40.4	25	I	NIFPDRPLTQKPLGV	R	-0.4	10.08	
1430	Cg3299	1	657.3697	0.5	69	74	0	38.0	32	Q	IQSIPT	L	0.4	6.02	
1431	Cg2578	1	656.3745	-0.5	166	171	0	27.6	27	A	DLVTLP	G	1.0	3.1	
1433	Cg1236	2	1731.8679	0.9	114	130	0	56.8	29	S	TFGEDNGIVLEGSPLKG	L	-0.2	3.82	
1437	Cg1291	2	915.4847	-2.5	51	60	0	27.2	27	G	AMLANAAAAL	F	1.7	6.02	
1442	Cg2625	1	1566.8869	-0.2	26	40	0	25.3	25	G	VPVEELATTVINAIV	E	1.3	3.12	
1447	Cg3211	1	532.2646	1.1	129	133	0	30.8	29	D	GTWGI	S	0.4	6.02	
1456	Cg1490	1	902.4605	0.2	208	215	0	33.8	29	Q	AEMLVPML	L	1.5	3.3	
1459	Cg2935	1	971.4811	-1.3	304	312	0	27.3	26	R	IDEPISDAI	S	0.3	2.88	
1462	Cg2620	1	553.3839	1.3	384	388	0	24.5	24	E	ILVPI	M	3.1	6.02	
1462	Cg2620	1	598.4418	1.7	217	221	0	28.1	17	A	LLKIL	E	2.4	10.1	
1464	Cg3308	1	601.3873	0.8	6	10	0	22.9	16	E	LMIIL	D	3.7	6.02	
1464	Cg3308	1	924.4626	0.4	3	9	0	32.1	27	R	QYELMII	L	0.9	3.3	Oxidation (M)
1467	Cg0153	1	755.3701	0.3	235	241	0	27.3	22	S	DLSDLPP	T	-0.5	2.92	
1468	Cg1176	2	1109.6332	1.5	77	87	0	26.8	24	G	IDVVVIEPGGI	A	1.5	3	
1476	Cg0154	1	676.416	1.2	11	16	0	40.4	25	D	LYGVLI	K	2.4	5.92	
1479	Cg0650	1	1057.5516	-1.4	61	69	0	30.9	27	T	RNTIQDQLA	S	-1.0	6.78	
1488	Cg1675	1	599.3894	1.5	11	15	0	30.2	19	F	IIEIL	A	2.8	3.3	
1498	Cg0156	1	579.338	2.6	352	356	0	22.2	21	R	LIPTH	R	0.6	7.84	
1505	Cg1206	1	1306.634	3.4	176	187	0	35.6	29	L	MEQAGARSVYPV	G	-0.1	6.88	
1506	Cg1842	2	1201.5687	-1.2	219	229	0	33.9	28	A	SAVGDDNIQQR	S	-1.2	3.88	
1508	Cg1962	1	601.3873	0.8	94	98	0	22.9	16	S	LMILI	I	3.7	6.02	
1509	Cg2952	2	931.3441	1.4	59	67	0	20.2	15	S	SMESSTTSS	S	-0.8	3.3	Oxidation (M)
1523	Cg0946	1	489.2587	0.2	75	79	0	31.3	29	A	GFPGI	T	1.0	6.02	
1532	Cg2567	1	640.416	2.0	72	77	0	31.4	23	P	LSVIPI	E	2.4	6.02	
1534	Cg2806	1	786.4851	-0.6	42	49	0	29.7	27	F	AVSLITAL	V	2.3	6.02	
1534	Cg2806	1	995.4811	-0.6	26	34	0	31.9	26	W	SPITSESYL	E	-0.1	3.3	
1539	Cg0109	1	641.3748	1.2	196	202	0	45.0	29	M	GGIVSPL	I	1.3	6.02	
1542	Cg3209	1	666.468	0.3	137	142	0	19.9	19	E	IPVLLI	W	3.2	6.02	
1547	Cg0620	2	1366.5524	-2.9	53	65	0	54.6	18	V	DYGADSEKEPEGA	C	-1.7	3.5	
1549	Cg2134	1	664.3584	2.1	33	37	0	25.1	24	K	WYLIA	G	1.6	5.92	
1550	Cg2350	1	1000.4349	-0.4	119	128	0	30.1	23	A	GIEEAPAEEG	A	-0.8	2.96	
1550	Cg2350	2	1297.6401	-0.2	4	15	0	40.7	28	V	ATDPEAPIEEKV	K	-0.8	3.68	
1565	Cg3155	1	686.3275	1.2	122	127	0	25.4	22	G	FSGYIT	L	0.7	5.92	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1568	Cg0680	1	532.2645	1.1	67	71	0	30.8	29	L	ASWGI	A	0.8	6.02	
1571	Cg1514	1	924.4626	0.4	122	129	0	27.9	27	I	YISGLEML	S	1.0	3.3	
1572	Cg3277	1	786.4851	-0.6	100	107	0	52.4	27	D	SAVLITIA	K	2.4	6.02	
1579	Cg1370	1	767.3813	-0.9	112	118	0	36.4	26	I	ELALDAH	G	0.1	4.06	
1584	Cg3249	1	1438.8031	-2.2	171	183	0	39.4	26	A	QLIAEEVIQNLGL	-	0.7	3.12	
1585	Cg2720	2	761.3344	-4.9	224	231	0	26.1	26	L	GGGVWGET	D	-0.3	3.3	
1590	Cg3280	2	2745.2724	-1.6	197	220	0	85.0	27	I	ALAEQVIEDQEAEIAEMEQMLNEL	-	-0.3	2.74	
1605	Cg0179	1	800.483	-4.5	37	44	0	33.9	30	G	CIVVAILA	L	3.4	5.32	
1617	Cg3293	1	959.5175	0.2	84	92	0	31.8	29	R	LDLSTLEAV	D	1.0	3	
1634	Cg0325	2	1303.5892	-1.6	116	127	0	39.7	26	R	SVTNPTDQEDKA	-	-1.6	3.7	
1643	Cg0415	1	1169.604	3.3	151	160	0	33.4	28	S	RSELNPLDNL	A	-1.0	4.08	
1645	Cg1597	1	526.3115	0.8	103	108	0	30.6	30	G	GPGLIA	V	1.3	6.02	
1649	Cg1033	1	1031.6055	-1.0	71	79	0	27.3	25	A	IPYFGLIPL	A	1.6	5.92	
1650	Cg2623	2	1565.8638	1.3	104	119	0	29.6	26	P	QGTLAERLRAGGAGIP	A	-0.2	10.88	
1662	Cg0530	1	1201.7144	-0.4	40	50	0	27.0	22	A	LIVAFPLSMLV	F	2.6	6.02	
1662	Cg0530	1	1217.7094	1.3	40	50	0	25.8	24	A	LIVAFPLSMLV	F	2.6	6.02	Oxidation (M)
1670	Cg0795	2	953.4277	1.6	276	285	0	25.3	25	M	AMVYGSAAQG	V	0.5	5.92	
1675	Cg0292	1	654.4064	-0.5	56	61	0	24.2	23	P	KPVLQA	V	0.1	10.1	
1681	Cg1893	1	887.46	-0.6	84	91	0	31.8	30	S	ESVQLEIA	E	0.4	3.12	
1696	Cg2113	1	632.3897	-1.3	110	115	0	28.4	27	V	IFAGIL	L	2.8	6.02	
1699	Cg2315	1	844.4542	-2.5	223	230	0	33.0	30	Y	DATVIVEV	I	1.4	3	
1704	Cg1130	1	690.3952	-1.3	94	99	0	31.0	26	L	LFDIIA	D	2.3	3.1	
1709	Cg2207	1	747.4895	-1.1	333	339	0	19.0	13	N	LVPLPPL	D	1.5	6.02	
1710	Cg0465	1	945.5688	-3.5	103	110	0	27.0	23	L	IWFLIAAI	S	2.9	6.02	
1712	Cg2861	1	739.4632	1.6	180	185	0	21.8	15	G	WLIVPL	V	2.3	6.02	
1720	Cg1682	1	656.3897	0.0	93	98	0	20.1	15	M	PLPLFA	D	1.5	6.02	
1728	Cg3412	1	751.5207	0.9	19	25	0	20.0	17	V	LIPIAII	T	3.1	6.02	
1741	Cg3223	1	672.4058	1.5	171	176	0	31.8	24	R	LLDSLL	T	1.8	3.1	
1748	Cg2942	1	858.4269	-0.2	31	38	0	29.7	28	T	MPNKDIAA	K	-0.3	6.76	
1750	Cg1652	2	800.4643	1.1	189	195	0	29.4	29	A	LDALEKI	E	0.4	4.08	
1751	Cg1630	1	1002.4618	-1.0	36	46	0	39.5	27	A	STGAENLPAGS	A	-0.4	3.3	
1770	Cg1884	2	2397.0972	-2.0	35	56	0	47.6	26	A	HDVVVDSNPENGSVVDEFPETI	E	-0.4	3.38	
1771	Cg2765	1	640.4523	0.3	12	17	0	30.8	25	S	LIGLIL	I	3.3	6.02	
1783	Cg2344	2	1417.7096	-4.2	90	102	0	40.3	29	H	CVVDSRANRNTIA	H	-0.2	9	
1801	Cg3357	2	723.4279	2.2	30	36	0	26.2	23	A	KLPGNPV	V	-0.4	10.1	
1801	Cg3357	1	891.3796	0.7	48	54	0	30.2	25	S	QELWDMA	H	-0.6	3	
1803	Cg0852	1	509.3213	-0.2	90	94	0	30.4	21	V	IPPAI	D	1.5	6.02	
1823	Cg2547	1	688.4523	0.1	92	97	0	24.4	21	L	ILFIIA	G	3.7	6.02	
1823	Cg2547	1	704.4473	0.6	90	95	0	22.7	22	V	SLILFI	I	3.1	6.02	
1824	Cg0240	2	2067.012	-0.9	78	97	0	53.3	29	I	RQEIGDLGVTPGPESDVDAI	T	-0.4	3.42	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1827	Cg1167	2	1170.588	-0.7	49	58	0	73.2	28	V	LIEQESERPA	T	-1.1	3.96	
1832	Cg1612	1	746.3884	1.9	178	183	0	40.8	28	D	EILEML	K	1.2	3.12	
1833	Cg3129	1	1198.6346	0.8	30	39	0	32.2	28	H	EQPLEFRAPI	T	-0.5	4.26	
1837	Cg1834	1	699.4167	0.3	93	99	0	31.8	30	V	ADLVLLG	R	1.9	3.1	
1840	Cg1783	1	695.4218	1.9	206	212	0	22.4	21	L	VPSIAPL	L	1.5	6.02	
1846	Cg2053	1	676.3948	0.0	68	72	0	25.6	19	L	FWIVI	S	3.0	6.02	
1847	Cg3139	2	1973.9847	-2.6	9	26	0	47.7	30	L	RLDPAVYDAIAKWAADEA	R	-0.2	3.96	
1866	Cg1348	1	704.4473	0.6	106	111	0	22.7	22	F	ILSLFI	V	3.1	6.02	
1871	Cg3345	1	747.3262	1.5	157	162	0	29.0	27	I	PWDMIA	N	0.4	3.1	Oxidation (M)
1875	Cg0374	1	656.3931	-4.4	58	63	0	25.4	20	T	LMPLLA	G	2.3	6.02	
1879	Cg3127	1	803.4429	0.5	141	147	0	26.7	25	E	FDIITVP	A	1.5	3.1	
1886	Cg0599	2	1832.8767	-1.0	61	77	0	56.6	29	V	FVDDAMVGHKLGEFAPT	K	0.2	4.3	
1892	Cg3324	1	1548.7824	-2.0	89	102	0	32.3	29	V	NIADPAPWEVVEPI	N	0.1	2.94	
1900	Cg3331	1	656.3897	0.0	122	127	0	20.1	15	N	PLPIFA	P	1.6	6.02	
1901	Cg0337	1	532.2646	0.2	82	86	0	35.2	29	V	WGGLT	E	0.3	6.02	
1902	Cg2607	1	688.4523	0.1	111	116	0	24.4	21	A	IIFIIA	W	3.8	6.02	
1904	Cg1796	2	1150.5255	-0.6	167	176	0	31.0	27	A	FQSRDGEDVV	R	-0.9	3.7	
1907	Cg1706	1	642.3701	-1.9	129	134	0	35.1	29	R	VQNLVA	E	1.2	6.02	
1911	Cg3052	2	1035.5237	1.5	306	315	0	37.1	29	S	YLLANGVSAE	F	0.6	3.3	
1925	Cg1326	1	557.3247	-0.7	69	73	0	27.7	19	Q	VMIPV	I	2.6	6.02	
1930	Cg1874	1	583.4309	-0.2	127	131	0	24.1	18	S	ILILL	V	4.1	6.02	
1937	Cg2824	2	668.3969	-0.1	88	93	0	25.1	24	V	RILNPG	G	-0.3	11.04	
1949	Cg2981	1	834.4487	-1.0	53	60	0	33.1	28	V	DYGALALL	V	1.2	3.1	
1954	Cg2121	2	1351.5263	-0.7	37	49	0	27.2	17	T	LVGSDDDEETDAS	S	-1.1	2.7	
1959	Cg2785	2	1009.6535	1.6	60	70	0	25.0	21	S	GALAVALLALV	A	2.8	6.02	
1991	Cg3105	1	583.4309	-0.2	106	110	0	24.1	18	L	IILIL	R	4.2	6.02	
1993	Cg1181	1	775.4844	0.9	183	189	0	24.6	23	Y	FAVIIIT	F	3.1	6.02	
1998	Cg2572	1	640.4523	0.3	130	135	0	30.8	25	A	ILGLLI	S	3.3	6.02	
2001	Cg0983	2	882.4923	0.9	164	171	0	26.4	26	Q	RAVPVEVN	D	0.2	6.98	
2036	Cg1804	1	767.3814	4.0	138	144	0	28.2	27	T	DHLDGVL	F	0.2	3.88	
2048	Cg2582	1	1064.539	0.6	115	123	0	28.3	28	I	EIEGLETFK	R	-0.5	3.96	
2049	Cg3257	1	950.5113	-0.8	29	36	0	33.3	27	T	LFDLLFPS	N	1.4	3.1	
2051	Cg2839	1	870.5062	0.2	223	230	0	33.0	27	L	LTPVELSL	R	1.1	3.3	
2078	Cg1469	1	632.3897	-1.3	11	16	0	29.0	27	L	FIALGL	V	2.7	6.02	
2110	Cg2033	2	715.448	1.7	9	15	0	29.2	25	A	LLAVSTL	M	2.3	6.02	
2119	Cg2850	1	577.3475	2.3	195	199	0	28.1	28	R	LYGLL	P	1.9	5.92	
2120	Cg0246	1	710.3792	-1.3	283	287	0	24.2	21	A	WFFLV	Q	2.5	6.02	
2123	Cg0500	1	1122.6649	-0.3	88	98	0	22.2	22	H	LITSINIGVPP	G	1.2	6.02	
2137	Cg0297	1	770.4538	-0.3	69	75	0	30.0	29	T	LQDLLLG	A	1.1	3.1	
2138	Cg0107	3	3416.8748	-0.4	156	186	0	30.6	28	T	FTIEVPGVGGVQLPDLYQIVQQFLAQFGIKI	-	0.7	4.08	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2148	Cg3110	1	598.4418	1.7	39	43	0	28.1	17	H	IIKLL	V	2.5	10.1	
2162	Cg0582	1	1625.8373	-1.2	117	132	0	31.0	29	I	ERLANELLDAANGLGA	S	0.0	3.82	
2163	Cg1635	2	1615.7002	1.2	27	40	0	26.1	24	A	DGYLDIDEFDTRTG	A	-1.0	3.36	
2191	Cg3423	2	990.4618	-0.5	57	65	0	34.5	28	A	SVDVDAERT	L	-0.7	3.7	
2202	Cg1085	1	763.3323	-0.3	17	22	0	36.3	25	N	NWVNMT	G	-0.4	6.02	
2223	Cg1894	1	726.3225	-1.7	151	156	0	25.3	24	K	AFDDFL	H	0.7	2.92	
2225	Cg0588	1	1093.7111	-2.1	232	241	0	19.3	19	E	LGVLEKIIPL	E	1.5	6.94	
2232	Cg1072	1	957.5019	-0.8	62	70	0	35.8	28	N	AVLELDIEG	Q	0.8	2.94	
2239	Cg0155	1	679.4268	-1.2	4	9	0	25.0	21	P	QPLILP	F	0.9	6.02	
2249	Cg0612	1	585.3737	1.5	94	98	0	27.8	25	I	DLLLI	H	2.5	3.1	
2249	Cg0612	1	698.4578	1.0	93	98	0	28.2	22	Y	IDLLLI	H	2.8	3.1	
2271	Cg2443	1	630.3775	-4.8	120	125	0	27.2	27	L	AVCLLL	Q	3.3	5.32	
2281	Cg2996	1	674.4367	1.5	2	7	0	24.6	24	M	FLAVIL	A	3.5	6.02	
2292	Cg1241	1	639.3268	0.6	42	46	0	25.2	23	T	FDVFL	N	2.0	3.1	
2295	Cg1708	2	2116.9841	-2.0	6	24	0	38.8	27	A	TFQPSVDEFISTLEEFATG	S	0.0	2.88	
2301	Cg2340	1	667.3945	-0.7	10	14	0	23.2	15	A	FYIII	C	3.0	5.92	
2331	Cg2071	1	635.3716	-4.9	221	225	0	20.5	19	S	MFILI	A	3.5	6.02	
2331	Cg2071	1	651.3666	0.6	221	225	0	24.1	17	S	MFILI	A	3.5	6.02	Oxidation (M)
2336	Cg0358	1	666.468	0.3	72	77	0	19.9	19	K	PLVLLI	H	3.1	6.02	
2346	Cg3267	1	676.3948	0.0	23	27	0	25.6	19	L	FWIVL	S	2.9	6.02	
2435	Cg0321	1	864.6048	-0.9	48	55	0	20.8	13	I	PLLIIALL	I	3.1	6.02	
2443	Cg1201	1	545.3247	2.0	36	40	0	29.9	28	S	LMVLA	G	3.1	6.02	
2447	Cg0366	1	949.5307	-3.1	36	44	0	29.0	28	A	ALAAVLYMV	V	2.4	5.92	
2457	Cg0087	1	1355.8249	-4.2	64	76	0	29.4	23	K	RVITRVSAGLTLA	I	1.0	12.4	
2468	Cg3433	1	678.3775	-0.1	2	7	0	23.3	23	M	LCAIFI	V	3.3	5.32	
2497	Cg2710	1	888.3614	-0.7	166	173	0	21.1	21	R	PWDATNAD	D	-1.3	2.92	
2632	Cg0380	2	668.397	-0.1	46	51	0	30.6	24	G	RLPQVG	I	-0.3	11.04	
2635	Cg2988	1	553.3839	1.1	59	63	0	26.4	24	A	LVILP	E	2.9	6.02	
2716	Cg0606	1	739.4632	1.6	27	32	0	21.8	15	V	LWLVPI	S	2.3	6.02	

END OF LIST I

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
II. Purple membrane; elastase digest, nLC-ESI MS/MS, no search specificity															
1	P02945|BACR	1	499.2278	-0.6	248	252	0	27.3	26	E	APEPS	A	-1.1	3.3	
1	P02945|BACR	1	505.29	-1.8	231	235	0	32.2	30	V	GFGLI	L	2.1	6.02	
1	P02945|BACR	1	542.27	-0.6	14	18	0	29.1	29	S	QAQIT	G	-0.3	6.02	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	543.3268	-0.7	109	113	0	32.6	30	L	DLALL	V	1.9	3.1	
1	P02945|BACR	1	555.3632	0.4	103	107	0	27.1	18	T	TPLLL	L	1.8	6.02	
1	P02945|BACR	1	568.3584	0.5	209	214	0	27.8	27	G	AGIVPL	N	2.1	6.02	
1	P02945|BACR	1	585.3737	1.0	106	110	0	29.2	20	L	LLLDL	A	2.3	3.1	
1	P02945|BACR	1	586.3479	0.2	201	205	0	27.1	21	V	VWLIG	S	2.2	6.02	
1	P02945|BACR	1	587.3643	0.3	138	143	0	33.0	25	V	GALTKV	Y	0.8	10.1	
1	P02945|BACR	1	609.3196	-0.8	157	161	0	25.4	22	A	AMLYI	L	2.1	5.92	
1	P02945|BACR	1	612.3847	-0.8	60	65	0	27.3	24	T	TLVPAI	A	2.0	6.02	
1	P02945|BACR	1	613.3112	0.3	55	59	0	29.0	21	K	FYAIT	T	1.4	5.92	
1	P02945|BACR	1	621.356	-0.3	220	224	0	27.2	13	L	LFMVL	D	3.3	6.02	
1	P02945|BACR	1	626.4479	0.3	234	238	0	14.5	13	G	LILLR	S	2.3	11.04	
1	P02945|BACR	1	628.2704	1.9	247	252	0	26.0	22	A	EAPEPS	A	-1.5	3.12	
1	P02945|BACR	1	628.416	0.0	120	125	0	42.4	25	G	TILALV	G	2.9	6.02	
1	P02945|BACR	1	642.3952	-0.5	109	114	0	44.7	27	L	DLALLV	D	2.3	3.1	
1	P02945|BACR	1	643.2709	0.5	69	73	0	26.6	15	T	MYLSM	L	1.1	5.92	
1	P02945|BACR	1	643.3541	0.3	124	130	0	46.5	31	A	LVGADGI	M	1.4	3.1	
1	P02945|BACR	1	653.3788	-1.8	38	42	0	26.5	23	T	LYFLV	K	2.7	5.92	
1	P02945|BACR	1	656.4109	1.1	106	111	0	43.1	21	L	LLLDLA	L	2.3	3.1	
1	P02945|BACR	1	659.3643	0.6	25	30	0	43.6	26	I	WLALGT	A	1.2	6.02	
1	P02945|BACR	1	661.3224	0.2	150	154	0	26.0	25	V	WWAIS	T	0.7	6.02	
1	P02945|BACR	1	668.4473	1.3	103	108	0	27.3	13	T	TPLLLL	D	2.2	6.02	
1	P02945|BACR	1	669.3737	1.5	160	164	0	24.4	13	L	YILYV	L	2.0	5.86	
1	P02945|BACR	1	673.3799	1.0	201	206	0	42.4	26	V	VWLIGS	E	1.7	6.02	
1	P02945|BACR	1	674.4367	-1.0	232	237	0	24.6	21	G	FGLILL	R	3.1	6.02	
1	P02945|BACR	1	680.317	-0.3	98	102	0	30.6	21	A	DWLFT	T	0.3	3.1	
1	P02945|BACR	1	683.4218	0.4	60	66	0	32.9	24	T	TLVPAIA	F	2.0	6.02	
1	P02945|BACR	1	689.3782	0.6	131	137	0	33.0	25	I	MIGTGLV	G	1.8	6.02	
1	P02945|BACR	2	693.4061	1.2	182	187	0	19.1	18	A	STFKVL	R	0.9	10.1	
1	P02945|BACR	1	701.3959	-1.0	215	220	0	38.2	29	L	NIETLL	F	0.7	3.3	
1	P02945|BACR	1	703.3905	0.1	191	196	0	28.0	27	V	TVVLWS	A	1.6	6.02	
1	P02945|BACR	1	703.3938	-0.1	32	38	0	41.1	27	A	LMGLGTL	Y	1.7	6.02	
1	P02945|BACR	1	704.317	0.9	166	171	0	31.6	24	L	FFGFTS	K	1.1	6.02	
1	P02945|BACR	1	705.3731	-1.7	131	137	0	29.5	29	I	MIGTGLV	G	1.8	6.02	Oxidation (M)
1	P02945|BACR	1	714.3588	-0.4	55	60	0	39.2	20	K	FYAITT	L	1.1	5.92	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	1	714.3912	0.0	123	130	0	29.3	29	L	ALVGADGI	M	1.5	3.1	
1	P02945|BACR	1	721.3435	-0.6	195	200	0	25.9	24	L	WSAYPV	V	0.2	5.92	
1	P02945|BACR	1	722.3673	-1.1	221	226	0	41.7	20	L	FMVLDV	S	2.2	3.1	
1	P02945|BACR	1	725.4476	-0.7	199	204	0	24.7	21	Y	PVVWLI	G	2.4	6.02	
1	P02945|BACR	1	730.4225	-1.2	134	141	0	34.0	28	G	TGLVGALT	K	1.4	6.02	
1	P02945|BACR	1	731.4582	-0.8	231	237	0	36.5	23	V	GFGLILL	R	2.6	6.02	
1	P02945|BACR	2	732.4534	0.4	229	235	0	35.7	16	A	KVGFGLI	L	1.5	10.1	
1	P02945|BACR	1	734.4401	0.1	219	224	0	22.5	13	T	LLFMVL	D	3.4	6.02	
1	P02945|BACR	1	738.3622	-2.8	221	226	0	41.1	21	L	FMVLDV	S	2.2	3.1	Oxidation (M)
1	P02945|BACR	1	739.3575	-0.7	76	82	0	30.6	25	L	GYGLTMV	P	1.0	5.92	
1	P02945|BACR	2	741.4061	1.8	54	59	0	17.0	17	K	KFYAIT	T	0.5	9.72	
1	P02945|BACR	1	754.4265	-0.3	37	42	0	23.9	15	G	TLYFLV	K	2.1	5.92	
1	P02945|BACR	1	755.4793	-0.8	108	114	0	30.0	23	L	LDLALLV	D	2.5	3.1	
1	P02945|BACR	1	756.355	-0.3	69	74	0	41.7	23	T	MYLSML	L	1.6	5.92	
1	P02945|BACR	1	759.3763	-0.7	8	15	0	33.4	30	T	AVEGVSQA	Q	0.5	3.3	
1	P02945|BACR	2	762.4024	1.8	240	246	0	40.2	27	S	RAIFGEA	E	0.4	6.98	
1	P02945|BACR	1	769.4949	-1.4	107	113	0	32.3	21	L	LLDLALL	V	2.5	3.1	
1	P02945|BACR	1	769.4949	0.3	105	111	0	44.4	21	P	LLLLDLA	L	2.5	3.1	
1	P02945|BACR	1	769.4949	-1.0	102	108	0	29.5	21	F	TTPLLLL	D	1.7	6.02	
1	P02945|BACR	1	774.431	-1.2	31	38	0	37.6	26	T	ALMGLGTL	Y	1.7	6.02	
1	P02945|BACR	1	781.3647	0.3	98	103	0	38.8	24	A	DWLFTT	P	0.1	3.1	
1	P02945|BACR	1	784.4695	-1.7	59	66	0	34.2	25	I	TTLVPAIA	F	1.6	6.02	
1	P02945|BACR	2	803.4905	2.9	228	235	0	34.3	13	S	AKVGFGLI	L	1.6	10.1	
1	P02945|BACR	2	820.4272	1.6	148	153	0	22.2	19	R	FVWWAI	S	1.9	6.02	
1	P02945|BACR	1	827.4753	1.2	122	130	0	26.9	26	I	LALVGADGI	M	1.7	3.1	
1	P02945|BACR	2	828.3918	-0.2	92	97	0	23.2	21	I	YWARYA	D	-0.7	9.58	
1	P02945|BACR	1	831.4127	0.1	202	209	0	44.2	31	V	WLIGSEGA	G	0.5	3.3	
1	P02945|BACR	2	834.4276	1.3	194	200	0	34.0	24	V	LWSAYPV	V	0.7	5.92	
1	P02945|BACR	1	835.4514	-1.0	220	226	0	53.1	17	L	LFMVLDV	S	2.5	3.1	
1	P02945|BACR	2	849.4783	1.8	40	47	0	20.4	20	Y	FLVKGMGV	S	1.5	10.1	
1	P02945|BACR	1	851.4463	-0.6	220	226	0	31.7	19	L	LFMVLDV	S	2.5	3.1	Oxidation (M)
1	P02945|BACR	2	856.5382	0.9	135	143	0	49.5	21	T	GLVGALTKV	Y	1.4	10.1	
1	P02945|BACR	1	859.444	1.4	201	208	0	47.7	26	V	VWLIGSEG	A	0.8	3.3	
1	P02945|BACR	1	866.5477	-0.1	104	111	0	52.2	16	T	PLLLLDLA	L	2.0	3.1	
1	P02945|BACR	2	869.4391	1.3	69	75	0	39.8	22	T	MYLSMLL	G	1.9	5.92	
1	P02945|BACR	1	882.579	-0.8	106	113	0	17.5	16	L	LLLDLALL	V	2.6	3.1	
1	P02945|BACR	2	887.5593	-0.2	231	238	0	56.6	16	V	GFGLILLR	S	1.7	11.04	
1	P02945|BACR	1	896.5583	-0.3	103	110	0	44.4	17	T	TPLLLLDL	A	1.7	3.1	
1	P02945|BACR	2	898.476	1.4	205	214	0	30.0	27	I	GSEGAGIVPL	N	0.7	3.3	
1	P02945|BACR	1	914.4174	0.1	96	102	0	30.2	25	R	YADWLFT	T	0.3	3.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	1	916.5634	-0.8	100	107	0	18.3	16	W	LFTTPLLL	L	1.9	6.02	
1	P02945|BACR	2	917.4276	0.4	174	181	0	41.5	26	A	ESMRPEVA	S	-0.8	4.26	
1	P02945|BACR	1	922.4834	-1.6	220	227	0	33.8	21	L	LFMVLDVS	A	2.1	3.1	
1	P02945|BACR	2	926.6025	0.9	233	240	0	34.1	14	F	GLILLRSR	A	0.7	12.4	
1	P02945|BACR	2	930.4811	0.9	201	209	0	71.6	26	V	VWLIGSEGA	G	0.9	3.3	
1	P02945|BACR	1	932.5001	-0.3	28	37	0	28.7	26	A	LGTALMGLGT	L	1.3	6.02	
1	P02945|BACR	1	948.5354	0.1	219	226	0	29.5	23	T	LLFMVLDV	S	2.6	3.1	
1	P02945|BACR	1	953.4892	-1.3	72	80	0	38.9	23	L	SMLLGYGLT	M	1.1	5.92	
1	P02945|BACR	1	957.4556	0.1	83	91	0	56.8	27	V	PFGGEQNPI	Y	-0.8	3.3	
1	P02945|BACR	2	957.5859	0.7	134	143	0	59.7	20	G	TGLVGALTKV	Y	1.2	10.1	
1	P02945|BACR	1	958.5157	0.7	123	132	0	35.3	28	L	ALVGADGIMI	G	1.8	3.1	
1	P02945|BACR	2	958.6215	0.7	229	237	0	29.1	13	A	KVGFGLILL	R	2.0	10.1	
1	P02945|BACR	2	959.548	1.4	197	204	0	31.3	20	S	AYPVVWLI	G	1.8	5.92	
1	P02945|BACR	1	964.5303	-0.1	217	224	0	40.9	23	I	ETLLFMVL	D	2.0	3.3	
1	P02945|BACR	1	967.5954	-0.5	103	111	0	57.2	18	T	TPLLLLDLA	L	1.7	3.1	
1	P02945|BACR	1	969.4841	-1.7	72	80	0	34.4	23	L	SMLLGYGLT	M	1.1	5.92	Oxidation (M)
1	P02945|BACR	2	969.5358	1.4	38	45	0	42.4	23	T	LYFLVKGM	G	1.4	9.72	
1	P02945|BACR	1	974.5107	-0.6	128	137	0	50.5	27	A	DGIMIGTGLV	G	1.4	3.1	
1	P02945|BACR	2	974.5913	0.1	231	239	0	44.6	19	V	GFGLILLRS	R	1.4	11.04	
1	P02945|BACR	1	979.5048	0.1	215	222	0	32.8	25	L	NIETLLFM	V	1.1	3.3	
1	P02945|BACR	2	981.6474	1.2	106	114	0	45.7	13	L	LLLDLALLV	D	2.8	3.1	
1	P02945|BACR	1	984.5354	0.8	157	164	0	30.1	25	A	AMLYILYV	L	2.2	5.86	
1	P02945|BACR	2	986.6277	0.6	230	238	0	81.9	13	K	VGFGLILLR	S	2.0	11.04	
1	P02945|BACR	2	991.5015	0.9	98	105	0	67.2	27	A	DWLFTTPL	L	0.4	3.1	
1	P02945|BACR	2	1001.5029	2.4	114	123	0	32.7	28	L	VDADQGTILA	L	0.5	2.92	
1	P02945|BACR	2	1012.5416	-0.5	39	47	0	47.1	26	L	YFLVKGMGV	S	1.2	9.72	
1	P02945|BACR	2	1014.6074	0.8	133	143	0	54.3	21	I	GTGLVGALTKV	Y	1.0	10.1	
1	P02945|BACR	2	1029.6586	0.6	228	237	0	43.9	13	S	AKVGFGLILL	R	2.0	10.1	
1	P02945|BACR	2	1031.5685	0.2	131	141	0	82.5	25	I	MIGTGLVGALT	K	1.6	6.02	
1	P02945|BACR	1	1032.44	-0.5	243	252	0	35.9	24	I	FGEAEAPEPS	A	-0.9	3.02	
1	P02945|BACR	1	1032.5856	-0.5	59	68	0	34.2	23	I	TTLVPAIAFT	M	1.5	6.02	
1	P02945|BACR	2	1043.5499	0.7	112	121	0	81.0	28	A	LLVDADQGTI	L	0.7	2.92	
1	P02945|BACR	1	1045.5478	0.5	124	134	0	33.3	27	A	LVGADGIMIGT	G	1.4	3.1	
1	P02945|BACR	1	1045.5842	-1.9	28	38	0	28.8	24	A	LGTALMGLGTL	Y	1.5	6.02	
1	P02945|BACR	2	1055.5552	0.6	19	26	0	33.4	26	T	GRPEWIWL	A	-0.4	6.98	
1	P02945|BACR	2	1062.5386	1.2	97	105	0	33.7	26	Y	ADWLFTTPL	L	0.5	3.1	
1	P02945|BACR	1	1067.6227	-2.4	210	219	0	27.7	21	A	GIVPLNIETL	L	1.1	3.3	
1	P02945|BACR	1	1070.5185	0.1	95	102	0	43.5	24	A	RYADWLFT	T	-0.3	6.7	
1	P02945|BACR	2	1078.5733	0.1	215	223	0	32.0	25	L	NIETLLFMV	L	1.5	3.3	
1	P02945|BACR	1	1094.5682	-0.5	215	223	0	47.8	26	L	NIETLLFMV	L	1.5	3.3	Oxidation (M)

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	2	1096.5661	-1.3	73	82	0	48.8	25	S	MLLGYGLTMV	P	1.7	5.92	
1	P02945|BACR	1	1097.5216	-0.2	76	86	0	27.3	26	L	GYGLTMVPFGG	E	0.7	5.92	
1	P02945|BACR	1	1102.5693	-0.4	126	137	0	32.8	27	V	GADGIMIGTGLV	G	1.2	3.1	
1	P02945|BACR	1	1103.6015	-0.3	197	206	0	26.5	26	S	AYPVVWLIGS	E	1.4	5.92	
1	P02945|BACR	2	1109.6485	-0.1	34	43	0	31.1	21	M	GLGTLYFLVK	G	1.2	9.72	
1	P02945|BACR	2	1112.561	-1.5	73	82	0	26.5	26	S	MLLGYGLTMV	P	1.7	5.92	Oxidation (M)
1	P02945|BACR	2	1114.587	-1.1	115	125	0	56.5	28	V	DADQGTILALV	G	0.8	2.92	
1	P02945|BACR	1	1114.587	1.3	113	123	0	34.2	27	L	LVDADQGTILA	L	0.8	2.92	
1	P02945|BACR	1	1116.5849	-1.3	123	134	0	32.8	27	L	ALVGADGIMIGT	G	1.4	3.1	
1	P02945|BACR	2	1116.6907	0.7	227	237	0	48.0	16	V	SAKVGFGLILL	R	1.7	10.1	
1	P02945|BACR	2	1117.5552	1.5	67	75	0	48.8	28	A	FTMYLSMLL	G	1.7	5.92	
1	P02945|BACR	2	1125.6256	-0.4	38	47	0	43.9	24	T	LYFLVKGMGV	S	1.5	9.72	
1	P02945|BACR	2	1126.5923	2.4	19	27	0	40.8	25	T	GRPEWIWLA	L	-0.2	6.98	
1	P02945|BACR	1	1126.6023	0.4	199	209	0	45.3	26	Y	PVVWLIGSEGA	G	1.0	3.3	
1	P02945|BACR	3	1130.6924	0.7	231	240	0	15.7	14	V	GFGLILLRSR	A	0.8	12.4	
1	P02945|BACR	2	1133.5501	-1.1	67	75	0	33.9	27	A	FTMYLSMLL	G	1.7	5.92	Oxidation (M)
1	P02945|BACR	2	1133.6121	1.3	191	200	0	67.2	27	V	TVVLWSAYPV	V	1.3	5.92	
1	P02945|BACR	2	1145.524	-0.7	242	252	0	85.9	26	A	IFGEAEAPEPS	A	-0.4	3.02	
1	P02945|BACR	2	1152.6179	2.3	50	59	0	36.7	24	D	PDAKKFYAIT	T	-0.4	9.62	
1	P02945|BACR	2	1156.634	1.0	112	122	0	105.9	26	A	LLVDADQGTIL	A	0.9	2.92	
1	P02945|BACR	2	1159.6635	0.5	131	142	0	89.8	23	I	MIGTGLVGALTK	V	1.1	10.1	
1	P02945|BACR	2	1166.67	0.3	34	44	0	81.2	22	M	GLGTLYFLVKG	M	1.0	9.72	
1	P02945|BACR	2	1171.5662	-0.6	95	103	0	29.1	25	A	RYADWLFTT	P	-0.4	6.7	
1	P02945|BACR	2	1173.7234	0.7	184	193	0	19.9	14	T	FKVLRNVTVV	L	1.1	11.48	
1	P02945|BACR	2	1180.7067	-0.2	210	220	0	38.5	19	A	GIVPLNIETLL	F	1.4	3.3	
1	P02945|BACR	2	1183.5981	0.3	72	82	0	68.8	26	L	SMLLGYGLTMV	P	1.4	5.92	
1	P02945|BACR	2	1185.687	0.8	187	196	0	23.3	23	V	LRNVTVVLWS	A	1.0	11.04	
1	P02945|BACR	2	1187.5645	0.3	81	91	0	76.5	27	T	MVPFGGEQNPI	Y	-0.1	3.3	
1	P02945|BACR	2	1191.6573	0.8	215	224	0	56.6	23	L	NIETLLFMVL	D	1.7	3.3	
1	P02945|BACR	2	1199.593	-0.8	72	82	0	36.2	26	L	SMLLGYGLTMV	P	1.4	5.92	Oxidation (M)
1	P02945|BACR	2	1199.655	2.1	201	212	0	61.8	26	V	VWLIGSEGAGIV	P	1.4	3.3	
1	P02945|BACR	2	1215.6533	1.3	128	140	0	76.5	26	A	DGIMIGTGLVGAL	T	1.4	3.1	
1	P02945|BACR	2	1215.7115	1.0	101	111	0	45.0	20	L	FTTPLLLLDLA	L	1.6	3.1	
1	P02945|BACR	2	1216.5612	0.9	241	252	0	78.8	26	R	AIFGEAEAPEPS	A	-0.2	3.02	
1	P02945|BACR	2	1217.6696	0.8	98	107	0	38.7	24	A	DWLFTTPLLL	L	1.1	3.1	
1	P02945|BACR	2	1225.6019	0.4	96	105	0	62.8	26	R	YADWLFTTPL	L	0.4	3.1	
1	P02945|BACR	2	1225.6781	0.8	32	42	0	36.5	25	A	LMGLGTLYFLV	K	1.9	5.92	
1	P02945|BACR	2	1227.64	0.5	18	27	0	29.7	28	I	TGRPEWIWLA	L	-0.2	6.98	
1	P02945|BACR	2	1227.6711	0.9	112	123	0	101.3	25	A	LLVDADQGTILA	L	1.0	2.92	
1	P02945|BACR	2	1241.673	0.5	32	42	0	28.0	26	A	LMGLGTLYFLV	K	1.9	5.92	Oxidation (M)

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	2	1242.6456	1.1	115	127	0	60.0	27	V	DADQGTILALVGA	D	0.7	2.92	
1	P02945|BACR	2	1253.6292	0.7	48	58	0	27.5	26	V	SDPDAKKFYAI	T	-0.7	6.8	
1	P02945|BACR	2	1258.7319	-1.0	131	143	0	106.6	23	I	MIGTGLVGALTKV	Y	1.4	10.1	
1	P02945|BACR	2	1274.7268	-1.6	131	143	0	92.6	23	I	MIGTGLVGALTKV	Y	1.4	10.1	Oxidation (M)
1	P02945|BACR	2	1274.7711	0.8	183	193	0	60.7	17	S	TFKVLRNVTVV	L	0.9	11.48	
1	P02945|BACR	2	1280.6513	1.0	14	24	0	34.8	26	S	QAQITGRPEWI	W	-0.7	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	2	1285.7316	0.5	120	132	0	56.2	23	G	TILALVGADGIMI	G	2.0	3.1	
1	P02945|BACR	1	1288.6122	-1.5	80	91	0	39.0	28	L	TMVPFGGEQNPI	Y	-0.2	3.3	
1	P02945|BACR	2	1296.7152	-0.2	31	42	0	55.9	24	T	ALMGLGTLYFLV	K	1.9	5.92	
1	P02945|BACR	2	1297.7104	-2.1	34	45	0	31.0	25	M	GLGTLYFLVKGM	G	1.1	9.72	
1	P02945|BACR	2	1301.7265	1.8	120	132	0	51.7	25	G	TILALVGADGIMI	G	2.0	3.1	Oxidation (M)
1	P02945|BACR	2	1310.7234	0.7	202	214	0	61.4	26	V	WLIGSEGAGIVPL	N	1.1	3.3	
1	P02945|BACR	1	1312.7101	-1.2	31	42	0	32.1	27	T	ALMGLGTLYFLV	K	1.9	5.92	Oxidation (M)
1	P02945|BACR	2	1314.7217	0.8	124	137	0	79.1	25	A	LVGADGIMIGTGLV	G	1.6	3.1	
1	P02945|BACR	2	1316.701	0.5	128	141	0	72.3	25	A	DGIMIGTGLVGALT	K	1.3	3.1	
1	P02945|BACR	2	1326.7395	1.3	113	125	0	40.7	24	L	LVDADQGTILALV	G	1.3	2.92	
1	P02945|BACR	1	1330.7167	-0.5	124	137	0	34.1	26	A	LVGADGIMIGTGLV	G	1.6	3.1	Oxidation (M)
1	P02945|BACR	2	1330.7537	2.0	98	108	0	46.6	23	A	DWLFTTPLLLL	D	1.3	3.1	
1	P02945|BACR	2	1338.7257	-1.1	60	71	0	31.0	25	T	TLVPAIAFTMYL	S	1.7	5.92	
1	P02945|BACR	2	1341.714	2.1	117	130	0	81.6	26	A	DQGTILALVGADGI	M	0.9	2.92	
1	P02945|BACR	1	1343.7119	0.7	126	140	0	26.8	26	V	GADGIMIGTGLVGAL	T	1.3	3.1	
1	P02945|BACR	2	1345.7434	1.0	194	204	0	55.7	24	V	LWSAYPVVWLI	G	1.5	5.92	
1	P02945|BACR	2	1353.773	-0.1	32	43	0	40.1	22	A	LMGLGTLYFLVK	G	1.5	9.72	
1	P02945|BACR	2	1354.6769	0.1	48	59	0	44.3	26	V	SDPDAKKFYAIT	T	-0.7	6.8	
1	P02945|BACR	2	1360.6771	0.2	69	80	0	67.0	28	T	MYLSMLLGYGLT	M	1.2	5.86	
1	P02945|BACR	1	1360.7027	-1.2	197	209	0	37.0	27	S	AYPVVWLIGSEGA	G	0.9	3.3	
1	P02945|BACR	2	1361.8031	-0.7	182	193	0	35.2	19	A	STFKVLRNVTVV	L	0.8	11.48	
1	P02945|BACR	2	1371.7432	-0.2	124	138	0	40.4	26	A	LVGADGIMIGTGLVG	A	1.5	3.1	
1	P02945|BACR	2	1372.6623	-1.0	240	252	0	87.2	27	S	RAIFGEAEAPEPS	A	-0.5	3.96	
1	P02945|BACR	1	1377.6353	-1.2	83	94	0	48.6	26	V	PFGGEQNPIYWA	R	-0.6	3.3	
1	P02945|BACR	2	1381.703	0.5	95	105	0	43.5	26	A	RYADWLFTTPL	L	-0.1	6.7	
1	P02945|BACR	2	1397.7456	-1.1	16	26	0	43.4	26	A	QITGRPEWIWL	A	-0.3	6.98	
1	P02945|BACR	2	1397.7629	0.1	30	42	0	37.9	25	G	TALMGLGTLYFLV	K	1.7	5.92	
1	P02945|BACR	2	1401.6962	-0.9	79	91	0	45.1	28	G	LTMVPFGGEQNPI	Y	0.2	3.3	
1	P02945|BACR	2	1405.7527	1.0	215	226	0	30.5	25	L	NIETLLFMVLDV	S	1.5	3	
1	P02945|BACR	2	1409.7191	-0.7	46	58	0	32.6	26	M	GVSDPDAKKFYAI	T	-0.3	6.8	
1	P02945|BACR	2	1409.7919	0.8	201	214	0	57.6	24	V	VWLIGSEGAGIVPL	N	1.3	3.3	
1	P02945|BACR	2	1421.7476	-0.6	215	226	0	35.4	26	L	NIETLLFMVLDV	S	1.5	3	Oxidation (M)
1	P02945|BACR	2	1424.8101	0.4	31	43	0	70.5	22	T	ALMGLGTLYFLVK	G	1.5	9.72	
1	P02945|BACR	3	1427.6755	1.3	45	57	0	42.7	27	G	MGVSDPDAKKFYA	I	-0.5	6.8	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	2	1439.8235	0.7	112	125	0	106.6	22	A	LLVDADQGTILALV	G	1.4	2.92	
1	P02945|BACR	2	1440.8051	0.5	31	43	0	77.3	25	T	ALMGLGTLYFLVK	G	1.5	9.72	Oxidation (M)
1	P02945|BACR	2	1442.7803	2.9	124	139	0	26.7	26	A	LVGADGIMIGTGLVGA	L	1.5	3.1	
1	P02945|BACR	2	1444.7596	1.0	126	141	0	83.2	27	V	GADGIMIGTGLVGALT	K	1.2	3.1	
1	P02945|BACR	2	1453.8003	-2.1	34	47	0	51.1	25	M	GLGTLYFLVKGMGV	S	1.2	9.72	
1	P02945|BACR	2	1455.7245	0.2	48	60	0	31.5	28	V	SDPDAKKFYAITT	L	-0.7	6.8	
1	P02945|BACR	2	1455.7821	0.7	109	122	0	35.4	26	L	DLALLVDADQGTIL	A	0.9	2.82	
1	P02945|BACR	2	1458.7752	1.0	124	139	0	36.3	27	A	LVGADGIMIGTGLVGA	L	1.5	3.1	Oxidation (M)
1	P02945|BACR	2	1459.6943	0.4	239	252	0	106.9	27	R	SRAIFGEAEAPEPS	A	-0.5	3.96	
1	P02945|BACR	2	1467.8185	0.7	106	119	0	37.7	22	L	LLLDLALLVDADQG	T	1.2	2.82	
1	P02945|BACR	2	1468.7773	-1.3	205	219	0	42.6	26	I	GSEGAGIVPLNIETL	L	0.5	3.12	
1	P02945|BACR	2	1468.7827	0.1	16	27	0	44.6	27	A	QITGRPEWIWLA	L	-0.1	6.98	
1	P02945|BACR	2	1481.8316	-0.1	31	44	0	60.1	23	T	ALMGLGTLYFLVKG	M	1.3	9.72	
1	P02945|BACR	2	1489.7969	0.3	194	206	0	57.7	26	V	LWSAYPVVWLIGS	E	1.2	5.92	
1	P02945|BACR	2	1492.7847	0.8	215	227	0	34.4	26	L	NIETLLFMVLDVS	A	1.3	3	
1	P02945|BACR	2	1498.7932	-0.1	18	30	0	54.0	27	I	TGRPEWIWLALGT	A	0.0	6.98	
1	P02945|BACR	2	1508.7796	0.4	215	227	0	28.5	26	L	NIETLLFMVLDVS	A	1.3	3	Oxidation (M)
1	P02945|BACR	2	1510.7668	-1.7	46	59	0	41.1	26	M	GVSDPDAKKFYAIT	T	-0.3	6.8	
1	P02945|BACR	2	1513.8174	-0.2	123	139	0	43.9	27	L	ALVGADGIMIGTGLVGA	L	1.5	3.1	
1	P02945|BACR	2	1533.7365	0.5	83	95	0	58.9	28	V	PFGGEQNPIYWAR	Y	-0.9	6.88	
1	P02945|BACR	3	1540.7596	0.8	45	58	0	43.2	27	G	MGVSDPDAKKFYAI	T	-0.1	6.8	
1	P02945|BACR	2	1543.8644	0.1	128	143	0	64.5	23	A	DGIMIGTGLVGALTKV	Y	1.1	6.76	
1	P02945|BACR	2	1559.8593	0.3	128	143	0	42.2	25	A	DGIMIGTGLVGALTKV	Y	1.1	6.76	Oxidation (M)
1	P02945|BACR	2	1567.8684	0.4	28	42	0	37.1	24	A	LGTALMGLGTLYFLV	K	1.7	5.92	
1	P02945|BACR	2	1567.8821	0.4	112	127	0	38.0	23	A	LLVDADQGTILALVGA	D	1.3	2.92	
1	P02945|BACR	2	1571.8593	-1.1	124	140	0	30.3	26	A	LVGADGIMIGTGLVGAL	T	1.7	3.1	Oxidation (M)
1	P02945|BACR	2	1583.8633	-0.2	28	42	0	35.7	26	A	LGTALMGLGTLYFLV	K	1.7	5.92	Oxidation (M)
1	P02945|BACR	2	1607.7442	-1.7	81	94	0	71.8	27	T	MVPFGGEQNPIYWA	R	-0.1	3.3	
1	P02945|BACR	2	1615.9086	-0.4	187	200	0	40.8	24	V	LRNVTVVLWSAYPV	V	0.9	9.84	
1	P02945|BACR	2	1623.7392	-1.4	81	94	0	40.6	26	T	MVPFGGEQNPIYWA	R	-0.1	3.3	Oxidation (M)
1	P02945|BACR	2	1629.9018	-0.1	98	111	0	33.1	25	A	DWLFTTPLLLLDLA	L	1.2	2.92	
1	P02945|BACR	2	1636.9188	0.8	201	216	0	27.9	23	V	VWLIGSEGAGIVPLNI	E	1.2	3.3	
1	P02945|BACR	2	1638.8882	0.8	16	29	0	29.4	25	A	QITGRPEWIWLALG	T	0.1	6.98	
1	P02945|BACR	2	1641.8072	-1.3	45	59	0	32.7	27	G	MGVSDPDAKKFYAIT	T	-0.2	6.8	
1	P02945|BACR	2	1644.928	0.8	191	204	0	48.6	23	V	TVVLWSAYPVVWLI	G	1.8	5.92	
1	P02945|BACR	2	1656.9121	0.5	124	141	0	73.1	26	A	LVGADGIMIGTGLVGALT	K	1.5	3.1	
1	P02945|BACR	2	1671.923	0.4	126	143	0	72.2	25	V	GADGIMIGTGLVGALTKV	Y	1.1	6.76	
1	P02945|BACR	2	1675.861	0.1	194	208	0	52.8	28	V	LWSAYPVVWLIGSEG	A	0.8	3.3	
1	P02945|BACR	2	1678.8025	-0.2	76	91	0	62.4	28	L	GYGLTMVPFGGEQNPI	Y	0.0	3.3	
1	P02945|BACR	2	1681.9502	-0.5	106	121	0	23.9	22	L	LLLDLALLVDADQGTI	L	1.3	2.82	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	2	1687.9179	-0.4	126	143	0	59.7	25	V	GADGIMIGTGLVGALTKV	Y	1.1	6.76	Oxidation (M)
1	P02945|BACR	2	1698.8287	0.0	44	59	0	45.5	28	K	GMGVSDPDAKKFYAIT	T	-0.2	6.8	
1	P02945|BACR	2	1720.9552	-1.5	95	108	0	39.3	24	A	RYADWLFTTPLLLL	D	0.7	6.7	
1	P02945|BACR	2	1722.9093	-0.4	16	30	0	28.0	26	A	QITGRPEWIWLALGT	A	0.1	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	2	1727.9492	0.1	123	141	0	27.3	25	L	ALVGADGIMIGTGLVGALT	K	1.5	3.1	
1	P02945|BACR	2	1738.9717	0.0	109	125	0	48.9	23	L	DLALLVDADQGTILALV	G	1.3	2.82	
1	P02945|BACR	2	1739.9359	-0.7	16	30	0	55.4	26	A	QITGRPEWIWLALGT	A	0.1	6.98	
1	P02945|BACR	2	1742.8549	0.5	45	60	0	46.9	28	G	MGVSDPDAKKFYAITT	L	-0.2	6.8	
1	P02945|BACR	2	1746.8981	0.5	194	209	0	100.4	27	V	LWSAYPVVWLIGSEGA	G	0.8	3.3	
1	P02945|BACR	3	1768.962	0.7	31	47	0	45.0	25	T	ALMGLGTLYFLVKGMGV	S	1.4	9.72	
1	P02945|BACR	2	1771.9026	0.5	115	132	0	68.6	28	V	DADQGTILALVGADGIMI	G	0.9	2.82	
1	P02945|BACR	3	1784.9569	0.3	31	47	0	40.7	26	T	ALMGLGTLYFLVKGMGV	S	1.4	9.72	Oxidation (M)
1	P02945|BACR	2	1785.007	0.4	124	142	0	54.0	23	A	LVGADGIMIGTGLVGALTK	V	1.2	6.76	
1	P02945|BACR	2	1791.8866	0.9	75	91	0	41.1	27	L	LGYGLTMVPFGGEQNPI	Y	0.2	3.3	
1	P02945|BACR	2	1801.8828	-0.7	92	105	0	35.2	28	I	YWARYADWLFTTPL	L	-0.1	6.64	
1	P02945|BACR	2	1826.9237	-1.5	43	59	0	51.7	28	V	KGMGVSDPDAKKFYAIT	T	-0.4	9.56	
1	P02945|BACR	2	1835.9669	1.8	48	64	0	32.0	27	V	SDPDAKKFYAITTLVPA	I	0.0	6.8	
1	P02945|BACR	2	1840.0135	0.1	197	214	0	47.9	26	S	AYPVVWLIGSEGAGIVPL	N	1.2	3.3	
1	P02945|BACR	2	1845.9665	-0.2	193	209	0	38.6	27	V	VLWSAYPVVWLIGSEGA	G	1.0	3.3	
1	P02945|BACR	2	1853.0146	0.5	112	130	0	123.6	24	A	LLVDADQGTILALVGADGI	M	1.2	2.82	
1	P02945|BACR	2	1856.0441	-0.3	123	142	0	77.4	23	L	ALVGADGIMIGTGLVGALTK	V	1.3	6.76	
1	P02945|BACR	2	1858.0393	0.1	189	204	0	50.3	24	R	NVTVVLWSAYPVVWLI	G	1.6	5.92	
1	P02945|BACR	2	1864.0022	0.8	96	111	0	62.1	25	R	YADWLFTTPLLLLDLA	L	1.1	2.92	
1	P02945|BACR	2	1866.0714	0.0	106	123	0	75.8	22	L	LLLDLALLVDADQGTILA	L	1.4	2.82	
1	P02945|BACR	2	1867.0091	1.0	201	218	0	47.0	26	V	VWLIGSEGAGIVPLNIET	L	0.9	3.12	
1	P02945|BACR	2	1884.0754	-0.5	124	143	0	130.4	22	A	LVGADGIMIGTGLVGALTKV	Y	1.4	6.76	
1	P02945|BACR	2	1885.0635	1.3	210	226	0	83.1	22	A	GIVPLNIETLLFMVLDV	S	1.7	3	
1	P02945|BACR	2	1900.0704	-1.4	124	143	0	79.2	22	A	LVGADGIMIGTGLVGALTKV	Y	1.4	6.76	Oxidation (M)
1	P02945|BACR	2	1911.0003	-0.9	11	27	0	34.7	27	E	GVSQAQITGRPEWIWLA	L	0.0	6.98	
1	P02945|BACR	2	1955.1125	-1.1	123	143	0	105.1	21	L	ALVGADGIMIGTGLVGALTKV	Y	1.4	6.76	
1	P02945|BACR	2	1955.1383	-1.5	98	114	0	29.8	19	A	DWLFTTPLLLLDLALLV	D	1.7	2.92	
1	P02945|BACR	2	1971.1075	-0.1	123	143	0	83.1	23	L	ALVGADGIMIGTGLVGALTKV	Y	1.4	6.76	Oxidation (M)
1	P02945|BACR	2	1972.0955	0.2	210	227	0	52.6	23	A	GIVPLNIETLLFMVLDVS	A	1.5	3	
1	P02945|BACR	2	1980.0932	0.1	201	219	0	47.0	23	V	VWLIGSEGAGIVPLNIETL	L	1.0	3.12	
1	P02945|BACR	2	2020.1033	-0.5	95	111	0	85.3	25	A	RYADWLFTTPLLLLDLA	L	0.7	3.88	
1	P02945|BACR	2	2036.0111	-0.4	73	91	0	66.7	28	S	MLLGYGLTMVPFGGEQNPI	Y	0.5	3.3	
1	P02945|BACR	2	2046.0826	0.6	191	209	0	43.8	27	V	TVVLWSAYPVVWLIGSEGA	G	1.1	3.3	
1	P02945|BACR	2	2052.006	-1.6	73	91	0	42.7	28	S	MLLGYGLTMVPFGGEQNPI	Y	0.5	3.3	Oxidation (M)
1	P02945|BACR	2	2072.1228	0.0	205	224	0	30.7	26	I	GSEGAGIVPLNIETLLFMVL	D	1.2	3.12	
1	P02945|BACR	3	2097.1391	1.0	112	132	0	59.8	25	A	LLVDADQGTILALVGADGIMI	G	1.4	2.82	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	2	2098.9823	-0.3	76	94	0	49.7	27	L	GYGLTMVPFGGEQNPIYWA	R	0.0	3.3	
1	P02945|BACR	2	2113.1341	-1.0	112	132	0	66.2	26	A	LLVDADQGTILALVGADGIMI	G	1.4	2.82	Oxidation (M)
1	P02945|BACR	2	2114.9772	-0.6	76	94	0	54.0	26	L	GYGLTMVPFGGEQNPIYWA	R	0.0	3.3	Oxidation (M)
1	P02945|BACR	2	2123.0431	-0.9	72	91	0	63.9	29	L	SMLLGYGLTMVPFGGEQNPI	Y	0.4	3.3	
1	P02945|BACR	2	2123.0973	0.8	45	64	0	35.4	28	G	MGVSDPDAKKFYAITTLVPA	I	0.2	6.8	
1	P02945|BACR	2	2127.2245	-0.5	187	204	0	70.4	21	V	LRNVTVVLWSAYPVVWLI	G	1.4	9.84	
1	P02945|BACR	2	2139.0381	-1.2	72	91	0	49.3	28	L	SMLLGYGLTMVPFGGEQNPI	Y	0.4	3.3	Oxidation (M)
1	P02945|BACR	2	2141.135	0.3	92	108	0	42.7	27	I	YWARYADWLFTTPLLLL	D	0.6	6.64	
1	P02945|BACR	2	2189.2388	-0.3	96	114	0	65.1	22	R	YADWLFTTPLLLLDLALLV	D	1.5	2.92	
1	P02945|BACR	3	2226.2089	0.3	194	214	0	39.0	25	V	LWSAYPVVWLIGSEGAGIVPL	N	1.1	3.3	
1	P02945|BACR	2	2274.2044	0.1	60	80	0	54.1	27	T	TLVPAIAFTMYLSMLLGYGLT	M	1.4	5.86	
1	P02945|BACR	3	2329.243	-1.0	231	252	0	28.8	27	V	GFGLILLRSRAIFGEAEAPEPS	A	0.3	4.56	
1	P02945|BACR	2	2440.2831	-0.3	92	111	0	52.3	27	I	YWARYADWLFTTPLLLLDLA	L	0.6	3.88	
1	P02945|BACR	2	2528.3791	-0.7	187	209	0	59.3	25	V	LRNVTVVLWSAYPVVWLIGSEGA	G	0.9	6.88	
1	P02945|BACR	3	2839.5623	0.3	98	123	0	26.8	24	A	DWLFTTPLLLLDLALLVDADQGTILA	L	1.1	2.74	
1	P02945|BACR	3	3051.7148	-1.9	98	125	0	25.8	23	A	DWLFTTPLLLLDLALLVDADQGTILALV	G	1.3	2.74	
1	P02945|BACR	3	3158.7267	-0.2	95	122	0	37.6	24	A	RYADWLFTTPLLLLDLALLVDADQGTIL	A	0.8	3.42	
1	P02945|BACR	2	3229.7638	-2.1	95	123	0	39.0	25	A	RYADWLFTTPLLLLDLALLVDADQGTILA	L	0.8	3.42	
2	P00772|ELA1	1	529.286	-0.2	260	264	0	33.1	27	I	NNVIA	S	0.7	6.02	
2	P00772|ELA1	1	532.2646	0.8	157	161	0	32.6	26	T	GWGLT	R	0.3	6.02	
2	P00772|ELA1	1	540.3384	0.4	138	142	0	24.8	24	L	GVLPR	A	0.3	11.04	
2	P00772|ELA1	1	543.3268	-0.7	119	123	0	32.6	30	Y	DIALL	R	2.1	3.1	
2	P00772|ELA1	1	633.3122	0.2	156	161	0	25.5	25	I	TGWGLT	R	0.1	6.02	
2	P00772|ELA1	1	642.3701	-2.6	259	264	0	33.2	26	W	INNVIA	S	1.3	6.02	
2	P00772|ELA1	1	649.2894	0.5	64	68	0	31.2	26	Q	NWVMT	A	0.2	6.02	
2	P00772|ELA1	1	653.4224	0.9	137	142	0	34.5	21	Q	LGVLPR	A	0.9	11.04	
2	P00772|ELA1	1	665.2843	-0.2	64	68	0	23.3	22	Q	NWVMT	A	0.2	6.02	Oxidation (M)
2	P00772|ELA1	2	668.397	1.0	138	144	0	34.8	22	L	GVLPRAG	T	0.4	11.04	
2	P00772|ELA1	2	672.3919	0.1	124	129	0	33.3	29	L	RLAQSV	T	0.2	11.04	
2	P00772|ELA1	1	680.3533	-0.7	255	259	0	22.8	18	A	YISWI	N	1.2	5.92	
2	P00772|ELA1	1	706.3901	-1.0	118	123	0	25.9	25	G	YDIALL	R	1.5	3.1	
2	P00772|ELA1	1	716.3493	0.3	37	42	0	28.5	26	N	SWPSQI	S	-0.5	6.02	
2	P00772|ELA1	1	720.3265	-0.3	64	69	0	32.3	26	Q	NWVMTA	A	0.5	6.02	
2	P00772|ELA1	1	722.3599	-0.1	132	137	0	26.5	26	L	NSYVQL	G	-0.2	5.92	
2	P00772|ELA1	1	730.3609	0.4	260	266	0	43.2	30	I	NNVIASN	-	-0.1	6.02	
2	P00772|ELA1	1	731.3602	0.0	257	262	0	37.8	26	I	SWINNV	I	0.0	6.02	
2	P00772|ELA1	1	736.3214	-0.1	64	69	0	28.3	23	Q	NWVMTA	A	0.5	6.02	Oxidation (M)
2	P00772|ELA1	2	751.3905	0.8	254	259	0	34.7	23	S	AYISWI	N	1.3	5.92	
2	P00772|ELA1	1	763.4116	0.1	117	123	0	41.6	26	A	GYDIALL	R	1.2	3.1	
2	P00772|ELA1	1	777.348	0.1	63	68	0	31.1	25	R	QNWVMT	A	-0.4	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	P00772|ELA1	1	781.481	0.5	137	144	0	29.5	21	Q	LGVLPRAG	T	0.8	11.04	
2	P00772|ELA1	1	781.481	-0.4	136	142	0	25.3	21	V	QLGVLPR	A	0.3	11.04	
2	P00772|ELA1	2	789.4133	1.6	156	162	0	40.0	26	I	TGWGLTR	T	-0.5	11.04	
2	P00772|ELA1	1	793.3429	-0.3	63	68	0	40.4	23	R	QNWVMT	A	-0.4	6.02	Oxidation (M)
2	P00772|ELA1	1	797.4759	-1.3	141	148	0	23.2	23	L	PRAGTILA	N	0.6	11.04	
2	P00772|ELA1	2	808.4443	-0.1	232	238	0	30.2	24	V	TSFVSRL	G	0.6	11.04	
2	P00772|ELA1	1	819.4127	-0.1	172	178	0	29.4	28	L	QQAYLPT	V	-0.7	5.92	
2	P00772|ELA1	1	828.4494	0.6	258	264	0	36.8	22	S	WINNVIA	S	1.0	6.02	
2	P00772|ELA1	1	830.3923	0.5	36	42	0	34.3	25	R	NSWPSQI	S	-0.9	6.02	
2	P00772|ELA1	1	834.4487	0.8	116	123	0	52.2	26	A	AGYDIALL	R	1.3	3.1	
2	P00772|ELA1	2	838.4225	1.0	253	259	0	41.0	24	V	SAYISWI	N	1.0	5.92	
2	P00772|ELA1	2	843.445	2.0	164	171	0	51.9	30	T	NGQLAQTL	Q	-0.3	6.02	
2	P00772|ELA1	2	844.4443	1.4	257	263	0	37.0	24	I	SWINNVI	A	0.6	6.02	
2	P00772|ELA1	1	848.3851	0.1	63	69	0	26.8	26	R	QNWVMTA	A	-0.1	6.02	
2	P00772|ELA1	2	862.4913	0.8	76	82	0	26.8	23	R	ELTFRVV	V	0.9	6.98	
2	P00772|ELA1	2	880.5494	0.2	135	142	0	29.1	17	Y	VQLGVLPR	A	0.8	11.04	
2	P00772|ELA1	2	882.5287	0.7	138	146	0	35.3	23	L	GVLPRAGTI	L	0.7	11.04	
2	P00772|ELA1	1	885.3869	0.2	187	194	0	28.1	24	S	SSYWGSTV	K	-0.2	5.92	
2	P00772|ELA1	2	890.461	-0.1	156	163	0	44.4	26	I	TGWGLTRT	N	-0.6	11.04	
2	P00772|ELA1	1	892.4654	0.1	131	138	0	29.5	27	T	LNSYVQLG	V	0.3	5.92	
2	P00772|ELA1	1	892.5131	-1.3	136	144	0	28.5	21	V	QLGVLPRAG	T	0.4	11.04	Gln->pyro-Glu (N-term Q)
2	P00772|ELA1	2	898.56	1.0	122	129	0	57.5	21	A	LLRLAQSV	T	1.1	11.04	
2	P00772|ELA1	1	909.5396	0.3	136	144	0	46.4	19	V	QLGVLPRAG	T	0.4	11.04	
2	P00772|ELA1	2	915.4814	1.4	257	264	0	52.6	24	I	SWINNVIA	S	0.8	6.02	
2	P00772|ELA1	2	936.4916	0.2	130	137	0	50.1	25	V	TLNSYVQL	G	0.3	5.92	
2	P00772|ELA1	2	940.4542	0.7	175	182	0	36.2	22	A	YLPTVDYA	I	0.2	3.1	
2	P00772|ELA1	2	943.4512	-1.0	223	231	0	52.6	26	V	NGQYAVHGV	T	-0.2	7.76	
2	P00772|ELA1	2	949.444	-0.5	62	68	0	29.5	28	I	RQNWVMT	A	-1.0	11.04	Oxidation (M)
2	P00772|ELA1	2	972.4189	-0.6	186	194	0	31.2	24	S	SSSYWGSTV	K	-0.3	5.92	
2	P00772|ELA1	2	993.5131	3.2	130	138	0	54.2	25	V	TLNSYVQLG	V	0.2	5.92	
2	P00772|ELA1	2	995.6128	-0.1	138	147	0	39.1	19	L	GVLPRAGTIL	A	1.1	11.04	
2	P00772|ELA1	2	1000.5665	-0.3	124	132	0	39.2	26	L	RLAQSVTLN	S	0.1	11.04	
2	P00772|ELA1	2	1002.5134	0.9	257	265	0	50.7	28	I	SWINNVIAS	N	0.6	6.02	
2	P00772|ELA1	1	1008.44	-0.8	112	121	0	30.1	27	T	DDVAAGYDIA	L	0.2	2.82	
2	P00772|ELA1	1	1008.608	-2.0	135	144	0	41.8	15	Y	VQLGVLPRAG	T	0.7	11.04	
2	P00772|ELA1	2	1009.6284	0.9	139	148	0	41.5	18	G	VLPRAGTILA	N	1.3	11.04	
2	P00772|ELA1	2	1013.4818	-0.1	187	195	0	49.0	26	S	SSYWGSTVK	N	-0.6	9.72	
2	P00772|ELA1	2	1020.4811	-1.1	62	69	0	35.7	27	I	RQNWVMTA	A	-0.7	11.04	Oxidation (M)
2	P00772|ELA1	2	1029.5203	1.0	27	36	0	84.2	28	R	VVGGTEAQRN	S	-0.6	6.98	
2	P00772|ELA1	1	1029.5243	1.7	258	266	0	38.6	25	S	WINNVIASN	-	0.3	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	P00772|ELA1	2	1043.6128	1.5	134	142	0	69.5	19	S	YVQLGVLPR	A	0.5	9.84	
2	P00772|ELA1	2	1056.5564	1.2	165	174	0	36.7	27	N	GQLAQTLQQA	Y	-0.4	6.02	
2	P00772|ELA1	2	1066.6499	0.5	138	148	0	53.2	19	L	GVLPRAGTILA	N	1.1	11.04	
2	P00772|ELA1	2	1078.5447	0.5	254	262	0	39.8	27	S	AYISWINNV	I	0.6	5.92	
2	P00772|ELA1	2	1093.592	0.5	251	259	0	45.1	25	T	RVSAYISWI	N	0.7	9.84	
2	P00772|ELA1	2	1100.5938	-0.8	162	171	0	27.7	27	T	RTNGQLAQTL	Q	-0.7	11.04	
2	P00772|ELA1	2	1103.6339	1.8	117	126	0	36.5	23	A	GYDIALLRLA	Q	1.0	6.7	
2	P00772|ELA1	1	1109.4877	-0.2	111	121	0	27.1	26	N	TDDVAAGYDIA	L	0.1	2.82	
2	P00772|ELA1	2	1116.5564	1.0	257	266	0	82.2	28	I	SWINNVIASN	-	0.2	6.02	
2	P00772|ELA1	2	1123.6713	0.4	136	146	0	34.9	20	V	QLGVLPRAGTI	L	0.6	11.04	
2	P00772|ELA1	2	1127.5247	-1.2	187	196	0	33.8	26	S	SSYWGSTVKN	S	-0.9	9.72	
2	P00772|ELA1	2	1130.6448	0.6	133	142	0	68.1	23	N	SYVQLGVLPR	A	0.4	9.84	
2	P00772|ELA1	2	1142.6196	1.1	57	66	0	41.7	27	C	GGTLIRQNWV	M	-0.1	11.04	
2	P00772|ELA1	2	1145.4778	2.2	106	114	0	53.2	22	V	HPYWNTDDV	A	-1.6	3.88	
2	P00772|ELA1	2	1170.5993	1.4	164	174	0	81.7	27	T	NGQLAQTLQQA	Y	-0.7	6.02	
2	P00772|ELA1	2	1171.6713	1.2	134	144	0	64.3	24	S	YVQLGVLPRAG	T	0.6	9.84	
2	P00772|ELA1	2	1191.6288	1.1	254	263	0	80.9	27	S	AYISWINNVI	A	1.0	5.92	
2	P00772|ELA1	2	1191.6288	0.7	255	264	0	61.0	26	A	YISWINNVIA	S	1.0	5.92	
2	P00772|ELA1	2	1201.6819	-0.6	133	143	0	48.3	23	N	SYVQLGVLPRA	G	0.5	9.84	
2	P00772|ELA1	2	1206.6033	0.5	225	235	0	42.8	27	G	QYAVHGVTSFV	S	0.7	7.76	
2	P00772|ELA1	2	1214.5568	0.9	187	197	0	34.0	25	S	SSYWGSTVKNS	M	-0.9	9.72	
2	P00772|ELA1	2	1222.7398	0.9	135	146	0	25.3	18	Y	VQLGVLPRAGTI	L	0.9	11.04	
2	P00772|ELA1	2	1226.7347	1.0	122	132	0	46.2	20	A	LLRLAQSVTLN	S	0.7	11.04	
2	P00772|ELA1	2	1230.6543	-0.2	60	69	0	41.4	25	T	LIRQNWVMTA	A	0.3	11.04	
2	P00772|ELA1	2	1240.5836	1.0	43	53	0	51.9	26	I	SLQYRSGSSWA	H	-0.7	9.84	
2	P00772|ELA1	2	1244.5462	1.0	105	114	0	52.7	25	V	VHPYWNTDDV	A	-1.0	3.88	
2	P00772|ELA1	2	1244.6877	0.6	132	142	0	108.4	25	L	NSYVQLGVLPR	A	0.0	9.84	
2	P00772|ELA1	2	1245.7081	0.5	115	126	0	52.1	22	V	AAGYDIALLRLA	Q	1.1	6.7	
2	P00772|ELA1	2	1250.6507	0.3	127	137	0	67.0	26	A	QSVTLNSYVQL	G	0.2	5.92	
2	P00772|ELA1	2	1258.7034	1.8	133	144	0	73.6	23	N	SYVQLGVLPRAG	T	0.4	9.84	
2	P00772|ELA1	2	1260.6649	-0.2	59	68	0	29.9	24	G	TLIRQNWVMT	A	0.1	11.04	
2	P00772|ELA1	2	1262.6659	1.0	254	264	0	92.5	27	S	AYISWINNVIA	S	1.0	5.92	
2	P00772|ELA1	2	1267.6085	0.6	172	182	0	56.2	26	L	QQAYLPTVDYA	I	-0.3	3.1	
2	P00772|ELA1	2	1271.647	0.2	163	174	0	63.2	27	R	TNGQLAQTLQQA	Y	-0.7	6.02	
2	P00772|ELA1	2	1278.6608	0.4	253	263	0	43.6	26	V	SAYISWINNVI	A	0.8	5.92	
2	P00772|ELA1	2	1307.6721	-0.6	127	138	0	41.4	26	A	QSVTLNSYVQLG	V	0.1	5.92	
2	P00772|ELA1	2	1307.7925	-1.5	136	148	0	64.9	18	V	QLGVLPRAGTILA	N	1.0	11.04	
2	P00772|ELA1	2	1314.6316	0.3	32	42	0	45.0	26	T	EAQRNSWPSQI	S	-1.5	6.98	
2	P00772|ELA1	2	1315.5833	0.2	105	115	0	29.1	25	V	VHPYWNTDDVA	A	-0.7	3.88	
2	P00772|ELA1	2	1331.702	-0.2	59	69	0	40.7	25	G	TLIRQNWVMTA	A	0.2	11.04	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	P00772|ELA1	2	1343.6146	1.1	104	114	0	66.0	26	I	VVHPYWNTDDV	A	-0.5	3.88	
2	P00772|ELA1	2	1347.6969	0.1	59	69	0	48.8	27	G	TLIRQNWVMTA	A	0.2	11.04	Oxidation (M)
2	P00772|ELA1	2	1349.6979	-0.1	254	265	0	62.3	26	S	AYISWINNVIAS	N	0.9	5.92	
2	P00772|ELA1	2	1349.6979	-0.7	253	264	0	68.4	26	V	SAYISWINNVIA	S	0.9	5.92	
2	P00772|ELA1	2	1349.7303	-1.0	124	135	0	52.7	25	L	RLAQSVTLNSYV	Q	0.2	9.84	
2	P00772|ELA1	2	1357.7718	0.1	131	142	0	83.7	22	T	LNSYVQLGVLPR	A	0.4	9.84	
2	P00772|ELA1	2	1360.7714	0.4	118	129	0	52.6	22	G	YDIALLRLAQSV	T	0.8	6.7	
2	P00772|ELA1	2	1372.7463	0.8	132	144	0	90.2	25	L	NSYVQLGVLPRAG	T	0.1	9.84	
2	P00772|ELA1	2	1373.7052	0.7	156	168	0	68.0	27	I	TGWGLTRTNGQLA	Q	-0.5	11.04	
2	P00772|ELA1	2	1377.6677	1.5	223	235	0	58.1	28	V	NGQYAVHGVTSFV	S	0.3	7.76	
2	P00772|ELA1	2	1385.8031	0.9	134	146	0	58.7	21	S	YVQLGVLPRAGTI	L	0.8	9.84	
2	P00772|ELA1	2	1386.6204	-0.5	105	116	0	50.9	24	V	VHPYWNTDDVAA	G	-0.5	3.88	
2	P00772|ELA1	2	1392.7037	0.6	255	266	0	47.9	28	A	YISWINNVIASN	-	0.4	5.92	
2	P00772|ELA1	2	1406.8609	0.3	135	148	0	40.2	16	Y	VQLGVLPRAGTILA	N	1.2	11.04	
2	P00772|ELA1	2	1414.6517	-2.1	104	115	0	62.1	25	I	VVHPYWNTDDVA	A	-0.3	3.88	
2	P00772|ELA1	2	1417.7929	0.6	117	129	0	52.0	23	A	GYDIALLRLAQSV	T	0.7	6.7	
2	P00772|ELA1	2	1434.7653	1.0	238	250	0	26.5	25	R	LGCNVTRKPTVFT	R	0.1	10.1	
2	P00772|ELA1	2	1436.7299	1.2	253	265	0	31.2	27	V	SAYISWINNVIAS	N	0.7	5.92	
2	P00772|ELA1	2	1444.6657	0.3	187	199	0	48.3	26	S	SSYWGSTVKNSMV	C	-0.3	9.72	
2	P00772|ELA1	2	1456.6987	0.3	103	114	0	63.9	27	K	IVVHPYWNTDDV	A	-0.1	3.88	
2	P00772|ELA1	2	1458.8195	0.4	130	142	0	84.8	23	V	TLNSYVQLGVLPR	A	0.3	9.84	
2	P00772|ELA1	2	1463.7408	-0.3	254	266	0	81.0	27	S	AYISWINNVIASN	-	0.5	5.92	
2	P00772|ELA1	2	1472.8351	2.6	133	146	0	95.8	22	N	SYVQLGVLPRAGTI	L	0.7	9.84	
2	P00772|ELA1	2	1481.7263	-0.1	41	53	0	63.6	26	S	QISLQYRSGSSWA	H	-0.6	9.84	
2	P00772|ELA1	2	1485.6889	-1.1	104	116	0	55.0	25	I	VVHPYWNTDDVAA	G	-0.2	3.88	
2	P00772|ELA1	2	1485.8304	-0.3	131	144	0	76.9	23	T	LNSYVQLGVLPRAG	T	0.4	9.84	
2	P00772|ELA1	2	1486.7165	-0.9	27	40	0	29.5	28	R	VVGGTEAQRNSWPS	Q	-0.7	6.98	
2	P00772|ELA1	2	1488.83	-0.2	116	129	0	27.7	23	A	AGYDIALLRLAQSV	T	0.8	6.7	
2	P00772|ELA1	2	1527.7358	0.3	103	115	0	27.9	27	K	IVVHPYWNTDDVA	A	0.1	3.88	
2	P00772|ELA1	2	1529.7223	-0.4	29	42	0	51.8	27	V	GGTEAQRNSWPSQI	S	-1.3	6.98	
2	P00772|ELA1	2	1529.8566	2.5	130	143	0	70.3	24	V	TLNSYVQLGVLPRA	G	0.4	9.84	
2	P00772|ELA1	1	1542.7103	-1.9	104	117	0	34.5	26	I	VVHPYWNTDDVAAG	Y	-0.2	3.88	
2	P00772|ELA1	2	1550.7729	0.5	253	266	0	87.7	27	V	SAYISWINNVIASN	-	0.4	5.92	
2	P00772|ELA1	2	1553.6706	-1.0	83	96	0	65.0	24	V	VGEHNLNQNDGTEQ	Y	-1.8	3.82	
2	P00772|ELA1	2	1559.8671	1.0	115	129	0	49.2	23	V	AAGYDIALLRLAQSV	T	0.9	6.7	
2	P00772|ELA1	2	1569.9243	-0.1	134	148	0	86.4	20	S	YVQLGVLPRAGTILA	N	1.0	9.84	
2	P00772|ELA1	2	1586.878	0.6	132	146	0	31.6	24	L	NSYVQLGVLPRAGTI	L	0.4	9.84	
2	P00772|ELA1	2	1586.878	0.4	130	144	0	109.8	24	V	TLNSYVQLGVLPRAG	T	0.3	9.84	
2	P00772|ELA1	2	1590.8729	0.4	124	137	0	85.0	25	L	RLAQSVTLNSYVQL	G	0.2	9.84	
2	P00772|ELA1	2	1598.7729	0.3	103	116	0	36.2	27	K	IVVHPYWNTDDVAA	G	0.2	3.88	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	P00772|ELA1	2	1602.8114	-0.2	156	170	0	74.8	28	I	TGWGLTRTNGQLAQT	L	-0.7	11.04	
2	P00772|ELA1	2	1604.8674	-0.2	251	264	0	57.3	25	T	RVSAYISWINNVIA	S	0.7	9.84	
2	P00772|ELA1	2	1609.7988	0.4	169	182	0	45.5	28	A	QTLQQAYLPTVDYA	I	-0.3	3.1	
2	P00772|ELA1	2	1628.7907	-1.9	28	42	0	56.5	28	V	VGGTEAQRNSWPSQI	S	-0.9	6.98	
2	P00772|ELA1	2	1644.8471	0.2	164	178	0	34.8	28	T	NGQLAQTLQQAYLPT	V	-0.5	5.92	
2	P00772|ELA1	2	1647.8944	-0.5	124	138	0	72.4	25	L	RLAQSVTLNSYVQLG	V	0.2	9.84	
2	P00772|ELA1	2	1649.8413	0.4	252	266	0	74.1	27	R	VSAYISWINNVIASN	-	0.7	5.92	
2	P00772|ELA1	2	1656.9563	1.7	133	148	0	89.5	21	N	SYVQLGVLPRAGTILA	N	0.9	9.84	
2	P00772|ELA1	2	1659.7125	-1.1	85	98	0	45.8	22	G	EHNLNQNDGTEQYV	G	-1.8	3.82	
2	P00772|ELA1	2	1685.9465	-1.4	129	144	0	39.2	23	S	VTLNSYVQLGVLPRAG	T	0.6	9.84	
2	P00772|ELA1	2	1691.8115	-1.1	89	103	0	27.3	27	L	NQNDGTEQYVGVQKI	V	-1.2	4.08	
2	P00772|ELA1	2	1695.8257	-2.1	101	114	0	58.0	27	V	QKIVVHPYWNTDDV	A	-0.6	5.1	Gln->pyro-Glu (N-term Q)
2	P00772|ELA1	2	1712.8522	0.2	101	114	0	48.2	28	V	QKIVVHPYWNTDDV	A	-0.6	5.1	
2	P00772|ELA1	2	1715.8955	1.5	156	171	0	58.2	27	I	TGWGLTRTNGQLAQTL	Q	-0.4	11.04	
2	P00772|ELA1	2	1727.8591	0.1	27	42	0	99.7	28	R	VVGGTEAQRNSWPSQI	S	-0.6	6.98	
2	P00772|ELA1	2	1770.9992	-0.3	132	148	0	110.7	23	L	NSYVQLGVLPRAGTILA	N	0.7	9.84	
2	P00772|ELA1	2	1772.9785	-0.2	127	142	0	110.8	24	A	QSVTLNSYVQLGVLPR	A	0.2	9.84	
2	P00772|ELA1	2	1801.0098	0.3	130	146	0	95.5	22	V	TLNSYVQLGVLPRAGTI	L	0.5	9.84	
2	P00772|ELA1	2	1805.9424	-1.4	251	266	0	92.1	27	T	RVSAYISWINNVIASN	-	0.4	9.84	
2	P00772|ELA1	2	1806.7849	-0.3	106	121	0	26.0	24	V	HPYWNTDDVAAGYDIA	L	-0.6	3.6	
2	P00772|ELA1	2	1814.8911	-0.3	27	43	0	48.4	28	R	VVGGTEAQRNSWPSQIS	L	-0.6	6.98	
2	P00772|ELA1	2	1815.8024	0.4	85	100	0	77.1	25	G	EHNLNQNDGTEQYVGV	Q	-1.4	3.82	
2	P00772|ELA1	2	1815.8024	0.2	83	98	0	63.2	25	V	VGEHNLNQNDGTEQYV	G	-1.4	3.82	
2	P00772|ELA1	2	1837.8999	-2.0	101	116	0	43.2	27	V	QKIVVHPYWNTDDVAA	G	-0.3	5.1	Gln->pyro-Glu (N-term Q)
2	P00772|ELA1	2	1844.0156	0.0	126	142	0	93.2	24	L	AQSVTLNSYVQLGVLPR	A	0.3	9.84	
2	P00772|ELA1	2	1854.9265	-2.4	101	116	0	40.5	28	V	QKIVVHPYWNTDDVAA	G	-0.3	5.1	
2	P00772|ELA1	2	1868.9421	-0.1	99	114	0	42.7	28	V	GVQKIVVHPYWNTDDV	A	-0.3	5.1	
2	P00772|ELA1	2	1872.8238	1.6	84	100	0	71.1	25	V	GEHNLNQNDGTEQYVGV	Q	-1.3	3.82	
2	P00772|ELA1	2	1884.0833	-0.4	131	148	0	62.4	21	T	LNSYVQLGVLPRAGTILA	N	0.8	9.84	
2	P00772|ELA1	2	1901.0371	-2.1	127	144	0	111.1	25	A	QSVTLNSYVQLGVLPRAG	T	0.3	9.84	
2	P00772|ELA1	2	1905.8533	-1.0	105	121	0	54.9	26	V	VHPYWNTDDVAAGYDIA	L	-0.3	3.6	
2	P00772|ELA1	2	1911.9479	-2.2	101	117	0	32.0	27	V	QKIVVHPYWNTDDVAAG	Y	-0.3	5.1	
2	P00772|ELA1	2	1914.0938	-1.4	130	147	0	57.8	21	V	TLNSYVQLGVLPRAGTIL	A	0.7	9.84	
2	P00772|ELA1	2	1914.8708	-0.6	82	98	0	77.6	26	V	VVGEHNLNQNDGTEQYV	G	-1.0	3.82	
2	P00772|ELA1	2	1914.8708	-0.9	81	97	0	27.6	26	R	VVVGEHNLNQNDGTEQY	V	-1.0	3.82	
2	P00772|ELA1	2	1918.9385	-1.5	87	103	0	76.7	29	H	NLNQNDGTEQYVGVQKI	V	-1.1	4.08	
2	P00772|ELA1	2	1933.8847	-1.9	104	120	0	51.7	27	I	VVHPYWNTDDVAAGYDI	A	-0.2	3.6	
2	P00772|ELA1	1	1971.8923	-2.8	83	100	0	83.1	26	V	VGEHNLNQNDGTEQYVGV	Q	-1.0	3.82	
2	P00772|ELA1	2	1971.8923	0.2	82	99	0	34.4	26	V	VVGEHNLNQNDGTEQYVG	V	-1.0	3.82	
2	P00772|ELA1	2	1972.0742	-0.6	126	144	0	69.7	25	L	AQSVTLNSYVQLGVLPRAG	T	0.3	9.84	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	P00772|ELA1	2	1985.131	2.2	130	148	0	78.2	22	V	TLNSYVQLGVLPRAGTILA	N	0.8	9.84	
2	P00772|ELA1	2	2004.9218	2.5	104	121	0	71.7	28	I	VVHPYWNTDDVAAGYDIA	L	-0.1	3.6	
2	P00772|ELA1	2	2013.9392	-0.4	81	98	0	54.9	27	R	VVVGEHNLNQNDGTEQYV	G	-0.7	3.82	
2	P00772|ELA1	2	2043.0498	-1.4	156	174	0	82.5	29	I	TGWGLTRTNGQLAQTLQQA	Y	-0.6	11.04	
2	P00772|ELA1	3	2054.977	0.6	79	96	0	41.7	28	T	FRVVVGEHNLNQNDGTEQ	Y	-1.0	4.42	
2	P00772|ELA1	2	2070.9607	-0.5	82	100	0	63.2	27	V	VVGEHNLNQNDGTEQYVGV	Q	-0.7	3.82	
2	P00772|ELA1	2	2093.0429	-1.0	164	182	0	93.2	28	T	NGQLAQTLQQAYLPTVDYA	I	-0.3	3.1	
2	P00772|ELA1	2	2098.1423	-1.7	127	146	0	57.1	25	A	QSVTLNSYVQLGVLPRAGTI	L	0.4	9.84	Gln->pyro-Glu (N-term Q)
2	P00772|ELA1	2	2099.9508	-1.0	83	101	0	76.2	26	V	VGEHNLNQNDGTEQYVGVQ	K	-1.1	3.82	
2	P00772|ELA1	2	2115.1688	0.0	127	146	0	86.6	23	A	QSVTLNSYVQLGVLPRAGTI	L	0.4	9.84	
2	P00772|ELA1	2	2118.0058	-0.3	103	121	0	73.7	28	K	IVVHPYWNTDDVAAGYDIA	L	0.2	3.6	
2	P00772|ELA1	2	2118.0058	-1.9	104	122	0	57.8	28	I	VVHPYWNTDDVAAGYDIAL	L	0.2	3.6	
2	P00772|ELA1	2	2132.0215	0.4	105	123	0	51.4	29	V	VHPYWNTDDVAAGYDIALL	R	0.1	3.6	
2	P00772|ELA1	3	2156.0247	-0.7	78	96	0	32.4	28	L	TFRVVVGEHNLNQNDGTEQ	Y	-1.0	4.42	
2	P00772|ELA1	2	2170.0291	-0.2	81	100	0	45.6	28	R	VVVGEHNLNQNDGTEQYVGV	Q	-0.5	3.82	
2	P00772|ELA1	3	2170.0403	-1.0	80	98	0	30.3	28	F	RVVVGEHNLNQNDGTEQYV	G	-0.9	4.42	
2	P00772|ELA1	3	2185.04	-1.0	85	103	0	61.2	28	G	EHNLNQNDGTEQYVGVQKI	V	-1.3	4.42	
2	P00772|ELA1	2	2199.0193	-0.3	82	101	0	74.7	27	V	VVGEHNLNQNDGTEQYVGVQ	K	-0.9	3.82	
2	P00772|ELA1	2	2231.0899	-1.3	104	123	0	50.0	29	I	VVHPYWNTDDVAAGYDIALL	R	0.3	3.6	
2	P00772|ELA1	3	2241.2593	0.0	124	144	0	47.5	23	L	RLAQSVTLNSYVQLGVLPRAG	T	0.3	11.14	
2	P00772|ELA1	3	2242.0614	-1.2	84	103	0	45.4	28	V	GEHNLNQNDGTEQYVGVQKI	V	-1.3	4.42	
2	P00772|ELA1	2	2299.29	-0.7	127	148	0	92.9	23	A	QSVTLNSYVQLGVLPRAGTILA	N	0.6	9.84	
2	P00772|ELA1	2	2317.1087	-2.1	79	98	0	84.0	29	T	FRVVVGEHNLNQNDGTEQYV	G	-0.8	4.42	
2	P00772|ELA1	3	2327.1142	-0.1	82	102	0	31.1	28	V	VVGEHNLNQNDGTEQYVGVQK	I	-1.0	4.42	
2	P00772|ELA1	2	2341.1299	-1.4	83	103	0	83.2	29	V	VGEHNLNQNDGTEQYVGVQKI	V	-1.0	4.42	
2	P00772|ELA1	2	2344.1739	-0.3	103	123	0	34.8	29	K	IVVHPYWNTDDVAAGYDIALL	R	0.5	3.6	
2	P00772|ELA1	2	2357.1328	-1.6	101	121	0	52.4	29	V	QKIVVHPYWNTDDVAAGYDIA	L	-0.2	4.16	Gln->pyro-Glu (N-term Q)
2	P00772|ELA1	2	2374.1594	0.5	101	121	0	41.4	29	V	QKIVVHPYWNTDDVAAGYDIA	L	-0.2	4.16	
2	P00772|ELA1	2	2440.1983	-1.5	82	103	0	94.6	28	V	VVGEHNLNQNDGTEQYVGVQKI	V	-0.8	4.42	
2	P00772|ELA1	3	2473.1986	-0.2	79	100	0	71.3	29	T	FRVVVGEHNLNQNDGTEQYVGV	Q	-0.5	4.42	
2	P00772|ELA1	3	2539.2667	0.2	81	103	0	56.4	28	R	VVVGEHNLNQNDGTEQYVGVQKI	V	-0.5	4.42	
2	P00772|ELA1	3	2574.2463	2.3	78	100	0	41.2	29	L	TFRVVVGEHNLNQNDGTEQYVGV	Q	-0.5	4.42	
3	Q9HM69|CSG	1	541.3112	0.7	740	744	0	26.5	26	S	VDVPL	S	1.4	3.1	
3	Q9HM69|CSG	1	636.3119	0.2	132	137	0	43.8	30	A	DFGVTV	Q	1.1	3.1	
3	Q9HM69|CSG	1	706.3901	-0.3	349	354	0	40.7	25	A	YAIVEI	D	1.7	3.3	
3	Q9HM69|CSG	1	830.4749	-1.3	679	686	0	26.9	24	R	LVDGLTTI	E	1.4	3.1	
3	Q9HM69|CSG	1	832.4178	-1.7	667	674	0	42.8	28	T	ASDDLIVT	Q	0.7	2.92	
3	Q9HM69|CSG	2	905.5334	-0.7	500	507	0	39.7	21	G	TYRLGIIA	K	1.0	9.84	
3	Q9HM69|CSG	1	943.4862	0.6	766	773	0	50.8	28	Q	NVEIVEEL	E	0.3	3.02	
3	Q9HM69|CSG	2	986.5761	0.8	678	686	0	53.3	24	F	RLVDGLTTI	E	0.7	6.78	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
3	Q9HM69|CSG	2	1025.5029	0.2	741	750	0	43.2	25	V	DVPLSNVEPG	N	-0.3	3	
3	Q9HM69|CSG	2	1074.5822	1.9	675	683	0	49.7	25	T	QQFRLVDGL	T	-0.1	6.78	
3	Q9HM69|CSG	2	1119.4931	0.4	632	641	0	67.0	25	A	NSISDLEDEV	G	-0.7	2.84	
3	Q9HM69|CSG	2	1120.5149	0.7	453	461	0	26.6	26	A	RDNNDFELV	T	-1.2	3.7	
3	Q9HM69|CSG	2	1124.5714	0.3	740	750	0	56.0	25	S	VDVPLSNVEPG	N	0.1	3	
3	Q9HM69|CSG	2	1175.6299	0.5	675	684	0	36.6	25	T	QQFRLVDGLT	T	-0.2	6.78	
3	Q9HM69|CSG	2	1186.6081	0.5	716	726	0	70.5	28	V	ELLQGDASIEI	N	0.3	2.94	
3	Q9HM69|CSG	2	1186.6557	-0.4	678	688	0	40.1	25	F	RLVDGLTTIEA	T	0.4	4.08	
3	Q9HM69|CSG	2	1191.552	-0.3	452	461	0	31.9	26	Y	ARDNNDFELV	T	-0.9	3.7	
3	Q9HM69|CSG	2	1200.5623	0.5	417	428	0	48.9	26	T	QGDITLDNPTGA	Y	-0.6	2.92	
3	Q9HM69|CSG	2	1204.6299	0.2	536	546	0	58.4	26	S	SIRVTDTELTA	S	0.0	4.08	
3	Q9HM69|CSG	2	1211.6034	-1.2	739	750	0	43.5	26	W	SVDVPLSNVEPG	N	0.1	3	
3	Q9HM69|CSG	1	1229.4572	0.8	406	416	0	17.7	13	V	STDDDTDFDVT	Q	-1.2	2.68	
3	Q9HM69|CSG	2	1261.703	-0.5	676	686	0	41.7	24	Q	QFRLVDGLTTI	E	0.5	6.78	
3	Q9HM69|CSG	1	1266.5252	0.9	238	249	0	37.7	23	V	EGVEDLDFGDAT	E	-0.5	2.76	
3	Q9HM69|CSG	2	1276.5783	0.8	687	700	0	54.8	26	I	EATEGGEAGGSLTV	M	-0.2	3.02	
3	Q9HM69|CSG	2	1287.7034	0.8	678	689	0	50.5	25	F	RLVDGLTTIEAT	E	0.3	4.08	
3	Q9HM69|CSG	2	1291.662	0.3	535	546	0	38.2	27	T	SSIRVTDTELTA	S	-0.1	4.08	
3	Q9HM69|CSG	2	1299.4627	0.6	593	603	0	33.1	13	V	DSDDTFDEEDI	D	-1.7	2.64	
3	Q9HM69|CSG	1	1313.4783	-2.6	472	482	0	31.6	14	V	DSDDTFEEEDI	T	-1.7	2.66	
3	Q9HM69|CSG	2	1320.631	-0.6	453	463	0	32.0	27	A	RDNNDFELVTV	D	-0.7	3.7	
3	Q9HM69|CSG	2	1327.6256	-0.5	486	499	0	42.8	26	S	DGDKGGDDILGLPG	T	-0.7	3.42	
3	Q9HM69|CSG	2	1342.6728	0.9	763	773	0	37.0	27	T	DRQNVEIVEEL	E	-0.8	3.68	
3	Q9HM69|CSG	2	1389.7616	-0.5	675	686	0	60.6	25	T	QQFRLVDGLTTI	E	0.2	6.78	
3	Q9HM69|CSG	2	1447.7341	1.3	312	325	0	32.0	28	V	MRSVGDTVDTGLVV	D	0.6	3.88	
3	Q9HM69|CSG	2	1467.6994	-2.5	450	461	0	38.6	27	V	LYARDNNDFELV	T	-0.6	3.7	
3	Q9HM69|CSG	1	1485.5631	0.9	591	603	0	38.4	16	I	SVDSDDTFDEEDI	D	-1.2	2.64	
3	Q9HM69|CSG	2	1527.659	0.1	39	50	0	35.6	24	S	DLNDYQRFNENT	N	-2.0	3.7	
3	Q9HM69|CSG	2	1527.7417	-0.5	484	499	0	35.6	27	T	LSDGDKGGDDILGLPG	T	-0.4	3.42	
3	Q9HM69|CSG	1	1565.6879	-0.9	687	703	0	41.2	25	I	EATEGGEAGGSLTVMGT	T	-0.1	3.02	
3	Q9HM69|CSG	2	1588.6965	-1.4	757	770	0	41.3	24	A	DDGDNTDRQNVEIV	E	-1.5	3.36	
3	Q9HM69|CSG	2	1603.857	-2.0	667	680	0	35.3	26	T	ASDDLIVTQQFRLV	D	0.4	3.88	
3	Q9HM69|CSG	2	1628.7894	0.1	483	499	0	29.9	27	I	TLSDGDKGGDDILGLPG	T	-0.4	3.42	
3	Q9HM69|CSG	2	1642.637	0.1	470	483	0	16.1	16	I	EVDSDDTFEEEDIT	L	-1.3	2.64	
3	Q9HM69|CSG	2	1710.7486	-0.9	220	234	0	75.4	24	L	RFDIDPNNVDAGDYT	V	-1.1	3.42	
3	Q9HM69|CSG	2	1750.8261	1.8	349	365	0	40.2	28	A	YAIVEIDDGNGVGSIET	Q	0.1	2.84	
3	Q9HM69|CSG	2	1751.7962	-1.6	516	532	0	42.1	26	S	GGVKDNIDTSDFNQGVS	S	-0.7	3.6	
3	Q9HM69|CSG	2	1751.7962	0.0	515	531	0	50.2	26	S	SGGVKDNIDTSDFNQGV	S	-0.7	3.6	
3	Q9HM69|CSG	2	1814.7595	0.3	547	562	0	71.4	21	A	SFETYNGQVADDDNQI	D	-1.1	2.78	
3	Q9HM69|CSG	3	1816.8915	-0.9	651	666	0	35.9	28	T	GDQIRDRILSNTVDDT	A	-1.0	3.88	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
3	Q9HM69|CSG	2	1838.8283	-1.3	515	532	0	68.1	26	S	SGGVKDNIDTSDFNQGVS	S	-0.8	3.6	
3	Q9HM69|CSG	2	1865.7664	-1.6	201	219	0	63.2	20	A	DQSGGAYEDGTGNNGPNTL	R	-1.4	2.88	
3	Q9HM69|CSG	2	1885.7966	-0.6	546	562	0	70.4	22	T	ASFETYNGQVADDDNQI	D	-0.9	2.78	
3	Q9HM69|CSG	2	1887.8446	2.4	754	770	0	29.8	25	T	VEADDGDNTDRQNVEIV	E	-1.1	3.32	
3	Q9HM69|CSG	2	1925.8603	-1.8	515	533	0	70.8	25	S	SGGVKDNIDTSDFNQGVSS	T	-0.8	3.6	
3	Q9HM69|CSG	2	1936.8035	0.2	200	219	0	87.4	21	A	ADQSGGAYEDGTGNNGPNTL	R	-1.2	2.88	
3	Q9HM69|CSG	2	1936.8796	-0.2	687	706	0	100.2	27	I	EATEGGEAGGSLTVMGTTNR	K	-0.5	3.96	
3	Q9HM69|CSG	2	1939.876	-1.2	516	534	0	59.5	26	S	GGVKDNIDTSDFNQGVSST	S	-0.7	3.6	
3	Q9HM69|CSG	2	1947.9326	-0.5	276	292	0	73.1	28	A	NLKYTIENSPEGNYHAV	T	-1.0	5.3	
3	Q9HM69|CSG	2	1959.8658	1.4	757	773	0	52.2	24	A	DDGDNTDRQNVEIVEEL	E	-1.4	3.28	
3	Q9HM69|CSG	2	1971.8658	-1.9	557	575	0	57.2	24	A	DDDNQIDVEGTAPGKDNVA	A	-1.2	3.26	
3	Q9HM69|CSG	2	1988.8923	-1.3	753	770	0	47.7	25	Y	TVEADDGDNTDRQNVEIV	E	-1.1	3.32	
3	Q9HM69|CSG	2	2026.908	-0.6	515	534	0	93.9	26	S	SGGVKDNIDTSDFNQGVSST	S	-0.8	3.6	
3	Q9HM69|CSG	2	2036.0208	-1.9	697	715	0	34.0	28	G	SLTVMGTTNRKADDNTITV	E	-0.4	6.9	
3	Q9HM69|CSG	2	2042.8328	-0.9	591	608	0	82.0	18	I	SVDSDDTFDEEDIDISEL	R	-0.8	2.58	
3	Q9HM69|CSG	2	2042.9029	-1.2	557	576	0	48.0	25	A	DDDNQIDVEGTAPGKDNVAA	I	-1.0	3.26	
3	Q9HM69|CSG	2	2113.94	-2.1	515	535	0	82.4	25	S	SGGVKDNIDTSDFNQGVSSTS	S	-0.8	3.6	
3	Q9HM69|CSG	2	2120.9247	0.1	198	219	0	73.7	24	I	LAADQSGGAYEDGTGNNGPNTL	R	-0.8	2.88	
3	Q9HM69|CSG	2	2204.1689	0.1	667	686	0	59.9	26	T	ASDDLIVTQQFRLVDGLTTI	E	0.4	3.6	
3	Q9HM69|CSG	3	2246.0775	-1.6	646	666	0	37.5	28	T	SGSPTGDQIRDRILSNTVDDT	A	-0.9	3.88	
3	Q9HM69|CSG	2	2315.9666	-0.2	547	567	0	97.1	20	A	SFETYNGQVADDDNQIDVEGT	A	-1.0	2.7	
3	Q9HM69|CSG	2	2384.0139	0.8	591	611	0	150.0	22	I	SVDSDDTFDEEDIDISELRQG	S	-1.1	3.12	
3	Q9HM69|CSG	2	2441.0943	-1.3	552	575	0	71.0	25	Y	NGQVADDDNQIDVEGTAPGKDNVA	A	-1.0	3.26	
3	Q9HM69|CSG	2	2471.046	-0.5	591	612	0	91.3	20	I	SVDSDDTFDEEDIDISELRQGS	A	-1.1	3.12	
3	Q9HM69|CSG	2	2512.1314	-0.4	552	576	0	55.0	26	Y	NGQVADDDNQIDVEGTAPGKDNVAA	I	-0.9	3.26	
3	Q9HM69|CSG	2	2542.0831	2.4	591	613	0	115.8	22	I	SVDSDDTFDEEDIDISELRQGSA	S	-1.0	3.12	
3	Q9HM69|CSG	3	2631.2988	-0.5	651	674	0	61.7	29	T	GDQIRDRILSNTVDDTASDDLIVT	Q	-0.4	3.58	
3	Q9HM69|CSG	3	2894.3564	-0.7	687	715	0	60.7	28	I	EATEGGEAGGSLTVMGTTNRKADDNTITV	E	-0.5	3.92	
3	Q9HM69|CSG	3	2910.3513	-0.6	687	715	0	66.1	28	I	EATEGGEAGGSLTVMGTTNRKADDNTITV	E	-0.5	3.92	Oxidation (M)
3	Q9HM69|CSG	3	2997.3112	-0.5	547	574	0	56.4	24	A	SFETYNGQVADDDNQIDVEGTAPGKDNV	A	-1.0	3.22	
3	Q9HM69|CSG	3	3060.4848	0.2	646	674	0	51.5	29	T	SGSPTGDQIRDRILSNTVDDTASDDLIVT	Q	-0.5	3.58	
3	Q9HM69|CSG	3	3068.3483	0.2	546	574	0	59.3	24	T	ASFETYNGQVADDDNQIDVEGTAPGKDNV	A	-0.9	3.22	
3	Q9HM69|CSG	3	3068.3483	-0.6	547	575	0	45.2	23	A	SFETYNGQVADDDNQIDVEGTAPGKDNVA	A	-0.9	3.22	
3	Q9HM69|CSG	3	3139.3854	-0.2	546	575	0	54.5	24	T	ASFETYNGQVADDDNQIDVEGTAPGKDNVA	A	-0.8	3.22	
3	Q9HM69|CSG	3	3210.4225	-0.4	546	576	0	59.7	24	T	ASFETYNGQVADDDNQIDVEGTAPGKDNVAA	I	-0.8	3.22	
4	Q9HMI3|Q9HMI3	1	923.4025	-0.5	160	167	0	38.0	26	T	FGDWVDSV	E	0.3	2.92	
4	Q9HMI3|Q9HMI3	1	1024.4502	-0.7	159	167	0	32.6	26	I	TFGDWVDSV	E	0.2	2.92	
4	Q9HMI3|Q9HMI3	2	1045.5557	0.7	554	563	0	40.2	27	T	SVGGPFLDRV	E	0.4	6.78	
4	Q9HMI3|Q9HMI3	1	1140.5299	0.4	209	219	0	39.8	25	A	DAQPELGTDPV	G	-0.8	2.88	
4	Q9HMI3|Q9HMI3	1	1162.5143	0.1	99	109	0	30.7	26	S	GLADDWTLDGT	T	-0.4	2.82	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
4	Q9HMI3|Q9HMI3	2	1172.6037	0.3	330	339	0	33.5	28	A	INRDEIVDSI	Y	-0.2	3.7	
4	Q9HMI3|Q9HMI3	2	1172.619	-0.9	556	566	0	36.4	28	V	GGPFLDRVELA	-	0.2	4.08	
4	Q9HMI3|Q9HMI3	2	1172.6401	-0.8	197	206	0	31.2	27	A	ILSRDQIESL	G	0.0	4.08	
4	Q9HMI3|Q9HMI3	2	1187.6146	-1.9	198	208	0	45.5	27	I	LSRDQIESLGA	D	-0.3	4.08	
4	Q9HMI3|Q9HMI3	2	1193.5928	-0.8	460	470	0	43.3	27	V	LLHPGTDIDDV	P	0.0	3.6	
4	Q9HMI3|Q9HMI3	2	1224.5663	0.5	157	167	0	41.0	26	A	SITFGDWVDSV	E	0.5	2.92	
4	Q9HMI3|Q9HMI3	2	1236.5874	-1.5	378	389	0	49.2	27	A	DAGVTDLSFELA	T	0.5	2.88	
4	Q9HMI3|Q9HMI3	2	1243.6772	0.2	196	206	0	43.3	26	A	AILSRDQIESL	G	0.2	4.08	
4	Q9HMI3|Q9HMI3	2	1268.5885	-1.2	207	219	0	45.5	26	L	GADAQPELGTDPV	G	-0.5	2.88	
4	Q9HMI3|Q9HMI3	2	1314.7143	0.3	195	206	0	62.3	26	A	AAILSRDQIESL	G	0.3	4.08	
4	Q9HMI3|Q9HMI3	2	1350.6932	1.9	178	188	0	33.3	27	I	DLTQQYAPFLR	N	-0.6	6.7	
4	Q9HMI3|Q9HMI3	2	1358.7194	-0.9	554	566	0	63.1	27	T	SVGGPFLDRVELA	-	0.5	4.08	
4	Q9HMI3|Q9HMI3	2	1370.5779	-0.1	240	252	0	44.5	23	T	AFDDYWGGAPSVS	A	-0.2	2.92	
4	Q9HMI3|Q9HMI3	2	1442.7729	0.6	195	208	0	32.6	26	A	AAILSRDQIESLGA	D	0.4	4.08	
4	Q9HMI3|Q9HMI3	2	1475.7157	-1.0	390	402	0	48.6	28	A	TFSNPRGYNPNPI	Q	-1.2	9.84	
4	Q9HMI3|Q9HMI3	2	1582.7223	-0.4	271	285	0	72.9	26	I	NGDAHITDNLDAQSI	Q	-0.6	3.6	
4	Q9HMI3|Q9HMI3	2	1632.7744	1.0	114	128	0	30.6	27	L	TLREDATFHSGADLT	A	-0.5	4.3	
4	Q9HMI3|Q9HMI3	2	1696.8056	-0.4	331	345	0	67.5	27	I	NRDEIVDSIYQGFAA	S	-0.3	3.7	
4	Q9HMI3|Q9HMI3	2	1718.8112	-1.9	460	475	0	36.7	28	V	LLHPGTDIDDVPADQN	Y	-0.7	3.42	
4	Q9HMI3|Q9HMI3	2	1740.8108	-0.1	237	252	0	58.2	27	V	RLTAFDDYWGGAPSVS	A	-0.3	3.88	
4	Q9HMI3|Q9HMI3	2	1761.7556	1.1	489	503	0	77.8	23	V	SAWVDTDYMEFVDKG	Q	-0.5	3.5	
4	Q9HMI3|Q9HMI3	2	1775.8591	-1.9	390	405	0	61.3	28	A	TFSNPRGYNPNPIQTA	T	-1.1	9.84	
4	Q9HMI3|Q9HMI3	2	1793.8221	2.3	222	236	0	99.2	27	T	GPFEFDQLDNETQRV	R	-1.2	3.58	
4	Q9HMI3|Q9HMI3	2	1806.7196	0.3	445	459	0	26.0	18	S	GWYTDNADPDNFMYV	L	-0.9	2.82	
4	Q9HMI3|Q9HMI3	2	1808.9309	-0.7	78	93	0	57.2	27	V	TNQIFDTLIQFKPGTS	G	-0.3	6.76	
4	Q9HMI3|Q9HMI3	2	1809.8897	-0.3	330	345	0	64.1	28	A	INRDEIVDSIYQGFAA	S	0.0	3.7	
4	Q9HMI3|Q9HMI3	2	1856.7741	0.1	139	153	0	83.7	20	R	FIDDEYDYYLGSDRS	G	-1.1	3.36	
4	Q9HMI3|Q9HMI3	2	1951.8912	-0.7	220	236	0	121.6	26	V	GTGPFEFDQLDNETQRV	R	-1.1	3.58	
4	Q9HMI3|Q9HMI3	3	1955.8762	-0.8	507	522	0	46.7	26	T	YDDAARQQYYHQASQI	A	-1.5	5.1	
4	Q9HMI3|Q9HMI3	2	1994.9585	0.4	460	477	0	44.3	28	V	LLHPGTDIDDVPADQNYI	A	-0.4	3.42	
4	Q9HMI3|Q9HMI3	2	2051.084	0.3	178	195	0	34.6	27	I	DLTQQYAPFLRNLAIFAA	A	0.4	6.7	
4	Q9HMI3|Q9HMI3	2	2065.0076	0.3	266	285	0	54.7	28	R	AQGLINGDAHITDNLDAQSI	Q	-0.2	3.6	
4	Q9HMI3|Q9HMI3	3	2146.963	1.9	489	506	0	53.0	26	V	SAWVDTDYMEFVDKGQRT	Y	-0.9	3.96	
4	Q9HMI3|Q9HMI3	2	2147.896	-0.4	139	156	0	71.5	20	R	FIDDEYDYYLGSDRSGYA	S	-0.9	3.36	
4	Q9HMI3|Q9HMI3	2	2209.1267	-1.2	78	97	0	80.9	28	V	TNQIFDTLIQFKPGTSGELT	S	-0.3	4.08	
4	Q9HMI3|Q9HMI3	2	2296.1587	-0.3	78	98	0	86.3	28	V	TNQIFDTLIQFKPGTSGELTS	G	-0.3	4.08	
4	Q9HMI3|Q9HMI3	2	2310.1339	0.2	198	219	0	79.5	28	I	LSRDQIESLGADAQPELGTDPV	G	-0.5	3.42	
4	Q9HMI3|Q9HMI3	2	2494.2551	-1.9	196	219	0	67.1	29	A	AILSRDQIESLGADAQPELGTDPV	G	-0.2	3.42	
4	Q9HMI3|Q9HMI3	2	2565.2922	0.0	195	219	0	94.1	29	A	AAILSRDQIESLGADAQPELGTDPV	G	-0.1	3.42	
4	Q9HMI3|Q9HMI3	3	2939.3322	0.2	346	372	0	59.9	26	A	SANQPLPPDVLGHNDDIDSYPHDPQQA	E	-1.2	3.7	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
5	Q9HQA6|Q9HQA6	1	795.3651	-1.8	287	293	0	53.8	26	A	YDLIDGT	R	-0.2	2.92	
5	Q9HQA6|Q9HQA6	2	956.4451	1.0	80	89	0	65.6	26	V	DLGPSAPSDV	S	-0.2	2.92	
5	Q9HQA6|Q9HQA6	1	1027.4862	-1.1	52	60	0	30.0	26	A	EYVAYVDVA	G	0.7	3	
5	Q9HQA6|Q9HQA6	1	1041.3961	-1.5	91	99	0	25.1	19	S	SMLDDFEDA	T	-0.5	2.78	
5	Q9HQA6|Q9HQA6	1	1055.4117	1.1	92	100	0	46.4	20	S	MLDDFEDAT	D	-0.5	2.78	
5	Q9HQA6|Q9HQA6	1	1098.4982	-2.1	212	222	0	24.5	24	S	AFEGVNGGSYV	Q	0.2	3.3	
5	Q9HQA6|Q9HQA6	1	1124.4622	-0.1	164	174	0	37.5	23	Y	SDDSLGGFDNV	L	-0.5	2.82	
5	Q9HQA6|Q9HQA6	1	1142.4438	-2.8	91	100	0	32.4	20	S	SMLDDFEDAT	D	-0.5	2.78	
5	Q9HQA6|Q9HQA6	2	1151.5822	0.4	287	296	0	66.4	26	A	YDLIDGTRSL	Y	-0.3	3.88	
5	Q9HQA6|Q9HQA6	2	1184.5561	0.5	78	89	0	40.8	25	A	EVDLGPSAPSDV	S	-0.1	2.88	
5	Q9HQA6|Q9HQA6	1	1198.5176	-0.1	134	144	0	27.8	24	T	TYDESGMVNAI	E	-0.1	3	
5	Q9HQA6|Q9HQA6	2	1287.5255	0.1	163	174	0	76.5	21	V	YSDDSLGGFDNV	L	-0.6	2.82	
5	Q9HQA6|Q9HQA6	2	1308.5834	0.8	164	176	0	74.9	25	Y	SDDSLGGFDNVLA	A	0.0	2.82	
5	Q9HQA6|Q9HQA6	2	1314.6456	0.5	287	297	0	41.4	28	A	YDLIDGTRSLY	A	-0.4	3.88	
5	Q9HQA6|Q9HQA6	2	1368.6773	0.4	76	89	0	45.6	26	T	LAEVDLGPSAPSDV	S	0.3	2.88	
5	Q9HQA6|Q9HQA6	2	1385.6827	0.4	287	298	0	32.7	28	A	YDLIDGTRSLYA	S	-0.2	3.88	
5	Q9HQA6|Q9HQA6	2	1386.5973	0.2	132	144	0	30.9	23	L	STTYDESGMVNAI	E	-0.2	3	
5	Q9HQA6|Q9HQA6	2	1414.5922	-0.5	134	146	0	29.1	22	T	TYDESGMVNAIES	S	-0.4	2.94	
5	Q9HQA6|Q9HQA6	2	1460.6572	0.1	212	225	0	44.0	27	S	AFEGVNGGSYVQYA	L	0.0	3.3	
5	Q9HQA6|Q9HQA6	2	1463.6893	0.4	178	191	0	96.0	28	A	LGDGEFVVGDRDSV	E	-0.1	3.5	
5	Q9HQA6|Q9HQA6	2	1503.7205	0.3	299	312	0	38.7	28	A	SVSPEELRPSFEAG	S	-0.6	3.96	
5	Q9HQA6|Q9HQA6	2	1519.6791	-0.3	93	105	0	98.3	25	M	LDDFEDATDINPR	K	-1.1	3.36	
5	Q9HQA6|Q9HQA6	2	1566.6798	-1.5	179	193	0	61.0	24	L	GDGEFVVGDRDSVES	M	-0.6	3.42	
5	Q9HQA6|Q9HQA6	2	1676.8369	-0.4	226	241	0	103.1	28	A	LSAPNGSDSLLGYERV	A	-0.2	4.08	
5	Q9HQA6|Q9HQA6	2	1679.7639	-1.4	178	193	0	72.9	27	A	LGDGEFVVGDRDSVES	M	-0.4	3.42	
5	Q9HQA6|Q9HQA6	2	1737.7516	0.5	91	105	0	93.0	24	S	SMLDDFEDATDINPR	K	-0.9	3.36	
5	Q9HQA6|Q9HQA6	2	1750.801	-1.0	177	193	0	78.0	27	A	ALGDGEFVVGDRDSVES	M	-0.2	3.42	
5	Q9HQA6|Q9HQA6	2	1760.8581	1.0	93	107	0	74.0	28	M	LDDFEDATDINPRKI	Q	-1.0	3.76	
5	Q9HQA6|Q9HQA6	2	1824.7836	1.3	90	105	0	90.6	23	V	SSMLDDFEDATDINPR	K	-0.9	3.36	
5	Q9HQA6|Q9HQA6	2	1840.7785	-0.8	90	105	0	90.9	22	V	SSMLDDFEDATDINPR	K	-0.9	3.36	Oxidation (M)
5	Q9HQA6|Q9HQA6	2	1978.9306	0.8	91	107	0	77.7	28	S	SMLDDFEDATDINPRKI	Q	-0.8	3.76	
5	Q9HQA6|Q9HQA6	3	1984.9272	-1.2	194	211	0	29.2	27	S	MLDVRSGDADHLEGDLRS	A	-0.7	4.12	
5	Q9HQA6|Q9HQA6	2	2038.879	-0.9	88	105	0	83.2	23	S	DVSSMLDDFEDATDINPR	K	-0.8	3.26	
5	Q9HQA6|Q9HQA6	2	2065.9626	-0.9	90	107	0	114.2	27	V	SSMLDDFEDATDINPRKI	Q	-0.8	3.76	
5	Q9HQA6|Q9HQA6	3	2081.9575	-0.1	90	107	0	57.9	27	V	SSMLDDFEDATDINPRKI	Q	-0.8	3.76	Oxidation (M)
5	Q9HQA6|Q9HQA6	3	2659.2977	0.2	299	323	0	36.7	29	A	SVSPEELRPSFEAGSIEQDGNTVIV	T	-0.3	3.58	
5	Q9HQA6|Q9HQA6	3	2666.158	-2.1	261	286	0	65.2	22	V	SFGTDDGDITSTEHVIADSEGSAERA	Y	-0.7	3.62	
5	Q9HQA6|Q9HQA6	2	2760.3454	-1.7	299	324	0	31.9	29	A	SVSPEELRPSFEAGSIEQDGNTVIVT	Y	-0.3	3.58	
6	Q9HMW9|Q9HMW9	1	666.3377	-0.3	494	499	0	21.4	19	T	GPFTFV	E	1.2	6.02	
6	Q9HMW9|Q9HMW9	1	701.3959	0.0	353	358	0	34.9	29	T	EITNLL	I	0.7	3.3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
6	Q9HMW9|Q9HMW9	1	1093.4386	-1.0	258	266	0	25.6	23	T	NMEEGIWES	A	-1.1	3.02	
6	Q9HMW9|Q9HMW9	2	1135.5584	0.2	336	345	0	50.0	26	A	KVMDLFDAPT	N	0.1	3.88	
6	Q9HMW9|Q9HMW9	1	1164.4757	-2.1	258	267	0	24.7	23	T	NMEEGIWESA	A	-0.8	3.02	
6	Q9HMW9|Q9HMW9	2	1179.5772	-1.1	435	444	0	34.3	27	V	EAVDDYTVRL	T	-0.3	3.7	
6	Q9HMW9|Q9HMW9	2	1212.6292	-1.3	636	645	0	36.0	26	A	FHLQPPQLFS	D	-0.1	7.84	
6	Q9HMW9|Q9HMW9	2	1235.6034	-1.7	315	326	0	29.3	28	S	GISSTFNSLDPV	A	0.3	3.1	
6	Q9HMW9|Q9HMW9	3	1241.7092	2.3	304	316	0	30.0	24	A	VAGIDGKGRLSGI	S	0.3	10.08	
6	Q9HMW9|Q9HMW9	2	1253.6768	0.8	269	279	0	28.9	25	A	LIPVYHNLAQS	F	0.4	7.76	
6	Q9HMW9|Q9HMW9	2	1268.5673	0.2	120	130	0	43.4	25	A	GYGPDNKYELN	W	-1.7	4.08	
6	Q9HMW9|Q9HMW9	2	1306.5102	0.4	512	523	0	36.0	18	A	DAFEDYHDGAPA	I	-1.0	3.5	
6	Q9HMW9|Q9HMW9	2	1324.7139	0.7	268	279	0	36.7	26	A	ALIPVYHNLAQS	F	0.5	7.76	
6	Q9HMW9|Q9HMW9	2	1362.7071	1.5	446	457	0	66.0	27	T	LESPFPYALDVL	T	0.7	3	
6	Q9HMW9|Q9HMW9	2	1406.6136	1.2	154	165	0	37.2	25	A	HIEMTINDANFS	S	-0.3	4.06	Oxidation (M)
6	Q9HMW9|Q9HMW9	2	1436.7147	0.5	432	444	0	114.8	26	A	TGVEAVDDYTVRL	T	0.0	3.7	
6	Q9HMW9|Q9HMW9	2	1457.6998	0.9	238	251	0	49.0	27	R	LVSNPGQSEDAIQT	R	-0.5	3	
6	Q9HMW9|Q9HMW9	2	1463.7548	0.1	445	457	0	36.7	27	L	TLESPFPYALDVL	T	0.6	3	
6	Q9HMW9|Q9HMW9	2	1568.7318	0.2	414	428	0	38.9	27	I	STLGIEHEVDENGAV	K	-0.3	3.68	
6	Q9HMW9|Q9HMW9	2	1601.7474	-0.4	538	550	0	77.7	27	A	RYNYFLNENADLA	G	-0.8	4.08	
6	Q9HMW9|Q9HMW9	2	1619.7144	0.2	92	104	0	61.1	25	T	DYQPDFDKYPYGI	D	-1.4	3.6	
6	Q9HMW9|Q9HMW9	3	1696.8268	0.2	414	429	0	43.6	27	I	STLGIEHEVDENGAVK	R	-0.5	4.16	
6	Q9HMW9|Q9HMW9	2	1714.6747	-1.5	508	523	0	62.0	16	G	SYSADAFEDYHDGAPA	I	-0.8	3.5	
6	Q9HMW9|Q9HMW9	2	1728.7301	0.2	116	130	0	73.4	22	V	MEEAGYGPDNKYELN	W	-1.5	3.68	
6	Q9HMW9|Q9HMW9	2	1735.7835	-1.6	252	266	0	52.6	26	T	RKDAATNMEEGIWES	A	-1.2	4.16	
6	Q9HMW9|Q9HMW9	2	1744.725	-2.8	116	130	0	37.6	20	V	MEEAGYGPDNKYELN	W	-1.5	3.68	Oxidation (M)
6	Q9HMW9|Q9HMW9	2	1802.905	1.3	166	181	0	48.3	29	S	SLLETTKQGEHEAFTL	G	-0.5	4.54	
6	Q9HMW9|Q9HMW9	2	1945.8305	1.3	280	295	0	60.1	23	S	FWYDRLDYNPPGAMDS	S	-1.0	3.6	
6	Q9HMW9|Q9HMW9	2	1964.8316	0.0	92	107	0	49.5	22	T	DYQPDFDKYPYGIDET	K	-1.6	3.36	
6	Q9HMW9|Q9HMW9	2	1996.92	-0.2	192	209	0	41.3	27	R	NFMQLVQPDNTIYGGETA	A	-0.4	3	
6	Q9HMW9|Q9HMW9	2	2017.9004	-1.9	356	372	0	90.9	25	T	NLLITDYETNDDLSEYT	L	-0.8	2.76	
6	Q9HMW9|Q9HMW9	2	2094.9283	-0.2	487	507	0	52.4	25	S	ASNPVGTGPFTFVEWDSGNGG	S	-0.3	3	
6	Q9HMW9|Q9HMW9	2	2338.9754	-0.8	88	107	0	52.1	18	T	GESTDYQPDFDKYPYGIDET	K	-1.6	3.32	
6	Q9HMW9|Q9HMW9	3	2637.1759	-0.1	88	110	0	59.6	25	T	GESTDYQPDFDKYPYGIDETKVA	E	-1.3	3.68	
6	Q9HMW9|Q9HMW9	3	2704.1942	-0.4	636	658	0	62.2	24	A	FHLQPPQLFSDGQEGYNNHYQGE	-	-1.4	4.4	
6	Q9HMW9|Q9HMW9	3	2837.2556	0.6	88	112	0	54.5	25	T	GESTDYQPDFDKYPYGIDETKVAEA	R	-1.2	3.62	
6	Q9HMW9|Q9HMW9	3	3223.4357	-0.5	82	110	0	42.7	25	T	DAPTTTGESTDYQPDFDKYPYGIDETKVA	E	-1.2	3.58	
6	Q9HMW9|Q9HMW9	3	3245.5128	-1.0	120	146	0	58.5	28	A	GYGPDNKYELNWLQYQSPTWKEMANTI	R	-1.2	4.44	
7	Q9HRU5|Q9HRU5	2	859.4593	-0.1	198	205	0	29.8	26	A	FVVGGWPV	G	1.5	6.02	
7	Q9HRU5|Q9HRU5	1	870.481	-0.3	162	169	0	44.9	26	V	NALQILEA	A	0.7	3.3	
7	Q9HRU5|Q9HRU5	1	941.5182	-1.1	162	170	0	63.2	25	V	NALQILEAA	G	0.8	3.3	
7	Q9HRU5|Q9HRU5	1	963.4661	2.2	181	189	0	28.4	27	A	SFAQAAEQL	R	0.1	3.3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
7	Q9HRU5|Q9HRU5	1	987.5178	-0.2	198	207	0	25.9	25	A	FVVGGWPVGA	I	1.4	6.02	
7	Q9HRU5|Q9HRU5	1	1050.4658	2.4	236	244	0	39.8	26	S	WFADDTIPS	G	-0.2	2.92	
7	Q9HRU5|Q9HRU5	2	1162.6485	-1.6	123	132	0	33.0	24	A	TLYPETITLI	T	0.8	3.3	
7	Q9HRU5|Q9HRU5	2	1208.535	-0.5	234	244	0	31.2	26	A	ASWFADDTIPS	G	-0.1	2.92	
7	Q9HRU5|Q9HRU5	2	1238.6143	1.0	247	257	0	55.5	26	T	YSGIDRSIETV	S	-0.2	4.08	
7	Q9HRU5|Q9HRU5	2	1261.615	0.0	149	161	0	35.0	28	A	TINTGDLGSGTQV	N	-0.2	3.1	
7	Q9HRU5|Q9HRU5	2	1263.6962	0.6	123	133	0	36.4	24	A	TLYPETITLIT	R	0.7	3.3	
7	Q9HRU5|Q9HRU5	2	1294.6921	0.3	92	102	0	42.8	25	A	LIQNDIAYFAK	N	0.3	6.68	
7	Q9HRU5|Q9HRU5	2	1326.5874	1.0	299	311	0	53.5	25	A	SAQDGMSIDLHPG	A	-0.4	3.88	
7	Q9HRU5|Q9HRU5	2	1396.6834	0.1	245	257	0	56.8	27	S	GTYSGIDRSIETV	S	-0.3	4.08	
7	Q9HRU5|Q9HRU5	2	1468.6616	0.4	299	313	0	78.2	26	A	SAQDGMSIDLHPGAA	A	-0.1	3.88	
7	Q9HRU5|Q9HRU5	2	1471.7711	0.9	198	211	0	51.3	27	A	FVVGGWPVGAIEEL	A	1.1	3.12	
7	Q9HRU5|Q9HRU5	2	1539.6987	0.8	299	314	0	79.3	26	A	SAQDGMSIDLHPGAAA	Y	0.0	3.88	
7	Q9HRU5|Q9HRU5	2	1542.8082	0.1	198	212	0	72.7	27	A	FVVGGWPVGAIEELA	N	1.1	3.12	
7	Q9HRU5|Q9HRU5	2	1560.7532	-1.5	108	122	0	46.8	28	I	DAFQDRAVDNLAGVA	T	0.0	3.6	
7	Q9HRU5|Q9HRU5	2	1688.8118	-1.7	182	197	0	43.2	28	S	FAQAAEQLRNGDIDAA	F	-0.4	3.7	
7	Q9HRU5|Q9HRU5	2	1736.9097	0.1	92	107	0	60.9	27	A	LIQNDIAYFAKNGTGI	D	0.2	6.68	
7	Q9HRU5|Q9HRU5	2	1775.8438	-1.1	181	197	0	69.2	27	A	SFAQAAEQLRNGDIDAA	F	-0.4	3.7	
7	Q9HRU5|Q9HRU5	2	1854.8959	-1.1	213	229	0	91.7	28	A	NTNDIEIVPIEGEARDA	A	-0.6	3.5	
7	Q9HRU5|Q9HRU5	2	1869.9261	-0.7	85	101	0	58.9	28	A	KGNADFALIQNDIAYFA	K	0.1	3.88	
7	Q9HRU5|Q9HRU5	2	1899.9538	0.1	151	169	0	70.2	28	I	NTGDLGSGTQVNALQILEA	A	0.0	3	
7	Q9HRU5|Q9HRU5	2	1970.9909	-1.2	151	170	0	38.0	29	I	NTGDLGSGTQVNALQILEAA	G	0.1	3	
7	Q9HRU5|Q9HRU5	2	2032.0153	-0.5	281	298	0	30.0	29	A	IFEHTGDLTIKPDFIDTA	S	0.0	3.96	
7	Q9HRU5|Q9HRU5	3	2034.9745	-0.9	162	180	0	64.4	28	V	NALQILEAAGVTDYEEQTA	S	-0.2	2.88	
7	Q9HRU5|Q9HRU5	2	2206.1733	-0.7	123	142	0	97.3	26	A	TLYPETITLITRADTGIETV	A	0.2	3.82	
7	Q9HRU5|Q9HRU5	3	2262.1015	-0.3	160	180	0	54.0	28	T	QVNALQILEAAGVTDYEEQTA	S	-0.2	2.88	
7	Q9HRU5|Q9HRU5	2	2538.2449	-2.1	206	229	0	77.8	29	V	GAIEELANTNDIEIVPIEGEARDA	A	-0.2	3.38	
7	Q9HRU5|Q9HRU5	2	2587.2078	-1.0	234	257	0	49.7	27	A	ASWFADDTIPSGTYSGIDRSIETV	S	-0.2	3.5	
7	Q9HRU5|Q9HRU5	3	3379.6936	-1.1	198	229	0	47.4	30	A	FVVGGWPVGAIEELANTNDIEIVPIEGEARDA	A	0.2	3.38	
8	Q9HH34|Q9HH34	1	727.448	-0.1	108	114	0	27.4	25	L	LDLALLA	K	2.2	3.1	
8	Q9HH34|Q9HH34	2	1191.6573	0.8	214	224	0	32.9	23	G	LGVETLAFMVL	D	2.0	3.3	
9	Q9HR20|Q9HR20	1	664.3068	1.2	267	272	0	44.1	29	S	DFADVV	L	1.0	2.92	
9	Q9HR20|Q9HR20	1	848.428	2.5	267	274	0	53.9	27	S	DFADVVLA	S	1.5	2.92	
9	Q9HR20|Q9HR20	2	1012.4713	0.6	340	349	0	34.8	25	I	AGDIDVPTEP	-	-0.4	2.88	
9	Q9HR20|Q9HR20	2	1074.5822	-0.3	248	257	0	37.9	25	A	QDIGRFAIGV	D	0.6	6.78	
9	Q9HR20|Q9HR20	2	1145.6193	0.9	247	257	0	67.1	25	A	AQDIGRFAIGV	D	0.7	6.78	
9	Q9HR20|Q9HR20	2	1241.6616	0.0	303	314	0	37.2	26	T	RLGLEDDGVVAV	Y	0.5	3.7	
9	Q9HR20|Q9HR20	2	1289.5789	-1.5	111	121	0	37.0	26	T	NAADFPDQRWA	L	-1.2	3.88	
9	Q9HR20|Q9HR20	2	1316.6096	-0.1	122	133	0	67.6	27	A	LVDETVDQDNVA	S	-0.3	2.78	
9	Q9HR20|Q9HR20	1	1474.7304	-0.4	314	327	0	50.7	28	A	VYGDQLGAEIPQSV	K	0.0	3	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
9	Q9HR20|Q9HR20	2	1526.6638	-0.9	207	221	0	46.1	24	S	YVGSFNDPSAGQSQA	R	-0.6	3.1	
9	Q9HR20|Q9HR20	2	1624.8308	-1.3	335	349	0	75.7	27	S	RTELIAGDIDVPTEP	-	-0.3	3.58	
9	Q9HR20|Q9HR20	2	1700.7278	-1.8	205	221	0	37.3	24	L	SSYVGSFNDPSAGQSQA	R	-0.7	3.1	
9	Q9HR20|Q9HR20	2	1842.8385	-0.1	38	56	0	96.5	26	V	GTVYGTGGLGDGSFNDQAK	Q	-0.6	3.88	
9	Q9HR20|Q9HR20	3	1918.9133	-0.4	44	62	0	44.3	28	T	GGLGDGSFNDQAKQGLERA	K	-1.0	4.3	
9	Q9HR20|Q9HR20	2	1919.9225	-0.1	295	313	0	60.2	28	G	NFAGGETTRLGLEDDGVVA	V	-0.1	3.58	
9	Q9HR20|Q9HR20	2	1961.9443	0.8	151	170	0	77.1	29	A	GLLTQREFSAGSGATNPDAA	T	-0.3	4.08	
9	Q9HR20|Q9HR20	3	2190.1168	-0.3	314	334	0	55.0	28	A	VYGDQLGAEIPQSVKDAVSKS	R	-0.3	4.3	
9	Q9HR20|Q9HR20	3	2240.0458	0.2	41	62	0	70.1	28	V	YGTGGLGDGSFNDQAKQGLERA	K	-0.9	4.3	
9	Q9HR20|Q9HR20	3	2426.1463	0.0	38	61	0	61.8	28	V	GTVYGTGGLGDGSFNDQAKQGLER	A	-0.8	4.3	
9	Q9HR20|Q9HR20	3	2497.1834	0.0	38	62	0	100.1	28	V	GTVYGTGGLGDGSFNDQAKQGLERA	K	-0.7	4.3	
9	Q9HR20|Q9HR20	2	2588.1779	-0.7	111	133	0	38.9	26	T	NAADFPDQRWALVDETVDQDNVA	S	-0.7	3.26	
9	Q9HR20|Q9HR20	3	2707.3453	-0.3	144	170	0	56.8	29	S	YLVGELAGLLTQREFSAGSGATNPDAA	T	0.1	3.82	
9	Q9HR20|Q9HR20	3	3339.3964	-2.0	69	97	0	20.0	18	I	TYEESQPENNSEFATDQQQYAQDGSFDLV	N	-1.4	2.7	
10	Q9HNI7|Q9HNI7	2	1016.5655	-0.8	36	44	0	26.7	25	A	DVRFVLTPA	E	0.7	6.78	
10	Q9HNI7|Q9HNI7	1	1064.451	-1.8	135	144	0	24.1	24	I	DSLSDLADET	V	-0.7	2.78	
10	Q9HNI7|Q9HNI7	2	1075.5736	0.4	155	164	0	32.0	26	S	GSLFPLQMLA	D	1.2	6.02	
10	Q9HNI7|Q9HNI7	2	1113.5554	-0.8	236	245	0	36.6	26	A	GTEDPELQLL	A	-0.5	2.94	
10	Q9HNI7|Q9HNI7	2	1148.6553	0.0	248	258	0	53.5	21	A	SDPIPRAPLLA	R	0.2	6.78	
10	Q9HNI7|Q9HNI7	1	1158.5081	-0.3	56	65	0	27.4	23	A	GVFDYLESET	G	-0.3	2.94	
10	Q9HNI7|Q9HNI7	2	1261.6376	0.7	155	166	0	35.5	27	S	GSLFPLQMLADA	G	0.8	3.1	
10	Q9HNI7|Q9HNI7	2	1290.7296	0.4	246	258	0	46.1	22	L	AASDPIPRAPLLA	R	0.4	6.78	
10	Q9HNI7|Q9HNI7	2	1299.6306	1.0	81	92	0	41.3	26	V	LQALENDQADIA	D	-0.3	2.88	
10	Q9HNI7|Q9HNI7	2	1527.8145	0.1	98	113	0	50.0	26	T	LAVVGDNASVTDVVGI	R	1.3	2.92	
10	Q9HNI7|Q9HNI7	2	1529.6845	-0.7	83	97	0	75.2	25	Q	ALENDQADIADASPT	L	-0.6	2.78	
10	Q9HNI7|Q9HNI7	2	1557.8151	0.3	212	225	0	50.7	28	V	SLPHVPQSQLPEQV	M	-0.5	5.12	
10	Q9HNI7|Q9HNI7	2	1903.8535	0.6	127	144	0	28.7	26	I	TTQPDSPIDSLSDLADET	V	-0.8	2.72	
10	Q9HNI7|Q9HNI7	2	1920.9177	0.4	75	92	0	97.0	28	A	ADHQAVLQALENDQADIA	D	-0.3	3.5	
10	Q9HNI7|Q9HNI7	2	1932.0105	-0.2	208	225	0	61.4	27	T	GAFVSLPHVPQSQLPEQV	M	0.0	5.12	
10	Q9HNI7|Q9HNI7	2	1974.9211	-0.9	47	63	0	39.5	28	S	DVNVKEQYAGVFDYLES	E	-0.5	3.58	
10	Q9HNI7|Q9HNI7	2	2090.0797	0.5	206	225	0	32.4	28	A	GTGAFVSLPHVPQSQLPEQV	M	0.0	5.12	
10	Q9HNI7|Q9HNI7	2	2205.0114	-0.5	47	65	0	93.2	27	S	DVNVKEQYAGVFDYLESET	G	-0.6	3.5	
10	Q9HNI7|Q9HNI7	2	2333.0699	-0.7	47	67	0	85.8	27	S	DVNVKEQYAGVFDYLESETGA	S	-0.5	3.5	
10	Q9HNI7|Q9HNI7	2	2386.2744	-0.3	236	258	0	54.2	26	A	GTEDPELQLLAASDPIPRAPLLA	R	0.0	3.58	
10	Q9HNI7|Q9HNI7	2	2392.1142	2.5	75	97	0	97.3	28	A	ADHQAVLQALENDQADIADASPT	L	-0.5	3.36	
10	Q9HNI7|Q9HNI7	2	2421.086	0.1	45	65	0	45.0	26	A	ESDVNVKEQYAGVFDYLESET	G	-0.8	3.44	
10	Q9HNI7|Q9HNI7	2	2549.1445	-0.9	45	67	0	44.3	25	A	ESDVNVKEQYAGVFDYLESETGA	S	-0.6	3.44	
10	Q9HNI7|Q9HNI7	2	2758.2821	0.0	120	144	0	44.0	28	A	SRYFSTITTQPDSPIDSLSDLADET	V	-0.6	3.36	
11	Q9HR99|Q9HR99	1	926.3658	-1.6	79	85	0	44.2	19	V	TWEFEES	S	-1.4	3.02	
11	Q9HR99|Q9HR99	1	1032.5162	-0.5	148	157	0	27.5	27	S	GMIGTVVVEE	-	1.1	3.12	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
11	Q9HR99|Q9HR99	2	1119.5482	0.5	147	157	0	58.1	27	A	SGMIGTVVVEE	-	0.9	3.12	
11	Q9HR99|Q9HR99	2	1150.5295	0.3	58	68	0	46.1	27	V	APDGGFKFEPS	E	-0.8	4.08	
11	Q9HR99|Q9HR99	3	1198.5441	-0.3	90	99	0	34.0	24	V	SAWPDMHDKI	S	-0.9	5.1	
11	Q9HR99|Q9HR99	2	1320.635	-0.2	56	68	0	59.9	27	I	AVAPDGGFKFEPS	E	-0.2	4.08	
11	Q9HR99|Q9HR99	2	1348.5783	0.5	122	133	0	58.3	24	V	DAGETLEHTFET	A	-0.9	3.68	
11	Q9HR99|Q9HR99	2	1392.6561	-0.2	58	70	0	57.7	27	V	APDGGFKFEPSEL	T	-0.6	3.82	
11	Q9HR99|Q9HR99	2	1419.6154	-1.8	122	134	0	53.4	24	V	DAGETLEHTFETA	G	-0.7	3.68	
11	Q9HR99|Q9HR99	2	1473.6195	-1.5	106	119	0	54.2	22	A	SGFGTMDKDGNQFA	V	-0.8	3.88	
11	Q9HR99|Q9HR99	2	1484.6307	0.8	73	85	0	35.8	23	V	SVGDTVTWEFEES	S	-0.5	2.88	
11	Q9HR99|Q9HR99	2	1491.7246	2.1	57	70	0	58.1	28	A	VAPDGGFKFEPSEL	T	-0.3	3.82	
11	Q9HR99|Q9HR99	2	1562.7617	2.2	56	70	0	65.9	29	I	AVAPDGGFKFEPSEL	T	-0.1	3.82	
11	Q9HR99|Q9HR99	2	1592.7722	-1.0	58	72	0	32.0	27	V	APDGGFKFEPSELTV	S	-0.3	3.82	
11	Q9HR99|Q9HR99	2	1671.7563	0.2	106	121	0	44.1	26	A	SGFGTMDKDGNQFAVV	D	-0.2	3.88	
11	Q9HR99|Q9HR99	2	1691.8407	0.0	57	72	0	40.8	28	A	VAPDGGFKFEPSELTV	S	0.0	3.82	
11	Q9HR99|Q9HR99	2	1738.7985	-0.5	90	105	0	37.8	27	V	SAWPDMHDKISIPDGA	S	-0.6	4.16	
11	Q9HR99|Q9HR99	2	1762.8778	-1.2	56	72	0	53.4	28	I	AVAPDGGFKFEPSELTV	S	0.1	3.82	
11	Q9HR99|Q9HR99	2	1869.7905	-0.2	122	138	0	64.7	22	V	DAGETLEHTFETAGEYT	Y	-0.9	3.58	
11	Q9HR99|Q9HR99	2	2004.9793	0.7	51	70	0	36.4	29	S	GGNTIAVAPDGGFKFEPSEL	T	-0.1	3.82	
11	Q9HR99|Q9HR99	2	2131.9222	-0.5	122	140	0	53.7	23	V	DAGETLEHTFETAGEYTYV	C	-0.7	3.58	
11	Q9HR99|Q9HR99	3	2176.0007	-2.3	86	105	0	39.2	27	S	SHNVSAWPDMHDKISIPDGA	S	-0.6	5.02	
11	Q9HR99|Q9HR99	2	2205.0954	-1.4	51	72	0	51.6	29	S	GGNTIAVAPDGGFKFEPSELTV	S	0.0	3.82	
11	Q9HR99|Q9HR99	2	2307.1019	-1.8	48	70	0	61.1	29	A	SQSGGNTIAVAPDGGFKFEPSEL	T	-0.3	3.82	
11	Q9HR99|Q9HR99	2	2507.218	-2.2	48	72	0	56.6	28	A	SQSGGNTIAVAPDGGFKFEPSELTV	S	-0.2	3.82	
11	Q9HR99|Q9HR99	3	3523.5362	-1.5	106	138	0	37.4	22	A	SGFGTMDKDGNQFAVVDAGETLEHTFETAGEYT	Y	-0.6	3.68	
12	P16102|BACH	1	558.3166	0.5	61	65	0	25.7	23	R	LIWGA	T	1.8	6.02	
12	P16102|BACH	1	609.3527	-1.6	171	175	0	26.1	23	A	FFVVV	L	3.6	6.02	
12	P16102|BACH	1	664.3796	-2.0	76	81	0	39.4	24	S	SYLGLL	S	1.5	5.92	
12	P16102|BACH	1	678.3952	-0.9	133	138	0	23.1	22	G	SLFTVI	A	2.3	6.02	
12	P16102|BACH	1	700.3908	-0.1	33	38	0	23.6	22	S	LWVNVA	L	1.6	6.02	
12	P16102|BACH	1	722.4367	0.7	171	176	0	37.5	13	A	FFVVVL	S	3.7	6.02	
12	P16102|BACH	1	872.5041	-1.0	66	73	0	28.9	20	A	TLMIPLVS	I	1.9	6.02	
12	P16102|BACH	1	883.5379	-1.0	121	129	0	32.5	23	L	LALGLLADV	D	2.1	3.1	
12	P16102|BACH	1	921.5171	-0.1	76	84	0	32.3	22	S	SYLGLLSGL	T	1.3	5.92	
12	P16102|BACH	1	939.5753	1.0	35	44	0	24.7	22	W	VNVALAGIAI	L	2.3	6.02	
12	P16102|BACH	1	963.5277	-0.5	130	138	0	25.8	23	V	DLGSLFTVI	A	1.5	3.1	
12	P16102|BACH	2	985.5882	0.8	66	74	0	45.9	22	A	TLMIPLVSI	S	2.2	6.02	
12	P16102|BACH	1	1001.5831	-2.0	66	74	0	28.2	20	A	TLMIPLVSI	S	2.2	6.02	Oxidation (M)
12	P16102|BACH	2	1022.5648	0.7	76	85	0	39.6	22	S	SYLGLLSGLT	V	1.1	5.92	
12	P16102|BACH	2	1072.6202	0.6	66	75	0	53.7	22	A	TLMIPLVSIS	S	1.9	6.02	
12	P16102|BACH	1	1088.6151	0.4	66	75	0	34.5	21	A	TLMIPLVSIS	S	1.9	6.02	Oxidation (M)

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
12	P16102|BACH	2	1121.6332	1.1	76	86	0	48.3	21	S	SYLGLLSGLTV	G	1.4	5.92	
12	P16102|BACH	2	1177.6231	0.8	128	138	0	49.6	25	A	DVDLGSLFTVI	A	1.3	2.92	
12	P16102|BACH	2	1178.6547	-0.1	76	87	0	71.3	23	S	SYLGLLSGLTVG	M	1.2	5.92	
12	P16102|BACH	2	1208.6653	-0.2	75	86	0	36.8	23	I	SSYLGLLSGLTV	G	1.2	5.92	
12	P16102|BACH	2	1403.8024	0.4	194	205	0	28.5	21	A	EIFDTLRVLTVV	L	1.2	4.08	
12	P16102|BACH	2	1628.9211	-0.2	61	75	0	26.7	23	R	LIWGATLMIPLVSIS	S	1.8	6.02	Oxidation (M)
12	P16102|BACH	2	1866.9471	-0.1	76	93	0	49.4	27	S	SYLGLLSGLTVGMIEMPA	G	1.1	3.3	Oxidation (M)
12	P16102|BACH	2	1937.9842	-0.1	75	93	0	36.2	27	I	SSYLGLLSGLTVGMIEMPA	G	1.0	3.3	
13	Q9HS51|Q9HS51	1	545.3213	0.4	169	173	0	25.1	24	A	LVAPF	T	2.2	6.02	
13	Q9HS51|Q9HS51	2	1204.5459	1.2	158	168	0	63.7	26	S	TIVDVDDEQTA	L	-0.4	2.78	
13	Q9HS51|Q9HS51	2	1237.6455	0.5	105	114	0	31.9	25	T	VREDPVIQPW	T	-0.6	4.08	
13	Q9HS51|Q9HS51	2	1294.5929	-1.2	138	149	0	33.1	27	S	DDTVYGDVLDLA	S	0.1	2.74	
13	Q9HS51|Q9HS51	2	1340.6725	0.1	106	116	0	43.8	26	V	REDPVIQPWTT	L	-1.1	4.08	
13	Q9HS51|Q9HS51	2	1439.7409	0.6	105	116	0	53.9	27	T	VREDPVIQPWTT	L	-0.6	4.08	
13	Q9HS51|Q9HS51	2	1453.7565	1.9	106	117	0	55.9	27	V	REDPVIQPWTTL	S	-0.7	4.08	
13	Q9HS51|Q9HS51	2	1552.825	-0.3	105	117	0	84.0	26	T	VREDPVIQPWTTL	S	-0.3	4.08	
13	Q9HS51|Q9HS51	2	1790.9163	-0.9	59	75	0	47.3	28	I	TFTQDQTTVSRGGVVPV	T	-0.1	6.78	
13	Q9HS51|Q9HS51	2	1860.849	-1.1	51	68	0	50.5	26	A	GASDGHPITFTQDQTTVS	R	-0.6	3.88	
13	Q9HS51|Q9HS51	2	1981.8654	3.7	76	93	0	81.7	24	V	TLGNDDADEIGLNPHDWT	V	-1.0	3.36	
13	Q9HS51|Q9HS51	3	2152.1277	0.0	105	123	0	54.2	27	T	VREDPVIQPWTTLSAGDRI	H	-0.4	4.3	
13	Q9HS51|Q9HS51	2	2243.9971	-0.4	76	95	0	61.4	25	V	TLGNDDADEIGLNPHDWTVY	R	-0.8	3.36	
13	Q9HS51|Q9HS51	2	2295.1159	-0.1	156	176	0	42.2	28	A	FSTIVDVDDEQTALVAPFTVE	-	0.4	2.76	
13	Q9HS51|Q9HS51	2	2308.0231	0.0	127	149	0	51.7	25	R	VGVGDADPDTSDDTVYGDVLDLA	S	-0.1	2.6	
14	Q9HHN1|Q9HHN1	1	653.4112	1.2	22	27	0	29.2	24	G	QALLPI	A	1.5	6.02	
14	Q9HHN1|Q9HHN1	1	782.4902	0.6	370	377	0	22.4	22	V	TALGPLVI	N	1.9	6.02	
14	Q9HHN1|Q9HHN1	1	926.4538	-0.3	110	116	0	29.4	25	M	YWGLEFL	T	0.6	3.3	
14	Q9HHN1|Q9HHN1	2	941.595	1.2	120	128	0	48.7	16	A	VFVPLAALL	S	2.7	6.02	
14	Q9HHN1|Q9HHN1	1	1050.6073	-1.1	152	163	0	27.1	21	V	GIGSGLGIPAPL	T	1.1	6.02	
14	Q9HHN1|Q9HHN1	2	1084.4826	1.7	192	200	0	27.8	24	V	SDVDLWDHV	R	-0.4	3.6	
14	Q9HHN1|Q9HHN1	1	1195.5914	-1.9	110	119	0	28.2	28	M	YWGLEFLTPA	V	0.4	3.3	
14	Q9HHN1|Q9HHN1	2	1333.7969	0.6	149	163	0	40.8	18	I	ALVGIGSGLGIPAPL	T	1.5	6.02	
14	Q9HHN1|Q9HHN1	2	1333.7969	0.6	148	162	0	41.7	18	G	IALVGIGSGLGIPAP	L	1.6	6.02	
14	Q9HHN1|Q9HHN1	2	1405.7453	0.1	301	314	0	52.1	25	I	IYSGTGPKTGVDLV	N	0.2	6.68	
14	Q9HHN1|Q9HHN1	2	1545.9171	0.6	120	134	0	48.3	19	A	VFVPLAALLSFVVAT	A	2.4	6.02	
14	Q9HHN1|Q9HHN1	2	1571.674	0.4	395	407	0	61.1	23	T	FRDLNDEYDLDGT	S	-1.3	3.36	
14	Q9HHN1|Q9HHN1	2	1581.8978	-1.6	361	377	0	22.8	22	V	DSVGGATLVTALGPLVI	N	1.4	3.1	
14	Q9HHN1|Q9HHN1	3	1672.7369	0.0	8	21	0	34.8	25	R	SYEDFDPEKRPSFG	Q	-1.7	4.06	
14	Q9HHN1|Q9HHN1	2	1803.7621	-2.7	393	407	0	53.3	22	G	MTFRDLNDEYDLDGT	S	-1.1	3.36	
14	Q9HHN1|Q9HHN1	2	2038.9881	-1.6	166	185	0	58.3	28	A	GAILSGVYMGDKQSPLSDTT	L	-0.1	3.88	
14	Q9HHN1|Q9HHN1	2	2336.1934	-0.5	166	188	0	45.4	28	A	GAILSGVYMGDKQSPLSDTTLLA	S	0.3	3.88	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
14	Q9HHN1|Q9HHN1	3	2430.1128	-0.2	2	21	0	38.6	27	M	VEFEPRSYEDFDPEKRPSFG	Q	-1.5	4.12	
14	Q9HHN1|Q9HHN1	3	2608.2302	0.3	411	434	0	47.2	28	S	RTLEETGTVSEPMIPWNSGGVFMA	S	-0.1	3.96	
15	Q9HMW4|Q9HMW4	1	1130.5033	1.5	406	415	0	54.4	26	T	WGPYAPENPT	T	-1.3	3.3	
15	Q9HMW4|Q9HMW4	2	1296.6463	-1.4	181	192	0	51.8	27	S	HLFNVGADNTPI	T	0.1	4.94	
15	Q9HMW4|Q9HMW4	2	1578.7467	-0.4	402	415	0	36.8	28	T	LHPTWGPYAPENPT	T	-1.1	5.12	
15	Q9HMW4|Q9HMW4	2	1682.8111	-0.4	62	76	0	84.0	27	T	SSPDTETLQPENIPR	G	-1.4	3.82	
15	Q9HMW4|Q9HMW4	2	1709.822	-1.9	63	78	0	64.8	28	S	SPDTETLQPENIPRGG	T	-1.3	3.82	
15	Q9HMW4|Q9HMW4	2	1796.8541	-1.2	62	78	0	71.2	27	T	SSPDTETLQPENIPRGG	T	-1.3	3.82	
15	Q9HMW4|Q9HMW4	2	1808.8653	-0.4	86	103	0	51.3	28	T	STTNGLNAFRIGDGQTSA	R	-0.5	6.78	
15	Q9HMW4|Q9HMW4	2	1828.9148	0.8	206	221	0	34.9	28	T	IPEPRPFFPYNEPLGG	M	-0.7	4.26	
15	Q9HMW4|Q9HMW4	2	1865.8948	0.1	176	192	0	56.7	28	T	AFTYSHLFNVGADNTPI	T	0.1	4.94	
15	Q9HMW4|Q9HMW4	2	1921.8959	-0.9	399	415	0	33.4	27	V	QNTLHPTWGPYAPENPT	T	-1.3	5.12	
15	Q9HMW4|Q9HMW4	2	2230.0237	-0.6	57	76	0	94.8	27	A	TSEETSSPDTETLQPENIPR	G	-1.5	3.58	
15	Q9HMW4|Q9HMW4	3	2784.1648	-1.3	505	529	0	21.8	20	G	FSGEPGYGDENRQPSDYNRGPQDEA	V	-2.0	3.76	
15	Q9HMW4|Q9HMW4	3	2883.2332	-1.1	505	530	0	74.7	21	G	FSGEPGYGDENRQPSDYNRGPQDEAV	S	-1.8	3.76	
15	Q9HMW4|Q9HMW4	3	3041.3023	-1.5	505	532	0	32.3	21	G	FSGEPGYGDENRQPSDYNRGPQDEAVSA	Q	-1.6	3.76	
16	Q48302|Q48302	1	613.3799	-0.2	28	34	0	41.8	29	A	AALAVGL	A	2.4	6.02	
16	Q48302|Q48302	1	684.417	0.4	28	35	0	40.0	27	A	AALAVGLA	A	2.3	6.02	
16	Q48302|Q48302	1	755.4541	1.3	28	36	0	25.5	25	A	AALAVGLAA	L	2.3	6.02	
16	Q48302|Q48302	1	805.4375	0.5	83	89	0	31.9	20	V	FVVPTPF	-	1.4	6.02	
16	Q48302|Q48302	1	882.5426	-1.1	69	76	0	27.5	17	T	VLPETLVI	L	1.8	3.3	
16	Q48302|Q48302	1	904.5059	-0.7	82	89	0	39.3	25	V	VFVVPTPF	-	1.8	6.02	
16	Q48302|Q48302	1	983.5903	-0.5	68	76	0	24.6	23	L	TVLPETLVI	L	1.6	3.3	
16	Q48302|Q48302	1	1003.5743	0.3	81	89	0	38.0	24	V	VVFVVPTPF	-	2.1	6.02	
16	Q48302|Q48302	1	1010.6124	0.4	28	39	0	38.4	22	A	AALAVGLAALAA	G	2.3	6.02	
16	Q48302|Q48302	1	1076.5026	-1.0	54	63	0	32.7	27	A	IAEDPDLFGT	G	0.0	2.88	
16	Q48302|Q48302	2	1348.6735	-0.7	39	53	0	36.4	27	A	AGYAERGIGSAAVGA	I	0.4	6.88	
16	Q48302|Q48302	2	1359.6922	1.0	54	66	0	43.2	28	A	IAEDPDLFGTGLI	L	0.6	2.88	
16	Q48302|Q48302	2	1871.9662	-0.3	9	27	0	55.5	28	L	STILAETGSNMPAITPKAA	A	0.2	6.94	
16	Q48302|Q48302	2	1901.037	-0.4	28	48	0	46.5	25	A	AALAVGLAALAAGYAERGIGS	A	1.1	6.88	
16	Q48302|Q48302	3	1972.0741	1.0	28	49	0	66.8	26	A	AALAVGLAALAAGYAERGIGSA	A	1.1	6.88	
16	Q48302|Q48302	3	2270.2382	-0.1	28	53	0	47.9	25	A	AALAVGLAALAAGYAERGIGSAAVGA	I	1.2	6.88	
17	Q9HSA8|Q9HSA8	1	569.4152	0.2	33	37	0	28.5	17	G	LLLLV	L	3.9	6.02	
17	Q9HSA8|Q9HSA8	1	830.4538	1.3	289	295	0	30.9	24	T	FVLPQEV	T	0.9	3.3	
17	Q9HSA8|Q9HSA8	2	1128.5339	-1.3	124	132	0	59.8	26	A	FLEVDDYKT	A	-0.6	3.7	
17	Q9HSA8|Q9HSA8	2	1199.571	0.3	124	133	0	62.4	26	A	FLEVDDYKTA	V	-0.4	3.7	
17	Q9HSA8|Q9HSA8	2	1200.551	-1.1	348	358	0	28.9	25	A	DVDPADLEEKA	E	-1.0	3.42	
17	Q9HSA8|Q9HSA8	2	1274.5965	-0.1	83	92	0	46.2	27	T	YTFDMRTQTI	D	-0.6	6.7	
17	Q9HSA8|Q9HSA8	2	1324.5089	0.2	308	321	0	21.9	17	A	GSDVGDGGSDLESM	A	-0.6	2.78	
17	Q9HSA8|Q9HSA8	2	1559.7104	0.8	166	178	0	39.6	26	I	RTELDEPTDEWGI	R	-1.4	3.5	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
17	Q9HSA8|Q9HSA8	2	1785.8632	-0.2	332	347	0	29.6	27	I	GLDNIDEILNQITEEA	D	-0.4	2.8	
17	Q9HSA8|Q9HSA8	2	1855.8912	0.0	359	376	0	67.8	28	A	EAVQRGEDAGLQDAGEVI	E	-0.5	3.5	
17	Q9HSA8|Q9HSA8	2	1898.9473	-0.5	331	347	0	55.1	28	L	IGLDNIDEILNQITEEA	D	-0.1	2.8	
17	Q9HSA8|Q9HSA8	2	1926.9283	-1.1	181	197	0	56.3	28	V	ESVEVREVNPSQEVQQA	M	-1.0	3.8	
17	Q9HSA8|Q9HSA8	3	1987.9884	1.1	145	161	0	44.1	29	A	VLGDMELDDTLNKRQEI	N	-0.7	3.84	
17	Q9HSA8|Q9HSA8	2	2091.0008	-0.7	322	339	0	52.0	28	M	AFDEETRELIGLDNIDEI	L	-0.4	3.32	
17	Q9HSA8|Q9HSA8	3	2182.0978	-0.7	179	197	0	36.5	28	I	RVESVEVREVNPSQEVQQA	M	-0.9	4.26	
17	Q9HSA8|Q9HSA8	2	2203.1677	-0.6	61	80	0	39.5	27	V	FGEYRGLLEPGINVIPPFVS	R	0.4	4.26	
18	Q9HRL3|Q9HRL3	1	685.4374	-0.9	252	258	0	26.3	26	F	SVVGLLV	L	2.7	6.02	
18	Q9HRL3|Q9HRL3	1	887.4752	1.7	2	10	0	26.1	25	M	AGALEFIPA	I	1.2	3.3	
18	Q9HRL3|Q9HRL3	1	991.4143	1.0	350	357	0	26.5	22	I	SQYGYMML	G	0.0	5.86	
18	Q9HRL3|Q9HRL3	2	1012.5375	-3.0	286	295	0	35.9	25	V	SALIHAATMV	A	1.5	7.84	
18	Q9HRL3|Q9HRL3	1	1103.5651	0.0	586	595	0	39.3	27	A	WLLYSGPAPT	K	0.2	5.92	
18	Q9HRL3|Q9HRL3	1	1221.5918	-0.2	411	421	0	32.5	27	V	TYYTFLSGSLA	L	0.6	5.86	
18	Q9HRL3|Q9HRL3	1	1301.7231	0.2	442	454	0	31.7	24	A	LIYGAGDSPILLA	A	1.2	3.1	
18	Q9HRL3|Q9HRL3	1	1311.6169	-1.1	274	285	0	31.9	27	T	WLPDAMEGPTPV	S	-0.2	3	
18	Q9HRL3|Q9HRL3	2	1561.7624	0.3	634	648	0	67.1	28	A	DTFDQGVIDGIVNAV	S	0.5	2.82	
18	Q9HRL3|Q9HRL3	2	1642.8719	-0.9	579	595	0	49.6	27	A	LGGAGLAWLLYSGPAPT	K	0.7	5.92	
18	Q9HRL3|Q9HRL3	2	1826.9931	-0.3	577	595	0	61.1	26	A	LALGGAGLAWLLYSGPAPT	K	0.9	5.92	
18	Q9HRL3|Q9HRL3	2	1916.9592	0.5	630	648	0	81.9	28	L	ARGADTFDQGVIDGIVNAV	S	0.3	3.6	
18	Q9HRL3|Q9HRL3	2	2093.9734	-0.7	607	622	0	56.1	27	T	LLYNNYYQDEYQVWLA	K	-0.6	3	
18	Q9HRL3|Q9HRL3	2	2106.0245	0.4	267	285	0	55.7	29	S	AQFPLHTWLPDAMEGPTPV	S	-0.1	4.06	
19	Q9HPQ5|Q9HPQ5	1	567.3996	-1.9	54	58	0	30.4	17	H	IPLLL	A	2.9	6.02	
19	Q9HPQ5|Q9HPQ5	1	617.3206	-3.9	306	312	0	34.7	27	D	AMAAIAA	S	2.2	6.02	
19	Q9HPQ5|Q9HPQ5	1	674.4367	-1.0	193	198	0	24.6	21	G	AFVLLL	A	3.4	6.02	
19	Q9HPQ5|Q9HPQ5	1	731.4582	0.7	192	198	0	24.3	23	H	GAFVLLL	A	2.8	6.02	
19	Q9HPQ5|Q9HPQ5	1	745.3792	0.3	462	468	0	43.3	27	T	NMLALNA	N	0.9	6.02	
19	Q9HPQ5|Q9HPQ5	1	1103.4982	-0.4	339	349	0	26.9	26	A	SEDADAGVVEI	E	0.1	2.84	
19	Q9HPQ5|Q9HPQ5	2	1181.702	-0.9	85	97	0	42.0	21	A	AELGIVGALVGLA	S	1.9	3.3	
19	Q9HPQ5|Q9HPQ5	2	1317.63	0.7	485	496	0	51.6	27	V	VADEVKDLAEET	R	-0.5	3.5	
19	Q9HPQ5|Q9HPQ5	2	1415.6351	-0.1	297	309	0	39.1	25	V	RLDPDVENDAMAA	I	-0.6	3.5	
19	Q9HPQ5|Q9HPQ5	2	1460.7107	-1.6	522	535	0	31.4	28	A	RTADESVQDAISAV	D	-0.2	3.7	
19	Q9HPQ5|Q9HPQ5	2	1517.7461	0.7	448	461	0	51.4	28	I	SEIVDLISDVAEQT	N	0.2	2.84	
19	Q9HPQ5|Q9HPQ5	2	1993.9117	0.5	533	552	0	75.6	26	I	SAVDAVVDAFGTVAENAEET	D	0.3	2.8	
19	Q9HPQ5|Q9HPQ5	3	2056.0072	-0.7	228	245	0	39.2	28	A	QQVEDLEARQAEIEAEKA	E	-1.1	3.88	
20	P33741|HTR1	2	1547.67	-0.1	244	257	0	76.7	24	A	NDQRTELDSAADDV	Q	-1.4	3.36	
20	P33741|HTR1	2	1734.7809	1.2	350	367	0	52.9	26	A	RAGGNADGDGFSVVADEV	K	-0.2	3.5	
20	P33741|HTR1	2	1902.8555	-1.8	244	260	0	104.4	26	A	NDQRTELDSAADDVQQV	S	-1.3	3.36	
20	P33741|HTR1	3	2096.0031	0.5	186	204	0	50.0	28	T	VGTAFNQMMDDLQATVRTV	T	0.1	3.88	
20	P33741|HTR1	2	2318.0258	-2.0	240	260	0	71.6	24	I	ESQANDQRTELDSAADDVQQV	S	-1.3	3.32	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
20	P33741|HTR1	3	2646.2369	-0.5	237	260	0	49.9	28	V	SKIESQANDQRTELDSAADDVQQV	S	-1.2	3.68	
21	Q9HN95|Q9HN95	1	657.301	0.5	58	62	0	25.3	22	A	DYFLT	Y	0.2	3.1	
21	Q9HN95|Q9HN95	2	940.5018	1.1	454	463	0	35.0	21	V	LAPGSPGFPV	-	0.6	6.02	
21	Q9HN95|Q9HN95	1	1034.547	-0.5	197	205	0	33.2	26	T	NTFMLLLPS	L	1.1	6.02	
21	Q9HN95|Q9HN95	1	1089.5859	-1.3	297	305	0	31.7	26	V	AYWLVPQIT	G	0.7	5.92	
21	Q9HN95|Q9HN95	2	1103.6379	0.5	143	151	0	44.6	22	A	WYTILPKLA	G	0.6	9.72	
21	Q9HN95|Q9HN95	2	1450.8224	-0.8	140	151	0	32.6	23	A	YLAWYTILPKLA	G	0.8	9.52	
21	Q9HN95|Q9HN95	2	1645.8716	0.8	9	24	0	39.7	27	A	AITILNGFAPELPFGS	A	0.8	3.3	
21	Q9HN95|Q9HN95	2	1716.9087	-0.3	9	25	0	48.9	27	A	AITILNGFAPELPFGSA	N	0.9	3.3	
21	Q9HN95|Q9HN95	2	1931.0404	-0.1	6	24	0	53.5	26	T	TLAAITILNGFAPELPFGS	A	1.0	3.3	
21	Q9HN95|Q9HN95	2	2002.0775	-0.7	6	25	0	34.9	26	T	TLAAITILNGFAPELPFGSA	N	1.0	3.3	
22	Q9HRL1|Q9HRL1	1	613.3112	0.3	16	20	0	29.0	21	E	FYALT	L	1.3	5.92	
22	Q9HRL1|Q9HRL1	1	628.416	0.0	379	384	0	29.5	25	G	TIALLV	A	2.9	6.02	
22	Q9HRL1|Q9HRL1	1	654.3377	0.9	259	264	0	30.0	22	N	TGAFLF	V	1.7	6.02	
22	Q9HRL1|Q9HRL1	1	685.4374	-0.9	378	384	0	26.4	26	V	GTIALLV	A	2.4	6.02	
22	Q9HRL1|Q9HRL1	1	850.4225	-1.1	184	190	0	45.8	28	I	DWSLLFA	A	1.0	3.1	
22	Q9HRL1|Q9HRL1	1	962.5107	-3.2	73	82	0	30.6	27	L	IGALSSGVML	Y	1.8	6.02	Oxidation (M)
22	Q9HRL1|Q9HRL1	2	1143.6328	0.8	309	318	0	31.2	26	A	GFLSKYVLFA	G	1.3	9.72	
22	Q9HRL1|Q9HRL1	2	1179.6362	1.8	296	306	0	37.3	24	T	VFMFSLAGLPV	G	2.0	6.02	
22	Q9HRL1|Q9HRL1	2	1235.4942	0.0	3	13	0	36.5	20	A	SHDYLDDADSV	A	-0.9	3.42	
22	Q9HRL1|Q9HRL1	2	1940.948	-1.4	350	366	0	66.2	28	A	LWIEDPRDDLSLSGQPT	G	-0.8	3.5	
22	Q9HRL1|Q9HRL1	2	2142.0211	0.0	130	149	0	65.4	28	T	ASVPFHFWAPEAYEGAPAPV	S	0.2	4.24	
23	Q9HPB1|SECY	1	870.5249	-0.7	291	298	0	32.2	16	A	SVLPMILV	R	2.5	6.02	
23	Q9HPB1|SECY	1	910.5852	0.3	430	439	0	44.0	21	T	VIGGALVGLL	A	2.5	6.02	
23	Q9HPB1|SECY	2	1086.4883	0.1	55	63	0	44.6	24	A	GNDFFGQFR	S	-0.8	6.78	
23	Q9HPB1|SECY	2	1112.5906	1.2	334	343	0	50.5	25	T	GGLFYYLAPI	Y	1.2	5.86	
23	Q9HPB1|SECY	2	1282.7683	0.5	430	443	0	27.3	20	T	VIGGALVGLLAVMA	N	2.5	6.02	
23	Q9HPB1|SECY	2	1309.7969	1.2	85	97	0	74.5	19	A	SIVLQLLGGANLL	G	1.6	6.02	
23	Q9HPB1|SECY	2	1870.8962	-0.3	55	72	0	71.4	27	A	GNDFFGQFRSLLAGGQGT	V	-0.2	6.78	
24	Q9HMH4|Q9HMH4	1	1172.5561	-0.6	154	164	0	29.5	27	M	VGEDENAIDVL	A	0.1	2.84	
24	Q9HMH4|Q9HMH4	1	1257.5037	1.4	57	67	0	39.0	20	S	FSYDDPDADTL	G	-0.9	2.74	
24	Q9HMH4|Q9HMH4	2	1278.6092	0.3	229	240	0	43.7	27	A	KDGIIEGDGNYV	D	-0.6	3.7	
24	Q9HMH4|Q9HMH4	1	1344.5358	-0.5	56	67	0	41.2	20	A	SFSYDDPDADTL	G	-0.9	2.74	
24	Q9HMH4|Q9HMH4	2	1376.7089	-0.6	276	287	0	38.6	27	T	RLQPYSDGPVFV	E	-0.2	6.7	
24	Q9HMH4|Q9HMH4	2	1541.7362	0.1	170	183	0	44.5	27	A	GSVLGYYSPSEDRI	A	-0.5	4.08	
24	Q9HMH4|Q9HMH4	2	1567.7114	-1.6	495	509	0	44.1	26	V	NAPTVDQLDAVHDSS	-	-0.6	3.6	
24	Q9HMH4|Q9HMH4	2	1612.7733	-0.2	169	183	0	81.9	27	R	AGSVLGYYSPSEDRI	A	-0.3	4.08	
24	Q9HMH4|Q9HMH4	3	1882.9173	-0.9	167	183	0	31.3	27	S	NRAGSVLGYYSPSEDRI	A	-0.7	6.9	
25	O54610|O54610	1	555.3996	1.1	243	247	0	28.5	20	V	VLLLV	S	4.0	6.02	
25	O54610|O54610	1	741.4272	0.5	17	23	0	41.1	24	A	LLSPEIA	S	1.1	3.3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
25	O54610|O54610	1	1008.44	-0.6	319	328	0	35.3	27	A	SGGDFDAEVI	G	0.1	2.88	
25	O54610|O54610	2	1243.6448	1.5	104	116	0	31.8	29	I	AGELIGGPLAFEA	K	0.8	3.12	
25	O54610|O54610	2	1389.6354	-1.2	90	101	0	33.9	26	M	SFQFGTNFPQFA	T	-0.1	6.02	
25	O54610|O54610	2	1457.7766	-0.4	102	116	0	61.2	26	A	TIAGELIGGPLAFEA	K	1.0	3.12	
25	O54610|O54610	2	1590.789	0.5	295	308	0	58.6	28	L	DALTDPRTENLFTV	S	-0.4	3.7	
25	O54610|O54610	2	1790.905	0.1	293	308	0	37.9	27	K	SLDALTDPRTENLFTV	S	-0.2	3.7	
25	O54610|O54610	2	1950.9575	0.9	309	328	0	73.3	28	V	SLPGIGSFLASGGDFDAEVI	G	0.7	2.88	
26	Q9HNV1|Q9HNV1	1	1013.4342	1.3	95	103	0	25.4	23	Q	AIEYDFDAA	T	0.1	2.88	
26	Q9HNV1|Q9HNV1	2	1268.5673	0.6	56	65	0	38.1	25	F	SDYEEWTLRA	E	-1.3	3.82	
26	Q9HNV1|Q9HNV1	2	1965.8552	-0.5	77	94	0	105.4	24	I	QTFDNAGNQVDEETLTGQ	A	-1.2	2.84	
26	Q9HNV1|Q9HNV1	2	2116.9662	0.2	137	156	0	82.0	26	A	SFEQTQRGGSTSQIGSAFET	R	-0.8	4.26	
26	Q9HNV1|Q9HNV1	2	2149.9764	-1.3	77	96	0	61.5	26	I	QTFDNAGNQVDEETLTGQAI	E	-0.8	2.84	
26	Q9HNV1|Q9HNV1	3	2735.2787	-1.4	137	161	0	29.9	28	A	SFEQTQRGGSTSQIGSAFETRPYTT	D	-1.0	7.04	
26	Q9HNV1|Q9HNV1	3	2855.2886	0.9	108	132	0	30.4	26	T	RADVQIEGTTPGTETFQWSYDPEQT	V	-1.2	3.5	
26	Q9HNV1|Q9HNV1	3	3259.5018	-0.2	181	211	0	78.2	27	A	TDAGGSVTGAERDVRDAIEFYNAGEFNQAVT	N	-0.5	3.76	
27	Q9HRL2|Q9HRL2	1	600.3635	0.3	152	156	0	26.7	21	F	LIGIW	G	2.3	6.02	
27	Q9HRL2|Q9HRL2	2	909.5072	-0.2	272	278	0	26.5	23	A	LLRFNFT	M	0.6	11.04	
27	Q9HRL2|Q9HRL2	2	1051.5736	0.6	262	271	0	30.4	24	A	GVLLKMGTYA	L	0.9	9.72	
27	Q9HRL2|Q9HRL2	2	1401.7041	0.4	244	256	0	46.1	29	T	WLPDAHVQAPTPA	S	-0.2	4.94	
28	Q9HS10|Q9HS10	1	1004.4662	-0.5	140	148	0	48.3	27	V	NTDLDIDSI	T	-0.3	2.82	
28	Q9HS10|Q9HS10	2	1293.5765	0.5	187	197	0	43.9	25	A	SGTYDYFIESI	L	0.0	3	
28	Q9HS10|Q9HS10	2	1321.703	2.4	271	282	0	42.2	24	S	GAYTPLSRPLFT	Y	0.0	9.84	
28	Q9HS10|Q9HS10	2	1385.715	0.7	325	336	0	32.8	27	A	QREQLDALTEAI	D	-0.6	3.82	
28	Q9HS10|Q9HS10	2	1698.7948	0.1	252	268	0	50.4	26	L	AVDDGDGEPVKPSLETA	R	-0.7	3.42	
28	Q9HS10|Q9HS10	2	1811.8789	-1.4	251	268	0	78.6	28	A	LAVDDGDGEPVKPSLETA	R	-0.4	3.42	
28	Q9HS10|Q9HS10	2	2330.1754	-0.4	316	336	0	41.5	28	V	GYVPLSQEAQREQLDALTEAI	D	-0.4	3.68	
29	Q9HHR4|Q9HHR4	1	567.3996	-1.9	262	266	0	30.4	17	L	IPLLI	T	3.0	6.02	
29	Q9HHR4|Q9HHR4	1	628.416	0.0	356	361	0	42.4	25	A	ITIALV	A	3.0	6.02	
29	Q9HHR4|Q9HHR4	1	684.417	-1.6	369	376	0	39.7	27	L	GVLGGVIA	V	2.2	6.02	
29	Q9HHR4|Q9HHR4	1	731.4582	-0.3	553	559	0	36.4	23	P	IFLGGLL	R	2.6	6.02	
29	Q9HHR4|Q9HHR4	1	755.4541	1.3	372	380	0	34.1	25	L	GGVIAVVAA	F	2.4	6.02	
29	Q9HHR4|Q9HHR4	2	845.5123	1.2	554	561	0	26.2	19	I	FLGGLLRA	G	1.3	11.04	
29	Q9HHR4|Q9HHR4	2	887.5593	1.2	553	560	0	18.9	15	P	IFLGGLLR	A	1.7	11.04	
29	Q9HHR4|Q9HHR4	1	910.5852	-0.1	632	641	0	23.3	21	L	LGGVALVALV	A	2.7	6.02	
30	Q9HMU9|Q9HMU9	1	617.3173	1.5	2	7	0	42.5	27	M	SWAAIA	R	1.4	6.02	
30	Q9HMU9|Q9HMU9	1	674.4367	-1.0	140	145	0	24.6	21	A	VFALLL	A	3.4	6.02	
30	Q9HMU9|Q9HMU9	1	700.4007	0.3	49	54	0	41.5	29	V	DLLDLL	S	1.4	2.92	
30	Q9HMU9|Q9HMU9	2	716.3527	-3.4	228	234	0	43.4	26	V	MNTPAAL	A	0.5	6.02	
30	Q9HMU9|Q9HMU9	1	971.5539	0.9	46	54	0	27.6	26	T	TAVDLLDLL	S	1.5	2.92	
30	Q9HMU9|Q9HMU9	1	1040.5754	-0.5	49	58	0	60.7	24	V	DLLDLLSGPV	N	1.0	2.92	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
30	Q9HMU9|Q9HMU9	1	1069.4393	-0.4	37	45	0	25.0	21	A	GYGYFFDTT	T	-0.3	3.1	
30	Q9HMU9|Q9HMU9	2	1311.7286	0.4	46	58	0	43.9	24	T	TAVDLLDLLSGPV	N	1.1	2.92	
31	Q9HR04|Q9HR04	2	1239.6248	0.2	76	87	0	53.6	25	S	IYLGGGEGGRYV	A	0.0	6.82	
31	Q9HR04|Q9HR04	2	1279.6085	-0.1	128	139	0	49.0	27	A	DVFWSIDAGSLA	Y	0.8	2.92	
31	Q9HR04|Q9HR04	2	1299.6459	0.3	277	288	0	52.0	27	V	FADRPDAPLDLA	F	-0.2	3.6	
31	Q9HR04|Q9HR04	2	1306.638	0.8	266	276	0	33.9	28	A	GLTNHYYPMLV	F	0.2	7.7	
31	Q9HR04|Q9HR04	2	1640.6988	0.6	114	127	0	28.1	23	A	NNIVTEYENDTMQA	D	-1.1	2.94	
31	Q9HR04|Q9HR04	2	1950.8344	-0.6	94	109	0	97.7	23	I	NQYYDDFSATQQTQRS	S	-1.9	3.88	
32	Q9HRT0|Q9HRT0	1	545.3247	-4.8	71	75	0	31.7	26	T	LMGLI	F	2.7	6.02	
32	Q9HRT0|Q9HRT0	1	858.5215	0.5	16	23	0	20.7	20	A	ALLVPFLS	R	2.2	6.02	
32	Q9HRT0|Q9HRT0	2	1071.556	0.6	558	567	0	55.7	28	G	RLLGDTDSPV	S	-0.3	3.88	
33	Q9HML5|Q9HML5	1	918.4083	-1.2	248	256	0	29.4	27	A	NVFGDPEAA	I	-0.2	3	
33	Q9HML5|Q9HML5	2	1240.5394	-0.1	104	113	0	33.7	23	A	NEYDTEMRLA	D	-1.3	3.82	
33	Q9HML5|Q9HML5	2	1303.662	0.3	193	204	0	67.7	27	A	SREIVDSGVETI	T	0.0	3.82	
33	Q9HML5|Q9HML5	2	1922.9473	0.1	60	78	0	35.4	28	S	SQLDTSVLTGDGSSTVFPI	T	0.3	2.92	
33	Q9HML5|Q9HML5	2	1927.9051	0.4	287	304	0	33.2	27	A	FVQPDGDTPPLDLEIDGT	T	-0.5	2.72	
33	Q9HML5|Q9HML5	2	2356.0707	0.3	163	185	0	47.6	26	S	AADELPDADSDTLDGFVDHVVGV	D	0.0	3.18	
33	Q9HML5|Q9HML5	3	3243.6272	-0.2	257	286	0	56.4	29	A	ISPDQRYGQNQQLQQAIGQADNAIGYIALA	F	-0.5	3.88	
34	Q9HN94|Q9HN94	2	1159.551	-0.6	66	76	0	44.0	27	T	SGDVTHGFELV	G	0.2	4.06	
34	Q9HN94|Q9HN94	2	1280.5786	0.6	18	28	0	42.5	26	A	DNFRDPGVYQA	D	-1.2	3.88	
34	Q9HN94|Q9HN94	1	1289.4936	-0.5	29	39	0	22.7	17	A	DDDSYDVYVEA	R	-1.0	2.72	
34	Q9HN94|Q9HN94	1	1360.5307	-0.4	28	39	0	30.9	18	Q	ADDDSYDVYVEA	R	-0.7	2.72	
34	Q9HN94|Q9HN94	2	1435.7096	-0.1	40	52	0	67.2	27	A	RQFAFSPGTSEPI	R	-0.4	6.98	
34	Q9HN94|Q9HN94	2	1755.8679	0.7	120	135	0	33.3	28	G	SIEVVPQSEFTPPQQA	A	-0.4	3.12	
34	Q9HN94|Q9HN94	2	2252.9135	-0.4	18	36	0	69.8	18	A	DNFRDPGVYQADDDSYDVY	V	-1.4	3.22	
34	Q9HN94|Q9HN94	2	2541.2534	-1.1	66	90	0	40.7	29	T	SGDVTHGFELVGTNVNTMVIPGQVA	Q	0.4	4.06	
35	Q9HRR2|Q9HRR2	2	1107.5699	0.1	42	50	0	37.0	26	V	DYLELLETL	Y	0.3	2.94	
35	Q9HRR2|Q9HRR2	2	1127.5764	-0.4	130	138	0	38.4	25	T	DLNFGFFLR	S	0.5	6.78	
35	Q9HRR2|Q9HRR2	2	1296.7078	1.2	212	223	0	48.0	26	L	SIPLVGDWVAQL	M	1.0	3.1	
35	Q9HRR2|Q9HRR2	2	1319.7224	-0.3	40	50	0	45.9	25	R	IVDYLELLETL	Y	1.0	2.94	
35	Q9HRR2|Q9HRR2	2	1496.8239	0.6	210	223	0	56.2	25	M	SLSIPLVGDWVAQL	M	1.0	3.1	
36	Q9HND8|VATI	1	555.3996	1.1	668	672	0	28.5	20	V	LVLLV	G	4.0	6.02	
36	Q9HND8|VATI	1	620.284	0.6	388	393	0	30.3	28	F	MIGDLG	Y	1.0	3.1	Oxidation (M)
36	Q9HND8|VATI	1	700.4007	0.3	131	136	0	41.5	29	G	IDLDLL	S	1.5	2.92	
36	Q9HND8|VATI	2	1912.8691	0.8	336	353	0	87.2	26	A	SFDETDSPPVIQDNPGPV	S	-0.8	2.78	
38	Q9HMY1|Q9HMY1	1	555.3632	0.4	306	310	0	19.4	18	H	LPTII	E	2.1	6.02	
38	Q9HMY1|Q9HMY1	1	572.3322	0.7	1281	1285	0	32.9	21	G	WAVVV	T	2.7	6.02	
38	Q9HMY1|Q9HMY1	1	656.4109	-0.3	536	541	0	26.2	26	T	LVELLA	E	2.3	3.3	
39	Q9HHI2|Q9HHI2	1	569.4152	0.2	37	41	0	28.5	17	D	IILIV	F	4.3	6.02	
39	Q9HHI2|Q9HHI2	1	731.4582	0.7	41	47	0	24.3	23	I	VFGAILL	M	2.9	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
39	Q9HHI2|Q9HHI2	1	743.4581	-0.1	206	212	0	22.5	21	I	APFALLL	G	2.3	6.02	
40	Q9HQF4|Q9HQF4	2	1031.4634	-1.9	208	215	0	26.8	24	A	DKEYFMTV	K	-0.5	4.08	
40	Q9HQF4|Q9HQF4	2	1047.5349	0.6	237	245	0	31.6	28	R	TRNPDVFTV	N	-0.4	6.78	
40	Q9HQF4|Q9HQF4	2	1155.5634	0.5	366	375	0	41.6	26	S	DIFGKLMDFA	G	0.6	3.88	
40	Q9HQF4|Q9HQF4	1	1182.5405	-0.5	102	113	0	27.5	25	A	TEDGDPSVPGPI	V	-0.7	2.88	
40	Q9HQF4|Q9HQF4	2	1276.6663	0.2	253	264	0	28.6	26	R	TLHPEDGSPIIV	E	0.1	4.06	
40	Q9HQF4|Q9HQF4	2	1665.8111	-0.3	232	245	0	34.2	27	V	DYSPRTRNPDVFTV	N	-1.1	6.84	
40	Q9HQF4|Q9HQF4	3	2268.0481	-0.8	226	245	0	39.4	27	S	MAGEDVDYSPRTRNPDVFTV	N	-0.7	3.96	
41	Q9HRU7|Q9HRU7	1	679.3363	-4.7	400	406	0	28.3	24	V	MGAAAFL	I	1.9	6.02	
41	Q9HRU7|Q9HRU7	1	684.417	-1.6	33	40	0	28.8	27	L	AVAAIGIA	F	2.5	6.02	
42	Q9HS86|Q9HS86	2	1488.7195	-0.2	369	382	0	55.4	28	I	DGITALIEDIAEET	N	0.1	2.8	
42	Q9HS86|Q9HS86	2	1589.7937	1.0	457	470	0	30.2	28	A	EGVLRDFEAIVDEV	A	0.2	3.5	
43	Q9HS47|Q9HS47	1	613.3799	-0.2	153	159	0	41.8	29	I	LAAAVGI	A	2.5	6.02	
43	Q9HS47|Q9HS47	1	684.417	0.4	153	160	0	40.0	27	I	LAAAVGIA	A	2.4	6.02	
43	Q9HS47|Q9HS47	1	755.4541	1.3	153	161	0	25.5	25	I	LAAAVGIAA	V	2.3	6.02	
43	Q9HS47|Q9HS47	1	868.5382	-0.5	152	161	0	26.5	23	A	ILAAAVGIAA	V	2.6	6.02	
44	P33518|COX1	1	714.468	-0.6	137	142	0	17.5	13	Y	FIPLLI	D	3.0	6.02	
44	P33518|COX1	1	714.4713	-3.6	261	266	0	32.7	13	A	LIMLLL	D	3.6	6.02	
44	P33518|COX1	1	991.5742	-0.8	135	142	0	28.4	21	G	NYFIPLLI	D	1.6	5.92	
44	P33518|COX1	1	1003.4135	-0.3	539	546	0	46.0	23	T	DPWDLEET	D	-1.7	2.84	
44	P33518|COX1	2	1266.7012	1.7	132	142	0	30.6	24	A	AFGNYFIPLLI	D	1.6	5.92	
45	Q9HP84|HTR4	1	555.3996	1.1	44	48	0	28.5	20	L	LVILV	I	4.1	6.02	
46	Q9HHP3|Q9HHP3	1	1185.519	0.7	100	110	0	39.8	24	A	LTPDEFGGSYT	S	-0.6	3	
46	Q9HHP3|Q9HHP3	2	1281.5514	0.4	339	349	0	63.3	24	A	DGTQFWLGEET	L	-1.0	2.94	
46	Q9HHP3|Q9HHP3	2	1330.7503	4.5	2	12	0	25.8	23	M	VDSICTRRRLL	A	0.0	10.8	
46	Q9HHP3|Q9HHP3	2	1610.8304	-0.7	76	89	0	41.0	26	S	TVLELFNLHPDSQV	M	0.2	4.06	
47	Q9HRL8|Q9HRL8	1	703.3938	0.0	103	109	0	28.0	27	I	ASLGLIM	G	2.1	6.02	
47	Q9HRL8|Q9HRL8	2	1319.7337	0.7	146	157	0	34.5	22	V	LFTGTLQLSEIV	A	1.1	3.3	
47	Q9HRL8|Q9HRL8	2	1854	0.3	25	42	0	110.7	26	I	SVNRVGPWGLGTIVVDSV	R	0.7	6.78	
48	P57684|ATKA	1	515.3319	1.4	15	19	0	30.5	29	F	TILAV	L	2.7	6.02	
48	P57684|ATKA	1	555.3996	1.1	556	560	0	28.5	20	G	VIIIV	S	4.4	6.02	
48	P57684|ATKA	1	621.356	-0.3	406	410	0	13.3	13	I	LMFVI	L	3.4	6.02	
48	P57684|ATKA	1	628.416	1.1	15	20	0	23.4	23	F	TILAVL	V	2.9	6.02	
48	P57684|ATKA	1	642.4105	0.9	91	95	0	26.1	13	C	IWVLL	F	3.1	6.02	
48	P57684|ATKA	1	731.4582	0.7	548	554	0	24.3	23	P	AFVGLLI	G	2.9	6.02	
49	Q9HR41|Q9HR41	1	755.4541	1.3	191	199	0	25.4	25	L	AGVVGVIAA	I	2.4	6.02	
50	Q9HN37|Q9HN37	1	657.301	0.5	512	516	0	25.3	22	R	YDFIT	R	0.4	3.1	
50	Q9HN37|Q9HN37	1	939.5753	1.0	123	132	0	28.4	22	W	QLGGVLVIAA	G	2.0	6.02	
50	Q9HN37|Q9HN37	1	1010.6124	-1.4	125	136	0	23.5	22	L	GGVLVIAAGLAA	L	2.2	6.02	
51	O54596|O54596	1	555.3632	0.4	261	265	0	19.4	18	A	LPTLL	T	1.8	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
51	O54596|O54596	1	626.4003	1.0	223	228	0	28.3	21	A	VLSLPV	A	2.3	6.02	
51	O54596|O54596	1	757.4738	-1.2	302	308	0	23.0	22	L	GFPVLLL	V	2.3	6.02	
51	O54596|O54596	1	771.4895	-1.0	136	142	0	22.1	20	S	VFAPLLL	G	2.7	6.02	
51	O54596|O54596	2	981.6474	1.2	261	269	0	23.2	13	A	LPTLLTLLV	A	2.2	6.02	
51	O54596|O54596	2	1218.7013	0.7	131	142	0	22.3	22	A	FVGGSVFAPLLL	G	2.0	6.02	
52	Q9HN25|Q9HN25	1	610.3326	0.3	96	101	0	28.7	23	V	LGPDPL	S	0.1	3.1	
52	Q9HN25|Q9HN25	1	1085.5241	-0.1	96	106	0	39.1	26	V	LGPDPLSADTT	V	-0.3	2.92	
52	Q9HN25|Q9HN25	1	1125.5342	-1.2	132	141	0	35.9	26	A	NFIEPGSLSY	V	-0.1	3.3	
52	Q9HN25|Q9HN25	1	1283.6609	0.3	96	108	0	46.4	26	V	LGPDPLSADTTVV	V	0.4	2.92	
52	Q9HN25|Q9HN25	2	1657.81	0.5	132	145	0	66.5	28	A	NFIEPGSLSYVYRN	M	-0.4	6.82	
53	P25964|BACS1	1	788.4221	0.0	177	183	0	43.6	24	L	VWLFGPA	G	1.4	6.02	
53	P25964|BACS1	1	905.595	-0.9	38	46	0	47.0	13	A	LAPLAIIPV	F	2.4	6.02	
53	P25964|BACS1	1	976.6321	0.7	37	46	0	21.9	13	S	ALAPLAIIPV	F	2.3	6.02	
53	P25964|BACS1	1	1123.7005	-1.0	38	48	0	28.4	20	A	LAPLAIIPVFA	G	2.3	6.02	
53	P25964|BACS1	2	1316.6765	-0.1	177	189	0	42.8	27	L	VWLFGPAGIGEAT	A	0.8	3.3	
55	O52005|O52005	1	555.3996	1.1	162	166	0	28.5	20	G	VLIIV	M	4.2	6.02	
55	O52005|O52005	2	1005.5648	0.6	35	44	0	29.0	23	I	KFGVAGPLFA	G	1.1	10.1	
56	Q9HS26|Q9HS26	1	555.3996	1.1	357	361	0	28.5	20	L	VLLIV	A	4.1	6.02	
56	Q9HS26|Q9HS26	1	973.5484	-1.0	320	328	0	34.5	25	L	SVLPFVEAI	N	1.7	3.3	
57	Q9HRR1|Q9HRR1	1	567.3996	-1.9	187	191	0	30.4	17	T	IPILI	I	3.1	6.02	
57	Q9HRR1|Q9HRR1	1	626.4479	0.3	189	193	0	14.5	13	P	ILIIR	S	2.6	11.04	
57	Q9HRR1|Q9HRR1	1	668.4473	-1.6	186	191	0	27.5	14	N	TIPILI	I	2.5	6.02	
57	Q9HRR1|Q9HRR1	3	1745.8472	-0.2	73	88	0	29.2	28	I	DDNGDIKGVFPDVKEV	E	-0.7	3.76	
57	Q9HRR1|Q9HRR1	2	2719.1198	-1.4	151	174	0	100.2	18	V	NIDEFDDYDTWENDYGDAGIGKPA	K	-1.3	3.16	
58	Q9HN17|Q9HN17	1	643.3541	0.6	295	300	0	41.3	31	E	VIQDGL	L	0.9	3.1	
58	Q9HN17|Q9HN17	1	656.4109	-0.3	300	305	0	43.9	26	G	LLDLLA	D	2.3	3.1	
60	Q9HR23|Q9HR23	1	600.3635	-0.3	138	142	0	22.8	21	V	WLVAL	G	2.5	6.02	
60	Q9HR23|Q9HR23	1	634.369	1.6	281	286	0	27.2	27	G	FIAIAT	Y	2.5	6.02	
60	Q9HR23|Q9HR23	1	769.4949	-0.9	75	81	0	28.9	21	G	LEGLLII	S	2.4	3.3	
61	Q9HNG4|Q9HNG4	1	690.4316	1.2	368	373	0	21.2	21	F	FLSLLV	V	2.9	6.02	
62	O54523|O54523	1	681.4425	0.9	81	87	0	26.0	22	L	PIAGVIL	V	2.4	6.02	
62	O54523|O54523	1	726.464	-1.5	326	332	0	27.7	25	L	IAQLAVL	L	2.3	6.02	
62	O54523|O54523	2	763.4116	0.4	100	106	0	29.3	26	G	ITTGYPI	A	0.6	5.92	
62	O54523|O54523	1	774.431	-1.2	94	101	0	27.5	26	A	GLMAIGIT	T	1.9	6.02	
63	Q9HS95|Q9HS95	1	543.3268	-0.7	41	45	0	32.6	30	I	IDAIL	F	2.2	3.1	
64	Q9HML7|Q9HML7	1	582.3741	0.5	49	54	0	25.3	25	A	VVGIPV	A	2.5	6.02	
64	Q9HML7|Q9HML7	1	782.4902	0.6	51	58	0	23.3	22	V	GIPVATLL	G	1.9	6.02	
65	Q9HRR3|Q9HRR3	1	641.3207	0.0	221	227	0	21.8	16	I	PPMAGAV	A	0.9	6.02	
65	Q9HRR3|Q9HRR3	1	690.3952	1.2	215	220	0	23.5	23	F	DLAFLI	P	2.2	3.1	
65	Q9HRR3|Q9HRR3	1	844.4517	0.8	218	225	0	31.2	29	A	FLIPPMAG	A	1.4	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
65	Q9HRR3|Q9HRR3	1	1014.5572	-0.1	218	227	0	33.2	27	A	FLIPPMAGAV	A	1.7	6.02	
65	Q9HRR3|Q9HRR3	2	1274.7387	-1.3	161	172	0	53.9	21	V	GFIAIVPFLNKG	S	1.2	10.1	
67	Q9HQY4|Q9HQY4	1	545.3247	-4.8	76	80	0	33.3	26	P	MLGLL	A	2.6	6.02	
67	Q9HQY4|Q9HQY4	1	555.3632	0.4	336	340	0	27.1	18	T	TPLLI	P	2.0	6.02	
67	Q9HQY4|Q9HQY4	2	1062.542	-2.0	329	338	0	36.6	26	P	MYAAVPTTPL	L	0.8	5.92	
68	P57699|ATKB	1	755.4793	-0.8	265	271	0	30.0	23	A	ELVALLV	A	2.6	3.3	
69	Q9HP66|Q9HP66	1	515.3319	1.4	254	258	0	30.5	29	A	TIIAV	L	2.9	6.02	
69	Q9HP66|Q9HP66	1	628.416	1.1	254	259	0	23.4	23	A	TIIAVL	S	3.0	6.02	
70	Q9HNT5|Q9HNT5	1	543.3268	0.2	814	818	0	31.8	29	N	EAVLL	L	2.0	3.3	
71	P71414|P71414	2	803.4905	2.9	12	18	0	13.5	13	A	AKFNVLL	L	1.3	10.1	
72	Q9HSL5|Q9HSL5	2	1229.6445	1.2	257	267	0	33.5	28	V	SWLPFVSVQPA	T	0.7	6.02	
73	Q9HNR0|Q9HNR0	2	1959.9385	-0.2	152	172	0	63.7	29	I	DATGLGGAEVKDIETSAGAQA	H	-0.2	3.58	
74	Q9HPQ1|Q9HPQ1	1	685.4374	-0.9	147	153	0	26.3	26	L	AITGLIV	V	2.5	6.02	
75	Q9HPT7|Q9HPT7	1	569.4152	0.2	28	32	0	28.5	17	G	LLILV	A	4.0	6.02	
75	Q9HPT7|Q9HPT7	1	771.4895	-1.0	245	251	0	22.1	20	S	AVFPILI	G	2.9	6.02	
76	Q9HRS9|Q9HRS9	1	676.416	1.3	469	474	0	23.0	22	A	VFLSLV	R	3.0	6.02	
76	Q9HRS9|Q9HRS9	1	924.5321	-1.3	360	367	0	32.3	23	K	YFLLIGTV	T	2.1	5.92	
76	Q9HRS9|Q9HRS9	1	976.523	-0.4	16	25	0	26.6	26	L	STFVPGVSLA	L	1.3	6.02	
76	Q9HRS9|Q9HRS9	1	1118.6223	0.0	216	225	0	38.0	23	V	LLDVYGIDLV	A	1.6	2.92	
77	Q9HNB9|Q9HNB9	1	730.3749	0.1	209	214	0	40.2	27	G	IEDLEL	S	0.3	2.94	
77	Q9HNB9|Q9HNB9	1	1003.4975	0.0	108	117	0	64.3	29	A	AFDVQVPAGT	A	0.5	3.1	
77	Q9HNB9|Q9HNB9	2	1254.6456	-1.7	110	122	0	28.1	26	F	DVQVPAGTAVGEL	E	0.5	3	
77	Q9HNB9|Q9HNB9	3	2627.2787	-2.4	71	97	0	53.4	29	A	RLSGPSEERVDGAEVAGQTGADGLSVA	L	-0.3	3.92	
79	Q9HSJ6|Q9HSJ6	2	1199.6622	-3.9	224	234	0	27.5	26	V	ERLAADRTGVL	K	-0.2	7.04	
80	Q9HSM2|MUTS1	1	643.3541	0.6	574	580	0	39.6	31	E	LVAGDGL	D	1.3	3.1	
81	Q9HP01|Q9HP01	1	668.4473	0.9	214	219	0	22.3	14	V	LLPLTL	P	2.2	6.02	
82	P82857|P82857	1	543.3268	0.2	389	393	0	31.8	29	T	EAVIL	E	2.2	3.3	
82	P82857|P82857	1	613.3799	-0.2	14	20	0	41.8	29	A	ALAAVGL	A	2.4	6.02	
82	P82857|P82857	1	684.417	0.4	14	21	0	40.0	27	A	ALAAVGLA	G	2.3	6.02	
83	Q9HME2|Q9HME2	1	1124.6077	-1.0	49	60	0	25.9	25	V	GGLISPLVPDSA	T	0.8	3.1	
83	Q9HME2|Q9HME2	2	1301.7054	1.3	2	12	0	70.0	26	M	VWIIDNLVTMV	E	1.7	3.1	
83	Q9HME2|Q9HME2	2	1317.7003	0.6	2	12	0	48.5	26	M	VWIIDNLVTMV	E	1.7	3.1	Oxidation (M)
83	Q9HME2|Q9HME2	2	1810.9829	0.6	41	60	0	35.8	25	A	GAFGALAVGGLISPLVPDSA	T	1.2	3.1	
83	Q9HME2|Q9HME2	2	1953.0571	0.9	39	60	0	35.2	26	A	AAGAFGALAVGGLISPLVPDSA	T	1.3	3.1	
84	Q9HNY2|Q9HNY2	1	543.3268	-0.7	227	231	0	32.6	30	T	DLALI	T	2.1	3.1	
84	Q9HNY2|Q9HNY2	1	678.3952	-0.9	85	90	0	23.1	22	T	AYLTVL	Q	1.9	5.92	
84	Q9HNY2|Q9HNY2	1	683.4218	0.6	147	153	0	24.5	24	A	LLSAPIA	V	1.9	6.02	
85	Q9HNR2|Q9HNR2	1	612.3847	1.0	408	413	0	30.2	24	S	IVTPIA	V	2.1	6.02	
85	Q9HNR2|Q9HNR2	2	763.4116	0.4	303	309	0	35.7	26	A	DYAVALI	V	1.6	3.1	
87	Q9HNF6|Q9HNF6	1	626.4003	-0.2	556	561	0	35.0	22	Y	LSLVPV	A	2.3	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
87	Q9HNF6|Q9HNF6	1	681.4425	0.9	268	274	0	26.0	22	F	GPIAVLL	A	2.3	6.02	
88	Q9HRQ9|Q9HRQ9	2	1017.4767	0.5	123	131	0	54.0	28	A	GWDAQTEIV	S	-0.2	3	
88	Q9HRQ9|Q9HRQ9	2	1615.7366	1.1	117	131	0	48.2	26	T	SVPDEAGWDAQTEIV	S	-0.4	2.84	
88	Q9HRQ9|Q9HRQ9	2	1626.8002	-1.5	79	93	0	42.3	27	V	KVGPNNQNVFDPAEV	Y	-0.8	4.08	
88	Q9HRQ9|Q9HRQ9	2	1674.8148	-0.3	175	191	0	45.5	29	S	GGGGPVERSPHEMGVPI	Q	-0.4	5.3	
88	Q9HRQ9|Q9HRQ9	2	1725.8686	-0.7	78	93	0	38.2	27	T	VKVGPNNQNVFDPAEV	Y	-0.4	4.08	
89	Q9HNN6|Q9HNN6	1	666.3588	1.2	455	460	0	22.4	21	S	AYLSTL	F	1.1	5.92	
89	Q9HNN6|Q9HNN6	1	703.3938	-0.1	579	585	0	28.0	27	T	TGIGLLM	L	1.8	6.02	
89	Q9HNN6|Q9HNN6	2	1508.8603	0.6	103	116	0	41.4	23	S	NVLVIPGVNDFLPL	S	1.2	3.1	
91	Q9HMS7|Q9HMS7	1	545.3247	-4.8	135	139	0	33.3	26	S	MIGLL	N	2.7	6.02	
91	Q9HMS7|Q9HMS7	1	617.3173	1.5	217	222	0	32.9	27	A	WGTAIA	N	1.0	6.02	
91	Q9HMS7|Q9HMS7	1	734.4367	3.7	278	283	0	17.5	14	F	PFLFVL	G	2.6	6.02	
92	Q9HNK5|Q9HNK5	1	543.3268	1.5	135	139	0	30.1	29	N	DLLLA	G	1.9	3.1	
93	Q9HN93|Q9HN93	1	766.4629	-4.4	263	268	0	20.0	20	V	YFLILV	G	3.0	5.92	
93	Q9HN93|Q9HN93	2	1239.5156	-0.4	118	128	0	26.0	21	A	DWGGHDPIENT	G	-1.5	3.7	
93	Q9HN93|Q9HN93	2	1832.7741	-1.1	239	254	0	27.1	21	D	AFEPDTELGHDEYDPV	G	-1.1	3.38	
93	Q9HN93|Q9HN93	2	1947.801	0.4	238	254	0	50.3	19	A	DAFEPDTELGHDEYDPV	G	-1.2	3.28	
93	Q9HN93|Q9HN93	2	2213.0389	-0.5	98	117	0	63.1	28	V	SFEWVSNTHNILIDAQPDGA	D	-0.3	3.7	
94	Q9HR54|Q9HR54	1	678.3952	-0.9	543	548	0	23.1	22	Q	FSLTVL	R	2.2	6.02	
95	Q9HMW2|Q9HMW2	1	628.416	0.0	71	76	0	42.4	25	G	TLIAIV	F	3.0	6.02	
95	Q9HMW2|Q9HMW2	1	664.3796	-2.0	36	41	0	39.4	24	L	SYLGLI	V	1.6	5.92	
95	Q9HMW2|Q9HMW2	1	714.4713	-3.9	229	234	0	26.4	13	F	MLLLLL	T	3.5	6.02	
96	Q9HRS0|Q9HRS0	2	1475.6067	-0.9	219	230	0	68.6	21	A	YFFMKYGGDYGE	-	-0.7	4.08	
97	Q9HNB6|Q9HNB6	1	690.4316	1.2	18	23	0	21.2	21	D	VTFLLV	L	3.0	6.02	
97	Q9HNB6|Q9HNB6	2	1162.5652	-0.2	295	305	0	61.7	28	V	GMVTLDDARSV	R	0.2	3.88	
98	Q9HN36|Q9HN36	1	731.4581	-0.8	259	264	0	36.5	23	T	FNLLLL	V	2.4	6.02	
98	Q9HN36|Q9HN36	1	830.5266	-0.4	259	265	0	23.3	21	T	FNLLLLV	M	2.7	6.02	
99	Q9HMI2|Q9HMI2	1	883.5379	-0.8	329	336	0	27.2	23	T	LVNLLVDV	T	2.1	3.1	
100	Q9HT01|Q9HT01	2	834.4276	0.5	192	198	0	27.6	24	H	VTAWYPV	V	0.8	5.92	
101	Q9HQ54|Q9HQ54	1	600.3483	1.8	68	73	0	38.0	30	A	TLTVAP	G	1.1	6.02	
102	O51965|O51965	2	1216.5611	0.9	322	331	0	48.0	26	A	EQLEEAWEAI	Q	-0.7	2.96	
103	Q9HNQ2|IF2P	1	543.3268	-0.7	103	107	0	32.6	30	A	DIAIL	V	2.2	3.1	
103	Q9HNQ2|IF2P	1	642.3952	-0.5	103	108	0	44.7	27	A	DIAILV	V	2.6	3.1	
104	Q9HNQ5|Q9HNQ5	1	684.417	-1.6	17	24	0	39.7	27	F	VVAGVGLA	A	2.4	6.02	
104	Q9HNQ5|Q9HNQ5	1	755.4541	1.3	17	25	0	25.5	25	F	VVAGVGLAA	T	2.3	6.02	
105	Q9HSW6|CDC61	1	515.3319	1.4	305	309	0	30.5	29	L	TLLAV	V	2.6	6.02	
105	Q9HSW6|CDC61	1	545.3247	-4.8	357	361	0	33.3	26	H	MLGIL	S	2.7	6.02	
106	Q9HP81|HTR2	1	628.416	0.0	17	22	0	42.4	25	K	LTLALV	V	2.8	6.02	
107	Q9HMV6|HELS	2	763.4116	0.1	399	405	0	31.7	26	P	YGEAVLL	A	1.2	3.3	
108	Q9HR16|Q9HR16	2	1089.5495	0.8	179	188	0	41.5	29	A	TWGLPFADLA	A	0.7	3.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
110	Q9HS12|Q9HS12	1	567.3996	-1.9	430	434	0	30.4	17	I	LPIII	I	3.1	6.02	
111	Q9HQT5|Q9HQT5	1	727.448	-0.1	73	79	0	27.4	25	G	DLLALLA	A	2.2	3.1	
111	Q9HQT5|Q9HQT5	1	834.4487	0.8	70	77	0	33.1	26	A	AYGDLLAL	L	1.2	3.1	
113	Q9HPN8|Q9HPN8	1	684.417	0.7	30	37	0	28.5	27	N	AALGLAVA	I	2.3	6.02	
114	Q9HHP2|Q9HHP2	2	762.4024	1.8	502	508	0	27.7	27	P	ARLFADA	P	0.6	6.78	
115	Q9HR05|Q9HR05	1	681.4425	0.7	512	518	0	28.6	22	A	AVPALVL	V	2.6	6.02	
118	Q9HHE7|Q9HHE7	2	1291.5528	1.3	73	86	0	62.2	24	A	GADVSENGDGTATV	T	-0.4	2.88	
118	Q9HHE7|Q9HHE7	2	1420.6722	0.7	87	99	0	35.8	27	V	TWISEGTASELEV	S	0.0	3.02	
118	Q9HHE7|Q9HHE7	2	1490.6485	0.7	71	86	0	28.4	24	V	QAGADVSENGDGTATV	T	-0.4	2.88	
118	Q9HHE7|Q9HHE7	2	2358.9572	0.2	120	140	0	39.3	18	I	QYNSDTDSDNKIDDDDNTITA	T	-1.7	3.14	
119	Q9HR13|Q9HR13	1	637.3475	4.2	455	459	0	25.2	18	Q	YPFVL	V	1.6	5.92	
121	O54662|O54662	1	505.29	-1.8	11	15	0	32.2	30	A	GFGLL	I	1.9	6.02	
121	O54662|O54662	1	612.3847	1.0	30	35	0	32.9	24	F	LVTPAL	L	1.9	6.02	
121	O54662|O54662	1	782.4902	-0.4	225	232	0	25.8	22	V	AIPVVATL	L	2.3	6.02	
122	Q9HRN3|Q9HRN3	2	1649.8009	0.1	84	100	0	81.1	28	V	SSPGGAVSGSEVQYRAV	K	-0.2	6.88	
122	Q9HRN3|Q9HRN3	2	1744.8843	-0.2	50	67	0	34.4	28	V	NIESAITGGTGDAVAKEL	R	0.1	3.82	
123	Q9HS59|Q9HS59	1	555.3996	1.1	163	167	0	28.5	20	G	IVLLV	F	4.1	6.02	
123	Q9HS59|Q9HS59	1	626.4003	-0.2	156	161	0	35.0	22	Q	TVLVPV	G	2.4	6.02	
123	Q9HS59|Q9HS59	2	1372.6544	4.4	42	54	0	35.4	27	D	PEDASVNCLLEAL	R	0.4	2.94	
124	Q9HMG7|Q9HMG7	1	626.4479	0.3	361	365	0	14.5	13	F	LLLLR	R	2.1	11.04	
124	Q9HMG7|Q9HMG7	1	684.417	0.7	18	25	0	28.5	27	G	ALAGIAVA	S	2.4	6.02	
125	Q9HNH6|Q9HNH6	1	612.3847	-0.8	382	387	0	27.3	24	E	TIVPAL	C	2.0	6.02	
126	Q9HSV6|Q9HSV6	1	668.4473	-1.6	91	96	0	27.5	14	F	ITPLLI	F	2.4	6.02	
127	Q9HP49|Q9HP49	2	1029.607	1.4	200	208	0	36.7	22	A	NTKLLVETL	A	0.4	6.94	
127	Q9HP49|Q9HP49	3	2466.2153	-0.3	119	139	0	58.1	28	R	TPSTWQAQQSQPRQPQFRQPA	Q	-1.8	12.4	
127	Q9HP49|Q9HP49	3	2986.5155	-1.2	28	54	0	44.4	29	A	QSGTVRQQQPAQQSIAQQQPMARPQPV	A	-1.2	12.4	
128	Q9HRF2|Q9HRF2	1	621.356	0.8	70	74	0	18.0	13	P	MVFLL	I	3.3	6.02	
128	Q9HRF2|Q9HRF2	2	734.4401	1.9	70	75	0	26.4	18	P	MVFLLI	S	3.5	6.02	
128	Q9HRF2|Q9HRF2	1	750.435	-2.3	70	75	0	20.2	14	P	MVFLLI	S	3.5	6.02	Oxidation (M)
128	Q9HRF2|Q9HRF2	2	941.595	1.2	309	317	0	19.2	16	S	VVFLPAIAI	A	2.9	6.02	
129	Q9HR62|Q9HR62	1	642.4105	0.9	222	226	0	26.1	13	V	WLVLL	A	2.9	6.02	
130	Q9HRT4|Q9HRT4	1	797.5011	-0.6	389	397	0	32.6	24	G	VAALAVALA	D	2.8	6.02	
131	Q9HQ23|Q9HQ23	1	755.4541	1.3	20	27	0	27.8	25	V	VVQVGALA	L	2.0	6.02	
133	Q9HNQ9|Q9HNQ9	2	1122.5094	0.8	209	218	0	27.2	25	S	GGFWESVDRA	M	-0.5	4.08	
135	Q9HP32|PYRG	1	765.4636	-1.0	421	427	0	23.6	16	Y	PVIDLLP	E	1.4	3.1	
135	Q9HP32|PYRG	1	1035.5601	2.4	117	125	0	24.1	24	G	DYLGKTVQI	I	-0.1	6.68	
136	Q9HS71|Q9HS71	1	628.416	0.0	167	172	0	42.4	25	A	LTIAIV	T	3.0	6.02	
137	Q9HNS6|Q9HNS6	1	674.4367	-1.0	19	24	0	24.6	21	P	FAVLLL	T	3.4	6.02	
137	Q9HNS6|Q9HNS6	1	771.4895	-1.0	18	24	0	23.2	20	E	PFAVLLL	T	2.7	6.02	
139	Q9HSQ7|Q9HSQ7	2	1329.7333	0.2	75	86	0	38.0	24	A	FLPFLPQSVVPS	S	1.0	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
139	Q9HSQ7|Q9HSQ7	2	1747.8013	-0.4	499	514	0	48.8	27	I	QNLPDGYDTEVGERGV	K	-1.1	3.58	
141	Q9HSN5|Q9HSN5	1	600.3635	0.5	731	735	0	23.0	21	I	WLAVL	A	2.5	6.02	
142	Q9HS03|Q9HS03	1	515.3319	1.4	266	270	0	30.5	29	G	LTLAV	A	2.6	6.02	
143	Q9HQJ9|Q9HQJ9	1	584.3533	0.5	105	109	0	26.0	26	E	EVKPL	T	-0.2	6.94	
144	Q9HQZ0|Q9HQZ0	1	545.3213	-1.7	438	442	0	28.1	24	Q	FGPLL	L	1.7	6.02	
145	Q9HQA7|Q9HQA7	1	621.356	0.8	248	252	0	15.9	13	V	VMFLL	L	3.3	6.02	
145	Q9HQA7|Q9HQA7	1	734.4401	-1.0	248	253	0	23.0	14	V	VMFLLL	G	3.4	6.02	
145	Q9HQA7|Q9HQA7	1	750.435	-2.3	248	253	0	20.2	14	V	VMFLLL	G	3.4	6.02	Oxidation (M)
147	Q9HS33|Q9HS33	1	545.3213	-1.7	168	172	0	28.1	24	G	FGPII	A	2.0	6.02	
147	Q9HS33|Q9HS33	1	674.4367	-1.0	301	306	0	24.6	21	A	GFIILI	P	3.3	6.02	
152	Q9HSB1|Q9HSB1	1	685.4374	-0.9	496	502	0	26.4	26	D	VATALLV	F	2.7	6.02	
152	Q9HSB1|Q9HSB1	1	910.5852	0.4	375	384	0	28.1	21	T	VLAGGVLVAL	S	2.7	6.02	
153	Q9HMT5|Q9HMT5	1	791.4582	-1.0	186	191	0	34.6	22	A	FLLWTI	H	2.2	6.02	
153	Q9HMT5|Q9HMT5	1	1178.5132	0.8	316	325	0	30.5	25	A	EYGYEPPEPV	R	-1.4	3.02	
153	Q9HMT5|Q9HMT5	2	1234.6016	-0.7	223	233	0	27.3	26	T	AFTEGERPMVV	S	0.1	4.26	
155	Q9HI34|Q9HI34	1	585.3737	1.0	177	181	0	29.2	20	L	ILLDL	A	2.5	3.1	
155	Q9HI34|Q9HI34	1	656.4109	1.1	177	182	0	43.1	21	L	ILLDLA	Y	2.4	3.1	
155	Q9HI34|Q9HI34	1	769.4949	0.3	176	182	0	44.4	21	R	LILLDLA	Y	2.6	3.1	
157	Q9HSC3|LONH	2	1145.5274	-3.6	529	538	0	26.2	26	G	QLKEMAEEAV	E	-0.4	3.96	Gln->pyro-Glu (N-term Q)
157	Q9HSC3|LONH	2	1146.6285	0.4	288	297	0	56.9	24	A	NKGVLFIDEI	N	0.5	4.08	
157	Q9HSC3|LONH	2	1812.7286	-0.1	22	38	0	53.4	18	S	VDHDDTDGLQDDPADSV	D	-1.2	3.14	
160	Q9HI06|Q9HI06	1	555.3632	0.4	147	151	0	19.4	18	D	LPTIL	E	2.0	6.02	
163	Q9HRD0|Q9HRD0	1	684.417	0.7	112	119	0	38.1	27	G	AIAGLGLA	R	2.1	6.02	
165	Q9HPV6|Q9HPV6	1	674.4367	-1.0	116	121	0	24.6	21	T	IGFLLL	F	3.1	6.02	
167	Q9HSM6|MUTL	2	1041.5818	-1.2	321	330	0	29.6	27	A	VEAGVRDALL	D	0.8	4.08	
168	Q9HN16|Q9HN16	1	684.417	-1.6	112	119	0	28.8	27	N	VAAALGLA	A	2.3	6.02	
171	Q9HP43|CARB	2	1010.6124	-1.7	866	876	0	28.9	22	K	ATGVPIAKLAA	K	1.2	10.1	
172	Q9HPX5|Q9HPX5	1	545.3213	-1.7	317	321	0	28.1	24	V	FGPLI	W	1.8	6.02	
172	Q9HPX5|Q9HPX5	1	545.3247	-4.8	237	241	0	31.7	26	T	LMGLL	T	2.6	6.02	
174	Q9HNT7|Q9HNT7	1	584.3533	0.5	503	507	0	26.0	26	A	VEKPI	P	-0.1	6.94	
174	Q9HNT7|Q9HNT7	1	741.3334	-0.5	75	81	0	35.9	27	T	GYGLDFA	P	0.4	3.1	
176	Q9HRM4|Q9HRM4	1	897.5535	-1.4	134	142	0	34.2	22	T	EVIALAGLL	A	2.2	3.3	
177	Q9HM71|Q9HM71	2	1306.5864	0.2	548	559	0	78.3	26	T	MFVADDTVAHTT	A	0.4	3.88	
178	O54630|O54630	1	567.3996	-1.9	96	100	0	30.4	17	P	LPIIL	I	3.0	6.02	
185	Q9HN44|Q9HN44	1	642.3952	-1.4	204	209	0	27.0	27	V	AVELLV	G	2.4	3.3	
186	Q9HHU7|Q9HHU7	1	690.4316	1.2	385	390	0	21.2	21	L	LSFIIV	N	3.2	6.02	
187	Q9HPF9|Q9HPF9	1	1137.519	-0.8	280	289	0	35.0	27	T	GLQVEDFETT	D	-0.5	2.94	
187	Q9HPF9|Q9HPF9	2	1300.6987	0.8	82	94	0	39.5	27	V	RAVGLESGLVEAT	R	0.4	4.26	
192	Q9HRT3|Q9HRT3	1	642.3952	-0.5	259	264	0	27.1	27	R	ADILLV	G	2.4	3.1	
193	Q9HQ81|Q9HQ81	1	690.3952	1.2	263	268	0	23.5	23	A	IDFALI	P	2.3	3.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
197	Q9HNK9|IF2G	1	756.4381	-0.4	137	143	0	39.9	27	I	IGIENIV	I	1.5	3.3	
199	O73955|CATA	1	642.3952	-1.4	519	524	0	27.0	27	S	LADLIV	L	2.4	3.1	
199	O73955|CATA	1	656.4109	-1.5	138	143	0	33.7	26	G	DLIILA	G	2.5	3.1	
200	Q9HMX2|Q9HMX2	1	543.3268	-0.7	220	224	0	32.6	30	R	DLAIL	F	2.1	3.1	
201	Q9HN70|THSA	1	681.4425	0.7	8	13	0	25.7	22	N	QPLIVL	S	1.9	6.02	
205	P71411|BACS2	1	643.3541	-0.2	210	216	0	35.8	31	A	VLGADAV	S	1.7	3.1	
205	P71411|BACS2	1	725.4476	-0.7	172	177	0	24.7	21	Y	PVVWLL	S	2.3	6.02	
206	Q9HQD6|HUTI	1	636.3119	1.7	192	197	0	33.6	30	D	AYVDAV	I	1.2	3.1	
207	O52009|O52009	1	544.3221	0.6	59	63	0	32.8	32	R	TQILA	S	1.2	6.02	
209	Q9HRJ3|Q9HRJ3	1	690.3952	0.3	50	55	0	24.0	23	L	LFADLI	A	2.2	3.1	
209	Q9HRJ3|Q9HRJ3	1	959.5692	-2.3	50	58	0	28.6	21	L	LFADLIAVV	N	2.6	3.1	
211	Q9HMU6|Q9HMU6	2	1221.6394	2.0	134	145	0	53.3	26	I	SFIPFSQLVGGA	V	1.0	6.02	
212	Q9HP06|Q9HP06	1	561.3163	0.5	78	82	0	25.0	25	E	PFVSL	V	1.7	6.02	
212	Q9HP06|Q9HP06	1	585.3737	1.0	266	270	0	29.2	20	D	LILDL	E	2.5	3.1	
212	Q9HP06|Q9HP06	2	981.6447	4.0	7	15	0	21.8	13	A	VRRVGALVL	A	1.4	12.4	
214	Q9HQ03|Q9HQ03	1	642.3952	-0.5	15	20	0	44.7	27	G	IDALLV	F	2.4	3.1	
215	Q9HPA2|Q9HPA2	1	666.3588	1.2	69	74	0	21.0	21	A	FSTSLL	A	1.4	6.02	
216	Q9HNG6|Q9HNG6	1	889.5273	-0.9	89	97	0	25.9	24	G	FLGIVIGTA	A	2.2	6.02	
218	Q9HRE4|Q9HRE4	2	869.4429	-3.1	155	162	0	23.3	22	L	HSIAAQMI	G	0.9	7.84	
219	Q9HRH7|Q9HRH7	2	995.6127	0.7	521	530	0	22.0	19	A	LRGASPGLLL	V	0.9	11.04	
224	Q9HRR0|Q9HRR0	1	706.3901	-0.4	69	74	0	27.0	25	I	DLSFIL	M	1.8	3.1	
224	Q9HRR0|Q9HRR0	2	1459.6653	0.3	109	120	0	63.8	26	T	SMFENTVEQFKT	A	-0.7	4.26	
224	Q9HRR0|Q9HRR0	2	1475.6602	-1.6	109	120	0	29.0	26	T	SMFENTVEQFKT	A	-0.7	4.26	Oxidation (M)
225	Q9HQ63|DHSD	1	654.3377	0.9	125	130	0	23.3	22	T	FLTGAF	-	1.7	6.02	
225	Q9HQ63|DHSD	2	1109.5757	0.3	120	130	0	39.8	26	V	ASVPTFLTGAF	-	1.2	6.02	
226	Q9HQN5|Q9HQN5	1	600.3635	0.5	455	459	0	26.7	21	C	WGLLL	A	2.0	6.02	
226	Q9HQN5|Q9HQN5	1	621.356	0.8	356	360	0	14.7	13	E	MFIVL	V	3.4	6.02	
232	Q9HQQ5|Q9HQQ5	1	681.4425	-0.1	432	438	0	26.1	22	S	LPAGIVL	V	2.3	6.02	
232	Q9HQQ5|Q9HQQ5	1	848.4314	-1.4	219	226	0	35.8	27	Q	SMDTLVLA	V	1.3	3.1	
236	Q9HRN5|Q9HRN5	1	664.3796	-2.0	11	16	0	39.4	24	A	YSLGLL	G	1.5	5.92	
239	Q9HRT5|Q9HRT5	1	634.369	1.6	310	315	0	31.0	27	A	LFAALT	A	2.2	6.02	
239	Q9HRT5|Q9HRT5	1	685.4374	-0.9	369	375	0	26.3	26	A	VVSGLLV	A	2.7	6.02	
244	Q9HP89|Q9HP89	2	956.4451	0.6	157	166	0	31.5	26	P	APDADALADV	H	0.3	2.82	
245	Q9HPD9|Q9HPD9	1	674.4367	-1.0	225	230	0	24.6	21	R	FGLLLL	A	2.9	6.02	
246	Q9HM75|Q9HM75	1	572.3322	0.7	9	13	0	30.8	21	L	AWVVV	A	2.7	6.02	
246	Q9HM75|Q9HM75	1	600.3635	0.5	48	52	0	26.7	21	F	WGLLI	E	2.2	6.02	
247	Q9HNC9|Q9HNC9	1	587.3716	1.4	1	5	0	14.7	13	-	MLLVL	C	3.5	6.02	
248	Q9HQ64|Q9HQ64	1	591.3017	-0.2	115	120	0	32.7	24	A	NALAGF	-	1.1	6.02	
248	Q9HQ64|Q9HQ64	1	621.356	0.8	63	67	0	14.7	13	T	MVLFL	V	3.3	6.02	
248	Q9HQ64|Q9HQ64	1	741.3333	-0.5	43	48	0	35.9	27	A	YNIDFA	G	0.1	3.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
248	Q9HQ64|Q9HQ64	1	754.4953	-0.4	105	111	0	26.8	24	V	LLIVQGI	R	2.4	6.02	
249	Q9HHR2|Q9HHR2	2	1156.6339	0.7	230	240	0	29.1	26	S	VDAVIEANTLL	S	1.2	3	
251	Q9HRW7|Q9HRW7	1	933.4994	-4.3	30	38	0	30.1	27	V	MTAVLFGVP	Y	1.8	6.02	
251	Q9HRW7|Q9HRW7	2	1618.7012	-0.1	2	15	0	54.0	24	M	SDALDAFDHDAWRT	A	-0.9	3.86	
252	Q9HN22|Q9HN22	2	1719.8104	0.6	149	165	0	27.4	27	A	AAFLADIDHSAYGTTPA	Q	0.3	3.88	
254	Q9HN92|Q9HN92	2	1066.646	0.9	11	20	0	19.9	19	T	VMPLLSLVPV	A	2.2	6.02	
254	Q9HN92|Q9HN92	2	1238.7308	0.6	9	20	0	44.3	20	I	ATVMPLLSLVPV	A	1.9	6.02	
258	Q9HPR5|Q9HPR5	1	700.4007	1.0	290	295	0	29.3	29	A	VEDLLI	L	1.6	3	
263	Q9HM70|Q9HM70	1	569.4152	0.2	600	604	0	28.5	17	V	ILLLV	V	4.0	6.02	
263	Q9HM70|Q9HM70	1	612.3847	1.0	432	437	0	32.9	24	E	LVTPAI	Q	2.0	6.02	
266	Q9HR01|Q9HR01	1	572.3322	0.7	134	138	0	25.2	21	E	WVAVV	F	2.7	6.02	
267	Q9HSL4|Q9HSL4	1	643.3541	-0.2	5	11	0	34.0	31	I	IVGAGDI	G	1.5	3.1	
268	O51984|O51984	1	643.3541	0.6	288	293	0	41.3	31	T	IVQDGL	A	0.9	3.1	
270	Q9HSF1|Q9HSF1	2	1009.6284	0.6	8	17	0	19.4	18	L	LAPRSLAVLA	G	1.4	11.04	
270	Q9HSF1|Q9HSF1	2	1501.6321	0.9	318	332	0	38.0	22	S	AFDHPEGLGGDTDTA	T	-0.7	3.5	
271	Q9HMM6|CSD	1	617.3425	-0.2	18	22	0	27.2	21	D	FPILE	R	1.2	3.3	
271	Q9HMM6|CSD	2	1468.7773	2.3	183	197	0	27.6	25	N	TLGTVNPVGELADIA	H	0.7	3	
272	Q9HRJ8|Q9HRJ8	1	751.3938	-3.3	426	432	0	23.5	23	N	AYLGCLL	V	2.0	5.32	
272	Q9HRJ8|Q9HRJ8	1	939.5753	-4.5	54	64	0	25.7	22	T	GLAVVGAAVLA	W	2.4	6.02	
273	Q9HPQ4|Q9HPQ4	1	706.3901	-0.3	233	238	0	26.6	25	E	EVAYLI	M	1.6	3.3	
276	Q9HPL9|Q9HPL9	1	685.4374	2.5	120	126	0	40.9	26	S	AIGLVTL	G	2.4	6.02	
277	Q9HRM6|Q9HRM6	1	543.3268	-0.7	115	119	0	32.6	30	D	EVALL	D	2.0	3.3	
278	Q9HNI3|Q9HNI3	1	684.417	-1.6	97	104	0	39.7	27	V	AVVGGVLA	V	2.4	6.02	
283	Q9HN79|Q9HN79	1	612.3847	1.0	20	25	0	27.8	24	L	VLTAPL	V	1.9	6.02	
286	Q9HSA1|Q9HSA1	1	832.4178	0.0	271	278	0	31.2	28	D	GEISDLVT	I	0.5	3	
287	Q9HQI5|Q9HQI5	1	832.4178	0.1	148	155	0	34.1	28	I	LSGDEIVT	H	0.5	3	
289	Q9HNP8|Q9HNP8	1	700.4007	0.7	569	574	0	40.6	29	A	LVEDIL	D	1.6	3	
291	Q9HPD4|RL3	3	2508.1558	1.0	178	201	0	33.2	27	A	DLIEDGGVHAFGDVFRAGEFTDAA	G	0.1	3.68	
293	Q9HQP1|Q9HQP1	1	628.416	0.0	14	19	0	29.5	25	G	TIALIV	G	3.0	6.02	
293	Q9HQP1|Q9HQP1	1	685.4374	-0.9	13	19	0	26.4	26	G	GTIALIV	G	2.5	6.02	
297	Q9HSR4|Q9HSR4	1	887.4786	-1.0	126	133	0	29.3	25	V	EVNLLGLM	N	1.3	3.3	
298	Q9HRJ7|Q9HRJ7	1	714.3588	-0.4	35	40	0	39.2	20	L	YFALTT	A	1.0	5.92	
301	Q9HMK3|SYFB	2	1187.571	-4.0	166	176	0	30.3	27	G	IDPDGDTFVPL	D	0.0	2.82	
303	O51978|O51978	1	587.3716	1.4	78	82	0	25.6	13	T	IMLLV	V	3.6	6.02	
303	O51978|O51978	1	668.4473	0.9	73	78	0	22.3	14	Y	ILPLTI	M	2.4	6.02	
303	O51978|O51978	1	757.4772	-4.6	79	85	0	19.6	19	I	MLLVVAL	A	3.4	6.02	
304	Q9HSG5|TRUD	1	617.3173	1.5	230	235	0	32.9	27	D	WTGALA	E	0.9	6.02	
304	Q9HSG5|TRUD	1	653.4112	1.1	427	432	0	25.6	24	F	LKPSPL	A	-0.1	10.1	
306	Q9HP92|Q9HP92	1	617.3425	-0.2	343	347	0	27.2	21	V	FLLEP	D	1.1	3.3	
306	Q9HP92|Q9HP92	1	727.448	-0.1	187	193	0	37.2	25	V	LLALDLA	F	2.2	3.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
308	Q9HP12|Q9HP12	1	684.417	0.3	165	172	0	40.0	27	A	VGVAGVLA	V	2.4	6.02	
309	Q9HRC9|Q9HRC9	2	1970.7138	1.0	249	267	0	16.1	13	A	DVQPGDDDEPGDDEDGAEP	-	-2.0	2.54	
309	Q9HRC9|Q9HRC9	2	2112.788	0.7	247	267	0	67.7	13	A	AADVQPGDDDEPGDDEDGAEP	-	-1.7	2.54	
311	Q9HPU7|Q9HPU7	1	600.3635	0.5	302	306	0	26.7	21	S	WAVLI	V	2.7	6.02	
311	Q9HPU7|Q9HPU7	1	642.4105	0.9	318	322	0	15.8	13	A	VLWLL	S	2.9	6.02	
312	Q9HRL4|Q9HRL4	1	706.4088	0.3	28	33	0	14.7	13	S	ALLFLM	S	3.0	6.02	
312	Q9HRL4|Q9HRL4	2	1054.5083	-0.7	83	90	0	37.1	27	T	LYRNFDDI	D	-0.7	3.88	
312	Q9HRL4|Q9HRL4	2	1369.6514	1.5	83	93	0	31.5	27	T	LYRNFDDIDVT	N	-0.5	3.6	
314	Q9HN02|Q9HN02	2	1096.5917	-0.9	163	171	0	30.9	25	V	LFDYLTRAV	N	0.7	6.7	
316	Q9HSC1|TRPC	1	735.4167	1.8	114	119	0	24.6	24	R	KDFLLT	E	0.4	6.76	
317	Q9HMK5|Q9HMK5	2	1299.6493	-2.2	250	261	0	38.7	27	T	DADLLAVLRDCP	A	0.4	3.6	
318	O51963|O51963	1	585.3737	1.0	192	196	0	29.2	20	E	LLIDL	R	2.5	3.1	
319	Q9HRN6|Q9HRN6	1	586.3479	0.3	130	134	0	31.6	21	I	WVLLG	L	2.1	6.02	
320	Q9HQT0|Q9HQT0	1	681.4425	-0.1	234	240	0	26.1	22	T	PIAGIVL	V	2.4	6.02	
322	Q9HMG3|Q9HMG3	2	2335.0717	-1.7	44	67	0	70.0	27	A	STVPETDFPEPYNRSIGGGGGAGA	V	-0.6	3.82	
323	Q9HMB7|Q9HMB7	1	700.4007	0.7	134	139	0	40.6	29	P	VLEDLI	D	1.6	3	
327	Q9HQV9|Q9HQV9	1	656.4109	-0.3	495	500	0	43.9	26	N	ILDLLA	L	2.4	3.1	
327	Q9HQV9|Q9HQV9	1	769.4949	-1.4	495	501	0	30.1	21	N	ILDLLAL	G	2.6	3.1	
328	Q9HR50|Q9HR50	1	745.4374	0.5	39	45	0	27.6	24	A	YAVPVVV	-	2.2	5.92	
328	Q9HR50|Q9HR50	2	1306.6227	3.7	14	25	0	32.4	28	T	APMQEFSIGQVT	N	0.1	3.3	
329	Q9HMZ1|Q9HMZ1	1	642.3952	-0.5	71	76	0	27.1	27	G	VEAIVL	F	2.5	3.3	
329	Q9HMZ1|Q9HMZ1	1	1027.4862	-0.8	315	323	0	26.7	26	I	ITYFAEDVA	E	0.7	3	
335	Q9HPQ2|Q9HPQ2	1	870.5249	-0.7	167	174	0	19.8	16	K	LMVPSILV	M	2.5	6.02	
337	Q9HMD8|Q9HMD8	1	755.4541	1.3	32	39	0	27.7	25	L	QVVGVALA	V	2.0	6.02	
337	Q9HMD8|Q9HMD8	1	868.5382	-1.6	31	39	0	32.2	23	R	LQVVGVALA	V	2.2	6.02	
339	Q9HHQ6|Q9HHQ6	2	1316.6976	3.0	148	159	0	42.1	25	A	DLGWTNTLLAIT	G	0.6	3.1	
343	Q9HQI9|ENO	1	962.5073	0.3	255	263	0	28.8	27	A	AQIEYVAGL	V	0.8	3.3	
349	Q9HRZ5|Q9HRZ5	1	543.3268	1.5	69	73	0	30.1	29	L	DILIA	L	2.2	3.1	
349	Q9HRZ5|Q9HRZ5	1	656.4109	-1.5	68	73	0	33.7	26	R	LDILIA	L	2.5	3.1	
350	Q9HR72|Q9HR72	1	621.356	0.8	62	66	0	18.0	13	I	MLFVL	F	3.3	6.02	
353	Q9HNE5|Q9HNE5	2	995.5804	0.6	17	25	0	33.7	22	T	GLWVQALPL	R	1.2	6.02	
355	Q9HMC6|Q9HMC6	2	887.5593	1.2	336	343	0	22.3	15	H	IARFLLGV	R	2.0	11.04	
357	Q9HRF8|Q9HRF8	1	610.4054	-1.5	221	226	0	23.4	22	D	LLGVPL	A	2.3	6.02	
360	Q9HQS6|Q9HQS6	1	636.3119	0.2	163	168	0	43.8	30	T	FDGVTV	L	1.1	3.1	
362	P13077|FLAB2	1	1100.5502	-0.5	102	111	0	48.9	28	S	TIQWIGPDTA	T	-0.1	3.1	
364	Q9HM89|EF1A	1	755.4541	1.3	110	117	0	35.2	25	D	NAVLVVAA	D	2.3	6.02	
365	Q9HSG1|Q9HSG1	1	681.4425	0.9	214	220	0	26.1	22	L	PVAVALL	A	2.6	6.02	
367	Q9HHR9|Q9HHR9	1	567.3996	-1.9	223	227	0	30.4	17	V	LPLLI	S	2.9	6.02	
370	O52039|O52039	1	681.4425	0.3	177	183	0	30.1	22	A	IPGIGII	A	2.2	6.02	
371	Q9HP02|Q9HP02	1	683.4218	0.4	186	192	0	24.5	24	D	VTLPAIA	P	2.0	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
372	Q9HMP2|Q9HMP2	2	851.4501	-3.3	7	14	0	26.0	25	R	QHAAVIVD	R	0.8	4.94	
373	P50562|RL18	2	1331.7561	1.0	82	94	0	38.8	22	A	AYLTGLLAGQRAV	D	0.8	9.84	
378	Q9HP11|Q9HP11	2	1100.59	2.3	221	231	0	29.2	27	R	GVPVMVAAQTL	K	1.4	6.02	Oxidation (M)
384	Q9HRE2|Q9HRE2	1	714.468	-0.6	22	27	0	22.5	13	I	LPFLLL	G	2.7	6.02	
385	Q9HQ25|Q9HQ25	1	714.468	-0.6	45	50	0	21.0	13	V	LLPFLI	G	2.9	6.02	
385	Q9HQ25|Q9HQ25	1	870.5579	-1.1	43	50	0	18.1	18	A	GVLLPFLI	G	2.6	6.02	
387	Q9HR91|Q9HR91	1	643.3541	-0.2	183	189	0	39.8	31	L	LVGADAV	E	1.7	3.1	
388	Q9HQF0|Q9HQF0	1	543.3268	-0.7	27	31	0	32.6	30	V	EVAII	V	2.3	3.3	
388	Q9HQF0|Q9HQF0	1	642.3952	-0.5	27	32	0	44.7	27	V	EVAIIV	E	2.6	3.3	
390	Q9HSA2|Q9HSA2	1	968.5906	-1.3	98	107	0	26.7	21	S	DVLAGVALLV	G	2.4	3.1	
393	Q9HRB8|Q9HRB8	1	889.5273	-0.9	14	22	0	29.8	24	V	GIVFGLLTA	A	2.2	6.02	
393	Q9HRB8|Q9HRB8	1	960.5644	-0.5	14	23	0	32.6	23	V	GIVFGLLTAA	A	2.1	6.02	
394	Q9HRL5|Q9HRL5	1	904.4906	-0.1	49	56	0	33.5	25	A	AFEIIDVV	L	1.9	3	
398	Q9HNG3|Q9HNG3	1	585.3737	1.0	193	197	0	29.2	20	E	LLLDI	A	2.5	3.1	
398	Q9HNG3|Q9HNG3	1	656.4109	1.1	193	198	0	43.1	21	E	LLLDIA	D	2.4	3.1	
399	Q9HS00|Q9HS00	1	684.417	0.0	535	542	0	28.6	27	V	ALAAVAVA	L	2.7	6.02	
399	Q9HS00|Q9HS00	1	868.5382	-0.6	264	273	0	26.6	23	V	VVAGAGVLLA	V	2.5	6.02	
401	P13078|FLAB3	2	1127.5975	1.5	98	107	0	48.0	26	S	TIQWIGPDKA	T	-0.4	6.76	
403	Q9HMW6|Q9HMW6	1	600.3635	0.7	44	48	0	26.6	21	G	WVLLA	T	2.5	6.02	
403	Q9HMW6|Q9HMW6	1	1114.5845	0.7	96	106	0	34.0	27	I	PLGSAAAMWLV	A	1.4	6.02	
404	Q9HRD4|Q9HRD4	1	765.4636	-1.0	172	178	0	23.6	16	Q	DPLVLLP	E	1.3	3.1	
411	Q9HRV6|Q9HRV6	2	1043.5723	3.6	312	321	0	28.7	27	T	ILKGRGATDN	H	-0.7	10.08	
415	Q9HSY7|Q9HSY7	1	699.4167	-1.0	176	182	0	39.5	28	A	LLGALDV	S	1.9	3.1	
415	Q9HSY7|Q9HSY7	2	1468.7773	3.7	131	144	0	29.4	27	L	DSGIEQEIGKVVVP	A	0.0	3.82	
417	Q9HQU0|Q9HQU0	1	731.4582	0.7	108	114	0	24.3	23	S	AGVFLLI	S	2.9	6.02	
417	Q9HQU0|Q9HQU0	1	818.4902	0.4	108	115	0	34.6	24	S	AGVFLLIS	S	2.5	6.02	
423	Q9HMK2|PYRD	2	672.3919	0.1	301	307	0	33.3	29	K	IRAGASV	V	0.9	11.04	
424	Q9HQP8|Q9HQP8	1	745.4375	0.4	5	11	0	25.1	24	S	PFVSVVV	P	2.5	6.02	
425	P05971|RL15	2	1332.5582	0.9	93	104	0	43.3	22	V	DARDVVDDGWDA	D	-0.9	3.3	
425	P05971|RL15	3	1863.8374	0.9	124	142	0	39.4	26	A	DAFSDAAVELIEGEGGDAV	V	0.2	2.72	
426	Q9HMH9|PYRC	1	567.3996	-1.9	318	322	0	30.4	17	A	LPLLL	G	2.7	6.02	
427	Q9HPR3|Q9HPR3	1	861.4596	-1.7	446	452	0	31.3	27	D	FQQDLLV	G	0.6	3.1	
428	Q9HR79|Q9HR79	1	543.3268	0.2	131	135	0	31.8	29	R	EAVLI	A	2.2	3.3	
432	Q9HR30|Q9HR30	1	653.4112	1.2	418	423	0	29.2	24	F	QAILPL	G	1.5	6.02	
433	Q9HRF4|Q9HRF4	3	2108.9134	-2.9	12	33	0	23.1	23	D	TPQSASSATQDDDGLAAADAFA	L	-0.3	2.74	
436	Q9HNA5|Q9HNA5	1	664.3068	1.2	753	758	0	44.1	29	E	FDADVV	E	1.0	2.92	
439	Q9HHY0|Q9HHY0	1	626.4003	-0.2	144	149	0	35.0	22	D	SILVPV	V	2.4	6.02	
440	Q9HRW2|Q9HRW2	1	910.5852	0.4	32	41	0	23.1	21	L	GGVLAVLAIV	L	2.8	6.02	
440	Q9HRW2|Q9HRW2	1	939.5753	1.0	30	39	0	29.7	22	L	QLGGVLAVLA	I	1.9	6.02	
442	Q9HHR8|Q9HHR8	1	585.3737	1.0	116	120	0	21.0	20	A	LLIEV	I	2.6	3.3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
445	Q9HML1|Q9HML1	1	543.3268	1.5	35	39	0	30.1	29	L	EVLLA	D	2.0	3.3	
445	Q9HML1|Q9HML1	1	656.4109	-0.3	34	39	0	26.2	26	L	LEVLLA	D	2.3	3.3	
445	Q9HML1|Q9HML1	1	769.4949	0.3	33	39	0	29.9	21	A	LLEVLLA	D	2.5	3.3	
446	Q9HMR2|Q9HMR2	1	567.3996	-1.9	425	429	0	30.4	17	G	LPILL	S	2.9	6.02	
451	Q9HQV6|Q9HQV6	1	505.29	-1.8	27	31	0	32.2	30	L	FGGLL	L	1.9	6.02	
451	Q9HQV6|Q9HQV6	1	731.4582	-0.8	27	33	0	36.5	23	L	FGGLLLI	P	2.6	6.02	
455	Q9HMB8|Q9HMB8	1	543.3268	-0.7	91	95	0	32.6	30	A	IDAII	R	2.4	3.1	
459	Q9HNB5|Q9HNB5	2	1409.7878	2.3	339	352	0	23.3	23	V	IDAVTAVRDALGLP	A	0.8	3.88	
461	Q9HN35|Q9HN35	2	1020.4764	3.4	193	202	0	29.9	27	E	AFVGVEVEGD	V	0.6	2.94	
462	Q9HNT1|ATGT	2	936.4916	0.6	59	66	0	28.9	25	L	ITNSYIIN	S	0.5	5.92	
465	Q9HQB9|Q9HQB9	1	868.5382	-0.6	77	86	0	31.9	23	A	VGGAGLVLAL	D	2.2	6.02	
468	Q9HS08|Q9HS08	2	1471.6579	0.3	108	120	0	27.3	25	V	YARNEDVGDYVTA	N	-0.8	3.7	
474	Q9HPD1|RL2	2	1390.6729	0.1	60	71	0	41.4	27	V	AFEDDDQRLVLA	S	-0.3	3.5	
480	Q9HSI4|Q9HSI4	1	654.3377	0.9	186	190	0	30.0	22	P	TQFLF	E	1.0	6.02	
487	Q9HQ91|Q9HQ91	1	584.3533	0.5	128	132	0	26.0	26	Y	DIKPL	Y	-0.1	6.76	
487	Q9HQ91|Q9HQ91	1	674.4367	-1.0	16	21	0	24.6	21	L	LFGLLL	V	2.9	6.02	
490	Q9HQZ1|Q9HQZ1	1	689.3782	-0.3	45	51	0	31.7	28	G	LASGIMV	S	2.1	6.02	
494	Q9HQ12|Q9HQ12	1	983.5876	2.2	49	56	0	23.7	23	A	QRRVVDVI	D	0.1	10.88	
497	Q9HHQ7|Q9HHQ7	1	726.464	-1.5	12	18	0	32.0	25	T	LQALGLL	L	1.9	6.02	
500	Q9HRK1|Q9HRK1	1	935.4541	0.1	29	35	0	29.7	24	A	SWWPFIT	A	0.3	6.02	
506	Q9HRA7|Q9HRA7	1	591.3017	0.5	19	24	0	25.7	24	A	NAALGF	L	1.1	6.02	
512	Q9HNH3|Q9HNH3	2	1409.7878	3.1	95	107	0	24.8	24	G	DIAKVVREDVGLP	D	0.1	4.3	
517	Q9HS50|Q9HS50	1	543.3268	1.5	235	239	0	30.1	29	M	LDLIA	D	2.1	3.1	
518	Q9HMW1|Q9HMW1	1	543.3268	1.5	102	106	0	30.1	29	P	DLLIA	D	2.1	3.1	
518	Q9HMW1|Q9HMW1	2	1062.5445	-4.3	2	11	0	33.7	26	M	DLTTLSETAL	Q	0.3	3	
522	Q9HP58|Q9HP58	2	1684.8349	0.5	21	35	0	36.1	28	T	TPDDTLPWYVAPLPT	R	-0.3	2.92	
524	Q9HMZ0|Q9HMZ0	1	703.3938	0.0	83	89	0	37.7	27	A	MLGSALL	F	2.0	6.02	
525	Q9HQV1|Q9HQV1	1	684.417	-1.6	44	50	0	30.7	27	F	LQAIGIA	S	1.8	6.02	
526	Q9HS82|Q9HS82	1	955.4803	-0.6	124	130	0	37.5	26	T	WYNLFTL	N	0.6	5.92	
528	Q9HN50|SAHH	1	730.3749	0.1	392	397	0	40.2	27	D	ELDIEI	A	0.4	2.94	
530	Q9HQQ6|Q9HQQ6	1	642.3952	1.1	263	268	0	34.1	24	H	EVIALV	A	2.5	3.3	
533	Q9HN47|PRIL	3	1645.6898	1.5	305	320	0	24.2	22	Y	TAPSCATMKAYGNCVN	P	0.0	8.28	Oxidation (M)
537	Q9HRJ0|Q9HRJ0	3	1525.7525	0.5	280	294	0	30.3	27	T	VLDDAGAVPHVEHPA	S	0.1	4.28	
541	Q9HPS5|Q9HPS5	2	750.435	2.3	183	188	0	27.2	21	Y	LMLYVL	Y	2.7	5.92	
545	Q9HPN1|Q9HPN1	2	1209.6605	0.1	171	182	0	24.2	24	N	LAVLDENLGPVA	R	0.9	3	
546	O51994|O51994	2	763.4116	0.4	137	143	0	27.2	26	D	VYADALL	V	1.5	3.1	
551	Q9HQ85|Q9HQ85	1	684.417	-1.6	54	61	0	28.8	27	T	GAIALGLA	A	2.1	6.02	
553	Q9HNS4|Q9HNS4	2	1261.6112	0.0	291	301	0	28.1	27	E	VDMVIDELAEL	I	0.9	2.84	Oxidation (M)
556	Q9HPP8|Q9HPP8	1	555.3632	0.4	429	433	0	19.4	18	G	IPTII	P	2.2	6.02	
558	Q9HRR5|Q9HRR5	1	600.3635	0.5	60	64	0	26.7	21	F	WVAII	G	2.8	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
558	Q9HRR5|Q9HRR5	2	1293.6639	-3.1	2	13	0	43.1	27	M	ADEFIKGLGMLT	G	0.5	4.08	
560	Q9HMZ4|Y2317	2	799.4916	1.4	2	8	0	27.1	25	M	LSVRNLV	H	1.0	11.04	
563	Q9HMW3|Q9HMW3	1	584.3533	0.5	62	66	0	26.0	26	N	LDKPI	T	-0.1	6.76	
565	Q9HRC1|Q9HRC1	1	1037.4666	-2.7	111	121	0	26.8	26	L	FVGGDGTATDV	A	0.3	2.92	
566	Q9HQW6|CHEB	1	555.3632	0.4	157	161	0	27.1	18	N	PTLLI	G	2.0	6.02	
584	Q9HSV2|Q9HSV2	1	711.4167	-1.5	241	247	0	27.3	24	A	GDVLVLP	S	1.5	3.1	
585	Q9HRB9|Q9HRB9	1	626.4479	0.3	180	184	0	20.9	13	V	LLLRL	I	2.1	11.04	
585	Q9HRB9|Q9HRB9	2	958.6215	0.8	175	182	0	16.1	13	A	NKIFVLLL	R	1.9	10.1	
586	Q9HP54|Q9HP54	1	642.3952	-0.5	208	213	0	27.6	27	R	LLDALV	E	2.3	3.1	
589	Q9HRL0|Q9HRL0	1	613.3799	-0.2	167	173	0	41.8	29	A	IAAAVGL	Q	2.5	6.02	
593	Q9HPA3|Q9HPA3	1	685.4374	-0.9	493	499	0	26.4	26	L	ATVALIV	L	2.8	6.02	
594	Q9HQX0|Q9HQX0	1	609.3196	-0.8	176	180	0	25.4	22	N	VCIYI	D	2.9	5.32	
597	Q9HRZ2|Q9HRZ2	1	757.4698	4.2	182	188	0	23.0	22	Q	SKLANLL	F	0.7	10.1	
598	Q9HMH3|Q9HMH3	2	991.5047	-2.1	148	156	0	25.3	24	R	LDTTSSRRG	D	-1.3	10.88	
599	Q9HHG1|Q9HHG1	1	545.3213	0.6	27	31	0	32.2	24	I	PFGLL	V	1.7	6.02	
604	Q9HHP9|Q9HHP9	1	515.3319	1.4	62	66	0	30.5	29	Y	ITLAV	V	2.7	6.02	
604	Q9HHP9|Q9HHP9	1	555.3632	0.4	71	75	0	27.1	18	D	TPLIL	V	2.0	6.02	
606	P08959|GVPA2	2	1051.4975	-0.2	47	55	0	46.9	27	A	SVDTFLHYA	E	0.3	4.94	
616	Q9HSG4|Q9HSG4	1	600.3635	0.7	81	85	0	26.6	21	G	WVLIA	G	2.7	6.02	
617	Q9HNV3|Q9HNV3	1	726.464	-1.7	74	80	0	28.0	25	A	VVNLVAL	S	2.6	6.02	
618	Q9HSG2|Q9HSG2	1	753.4385	0.7	158	165	0	25.0	23	Q	IPAVGANL	V	1.3	6.02	
619	O54654|O54654	2	763.4116	0.4	186	191	0	32.4	26	Y	DLYQLL	E	0.5	3.1	
620	Q9HSW4|Q9HSW4	1	1012.4713	-0.2	130	138	0	26.2	25	T	DVVEKPDDP	P	-1.4	3.5	
623	Q9HSR9|Q9HSR9	2	1035.5601	-1.4	220	228	0	25.7	24	S	KLTFTGQEI	N	-0.2	6.94	
628	Q9HHJ7|CDC66	1	585.3737	1.0	156	160	0	21.0	20	V	IIILD	E	2.8	3.1	
628	Q9HHJ7|CDC66	1	656.4221	2.1	310	316	0	24.6	19	Q	AKAALLA	L	1.6	10.1	
632	Q9HPZ7|Q9HPZ7	1	532.2646	0.8	136	140	0	32.6	26	S	GWGIT	L	0.4	6.02	
633	Q9HRJ5|Q9HRJ5	2	2016.0932	-0.4	172	190	0	57.2	25	A	SNGIALPLLFLSETFVQPA	L	0.9	3.3	
635	Q9HN45|PCNA	1	730.3749	0.1	212	217	0	31.6	27	A	EVELEL	G	0.2	3.02	
640	P15756|RS12	2	1089.4615	0.2	90	98	0	30.1	25	I	SFIDEHDEV	T	-0.7	3.58	
642	Q9HSR5|Q9HSR5	1	727.448	-0.4	4	10	0	27.4	25	I	VAEILLA	D	2.3	3.3	
647	Q9HSQ2|HTPX	1	544.3221	0.6	27	31	0	32.8	32	N	QTILA	I	1.2	6.02	
655	Q9HQE5|Q9HQE5	1	765.4636	-1.0	177	183	0	23.6	16	R	VLDPLLP	A	1.3	3.1	
660	Q9HPQ7|Q9HPQ7	3	1157.4958	0.1	52	62	0	30.0	22	A	SGAMNTCGVYR	V	-0.1	8.9	
664	Q9HSK1|Q9HSK1	1	673.3799	0.1	56	61	0	29.0	26	T	WVIGLS	G	1.7	6.02	
665	Q9HHX5|Q9HHX5	1	765.4636	-1.0	33	39	0	23.6	16	Y	DLLVPLP	D	1.3	3.1	
669	Q9HMT1|Q9HMT1	1	600.3635	0.7	31	35	0	26.6	21	E	VWLLA	S	2.5	6.02	
670	Q9HQV2|Q9HQV2	1	757.4772	-3.8	12	18	0	20.5	19	V	ILALCLL	T	3.4	5.32	
670	Q9HQV2|Q9HQV2	3	2011.9923	0.6	40	56	0	35.1	28	T	QLTVEDDRVQVQQDSPR	L	-1.4	3.96	
677	Q9HQH4|Q9HQH4	1	741.4272	0.5	166	172	0	26.4	24	V	LEPSLIA	A	1.1	3.3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
679	Q9HSW8|Q9HSW8	1	714.3588	-0.4	110	115	0	21.0	20	G	YFLATT	G	1.0	5.92	
683	Q9HN66|SYW2	1	612.3847	-1.0	204	209	0	27.1	24	E	TLVPIA	V	2.0	6.02	
689	Q9HR96|Q9HR96	1	628.416	1.1	52	57	0	23.4	23	S	TLLAVL	G	2.8	6.02	
707	Q9HPT8|Q9HPT8	1	683.4218	0.0	513	519	0	24.9	24	G	LTVGVPV	S	2.0	6.02	
712	Q9HQ62|Q9HQ62	1	664.3068	4.4	58	63	0	31.0	29	V	FDAVDV	T	1.0	2.92	
719	Q9HR47|Q9HR47	1	653.4112	1.2	193	198	0	36.8	24	V	QIALPL	F	1.5	6.02	
720	Q9HSE6|Q9HSE6	2	1401.7113	-4.7	310	322	0	29.0	29	A	GETPAQRGVNFAR	S	-0.9	10.88	
730	Q9HNG1|Y2119	1	612.3847	1.0	158	163	0	32.9	24	A	VLTPAL	H	1.9	6.02	
731	Q9HS84|Q9HS84	2	1161.6798	0.6	71	81	0	42.4	21	A	VFVGIFTVLPA	N	2.3	6.02	
739	Q9HPZ6|Y1401	1	555.3632	0.4	2	6	0	19.4	18	M	PITLL	G	2.0	6.02	
739	Q9HPZ6|Y1401	1	686.4037	0.6	1	6	0	23.8	13	-	MPITLL	G	2.0	6.02	
742	Q9HMQ2|ASSY	1	682.4238	2.9	341	346	0	23.2	20	G	RARPIA	R	-0.4	12.4	
745	Q9HQ19|Q9HQ19	1	782.4902	0.6	344	351	0	23.6	22	P	PVGIITAL	I	2.0	6.02	
748	Q9HNW9|Q9HNW9	1	686.4003	5.0	3	8	0	21.0	15	V	FTPLPL	V	1.1	6.02	
750	Q9HS91|Q9HS91	1	727.448	-0.4	69	75	0	27.4	25	A	EAVLLIA	A	2.3	3.3	
752	P57697|PSMA	1	731.4582	0.7	134	140	0	24.3	23	P	FGVALLI	A	2.9	6.02	
753	Q9HPR9|Q9HPR9	2	1135.5622	-3.2	146	156	0	40.9	26	E	QVVQAHADAPT	T	-0.2	4.94	
754	Q9HQF7|Q9HQF7	3	1936.8551	-0.4	51	67	0	26.9	25	D	GLPERNDEFRGEEGAFD	A	-1.5	3.82	
762	Q9HRL6|Q9HRL6	1	733.4374	-1.8	10	16	0	26.7	25	A	LFAALTV	A	2.5	6.02	
769	Q9HNX6|Y1901	1	543.3268	1.5	130	134	0	30.1	29	T	IDIIA	S	2.4	3.1	
773	Q9HPR7|Q9HPR7	2	1041.5818	-1.3	238	247	0	31.0	26	H	IARDGLGVEL	-	0.6	4.08	
774	Q9HSQ5|Q9HSQ5	2	1187.567	-0.7	42	53	0	28.0	27	W	EVDDGGNTLGVL	N	0.0	2.88	
776	Q9HS66|TRPE2	1	741.4272	-0.7	276	282	0	27.8	24	A	SPELLLA	R	1.0	3.3	
778	Q9HHV9|Q9HHV9	2	910.5851	0.3	56	64	0	46.7	21	L	VANLVLGLL	L	2.4	6.02	
795	Q9HQP0|Q9HQP0	3	943.4359	-2.4	178	187	0	24.9	22	D	AASPADADAR	-	-0.5	3.88	
805	Q9HQJ4|RPOD	1	610.4054	-1.5	67	72	0	25.3	22	R	LGLVPL	T	2.3	6.02	
811	Q9HS73|Q9HS73	1	656.4109	-0.3	92	97	0	26.2	26	D	IVELIA	G	2.6	3.3	
814	Q9HMC5|Q9HMC5	1	668.4473	-1.6	200	205	0	27.5	14	S	LTPLLI	N	2.3	6.02	
817	Q9HME6|Q9HME6	1	727.448	-0.4	180	186	0	27.4	25	T	IEGLLLA	D	2.0	3.3	
818	Q9HSV1|Q9HSV1	1	757.4585	1.5	252	258	0	30.4	23	N	IDILTLA	E	2.0	3.1	
820	Q9HSF8|PCRB	1	745.4374	0.5	98	104	0	27.6	24	D	GYLVPVV	L	1.9	5.92	
824	Q9HQF5|Q9HQF5	1	724.4483	0.0	150	156	0	26.3	23	E	LGVPLQV	N	1.5	6.02	
828	Q9HPN5|Q9HPN5	1	656.4109	1.1	24	29	0	25.3	21	Q	ILVEIA	E	2.6	3.3	
831	Q9HQT2|Q9HQT2	2	668.3969	0.6	145	151	0	24.6	22	S	RLAAPAA	D	0.7	11.04	
832	Q9HSZ9|Q9HSZ9	2	1187.567	-1.6	329	340	0	34.3	27	T	VEGGQTDVVLGD	T	0.0	2.88	
834	Q9HP41|Q9HP41	1	555.3996	1.1	98	102	0	28.5	20	D	IVLIV	D	4.2	6.02	
837	Q9HNX1|Q9HNX1	2	672.3919	0.1	59	64	0	33.3	29	S	RLQASV	A	0.2	11.04	
846	Q9HRM1|Q9HRM1	2	874.4953	2.7	75	81	0	22.8	21	V	LIFPWTV	I	1.7	6.02	
859	Q9HPK2|Y1595	1	666.3588	1.2	257	262	0	21.0	21	T	YATTVL	N	1.2	5.92	
859	Q9HPK2|Y1595	2	991.5049	-2.3	116	124	0	30.5	24	G	ICYVPSTPL	G	1.0	5.32	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
876	Q9HQ46|PHR	1	779.3887	-4.4	57	63	0	25.4	23	V	AFMLDAL	A	1.8	3.1	
879	Q9HT00|GLMS	1	906.5175	-0.8	122	129	0	20.6	19	D	TEVVPHLI	E	1.0	5.12	
885	Q9HMH2|Y2543	1	730.3749	0.1	129	134	0	40.2	27	P	IEDIEL	G	0.4	2.94	
886	Q9HNK7|Q9HNK7	1	626.4003	-0.2	145	150	0	35.0	22	D	VTLVPV	D	2.4	6.02	
894	Q9HR70|Q9HR70	2	1009.6324	-3.5	141	149	0	23.5	18	P	FHIVVLVLA	V	2.9	7.84	
906	Q9HNH8|Q9HNH8	1	617.3207	-3.9	13	19	0	40.8	27	W	GCIAALA	F	2.3	5.32	
919	Q9HHU8|Q9HHU8	1	543.3268	1.5	6	10	0	30.1	29	R	DLIIA	G	2.2	3.1	
924	O54605|O54605	1	600.3635	0.3	112	116	0	26.7	21	D	LLGLW	A	2.0	6.02	
953	Q9HQS8|Q9HQS8	1	544.3221	0.6	163	167	0	32.8	32	T	TQLLA	S	1.0	6.02	
954	Q9HHK7|Q9HHK7	1	585.3737	1.0	76	80	0	29.2	20	S	IILDL	H	2.6	3.1	
958	Q9HN71|Q9HN71	1	543.3268	1.5	198	202	0	30.1	29	D	DILLA	G	2.1	3.1	
959	Q9HHL5|Q9HHL5	1	626.4003	-0.2	171	176	0	23.7	22	R	SLVIPV	E	2.4	6.02	
965	Q9HPH2|Q9HPH2	1	653.4112	1.1	369	374	0	26.3	24	D	LQALIP	D	1.5	6.02	
977	Q9HQY9|Q9HQY9	1	905.595	-0.9	197	205	0	18.3	13	G	IPVLGVLPV	E	2.3	6.02	
978	Q9HHF3|Q9HHF3	1	745.4375	0.4	10	16	0	25.1	24	V	PVFSVVV	G	2.5	6.02	
985	Q9HNH1|Q9HNH1	1	642.3952	-1.4	77	82	0	27.0	27	A	GEILIV	G	2.2	3.3	
986	P33963|GVPK2	1	983.5903	-2.1	24	32	0	24.0	23	T	VVELLVEAL	E	2.1	3.12	
1009	Q9HHZ7|Q9HHZ7	1	543.3268	1.5	246	250	0	30.1	29	D	LDILA	V	2.1	3.1	
1010	Q9HSV9|Q9HSV9	1	681.4425	-0.1	20	26	0	24.7	22	A	LGPIAVI	S	2.4	6.02	
1024	Q9HSB5|Q9HSB5	1	706.3901	-0.3	48	53	0	26.6	25	T	LDAYIL	A	1.5	3.1	
1027	Q9HSG7|Q9HSG7	1	681.4425	0.3	41	47	0	30.4	22	G	LPGLAVL	T	2.2	6.02	
1040	Q9HSA9|Q9HSA9	1	882.5426	-1.1	170	177	0	31.7	17	E	PETLVVLL	V	1.8	3.3	
1041	Q9HPH8|Q9HPH8	1	567.3996	-1.9	41	45	0	30.4	17	Y	LPLII	M	3.0	6.02	
1060	Q9HMD5|Q9HMD5	1	1010.6124	0.4	84	95	0	38.4	22	P	IGVLGVGAALAA	L	2.2	6.02	
1062	Q9HR40|Q9HR40	1	591.3017	-0.2	7	13	0	27.7	24	V	AGGLAGF	L	1.3	6.02	
1070	Q9HQR3|Q9HQR3	1	690.3952	1.2	91	96	0	23.5	23	V	VEAFLL	A	2.2	3.3	
1076	O54608|Y3061	1	656.4109	1.1	37	42	0	25.3	21	E	ILEVLA	T	2.4	3.3	
1085	Q9HS14|Q9HS14	1	543.3268	1.5	46	50	0	30.1	29	C	IDLLA	L	2.1	3.1	
1090	Q9HML3|Q9HML3	1	685.4374	-0.7	157	163	0	26.4	26	P	SALALLV	L	2.6	6.02	
1094	Q9HMI5|Q9HMI5	1	642.3952	-1.4	66	71	0	27.0	27	G	GIELLV	P	2.1	3.3	
1096	Q9HPB8|RL6	2	1211.6034	-1.2	13	23	0	36.6	26	V	TAEVDHLDLTV	E	0.2	3.7	
1100	Q9HR94|Q9HR94	1	757.4772	-4.6	18	24	0	22.6	19	E	MAVVLLI	A	3.5	6.02	
1105	Q9HPD8|Q9HPD8	1	529.286	-0.2	505	509	0	33.1	27	A	NNVLA	D	0.6	6.02	
1107	Q9HMF0|Q9HMF0	1	642.3952	1.1	35	40	0	34.1	24	A	DLLAIV	R	2.4	3.1	
1109	Q9HMI7|Q9HMI7	1	1114.587	-1.6	12	23	0	41.2	27	V	LVGIGGADDSLV	A	1.1	2.92	
1113	Q9HMJ1|Q9HMJ1	1	771.4854	4.1	340	346	0	21.4	20	T	TAKQVIL	D	0.9	10.1	
1120	P15008|RL22	2	1066.6498	0.0	24	33	0	21.2	19	S	ISLKHSKAIA	R	0.4	10.6	
1128	Q9HRY0|GRPE	2	1529.6845	-0.7	44	59	0	28.1	25	R	ALDADNADALADDVAA	L	0.2	2.68	
1149	Q9HHN6|Q9HHN6	1	789.412	0.3	51	57	0	31.9	26	Y	EISVEIT	G	0.7	3.12	
1153	Q9HS42|Q9HS42	2	859.4698	2.6	71	77	0	22.8	19	L	MRARVEV	E	-0.1	10.88	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1154	Q9HRU9|Q9HRU9	1	644.3567	0.3	37	42	0	24.2	20	I	IPVSMV	N	2.1	6.02	
1159	O54646|O54646	1	656.4109	1.1	119	124	0	25.3	21	K	IIEVIA	Q	2.7	3.3	
1163	Q9HMJ9|Q9HMJ9	1	973.5597	-1.6	15	25	0	26.4	24	S	VGAFVALVGAA	T	2.3	6.02	
1167	P15763|RS7	2	1117.6132	1.3	135	145	0	29.9	25	L	KYGGISVPQAV	D	0.3	9.72	
1170	Q9HRZ7|Q9HRZ7	1	939.5753	-0.3	85	94	0	28.0	22	L	QIAGVVGLLA	M	2.0	6.02	
1191	P13044|GVPE1	1	690.4316	1.2	164	169	0	21.1	21	L	LLFSLV	L	2.9	6.02	
1193	O52020|O52020	2	1025.5393	0.7	156	164	0	33.8	26	R	LLVDEQVNP	R	0.0	3	
1204	Q9HPT5|Q9HPT5	1	676.416	1.3	5	10	0	23.0	22	T	FVVTIV	V	3.2	6.02	
1210	Q9HHL1|Q9HHL1	1	674.4367	-1.0	65	70	0	24.6	21	T	GLFIIL	G	3.2	6.02	
1216	Q9HRK5|Q9HRK5	1	1010.6124	-0.9	60	71	0	41.5	22	C	AVGALLGVGLAA	I	2.2	6.02	
1225	Q9HQC2|AROC	1	851.4463	-1.8	359	365	0	22.1	19	C	TILDFML	L	1.8	3.1	
1227	Q9HN85|Q9HN85	2	1186.6081	0.4	256	267	0	29.4	28	G	DATLAALAEAEL	D	0.8	2.94	
1233	Q9HQ04|Q9HQ04	1	726.464	1.1	154	161	0	26.1	25	V	LAAGLVAL	S	2.6	6.02	
1246	Q9HPE9|RS8E	2	1592.6954	-0.3	73	87	0	42.9	24	A	TIEDVSANDANPNYA	R	-0.8	2.88	
1254	Q9HQV5|Q9HQV5	1	584.3533	0.5	4	8	0	26.0	26	T	DLKPI	D	-0.1	6.76	
1256	Q9HQK8|Q9HQK8	2	1861.8694	0.3	209	224	0	43.8	27	A	DSLQDDWATLLERETA	D	-0.9	3.42	
1264	Q9HR06|Q9HR06	1	585.3737	1.0	179	183	0	21.0	20	D	ILLLD	E	2.5	3.1	
1267	Q9HMD3|Q9HMD3	2	1185.683	4.2	74	84	0	27.7	23	G	GRVDRVVISSV	E	0.6	10.88	
1280	Q9HQ35|Q9HQ35	2	763.4084	4.6	1	6	0	27.3	26	-	MTMRLL	V	1.0	11.04	
1294	Q9HQC3|Q9HQC3	1	681.4425	0.7	8	14	0	28.6	22	I	GLPALVL	G	2.2	6.02	
1298	Q9HN39|Q9HN39	1	620.3534	-0.3	111	116	0	28.6	28	D	AFATVL	L	2.3	6.02	
1345	O52038|O52038	1	745.4408	-4.0	1	7	0	25.1	24	-	MVLSVVV	V	3.1	6.02	
1363	Q9HN99|Q9HN99	1	674.4367	-1.0	63	68	0	24.6	21	F	LFGILL	P	3.1	6.02	
1384	Q9HRS3|Q9HRS3	1	642.3952	1.1	32	37	0	34.1	24	A	LDIAIV	Y	2.6	3.1	
1402	Q9HHH6|Q9HHH6	1	722.4367	0.7	104	109	0	13.5	13	A	FVFVLV	Q	3.7	6.02	
1419	Q9HQV0|Q9HQV0	1	543.3268	-0.7	52	56	0	32.6	30	H	IDALI	A	2.2	3.1	
1425	Q9HSN8|Q9HSN8	1	668.4473	-0.3	49	54	0	35.0	14	L	PLLTLL	R	2.2	6.02	
1466	Q9HPI3|Q9HPI3	1	681.4425	0.9	100	105	0	26.0	22	L	PLQVIL	G	1.9	6.02	
1490	Q9HPQ9|KITH	1	555.3632	0.4	78	82	0	19.4	18	S	IPTLL	N	2.0	6.02	
1548	Q9HHS4|Q9HHS4	1	642.3952	1.1	21	26	0	27.5	24	E	LIADLV	E	2.4	3.1	
1588	Q9HSE3|Q9HSE3	1	726.464	1.1	5	12	0	25.6	25	D	ALAGIVAL	F	2.7	6.02	
1633	Q9HNR9|Q9HNR9	1	755.4541	1.3	19	26	0	26.4	25	Q	ASPKIVAA	N	1.0	10.1	
1647	Q9HHL8|Q9HHL8	1	584.3533	0.5	23	27	0	26.0	26	S	LDKPL	L	-0.3	6.76	
1665	Q9V2W4|RS13	2	822.4024	1.8	80	86	0	22.8	21	T	EHAPAWL	A	-0.3	5.12	
1668	Q9HHG7|Q9HHG7	1	683.4694	-0.1	32	37	0	22.7	19	V	LIGLLR	D	1.8	11.04	
1677	Q9HM72|Q9HM72	1	666.3588	1.2	135	140	0	22.4	21	A	SFISTL	L	1.5	6.02	
1680	Q9HPG0|Q9HPG0	1	830.5266	-0.4	88	94	0	22.2	21	A	FNLVILL	A	2.8	6.02	
1707	Q9HR95|Q9HR95	1	745.4408	0.9	91	97	0	21.3	21	A	ITAVMLV	A	2.8	6.02	

END OF LIST II

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
III. Corynebacterium glutmicum membrane; elastase digest; nLC-MALDI MS/MS; no search specificity															
1	P00772|ELA1	1	711.3228	6.2	189	194	0	36.8	32	S	YWGSTV	K	0.0	5.92	
1	P00772|ELA1	1	747.3698	5.9	236	242	0	37.6	36	V	SRLGCNV	T	0.2	9	
1	P00772|ELA1	1	752.3817	5.6	43	48	0	36.6	33	I	SLQYRS	G	-1.2	9.84	
1	P00772|ELA1	1	761.3854	6.0	237	243	0	45.6	35	S	RLGCNVT	R	0.2	9	
1	P00772|ELA1	1	772.3868	8.5	225	231	0	48.4	36	G	QYAVHGV	T	0.3	7.76	
1	P00772|ELA1	1	798.3548	-7.3	188	194	0	35.3	31	S	SYWGSTV	K	-0.1	5.92	
1	P00772|ELA1	1	800.3851	6.9	54	61	0	56.0	34	A	HTCGGTLI	R	0.7	7.16	
1	P00772|ELA1	1	809.3378	1.6	149	155	0	40.6	32	A	NNSPCYI	T	-0.5	5.32	
1	P00772|ELA1	1	809.4032	6.1	43	49	0	38.7	33	I	SLQYRSG	S	-1.1	9.84	
1	P00772|ELA1	1	816.3555	5.6	106	111	0	32.6	32	V	HPYWNT	D	-1.9	7.76	
1	P00772|ELA1	1	825.5072	6.7	139	146	0	35.0	30	G	VLPRAGTI	L	0.9	11.04	
1	P00772|ELA1	1	828.4494	-5.7	258	264	0	39.8	35	S	WINNVIA	S	1.0	6.02	
1	P00772|ELA1	1	848.4174	11.4	236	243	0	45.0	36	V	SRLGCNVT	R	0.1	9	
1	P00772|ELA1	1	873.4093	18.0	34	40	0	41.9	36	A	QRNSWPS	Q	-2.2	11.04	
1	P00772|ELA1	1	882.5287	9.2	138	146	0	39.7	30	L	GVLPRAGTI	L	0.7	11.04	
1	P00772|ELA1	1	885.3869	1.7	187	194	0	63.5	31	S	SSYWGSTV	K	-0.2	5.92	
1	P00772|ELA1	1	890.461	5.1	156	163	0	51.2	36	I	TGWGLTRT	N	-0.6	11.04	
1	P00772|ELA1	1	896.4352	5.4	43	50	0	40.5	34	I	SLQYRSGS	S	-1.0	9.84	
1	P00772|ELA1	1	898.56	6.6	122	129	0	36.3	31	A	LLRLAQSV	T	1.1	11.04	
1	P00772|ELA1	1	909.5396	12.9	136	144	0	64.3	29	V	QLGVLPRAG	T	0.4	11.04	
1	P00772|ELA1	1	915.4239	0.1	105	111	0	43.6	33	V	VHPYWNT	D	-1.0	7.76	
1	P00772|ELA1	1	915.4814	-4.2	257	264	0	54.0	37	I	SWINNVIA	S	0.8	6.02	
1	P00772|ELA1	1	933.4491	10.1	62	68	0	52.3	36	I	RQNWVMT	A	-1.0	11.04	
1	P00772|ELA1	1	936.4916	-9.9	130	137	0	49.7	35	V	TLNSYVQL	G	0.3	5.92	
1	P00772|ELA1	1	940.4542	-6.8	175	182	0	51.3	33	A	YLPTVDYA	I	0.2	3.1	
1	P00772|ELA1	1	943.4512	5.5	223	231	0	60.3	35	V	NGQYAVHGV	T	-0.2	7.76	
1	P00772|ELA1	1	948.5393	7.8	243	250	0	34.6	31	V	TRKPTVFT	R	-0.6	11.48	
1	P00772|ELA1	1	972.4189	-7.7	186	194	0	31.7	30	S	SSSYWGSTV	K	-0.3	5.92	
1	P00772|ELA1	1	974.4968	0.7	239	247	0	45.2	36	L	GCNVTRKPT	V	-1.0	10.1	
1	P00772|ELA1	1	993.5131	-13.2	130	138	0	43.6	35	V	TLNSYVQLG	V	0.2	5.92	
1	P00772|ELA1	1	996.4699	6.9	213	222	0	68.1	34	G	DSGGPLHCLV	N	0.4	4.94	
1	P00772|ELA1	1	1000.5665	8.8	124	132	0	55.3	35	L	RLAQSVTLN	S	0.1	11.04	
1	P00772|ELA1	1	1004.4862	10.0	62	69	0	61.9	36	I	RQNWVMTA	A	-0.7	11.04	
1	P00772|ELA1	1	1014.4923	10.5	104	111	0	50.0	35	I	VVHPYWNT	D	-0.4	7.76	
1	P00772|ELA1	1	1029.5203	4.2	27	36	0	56.9	36	R	VVGGTEAQRN	S	-0.6	6.98	
1	P00772|ELA1	1	1040.4675	4.0	45	53	0	44.4	33	L	QYRSGSSWA	H	-1.2	9.84	
1	P00772|ELA1	1	1042.4866	2.7	70	78	0	54.5	34	A	AHCVDRELT	F	-0.3	5.22	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P00772|ELA1	1	1050.5458	3.1	41	49	0	45.4	35	S	QISLQYRSG	S	-0.7	9.84	
1	P00772|ELA1	1	1066.6499	7.7	138	148	0	55.2	28	L	GVLPRAGTILA	N	1.1	11.04	
1	P00772|ELA1	1	1087.5986	-1.2	124	133	0	61.0	36	L	RLAQSVTLNS	Y	0.0	11.04	
1	P00772|ELA1	1	1093.592	2.7	251	259	0	50.5	34	T	RVSAYISWI	N	0.7	9.84	
1	P00772|ELA1	1	1114.5519	9.6	34	42	0	50.8	36	A	QRNSWPSQI	S	-1.6	11.04	
1	P00772|ELA1	1	1123.6713	1.7	136	146	0	49.6	30	V	QLGVLPRAGTI	L	0.6	11.04	
1	P00772|ELA1	1	1127.5247	1.4	187	196	0	72.8	34	S	SSYWGSTVKN	S	-0.9	9.72	
1	P00772|ELA1	1	1133.6193	3.4	74	82	0	46.2	35	V	DRELTFRVV	V	-0.2	7.04	
1	P00772|ELA1	1	1145.4778	1.4	106	114	0	63.7	30	V	HPYWNTDDV	A	-1.6	3.88	
1	P00772|ELA1	1	1153.5516	2.0	44	53	0	45.3	35	S	LQYRSGSSWA	H	-0.7	9.84	
1	P00772|ELA1	1	1155.6037	-1.0	221	231	0	75.5	35	C	LVNGQYAVHGV	T	0.5	7.76	
1	P00772|ELA1	1	1170.5993	-5.0	164	174	0	87.7	36	T	NGQLAQTLQQA	Y	-0.7	6.02	
1	P00772|ELA1	1	1171.6713	3.8	134	144	0	85.0	34	S	YVQLGVLPRAG	T	0.6	9.84	
1	P00772|ELA1	1	1206.6033	3.3	225	235	0	72.4	36	G	QYAVHGVTSFV	S	0.7	7.76	
1	P00772|ELA1	1	1214.5568	-1.2	187	197	0	84.1	34	S	SSYWGSTVKNS	M	-0.9	9.72	
1	P00772|ELA1	1	1226.7347	1.1	122	132	0	59.0	32	A	LLRLAQSVTLN	S	0.7	11.04	
1	P00772|ELA1	1	1240.5836	15.1	43	53	0	74.4	35	I	SLQYRSGSSWA	H	-0.7	9.84	
1	P00772|ELA1	1	1244.5462	-0.4	105	114	0	79.8	32	V	VHPYWNTDDV	A	-1.0	3.88	
1	P00772|ELA1	1	1250.6507	-6.7	127	137	0	42.6	36	A	QSVTLNSYVQL	G	0.2	5.92	
1	P00772|ELA1	1	1258.7034	12.9	133	144	0	104.9	34	N	SYVQLGVLPRAG	T	0.4	9.84	
1	P00772|ELA1	1	1262.6659	-9.2	254	264	0	73.2	36	S	AYISWINNVIA	S	1.0	5.92	
1	P00772|ELA1	1	1267.6085	-11.6	172	182	0	86.0	35	L	QQAYLPTVDYA	I	-0.3	3.1	
1	P00772|ELA1	1	1271.647	-3.4	163	174	0	67.7	36	R	TNGQLAQTLQQA	Y	-0.7	6.02	
1	P00772|ELA1	1	1287.552	6.2	106	116	0	75.4	32	V	HPYWNTDDVAA	G	-0.9	3.88	
1	P00772|ELA1	1	1307.7925	-15.5	136	148	0	56.2	30	V	QLGVLPRAGTILA	N	1.0	11.04	
1	P00772|ELA1	1	1315.5833	0.4	105	115	0	83.5	33	V	VHPYWNTDDVA	A	-0.7	3.88	
1	P00772|ELA1	1	1321.6813	-0.8	239	250	0	52.2	36	L	GCNVTRKPTVFT	R	-0.2	10.1	
1	P00772|ELA1	1	1343.6146	4.3	104	114	0	75.7	34	I	VVHPYWNTDDV	A	-0.5	3.88	
1	P00772|ELA1	1	1372.7463	0.9	132	144	0	83.4	36	L	NSYVQLGVLPRAG	T	0.1	9.84	
1	P00772|ELA1	1	1373.7052	-2.2	156	168	0	57.0	37	I	TGWGLTRTNGQLA	Q	-0.5	11.04	
1	P00772|ELA1	1	1374.7078	-0.5	57	68	0	44.3	37	C	GGTLIRQNWVMT	A	0.0	11.04	
1	P00772|ELA1	1	1385.8031	-16.5	134	146	0	81.3	35	S	YVQLGVLPRAGTI	L	0.8	9.84	
1	P00772|ELA1	1	1386.6204	-1.4	105	116	0	101.4	33	V	VHPYWNTDDVAA	G	-0.5	3.88	
1	P00772|ELA1	1	1393.611	9.0	87	98	0	57.6	34	H	NLNQNDGTEQYV	G	-1.6	3	
1	P00772|ELA1	1	1414.6517	-0.5	104	115	0	84.5	34	I	VVHPYWNTDDVA	A	-0.3	3.88	
1	P00772|ELA1	1	1417.7929	-0.6	117	129	0	55.5	34	A	GYDIALLRLAQSV	T	0.7	6.7	
1	P00772|ELA1	1	1427.7481	2.3	162	174	0	109.5	36	T	RTNGQLAQTLQQA	Y	-1.0	11.04	
1	P00772|ELA1	1	1443.6419	1.2	105	117	0	88.4	33	V	VHPYWNTDDVAAG	Y	-0.5	3.88	
1	P00772|ELA1	1	1444.6657	2.0	187	199	0	45.1	35	S	SSYWGSTVKNSMV	C	-0.3	9.72	
1	P00772|ELA1	1	1445.7449	-0.1	57	69	0	56.5	37	C	GGTLIRQNWVMTA	A	0.1	11.04	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P00772|ELA1	1	1458.8195	-0.5	130	142	0	96.8	35	V	TLNSYVQLGVLPR	A	0.3	9.84	
1	P00772|ELA1	1	1463.7408	8.9	254	266	0	40.8	36	S	AYISWINNVIASN	-	0.5	5.92	
1	P00772|ELA1	1	1472.8351	-0.4	133	146	0	100.9	34	N	SYVQLGVLPRAGTI	L	0.7	9.84	
1	P00772|ELA1	1	1478.6902	0.2	43	55	0	42.8	35	I	SLQYRSGSSWAHT	C	-0.9	9.84	
1	P00772|ELA1	1	1481.7263	-5.1	41	53	0	45.3	36	S	QISLQYRSGSSWA	H	-0.6	9.84	
1	P00772|ELA1	1	1485.6889	4.2	104	116	0	89.7	35	I	VVHPYWNTDDVAA	G	-0.2	3.88	
1	P00772|ELA1	1	1486.7165	1.8	27	40	0	83.0	36	R	VVGGTEAQRNSWPS	Q	-0.7	6.98	
1	P00772|ELA1	1	1507.7419	-0.3	37	49	0	43.0	36	N	SWPSQISLQYRSG	S	-0.8	9.84	
1	P00772|ELA1	1	1529.7223	5.0	29	42	0	69.9	36	V	GGTEAQRNSWPSQI	S	-1.3	6.98	
1	P00772|ELA1	1	1542.7103	5.4	104	117	0	106.1	35	I	VVHPYWNTDDVAAG	Y	-0.2	3.88	
1	P00772|ELA1	1	1543.7929	0.3	70	82	0	58.1	37	A	AHCVDRELTFRVV	V	0.3	7.16	
1	P00772|ELA1	1	1549.7009	-3.4	87	100	0	102.4	34	H	NLNQNDGTEQYVGV	Q	-1.1	3	
1	P00772|ELA1	1	1553.6706	1.0	83	96	0	92.2	32	V	VGEHNLNQNDGTEQ	Y	-1.8	3.82	
1	P00772|ELA1	1	1559.8671	-4.3	115	129	0	69.4	35	V	AAGYDIALLRLAQSV	T	0.9	6.7	
1	P00772|ELA1	1	1560.6441	3.8	85	97	0	59.8	29	G	EHNLNQNDGTEQY	V	-2.3	3.82	
1	P00772|ELA1	1	1586.878	3.8	130	144	0	125.5	35	V	TLNSYVQLGVLPRAG	T	0.3	9.84	
1	P00772|ELA1	1	1590.8729	-2.7	124	137	0	116.6	35	L	RLAQSVTLNSYVQL	G	0.2	9.84	
1	P00772|ELA1	1	1602.8114	-3.2	156	170	0	46.9	37	I	TGWGLTRTNGQLAQT	L	-0.7	11.04	
1	P00772|ELA1	1	1604.8674	2.6	251	264	0	77.9	36	T	RVSAYISWINNVIA	S	0.7	9.84	
1	P00772|ELA1	1	1614.83	-2.0	69	82	0	44.7	37	T	AAHCVDRELTFRVV	V	0.4	7.16	
1	P00772|ELA1	1	1628.7907	-2.3	28	42	0	47.6	36	V	VGGTEAQRNSWPSQI	S	-0.9	6.98	
1	P00772|ELA1	1	1647.8944	-4.9	124	138	0	111.4	36	L	RLAQSVTLNSYVQLG	V	0.2	9.84	
1	P00772|ELA1	1	1652.739	-0.2	82	96	0	118.3	33	V	VVGEHNLNQNDGTEQ	Y	-1.4	3.82	
1	P00772|ELA1	1	1656.9563	-2.5	133	148	0	80.6	34	N	SYVQLGVLPRAGTILA	N	0.9	9.84	
1	P00772|ELA1	1	1659.7125	-2.9	85	98	0	132.7	30	G	EHNLNQNDGTEQYV	G	-1.8	3.82	
1	P00772|ELA1	1	1677.8985	-1.0	236	250	0	41.7	36	V	SRLGCNVTRKPTVFT	R	-0.3	11.32	
1	P00772|ELA1	1	1698.9013	-0.5	159	174	0	107.9	36	W	GLTRTNGQLAQTLQQA	Y	-0.6	11.04	
1	P00772|ELA1	1	1705.7737	0.1	104	118	0	102.0	34	I	VVHPYWNTDDVAAGY	D	-0.2	3.88	
1	P00772|ELA1	1	1712.8522	-4.1	101	114	0	105.9	36	V	QKIVVHPYWNTDDV	A	-0.6	5.1	
1	P00772|ELA1	1	1715.8955	8.7	156	171	0	124.3	37	I	TGWGLTRTNGQLAQTL	Q	-0.4	11.04	
1	P00772|ELA1	1	1716.7339	0.8	83	97	0	113.1	31	V	VGEHNLNQNDGTEQY	V	-1.7	3.82	
1	P00772|ELA1	1	1727.8591	0.8	27	42	0	104.6	37	R	VVGGTEAQRNSWPSQI	S	-0.6	6.98	
1	P00772|ELA1	1	1770.9992	-5.5	132	148	0	102.7	35	L	NSYVQLGVLPRAGTILA	N	0.7	9.84	
1	P00772|ELA1	1	1783.8893	-0.7	101	115	0	88.5	37	V	QKIVVHPYWNTDDVA	A	-0.4	5.1	
1	P00772|ELA1	1	1786.8607	-3.6	54	69	0	58.4	36	A	HTCGGTLIRQNWVMTA	A	0.0	9.02	
1	P00772|ELA1	1	1801.0098	-0.6	130	146	0	134.4	35	V	TLNSYVQLGVLPRAGTI	L	0.5	9.84	
1	P00772|ELA1	1	1805.9424	-4.1	251	266	0	72.9	37	T	RVSAYISWINNVIASN	-	0.4	9.84	
1	P00772|ELA1	1	1806.7849	0.9	106	121	0	115.8	32	V	HPYWNTDDVAAGYDIA	L	-0.6	3.6	
1	P00772|ELA1	1	1815.8024	4.0	83	98	0	120.8	33	V	VGEHNLNQNDGTEQYV	G	-1.4	3.82	
1	P00772|ELA1	1	1854.9265	-2.5	101	116	0	92.7	37	V	QKIVVHPYWNTDDVAA	G	-0.3	5.1	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P00772|ELA1	1	1872.8238	3.3	84	100	0	115.9	33	V	GEHNLNQNDGTEQYVGV	Q	-1.3	3.82	
1	P00772|ELA1	1	1872.8238	0.7	83	99	0	67.2	32	V	VGEHNLNQNDGTEQYVG	V	-1.3	3.82	
1	P00772|ELA1	1	1901.0371	-3.3	127	144	0	118.8	36	A	QSVTLNSYVQLGVLPRAG	T	0.3	9.84	
1	P00772|ELA1	1	1905.8533	0.1	105	121	0	132.8	34	V	VHPYWNTDDVAAGYDIA	L	-0.3	3.6	
1	P00772|ELA1	1	1914.0938	-5.6	130	147	0	67.6	34	V	TLNSYVQLGVLPRAGTIL	A	0.7	9.84	
1	P00772|ELA1	1	1914.8708	0.1	82	98	0	156.7	34	V	VVGEHNLNQNDGTEQYV	G	-1.0	3.82	
1	P00772|ELA1	1	1927.9752	-1.7	27	44	0	62.4	37	R	VVGGTEAQRNSWPSQISL	Q	-0.4	6.98	
1	P00772|ELA1	1	1933.8847	-2.1	104	120	0	56.0	34	I	VVHPYWNTDDVAAGYDI	A	-0.2	3.6	
1	P00772|ELA1	1	1938.9224	-3.1	37	53	0	86.4	36	N	SWPSQISLQYRSGSSWA	H	-0.7	9.84	
1	P00772|ELA1	1	1971.8923	4.1	83	100	0	147.5	34	V	VGEHNLNQNDGTEQYVGV	Q	-1.0	3.82	
1	P00772|ELA1	1	1971.8923	-5.9	82	99	0	50.7	33	V	VVGEHNLNQNDGTEQYVG	V	-1.0	3.82	
1	P00772|ELA1	1	1985.131	-0.8	130	148	0	118.0	33	V	TLNSYVQLGVLPRAGTILA	N	0.8	9.84	
1	P00772|ELA1	1	2004.9218	24.9	104	121	0	140.4	37	I	VVHPYWNTDDVAAGYDIA	L	-0.1	3.6	
1	P00772|ELA1	1	2013.9392	-9.5	81	98	0	35.7	35	R	VVVGEHNLNQNDGTEQYV	G	-0.7	3.82	
1	P00772|ELA1	1	2022.9582	-2.5	43	61	0	50.2	36	I	SLQYRSGSSWAHTCGGTLI	R	-0.1	8.9	
1	P00772|ELA1	1	2043.0498	-0.6	156	174	0	159.4	37	I	TGWGLTRTNGQLAQTLQQA	Y	-0.6	11.04	
1	P00772|ELA1	1	2070.9607	12.8	82	100	0	174.0	36	V	VVGEHNLNQNDGTEQYVGV	Q	-0.7	3.82	
1	P00772|ELA1	1	2099.9508	-1.6	83	101	0	145.8	34	V	VGEHNLNQNDGTEQYVGVQ	K	-1.1	3.82	
1	P00772|ELA1	1	2115.1688	-8.6	127	146	0	126.1	36	A	QSVTLNSYVQLGVLPRAGTI	L	0.4	9.84	
1	P00772|ELA1	1	2170.0291	1.8	81	100	0	121.4	36	R	VVVGEHNLNQNDGTEQYVGV	Q	-0.5	3.82	
1	P00772|ELA1	1	2185.04	1.9	85	103	0	154.7	37	G	EHNLNQNDGTEQYVGVQKI	V	-1.3	4.42	
1	P00772|ELA1	1	2186.2059	-4.6	126	146	0	80.9	36	L	AQSVTLNSYVQLGVLPRAGTI	L	0.5	9.84	
1	P00772|ELA1	1	2199.0193	-3.2	82	101	0	150.9	35	V	VVGEHNLNQNDGTEQYVGVQ	K	-0.9	3.82	
1	P00772|ELA1	1	2231.0899	3.8	104	123	0	104.0	37	I	VVHPYWNTDDVAAGYDIALL	R	0.3	3.6	
1	P00772|ELA1	1	2241.2593	-9.6	124	144	0	151.2	35	L	RLAQSVTLNSYVQLGVLPRAG	T	0.3	11.14	
1	P00772|ELA1	1	2299.29	-4.0	127	148	0	116.1	35	A	QSVTLNSYVQLGVLPRAGTILA	N	0.6	9.84	
1	P00772|ELA1	1	2317.1087	6.6	79	98	0	119.2	37	T	FRVVVGEHNLNQNDGTEQYV	G	-0.8	4.42	
1	P00772|ELA1	1	2341.1299	8.1	83	103	0	187.3	37	V	VGEHNLNQNDGTEQYVGVQKI	V	-1.0	4.42	
1	P00772|ELA1	1	2370.3271	-4.4	126	148	0	98.1	35	L	AQSVTLNSYVQLGVLPRAGTILA	N	0.7	9.84	
1	P00772|ELA1	1	2374.1594	3.5	101	121	0	156.0	37	V	QKIVVHPYWNTDDVAAGYDIA	L	-0.2	4.16	
1	P00772|ELA1	1	2440.1983	-1.2	82	103	0	198.5	37	V	VVGEHNLNQNDGTEQYVGVQKI	V	-0.8	4.42	
1	P00772|ELA1	1	2455.3911	-7.0	124	146	0	124.0	35	L	RLAQSVTLNSYVQLGVLPRAGTI	L	0.4	11.14	
1	P00772|ELA1	1	2467.4275	-3.1	122	144	0	95.3	32	A	LLRLAQSVTLNSYVQLGVLPRAG	T	0.6	11.14	
1	P00772|ELA1	1	2473.1986	-4.6	79	100	0	142.6	37	T	FRVVVGEHNLNQNDGTEQYVGV	Q	-0.5	4.42	
1	P00772|ELA1	1	2519.2517	-3.0	27	49	0	91.7	38	R	VVGGTEAQRNSWPSQISLQYRSG	S	-0.7	9.84	
1	P00772|ELA1	1	2574.2463	-5.3	78	100	0	88.0	37	L	TFRVVVGEHNLNQNDGTEQYVGV	Q	-0.5	4.42	
1	P00772|ELA1	1	2606.2837	-0.2	27	50	0	106.0	38	R	VVGGTEAQRNSWPSQISLQYRSGS	S	-0.7	9.84	
1	P00772|ELA1	1	2639.5123	-6.0	124	148	0	139.9	34	L	RLAQSVTLNSYVQLGVLPRAGTILA	N	0.6	11.14	
1	P00772|ELA1	1	2681.5592	-4.7	122	146	0	93.6	32	A	LLRLAQSVTLNSYVQLGVLPRAGTI	L	0.7	11.14	
1	P00772|ELA1	1	2842.4362	-3.1	79	103	0	52.5	38	T	FRVVVGEHNLNQNDGTEQYVGVQKI	V	-0.6	5.34	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P00772|ELA1	1	2865.6804	-8.2	122	148	0	83.9	32	A	LLRLAQSVTLNSYVQLGVLPRAGTILA	N	0.8	11.14	
1	P00772|ELA1	1	2885.4712	-3.3	104	129	0	139.0	38	I	VVHPYWNTDDVAAGYDIALLRLAQSV	T	0.3	4.16	
1	P00772|ELA1	1	2950.4322	-7.1	27	53	0	47.8	37	R	VVGGTEAQRNSWPSQISLQYRSGSSWA	H	-0.7	9.84	
1	P00772|ELA1	1	3128.7346	-12.4	115	144	0	71.8	37	V	AAGYDIALLRLAQSVTLNSYVQLGVLPRAG	T	0.6	9.58	
1	P00772|ELA1	1	3200.7921	-3.5	117	146	0	76.3	35	A	GYDIALLRLAQSVTLNSYVQLGVLPRAGTI	L	0.6	9.58	
1	P00772|ELA1	1	3254.7088	-1.1	101	129	0	59.6	38	V	QKIVVHPYWNTDDVAAGYDIALLRLAQSV	T	0.2	5.2	
1	P00772|ELA1	1	3342.8663	-8.6	115	146	0	67.1	36	V	AAGYDIALLRLAQSVTLNSYVQLGVLPRAGTI	L	0.7	9.58	
1	P00772|ELA1	1	3384.9133	1.6	117	148	0	43.2	33	A	GYDIALLRLAQSVTLNSYVQLGVLPRAGTILA	N	0.8	9.58	
1	P00772|ELA1	1	3666.7339	-10.1	83	114	0	62.8	36	V	VGEHNLNQNDGTEQYVGVQKIVVHPYWNTDDV	A	-0.8	4.2	
2	Cg0446	1	772.4119	8.7	487	493	0	52.5	37	I	PNYLGPL	L	-0.1	5.92	
2	Cg0446	1	819.3763	9.8	647	654	0	52.8	35	E	PGENGTFV	R	-0.4	3.3	
2	Cg0446	1	820.3504	8.9	457	463	0	39.2	34	A	SWTYHGA	N	-0.8	7.76	
2	Cg0446	1	888.4494	3.6	292	298	0	51.3	37	S	FIQFHPT	G	0.2	7.84	
2	Cg0446	1	935.4825	3.3	171	179	0	73.6	35	T	RSFGGVQVS	R	0.1	11.04	
2	Cg0446	1	942.5175	7.5	487	495	0	56.7	36	I	PNYLGPLLG	S	0.3	5.92	
2	Cg0446	1	944.4352	3.0	182	189	0	35.3	34	T	YYTRGQTG	Q	-1.6	9.58	
2	Cg0446	1	966.4559	3.3	159	167	0	40.2	35	A	PFAREYGGA	L	-0.6	6.88	
2	Cg0446	1	987.4596	7.4	521	528	0	41.4	35	L	MGNRPEWV	G	-1.0	6.98	
2	Cg0446	1	993.5396	-7.0	9	16	0	41.8	34	T	RPEFIHPV	S	-0.4	7.84	
2	Cg0446	1	994.5236	-2.7	294	302	0	37.1	34	I	QFHPTGLPV	N	0.0	7.84	
2	Cg0446	1	1036.5302	3.2	170	179	0	49.3	35	A	TRSFGGVQVS	R	0.0	11.04	
2	Cg0446	1	1045.4577	3.2	115	123	0	45.5	32	V	DNDGAYRHV	K	-1.5	5.1	
2	Cg0446	1	1066.5335	-7.1	661	669	0	53.4	35	L	FFESVPLQT	R	0.4	3.3	
2	Cg0446	1	1094.5145	7.4	157	167	0	61.1	35	I	GAPFAREYGGA	L	-0.4	6.88	
2	Cg0446	1	1094.5873	0.1	8	16	0	46.4	34	T	TRPEFIHPV	S	-0.4	7.84	
2	Cg0446	1	1095.5673	-4.9	372	383	0	83.0	35	I	NAGLGVGPLNNA	A	0.2	6.02	
2	Cg0446	1	1110.5418	2.1	98	109	0	111.9	35	A	HSIAAQGGVNSA	R	0.1	7.84	
2	Cg0446	1	1134.5921	-1.8	77	87	0	49.7	36	A	ALGELGYDVKA	F	0.2	4.08	
2	Cg0446	1	1184.4921	4.3	256	266	0	64.1	30	A	TGGYGNVYHMS	T	-0.5	7.7	
2	Cg0446	1	1205.5353	-6.3	644	654	0	61.1	33	S	AWEPGENGTFV	R	-0.5	3.12	
2	Cg0446	1	1207.5986	2.0	156	167	0	83.6	36	A	IGAPFAREYGGA	L	0.0	6.88	
2	Cg0446	1	1216.6815	-2.3	489	499	0	69.3	35	N	YLGPLLGSERL	S	0.2	6.88	
2	Cg0446	1	1223.5757	3.7	569	577	0	39.6	35	A	LRDDFWKNM	R	-1.3	6.9	
2	Cg0446	1	1232.605	1.8	88	97	0	50.4	37	A	FTYHDAPRRA	H	-1.3	9.84	
2	Cg0446	1	1254.6761	-1.3	292	302	0	84.2	35	S	FIQFHPTGLPV	N	0.6	7.84	
2	Cg0446	1	1285.5397	2.0	256	267	0	76.7	30	A	TGGYGNVYHMST	L	-0.6	7.7	
2	Cg0446	1	1292.5673	-3.9	643	654	0	94.8	33	V	SAWEPGENGTFV	R	-0.5	3.12	
2	Cg0446	1	1298.6156	-8.2	533	542	0	53.3	34	V	HGPEYYHRQL	G	-1.9	7.84	
2	Cg0446	1	1313.6364	1.6	182	192	0	82.7	35	T	YYTRGQTGQQL	Q	-1.5	9.58	
2	Cg0446	1	1355.6371	5.8	533	543	0	42.7	35	V	HGPEYYHRQLG	D	-1.7	7.84	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	Cg0446	1	1368.6132	-3.5	254	266	0	52.4	33	I	LATGGYGNVYHMS	T	0.0	7.7	
2	Cg0446	1	1372.6194	1.7	521	532	0	63.6	34	L	MGNRPEWVGDNV	H	-1.0	4.08	
2	Cg0446	1	1381.6918	-1.9	475	486	0	76.8	36	A	SVDGWFTLPFTI	P	0.8	3.1	
2	Cg0446	1	1397.6939	-9.3	385	395	0	44.3	36	A	YLDFRDATERL	G	-0.8	4.3	
2	Cg0446	1	1400.6896	-0.1	551	563	0	57.3	36	C	GVSRNVEDLQDGI	N	-0.5	3.7	
2	Cg0446	1	1427.7772	-8.3	487	499	0	50.3	36	I	PNYLGPLLGSERL	S	-0.2	6.88	
2	Cg0446	1	1450.7139	4.7	567	577	0	44.4	36	I	RALRDDFWKNM	R	-1.3	10.08	
2	Cg0446	1	1455.6188	-6.1	581	593	0	48.4	30	T	GSTDEMNQVLEYA	A	-0.7	2.94	
2	Cg0446	1	1468.731	-1.8	384	395	0	55.8	36	A	AYLDFRDATERL	G	-0.6	4.3	
2	Cg0446	1	1469.6609	13.4	254	267	0	64.3	34	I	LATGGYGNVYHMST	L	-0.1	7.7	
2	Cg0446	1	1469.6609	-23.1	256	269	0	39.4	31	A	TGGYGNVYHMSTLA	K	-0.1	7.7	
2	Cg0446	1	1492.7609	2.2	569	579	0	65.0	36	A	LRDDFWKNMRI	T	-1.0	10.08	
2	Cg0446	1	1509.638	-5.2	39	49	0	80.8	29	T	KDMWEYQKDHM	N	-2.1	5.28	
2	Cg0446	1	1526.6386	-1.4	620	632	0	41.5	30	A	HFRDDHLSEDGEA	E	-1.6	4.2	
2	Cg0446	1	1540.8038	-0.1	655	667	0	85.3	36	V	RHAEPLFFESVPL	Q	0.0	5.3	
2	Cg0446	1	1593.8086	-1.1	569	580	0	54.8	36	A	LRDDFWKNMRIT	G	-1.0	10.08	
2	Cg0446	1	1641.8111	0.7	182	195	0	106.8	36	T	YYTRGQTGQQLQLS	T	-1.2	9.58	
2	Cg0446	1	1653.7821	-0.4	254	269	0	72.4	35	I	LATGGYGNVYHMSTLA	K	0.3	7.7	
2	Cg0446	1	1673.8121	-1.1	115	129	0	89.3	36	V	DNDGAYRHVKDTVKG	G	-1.5	7.72	
2	Cg0446	1	1696.8321	0.1	533	546	0	78.2	36	V	HGPEYYHRQLGDIL	Y	-1.0	6.02	
2	Cg0446	1	1724.8832	-18.3	17	34	0	52.9	37	V	SVLPEVSAGTVLDAAEPA	G	0.6	2.94	
2	Cg0446	1	1730.8336	-2.1	115	130	0	91.7	36	V	DNDGAYRHVKDTVKGG	D	-1.4	7.72	
2	Cg0446	1	1736.8482	-4.0	2	16	0	61.8	36	M	STHSETTRPEFIHPV	S	-0.9	6.02	
2	Cg0446	1	1756.8315	3.5	518	532	0	46.0	36	I	DRLMGNRPEWVGDNV	H	-1.0	4.3	
2	Cg0446	1	1767.8639	0.6	491	507	0	49.5	37	L	GPLLGSERLSEDAPEAQ	A	-0.7	3.68	
2	Cg0446	1	1769.9101	0.2	655	669	0	79.5	37	V	RHAEPLFFESVPLQT	R	-0.2	5.3	
2	Cg0446	1	1835.8335	1.9	39	52	0	37.1	35	T	KDMWEYQKDHMNLV	S	-1.4	5.28	
2	Cg0446	1	1938.951	-20.2	205	221	0	66.4	36	I	HLGSVEIFTHNEMVDVI	V	0.5	4.4	
2	Cg0446	1	1954.9173	-2.8	339	353	0	38.8	35	I	PEDERDYFLERRYPA	F	-1.9	4.28	
2	Cg0446	1	1968.9078	-3.3	529	545	0	41.5	35	V	GDNVHGPEYYHRQLGDI	L	-1.3	5.12	
2	Cg0446	1	2044.0113	14.7	489	507	0	87.2	38	N	YLGPLLGSERLSEDAPEAQ	A	-0.5	3.68	
2	Cg0446	1	2081.9919	-6.2	529	546	0	77.7	36	V	GDNVHGPEYYHRQLGDIL	Y	-1.0	5.12	
2	Cg0446	1	2133.0023	1.5	39	55	0	77.6	36	T	KDMWEYQKDHMNLVSPL	N	-1.0	5.28	
2	Cg0446	1	2144.0585	-0.5	148	167	0	50.4	37	V	RVIDHMNAIGAPFAREYGGA	L	-0.1	7.76	
2	Cg0446	1	2255.1069	-5.9	487	507	0	82.1	37	I	PNYLGPLLGSERLSEDAPEAQ	A	-0.7	3.68	
2	Cg0446	1	2349.1866	-0.6	77	97	0	113.9	38	A	ALGELGYDVKAFTYHDAPRRA	H	-0.5	7.68	
2	Cg0446	1	2418.0025	0.1	598	619	0	29.3	27	A	DYIDLGELMCVDALDRDESCGA	H	-0.1	3.22	Oxidation (M)
2	Cg0446	1	2420.2237	-1.5	76	97	0	60.0	38	A	AALGELGYDVKAFTYHDAPRRA	H	-0.4	7.68	
2	Cg0446	1	2605.3581	-4.9	477	499	0	58.3	38	V	DGWFTLPFTIPNYLGPLLGSERL	S	0.2	4.08	
2	Cg0446	1	2791.4585	0.3	475	499	0	111.3	38	A	SVDGWFTLPFTIPNYLGPLLGSERL	S	0.3	4.08	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	Cg0446	1	3618.7882	-1.6	475	507	0	40.9	39	A	SVDGWFTLPFTIPNYLGPLLGSERLSEDAPEAQ	A	-0.2	3.5	
3	Cg1537	1	721.3911	-1.1	320	325	0	33.9	33	L	GLHWPL	N	0.3	7.84	
3	Cg1537	1	775.4302	-3.0	220	226	0	43.3	34	V	FGLPMVL	N	2.1	6.02	
3	Cg1537	1	798.4316	-9.0	173	178	0	38.4	33	V	FYFLPI	M	1.8	5.92	
3	Cg1537	1	832.4331	22.9	205	212	0	41.7	35	T	PEFLALGS	A	0.7	3.3	
3	Cg1537	1	862.4953	7.8	277	284	0	60.6	32	A	FLLGPFGI	G	1.9	6.02	
3	Cg1537	1	864.4858	3.0	403	409	0	45.7	31	T	YFRLLPG	C	0.4	9.84	
3	Cg1537	1	902.5113	-5.4	201	208	0	58.6	35	A	ALLTPEFL	A	1.3	3.3	
3	Cg1537	1	941.4494	-7.4	334	341	0	45.7	34	I	NTLGYDFI	Q	0.2	3.1	
3	Cg1537	1	950.4862	2.9	242	249	0	53.3	35	I	GLYWVEKG	L	-0.3	6.86	
3	Cg1537	1	950.4862	0.0	298	305	0	63.2	35	I	NNFSPFIL	S	0.6	6.02	
3	Cg1537	1	960.5684	-5.0	312	319	0	47.5	32	L	LYPFLVPL	G	1.7	5.92	
3	Cg1537	1	975.5463	-7.9	218	226	0	47.5	34	V	TVFGLPMVL	N	2.0	6.02	
3	Cg1537	1	991.5413	-2.3	218	226	0	54.5	34	V	TVFGLPMVL	N	2.0	6.02	Oxidation (M)
3	Cg1537	1	1018.5852	-4.0	277	286	0	60.0	33	A	FLLGPFGIGV	G	1.9	6.02	
3	Cg1537	1	1019.5552	7.0	320	328	0	53.7	34	L	GLHWPLNAI	M	0.5	7.84	
3	Cg1537	1	1100.5365	-2.7	259	267	0	55.3	35	V	QMVFVPFFS	L	1.4	6.02	
3	Cg1537	1	1113.6394	1.4	591	600	0	43.4	34	A	LRLDSGVEIL	V	0.7	4.08	
3	Cg1537	1	1134.6073	1.9	240	249	0	71.1	35	A	AIGLYWVEKG	L	0.4	6.86	
3	Cg1537	1	1143.6539	-11.4	201	211	0	47.9	35	A	ALLTPEFLALG	S	1.4	3.3	
3	Cg1537	1	1154.5067	-4.0	337	347	0	88.8	32	L	GYDFIQGPMGA	W	0.0	3.1	
3	Cg1537	1	1182.6284	-1.7	74	82	0	55.2	35	A	NYYQEILKL	D	-0.5	6.8	
3	Cg1537	1	1213.6567	-3.8	186	196	0	87.4	36	A	RKLGANEWIGA	A	-0.5	10.08	
3	Cg1537	1	1230.686	-7.9	201	212	0	76.6	35	A	ALLTPEFLALGS	A	1.2	3.3	
3	Cg1537	1	1237.7394	-0.5	640	650	0	61.9	31	I	RSKDLPLITPV	V	0.0	10.08	
3	Cg1537	1	1322.6394	-4.3	628	639	0	63.8	36	A	GDPLITFDADFI	R	0.6	2.82	
3	Cg1537	1	1336.8231	1.1	392	402	0	31.1	27	S	LYGVLLRFKKT	Y	0.3	10.7	
3	Cg1537	1	1359.7551	-1.5	277	290	0	63.7	35	A	FLLGPFGIGVGNGI	S	1.4	6.02	
3	Cg1537	1	1370.6871	-2.6	116	126	0	76.8	36	A	FEFLSDTFRPI	L	0.2	4.08	
3	Cg1537	1	1373.6827	-10.6	657	669	0	50.1	36	A	KFGEIEGIPADQA	N	-0.4	3.82	
3	Cg1537	1	1382.5698	1.8	463	473	0	73.5	30	L	DYRSNEERDEA	R	-2.8	3.92	
3	Cg1537	1	1396.6445	-0.1	144	155	0	42.4	34	A	DTFGLQDFRAPM	D	-0.4	3.88	
3	Cg1537	1	1418.7154	-4.1	10	22	0	88.1	37	S	QHILENLGGPDNI	T	-0.5	4.06	
3	Cg1537	1	1419.7034	-3.4	227	239	0	70.8	37	L	NDYSGQVFPPLIA	A	0.1	3.1	
3	Cg1537	1	1439.8136	-2.8	553	567	0	114.0	34	I	FAAGKLGPGIAIQPT	G	0.6	10.1	
3	Cg1537	1	1482.6813	-8.0	334	347	0	42.9	34	I	NTLGYDFIQGPMGA	W	0.0	3.1	
3	Cg1537	1	1495.6539	-0.6	462	473	0	65.1	33	A	LDYRSNEERDEA	R	-2.2	3.92	
3	Cg1537	1	1505.7474	-1.7	9	22	0	95.2	37	T	SQHILENLGGPDNI	T	-0.5	4.06	
3	Cg1537	1	1673.8876	1.6	201	217	0	139.5	37	A	ALLTPEFLALGSAGDTV	T	0.9	3	
3	Cg1537	1	1693.8271	-4.0	9	24	0	84.7	36	T	SQHILENLGGPDNITS	M	-0.6	4.06	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
3	Cg1537	1	1719.8144	3.3	113	126	0	60.9	36	I	DYAFEFLSDTFRPI	L	-0.1	3.7	
3	Cg1537	1	1772.0236	1.2	244	258	0	103.8	32	L	YWVEKGLKKIIPEAV	Q	0.0	9.56	
3	Cg1537	1	1793.8777	-4.4	106	119	0	38.2	36	V	RGKYSWIDYAFEFL	S	-0.3	6.88	
3	Cg1537	1	1806.0139	0.8	528	545	0	129.0	34	A	AGEVVDIVSPLEGKAIPL	S	0.8	3.82	
3	Cg1537	1	1810.7832	-1.0	149	163	0	57.6	31	L	QDFRAPMDEQPDTYV	F	-1.3	3.5	
3	Cg1537	1	1810.9941	-8.1	553	571	0	54.8	36	I	FAAGKLGPGIAIQPTGNTV	V	0.4	10.1	
3	Cg1537	1	1831.9428	-4.1	33	47	0	104.5	37	L	RFQVKDQSIVDQQEI	D	-0.9	4.3	
3	Cg1537	1	1939.0024	-7.3	609	625	0	46.2	37	V	QLGGEGFTVHVERRQQV	K	-0.7	7.86	
3	Cg1537	1	1942.1291	-6.9	242	258	0	89.6	33	I	GLYWVEKGLKKIIPEAV	Q	0.2	9.56	
3	Cg1537	1	1980.8524	1.1	144	160	0	84.8	31	A	DTFGLQDFRAPMDEQPD	T	-1.2	3.36	
3	Cg1537	1	2076.0375	-1.6	657	676	0	141.1	37	A	KFGEIEGIPADQANSSTTVI	K	-0.1	3.82	
3	Cg1537	1	2126.2503	2.4	240	258	0	90.6	30	A	AIGLYWVEKGLKKIIPEAV	Q	0.5	9.56	
3	Cg1537	1	2149.1895	-4.2	553	575	0	79.5	35	I	FAAGKLGPGIAIQPTGNTVVAPA	D	0.6	10.1	
3	Cg1537	1	2244.9634	3.2	144	162	0	44.5	31	A	DTFGLQDFRAPMDEQPDTY	V	-1.2	3.36	
3	Cg1537	1	2333.1135	-0.1	33	52	0	88.9	37	L	RFQVKDQSIVDQQEIDSDPS	V	-1.2	3.76	
3	Cg1537	1	2344.0318	6.5	144	163	0	124.8	33	A	DTFGLQDFRAPMDEQPDTYV	F	-0.9	3.36	
3	Cg1537	1	2360.0267	-9.4	144	163	0	51.7	29	A	DTFGLQDFRAPMDEQPDTYV	F	-0.9	3.36	Oxidation (M)
3	Cg1537	1	2528.153	-5.1	142	163	0	60.1	34	V	LADTFGLQDFRAPMDEQPDTYV	F	-0.6	3.36	
3	Cg1537	1	2543.3734	2.8	528	552	0	82.2	36	A	AGEVVDIVSPLEGKAIPLSEVPDPI	F	0.5	3.5	
3	Cg1537	1	2604.1843	-4.3	144	165	0	91.8	34	A	DTFGLQDFRAPMDEQPDTYVFL	H	-0.5	3.36	
3	Cg1537	1	2658.2271	6.3	74	96	0	78.7	36	A	NYYQEILKLDGMKHFADGEATES	S	-0.9	4.28	
3	Cg1537	1	2828.2752	-11.5	144	167	0	35.3	32	A	DTFGLQDFRAPMDEQPDTYVFLHS	M	-0.6	3.76	
4	Cg2705	1	921.4596	-0.8	338	344	0	35.9	35	T	KDFVDWL	F	-0.1	3.88	
4	Cg2705	1	975.4662	-0.6	38	45	0	49.2	36	L	NFKPEQDV	A	-1.6	4.08	
4	Cg2705	1	1159.6237	-1.3	418	427	0	49.9	36	A	SGKLKWEDVV	K	-0.5	6.98	
4	Cg2705	1	1163.4996	1.7	199	207	0	35.6	33	T	SGEDWRWQT	H	-2.1	4.08	
4	Cg2705	1	1222.6234	-3.6	356	366	0	62.5	35	V	KDLGFIAPFES	Y	0.2	4.08	
4	Cg2705	1	1318.6081	3.5	143	152	0	69.8	35	I	IYNDEIFDKY	I	-0.9	3.7	
4	Cg2705	1	1339.6078	-1.3	260	272	0	78.7	34	T	VSDSMAEFAQGKA	A	-0.2	4.08	
4	Cg2705	1	1389.6452	-2.2	144	154	0	86.8	35	I	YNDEIFDKYIA	T	-0.6	3.7	
4	Cg2705	1	1426.6365	2.7	403	414	0	111.2	33	S	QQFKDDFGQDLS	Q	-1.4	3.6	
4	Cg2705	1	1464.6634	-0.5	196	207	0	65.2	34	T	SLTSGEDWRWQT	H	-1.4	4.08	
4	Cg2705	1	1464.6885	1.9	333	344	0	58.6	36	V	DQQATKDFVDWL	F	-0.9	3.6	
4	Cg2705	1	1484.6797	0.8	199	210	0	69.2	34	T	SGEDWRWQTHLA	N	-1.4	5.22	
4	Cg2705	1	1490.6929	-1.2	144	155	0	88.5	35	I	YNDEIFDKYIAT	S	-0.6	3.7	
4	Cg2705	1	1496.642	3.4	215	226	0	65.4	32	I	WQEYQDKGVEDT	N	-2.0	3.58	
4	Cg2705	1	1502.7293	1.5	143	154	0	86.2	37	I	IYNDEIFDKYIA	T	-0.2	3.7	
4	Cg2705	1	1574.7113	1.0	428	440	0	110.0	34	V	KHFNDNWAAEKES	N	-1.8	5.34	
4	Cg2705	1	1603.777	-14.5	143	155	0	103.3	36	I	IYNDEIFDKYIAT	S	-0.2	3.7	
4	Cg2705	1	1747.7901	0.1	367	382	0	104.7	34	S	YTAENTPNDPLSEQVA	E	-1.0	2.94	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
4	Cg2705	1	1785.8434	-8.3	196	210	0	51.1	35	T	SLTSGEDWRWQTHLA	N	-0.9	5.22	
4	Cg2705	1	1852.8115	4.3	215	229	0	123.5	33	I	WQEYQDKGVEDTNEI	E	-1.8	3.5	
4	Cg2705	1	1871.9781	-3.2	350	366	0	71.3	37	A	GKEHVVKDLGFIAPFES	Y	0.0	5.34	
4	Cg2705	1	1891.8588	1.4	211	226	0	110.2	35	A	NAPIWQEYQDKGVEDT	N	-1.4	3.58	
4	Cg2705	1	1964.9519	7.8	233	247	0	96.7	37	S	YNKEYKNLFDLYLEN	S	-1.2	4.44	
4	Cg2705	1	1973.9232	0.3	194	210	0	96.3	36	A	STSLTSGEDWRWQTHLA	N	-0.9	5.22	
4	Cg2705	1	2003.9849	-3.2	299	315	0	38.4	37	I	KFLPMYMGLPDEEKHGI	N	-0.5	5.34	
4	Cg2705	1	2051.984	-0.1	233	248	0	137.3	37	S	YNKEYKNLFDLYLENS	T	-1.2	4.44	
4	Cg2705	1	2056.9953	-13.6	117	135	0	46.4	36	L	TDDIPPLTTEDGEVRGVPF	A	-0.5	3.42	
4	Cg2705	1	2090.9738	0.3	386	402	0	89.6	36	I	ANKDLTTYPWNFQYFPS	Q	-0.9	6.62	
4	Cg2705	1	2107.015	-2.6	138	155	0	84.8	36	V	EGFGIIYNDEIFDKYIAT	S	0.0	3.58	
4	Cg2705	1	2140.0437	5.5	306	325	0	83.9	37	M	GLPDEEKHGINVGTENYLGV	N	-0.6	4.16	
4	Cg2705	1	2153.0316	8.5	233	249	0	77.8	37	S	YNKEYKNLFDLYLENST	V	-1.2	4.44	
4	Cg2705	1	2182.1118	-14.5	114	133	0	116.6	37	A	KQLTDDIPPLTTEDGEVRGV	P	-0.8	3.84	
4	Cg2705	1	2194.047	1.3	138	156	0	99.7	37	V	EGFGIIYNDEIFDKYIATS	G	0.0	3.58	
4	Cg2705	1	2215.9546	12.2	215	232	0	85.8	33	I	WQEYQDKGVEDTNEIEFS	Y	-1.6	3.44	
4	Cg2705	1	2227.1009	0.6	117	137	0	98.0	37	L	TDDIPPLTTEDGEVRGVPFAV	E	-0.2	3.42	
4	Cg2705	1	2248.0284	0.9	211	229	0	94.1	35	A	NAPIWQEYQDKGVEDTNEI	E	-1.3	3.5	
4	Cg2705	1	2252.1001	-5.2	233	250	0	155.5	37	S	YNKEYKNLFDLYLENSTV	E	-0.9	4.44	
4	Cg2705	1	2426.2329	-4.0	114	135	0	148.5	38	A	KQLTDDIPPLTTEDGEVRGVPF	A	-0.6	3.84	
4	Cg2705	1	2596.2696	4.4	233	253	0	120.1	38	S	YNKEYKNLFDLYLENSTVEKS	L	-1.1	4.64	
4	Cg2705	1	2596.3385	2.1	114	137	0	136.9	38	A	KQLTDDIPPLTTEDGEVRGVPFAV	E	-0.3	3.84	
4	Cg2705	1	2611.1714	7.2	211	232	0	138.7	35	A	NAPIWQEYQDKGVEDTNEIEFS	Y	-1.2	3.44	
4	Cg2705	1	2615.2431	6.4	230	250	0	75.6	37	I	EFSYNKEYKNLFDLYLENSTV	E	-0.8	4.16	
4	Cg2705	1	2679.3425	-9.0	168	191	0	95.9	38	T	SYQKLKEVAEDMQAKKDELGIEGA	F	-1.0	4.44	
4	Cg2705	1	2780.3902	2.8	167	191	0	104.7	38	I	TSYQKLKEVAEDMQAKKDELGIEGA	F	-0.9	4.44	
4	Cg2705	1	3050.4881	0.7	299	325	0	64.5	38	I	KFLPMYMGLPDEEKHGINVGTENYLGV	N	-0.3	4.62	
4	Cg2705	1	3453.7184	-18.5	161	191	0	45.1	37	I	KSTDEITSYQKLKEVAEDMQAKKDELGIEGA	F	-1.0	4.34	
5	Cg2409	1	802.4225	4.2	232	238	0	63.3	37	T	PIEFNLA	S	0.6	3.3	
5	Cg2409	1	930.4382	7.8	43	50	0	39.4	35	L	RMGWPDGI	T	-0.6	6.78	
5	Cg2409	1	936.4745	0.1	246	252	0	41.4	35	S	FWVPEFL	F	1.1	3.3	
5	Cg2409	1	1017.5131	-10.3	230	238	0	62.7	36	V	NTPIEFNLA	S	0.0	3.3	
5	Cg2409	1	1114.4931	-1.4	304	312	0	41.2	32	V	DRDSFAEYI	S	-0.9	3.7	
5	Cg2409	1	1135.5121	8.6	40	48	0	37.5	35	G	DFLRMGWPD	G	-0.7	3.88	
5	Cg2409	1	1137.5675	5.7	295	303	0	57.2	35	A	MMNFELRVV	D	0.8	6.98	
5	Cg2409	1	1160.5655	6.3	244	252	0	67.8	36	A	HSFWVPEFL	F	0.4	5.12	
5	Cg2409	1	1198.556	-1.2	150	158	0	61.4	34	T	AYQWNWKFG	Y	-1.1	9.72	
5	Cg2409	1	1257.5812	2.5	43	53	0	36.0	34	L	RMGWPDGITPE	A	-1.0	4.08	
5	Cg2409	1	1296.6714	1.2	207	216	0	52.7	35	S	YLEFNRIETL	G	-0.2	4.26	
5	Cg2409	1	1303.6309	2.1	253	263	0	53.3	36	L	FKRDAYAHPEA	N	-1.2	7.74	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
5	Cg2409	1	1305.6176	-2.4	40	50	0	60.6	36	G	DFLRMGWPDGI	T	-0.2	3.88	
5	Cg2409	1	1305.6176	2.5	38	48	0	74.1	36	V	LGDFLRMGWPD	G	-0.2	3.88	
5	Cg2409	1	1383.7034	-0.2	206	216	0	60.2	36	V	SYLEFNRIETL	G	-0.3	4.26	
5	Cg2409	1	1397.6939	-1.9	325	337	0	125.5	36	A	QALEHIGQAPYAT	S	-0.3	5.12	
5	Cg2409	1	1416.7361	4.3	92	103	0	73.1	37	A	EKRGEGEFPKQL	Q	-1.8	7.16	
5	Cg2409	1	1417.6738	0.3	253	264	0	82.0	36	L	FKRDAYAHPEAN	K	-1.4	7.74	
5	Cg2409	1	1427.6867	-3.8	43	55	0	95.0	35	L	RMGWPDGITPEAV	A	-0.4	4.08	
5	Cg2409	1	1449.612	5.9	170	182	0	45.3	31	G	GQDYQGSDPERQA	A	-2.2	3.7	
5	Cg2409	1	1553.8031	-6.2	246	257	0	45.5	36	S	FWVPEFLFKRDA	Y	0.0	7.02	
5	Cg2409	1	1576.7733	-1.6	267	279	0	94.0	37	S	QRVFQIEEITEEG	A	-0.8	3.8	
5	Cg2409	1	1582.7739	-1.8	323	337	0	131.8	36	T	NAQALEHIGQAPYAT	S	-0.4	5.12	
5	Cg2409	1	1597.7988	-7.0	204	216	0	84.6	36	S	DVSYLEFNRIETL	G	-0.2	3.82	
5	Cg2409	1	1632.8008	-2.7	253	266	0	74.9	37	L	FKRDAYAHPEANKS	Q	-1.5	9.62	
5	Cg2409	1	1647.8104	0.1	267	280	0	94.2	37	S	QRVFQIEEITEEGA	F	-0.6	3.8	
5	Cg2409	1	1690.778	0.7	150	162	0	95.0	35	T	AYQWNWKFGYSEI	D	-0.8	6.8	
5	Cg2409	1	1716.7703	-2.3	166	181	0	47.5	33	S	LAPGGQDYQGSDPERQ	A	-1.7	3.7	
5	Cg2409	1	1766.8547	-4.6	187	203	0	71.3	36	A	SKKDPSGDNPIHGNSKS	D	-1.9	9.76	
5	Cg2409	1	1787.8074	-0.7	166	182	0	106.0	34	S	LAPGGQDYQGSDPERQA	A	-1.4	3.7	
5	Cg2409	1	1802.8662	-5.4	40	55	0	105.1	36	G	DFLRMGWPDGITPEAV	A	-0.1	3.7	
5	Cg2409	1	1832.9156	-8.0	209	224	0	42.7	37	L	EFNRIETLGTTDEIPV	M	-0.4	3.68	
5	Cg2409	1	1859.8876	-2.6	39	55	0	45.9	36	L	GDFLRMGWPDGITPEAV	A	-0.1	3.7	
5	Cg2409	1	1874.8395	-6.6	165	182	0	70.9	32	G	SLAPGGQDYQGSDPERQA	A	-1.4	3.7	
5	Cg2409	1	1949.8584	5.0	150	165	0	98.2	33	T	AYQWNWKFGYSEIDGS	L	-1.0	4.08	
5	Cg2409	1	1972.9717	-2.5	38	55	0	69.4	37	V	LGDFLRMGWPDGITPEAV	A	0.1	3.7	
5	Cg2409	1	1975.8508	-0.4	163	181	0	76.2	31	I	DGSLAPGGQDYQGSDPERQ	A	-1.6	3.5	
5	Cg2409	1	2046.8879	-1.5	163	182	0	141.0	31	I	DGSLAPGGQDYQGSDPERQA	A	-1.5	3.5	
5	Cg2409	1	2109.063	-1.3	207	224	0	92.7	37	S	YLEFNRIETLGTTDEIPV	M	-0.2	3.68	
5	Cg2409	1	2129.9614	-0.1	166	186	0	66.4	34	S	LAPGGQDYQGSDPERQAAAEA	S	-1.1	3.58	
5	Cg2409	1	2196.095	1.2	206	224	0	78.8	37	V	SYLEFNRIETLGTTDEIPV	M	-0.2	3.68	
5	Cg2409	1	2336.1378	-4.1	246	264	0	63.9	37	S	FWVPEFLFKRDAYAHPEAN	K	-0.5	5.34	
5	Cg2409	1	2340.0578	-1.4	338	359	0	41.8	34	T	STSPFVSDRTATRDGENTQSNA	-	-1.2	4.3	
5	Cg2409	1	2389.0418	1.5	163	186	0	74.8	32	I	DGSLAPGGQDYQGSDPERQAAAEA	S	-1.1	3.42	
5	Cg2409	1	2410.1904	-0.3	204	224	0	92.6	37	S	DVSYLEFNRIETLGTTDEIPV	M	-0.2	3.5	
5	Cg2409	1	2539.1099	0.5	159	182	0	153.5	32	G	YSEIDGSLAPGGQDYQGSDPERQA	A	-1.3	3.42	
5	Cg2409	1	3719.6553	-7.6	150	182	0	71.7	31	T	AYQWNWKFGYSEIDGSLAPGGQDYQGSDPERQA	A	-1.2	3.84	
6	Cg0587	1	739.4592	-5.4	293	299	0	32.5	29	G	QVIVKPG	A	0.5	10.1	
6	Cg0587	1	817.4446	9.3	126	132	0	41.3	35	A	RQVGVPY	I	-0.4	9.84	
6	Cg0587	1	833.4072	6.8	333	338	0	46.1	36	Q	FYFRTT	D	-0.3	9.84	
6	Cg0587	1	938.4246	1.1	326	332	0	40.3	34	F	FDNYRPQ	F	-2.2	6.7	
6	Cg0587	1	1008.4698	1.3	370	378	0	43.1	35	V	AMDEGLRFA	I	0.0	4.08	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
6	Cg0587	1	1043.6128	1.0	126	134	0	47.3	34	A	RQVGVPYIL	V	0.6	9.84	
6	Cg0587	1	1142.6812	11.7	126	135	0	84.8	31	A	RQVGVPYILV	A	1.0	9.84	
6	Cg0587	1	1166.488	5.0	301	310	0	45.2	32	A	YTPHTEFEGS	V	-1.3	4.24	
6	Cg0587	1	1182.5458	-4.7	324	332	0	53.6	34	T	PFFDNYRPQ	F	-1.5	6.7	
6	Cg0587	1	1237.5251	-0.9	300	310	0	58.9	31	G	AYTPHTEFEGS	V	-1.0	4.24	
6	Cg0587	1	1323.6207	2.3	71	80	0	50.1	35	V	EYQTEKRHYA	H	-2.4	7.68	
6	Cg0587	1	1345.7064	1.3	206	216	0	57.7	36	V	RETDKPFLMPI	E	-0.6	7.02	
6	Cg0587	1	1361.7013	0.1	206	216	0	48.1	37	V	RETDKPFLMPI	E	-0.6	7.02	Oxidation (M)
6	Cg0587	1	1367.7673	-1.9	5	15	0	51.6	34	A	KFERTKPHVNI	G	-1.2	10.58	
6	Cg0587	1	1378.7278	1.7	260	271	0	82.3	35	T	GIEMFRKLLDSA	E	0.2	7.02	
6	Cg0587	1	1479.7755	0.9	259	271	0	66.3	36	V	TGIEMFRKLLDSA	E	0.1	7.02	
6	Cg0587	1	1598.7253	-0.6	300	313	0	73.6	34	G	AYTPHTEFEGSVYV	L	-0.3	4.24	
6	Cg0587	1	1646.7801	1.2	68	80	0	80.3	36	I	SHVEYQTEKRHYA	H	-1.8	7.84	
6	Cg0587	1	1677.8688	0.7	209	222	0	90.8	37	T	DKPFLMPIEDIFTI	T	0.5	3.7	
6	Cg0587	1	1693.8637	0.0	209	222	0	38.9	37	T	DKPFLMPIEDIFTI	T	0.5	3.7	Oxidation (M)
6	Cg0587	1	1732.8631	-0.6	49	63	0	74.8	37	A	FDSIDKAPEEKERGI	T	-1.3	4.28	
6	Cg0587	1	1734.8723	-0.8	110	125	0	55.0	37	A	ATDGPMPQTREHVLLA	R	-0.4	5.22	
6	Cg0587	1	1778.9165	-0.1	209	223	0	86.3	37	T	DKPFLMPIEDIFTIT	G	0.4	3.7	
6	Cg0587	1	1787.9127	-2.3	180	194	0	103.3	37	A	LEGDEKWGKQILELM	Q	-0.6	4.16	
6	Cg0587	1	1789.837	-1.7	157	171	0	117.4	35	V	RELLAEQDYDEEAPI	V	-1.1	3.44	
6	Cg0587	1	1803.9077	2.9	180	194	0	55.4	37	A	LEGDEKWGKQILELM	Q	-0.6	4.16	Oxidation (M)
6	Cg0587	1	1867.9713	-5.5	255	271	0	53.2	37	T	STTVTGIEMFRKLLDSA	E	0.2	7.02	
6	Cg0587	1	1882.9074	3.0	68	82	0	84.3	37	I	SHVEYQTEKRHYAHV	D	-1.5	7.92	
6	Cg0587	1	1883.9701	-18.9	231	247	0	82.6	37	T	GRVERGTLNVNDDVDII	G	-0.4	3.96	
6	Cg0587	1	1946.9949	-4.6	49	65	0	65.9	37	A	FDSIDKAPEEKERGITI	N	-0.9	4.28	
6	Cg0587	1	1950.9687	1.0	47	63	0	95.1	37	A	FAFDSIDKAPEEKERGI	T	-0.8	4.28	
6	Cg0587	1	1950.9761	-9.9	206	221	0	37.1	37	V	RETDKPFLMPIEDIFT	I	-0.4	4.06	
6	Cg0587	1	1987.0084	5.2	180	196	0	50.0	37	A	LEGDEKWGKQILELMQA	C	-0.6	4.16	
6	Cg0587	1	2062.9609	-1.6	316	332	0	103.0	35	S	KDEGGRHTPFFDNYRPQ	F	-2.0	7.74	
6	Cg0587	1	2064.0601	1.9	206	222	0	105.4	37	V	RETDKPFLMPIEDIFTI	T	-0.1	4.06	
6	Cg0587	1	2149.993	2.5	315	332	0	50.7	35	L	SKDEGGRHTPFFDNYRPQ	F	-1.9	7.74	
6	Cg0587	1	2165.1004	-1.2	47	65	0	102.2	37	A	FAFDSIDKAPEEKERGITI	N	-0.6	4.28	
6	Cg0587	1	2165.1078	1.1	206	223	0	94.2	37	V	RETDKPFLMPIEDIFTIT	G	-0.2	4.06	
6	Cg0587	1	2248.0426	22.8	344	364	0	37.7	37	V	VKLPEGTEMVMPGDNVDMSVT	L	-0.1	3.58	
6	Cg0587	1	2263.077	-5.0	314	332	0	48.6	36	V	LSKDEGGRHTPFFDNYRPQ	F	-1.6	7.74	
6	Cg0587	1	2278.0311	1.7	153	171	0	51.8	34	V	EMEVRELLAEQDYDEEAPI	V	-0.9	3.32	
6	Cg0587	1	2319.0861	3.8	141	159	0	111.2	36	C	DMVEDEEIIELVEMEVREL	L	-0.2	3.28	
6	Cg0587	1	2348.245	-4.8	209	229	0	50.2	37	T	DKPFLMPIEDIFTITGRGTVV	T	0.4	4.3	
6	Cg0587	1	2449.2927	-5.5	209	230	0	89.6	38	T	DKPFLMPIEDIFTITGRGTVVT	G	0.3	4.3	
6	Cg0587	1	2734.4364	-3.7	206	229	0	42.3	38	V	RETDKPFLMPIEDIFTITGRGTVV	T	0.0	4.56	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
6	Cg0587	1	2835.4841	-3.2	206	230	0	59.6	38	V	RETDKPFLMPIEDIFTITGRGTVVT	G	0.0	4.56	
7	Cg3138	1	1132.5513	-0.4	146	155	0	57.4	36	A	KVNDYNGNPI	N	-1.3	6.68	
7	Cg3138	1	1158.5881	-1.3	2	12	0	37.2	36	M	STIEERTPGAV	A	-0.5	4.26	
7	Cg3138	1	1200.6292	1.0	107	116	0	41.8	36	V	QFFGRYIGTL	R	0.3	9.84	
7	Cg3138	1	1285.5575	1.5	194	205	0	75.4	32	V	ATQHPYDSPVDG	R	-1.2	3.88	
7	Cg3138	1	1312.6987	-11.4	280	290	0	44.5	36	T	ALDQLEQREIV	D	-0.4	3.82	
7	Cg3138	1	1341.6677	-3.8	27	39	0	52.5	36	I	NEKNVWSLGAGPA	A	-0.5	6.94	
7	Cg3138	1	1368.6422	-1.9	196	207	0	40.0	35	T	QHPYDSPVDGRV	S	-1.3	5.1	
7	Cg3138	1	1442.7664	-0.8	251	263	0	69.1	36	A	QAMLQRQQASAIV	D	0.0	11.04	
7	Cg3138	1	1484.646	4.8	172	183	0	90.8	33	A	SFSVEDFEEFLH	Q	-0.2	3.68	
7	Cg3138	1	1540.727	-0.6	194	207	0	83.1	35	V	ATQHPYDSPVDGRV	S	-1.0	5.1	
7	Cg3138	1	1541.7838	-5.4	25	39	0	82.6	36	V	SINEKNVWSLGAGPA	A	-0.2	6.94	
7	Cg3138	1	1542.7889	-4.1	278	290	0	56.4	37	V	ETALDQLEQREIV	D	-0.6	3.68	
7	Cg3138	1	1612.7046	4.5	172	184	0	85.1	33	A	SFSVEDFEEFLHQ	Q	-0.5	3.68	
7	Cg3138	1	1676.8006	0.4	310	325	0	83.0	36	C	SDTNAQPIVNAGSLYQ	-	-0.4	3.1	
7	Cg3138	1	1724.7682	-7.8	173	186	0	69.4	32	S	FSVEDFEEFLHQQA	E	-0.5	3.68	
7	Cg3138	1	1740.7631	0.2	172	185	0	100.6	32	A	SFSVEDFEEFLHQQ	A	-0.7	3.68	
7	Cg3138	1	1811.8002	2.8	172	186	0	127.1	33	A	SFSVEDFEEFLHQQA	E	-0.5	3.68	
7	Cg3138	1	1818.8483	-3.4	208	224	0	113.9	35	V	SLRGATDEVSEELADEV	A	-0.5	3.44	
7	Cg3138	1	2010.8959	-1.3	170	186	0	50.7	33	A	QASFSVEDFEEFLHQQA	E	-0.5	3.68	
7	Cg3138	1	2027.8749	0.1	172	188	0	103.8	31	A	SFSVEDFEEFLHQQAES	A	-0.7	3.58	
7	Cg3138	1	2098.912	0.0	172	189	0	109.4	32	A	SFSVEDFEEFLHQQAESA	L	-0.6	3.58	
7	Cg3138	1	2117.0766	-3.9	189	207	0	53.3	38	S	ALRHVATQHPYDSPVDGRV	S	-0.6	7.92	
7	Cg3138	1	2194.1342	0.1	281	298	0	91.8	37	A	LDQLEQREIVDLDPERRA	A	-1.2	4.06	
7	Cg3138	1	2265.1713	-3.1	280	298	0	107.4	37	T	ALDQLEQREIVDLDPERRA	A	-1.0	4.06	
7	Cg3138	1	2336.2084	-3.5	280	299	0	58.2	37	T	ALDQLEQREIVDLDPERRAA	M	-0.9	4.06	
7	Cg3138	1	2495.2616	-4.3	278	298	0	48.3	38	V	ETALDQLEQREIVDLDPERRA	A	-1.1	3.96	
8	Cg2911	1	1256.531	19.2	65	76	0	57.1	33	T	GGDIDPHSFEPS	A	-1.0	3.7	
8	Cg2911	1	1541.6668	-0.4	218	231	0	53.3	32	H	SDMVESTPEGYRAT	T	-1.0	3.82	
8	Cg2911	1	1839.8891	1.0	294	310	0	134.2	36	T	ENFLDAFTKAVDDLTAA	T	0.1	3.5	
8	Cg2911	1	1940.9367	-0.8	294	311	0	169.3	36	T	ENFLDAFTKAVDDLTAAT	N	0.1	3.5	
8	Cg2911	1	1945.9633	-1.0	53	71	0	111.0	37	A	VAPDVDIEAIITGGDIDPH	S	0.2	3.36	
8	Cg2911	1	2028.0574	-6.2	188	204	0	44.1	37	T	KMDELHNQIHDLPAVRI	A	-0.6	6.02	
8	Cg2911	1	2099.0946	-5.8	188	205	0	72.6	37	T	KMDELHNQIHDLPAVRIA	Q	-0.4	6.02	
8	Cg2911	1	2115.0895	4.4	188	205	0	43.6	37	T	KMDELHNQIHDLPAVRIA	Q	-0.4	6.02	Oxidation (M)
8	Cg2911	1	2156.0273	11.6	292	311	0	64.2	37	Q	NTENFLDAFTKAVDDLTAAT	N	-0.2	3.5	
8	Cg2911	1	2200.9913	1.6	92	111	0	160.6	34	V	GGGGYDSWLYGTLEDDDRII	H	-0.6	3.36	
8	Cg2911	1	2300.8704	-8.3	135	153	0	89.7	15	A	HEHDHDEEGHDHDVDNEHV	W	-2.4	4.32	
8	Cg2911	1	2413.1438	-5.8	90	111	0	101.5	36	I	IVGGGGYDSWLYGTLEDDDRII	H	-0.2	3.36	
8	Cg2911	1	2493.1911	0.0	53	76	0	119.2	37	A	VAPDVDIEAIITGGDIDPHSFEPS	A	0.0	3.32	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
8	Cg2911	1	2522.1714	-9.9	92	114	0	139.9	34	V	GGGGYDSWLYGTLEDDDRIIHAL	D	-0.4	3.76	
8	Cg2911	1	2673.2446	-0.4	287	310	0	92.9	36	I	YETPQNTENFLDAFTKAVDDLTAA	T	-0.5	3.42	
8	Cg2911	1	2774.2923	11.1	287	311	0	71.2	37	I	YETPQNTENFLDAFTKAVDDLTAAT	N	-0.5	3.42	
8	Cg2911	1	2837.3144	7.1	92	117	0	85.0	36	V	GGGGYDSWLYGTLEDDDRIIHALDLS	E	-0.4	3.62	
8	Cg2911	1	2954.3716	1.0	205	231	0	124.3	36	I	AQTEPIADHILSHSDMVESTPEGYRAT	T	-0.6	4.28	
8	Cg2911	1	3014.4397	3.5	284	310	0	87.4	37	V	VEIYETPQNTENFLDAFTKAVDDLTAA	T	-0.3	3.38	
8	Cg2911	1	3049.4669	9.6	90	117	0	43.6	38	I	IVGGGGYDSWLYGTLEDDDRIIHALDLS	E	-0.1	3.62	
8	Cg2911	1	3115.4873	6.0	284	311	0	42.8	38	V	VEIYETPQNTENFLDAFTKAVDDLTAAT	N	-0.3	3.38	
8	Cg2911	1	4495.2534	15.2	271	311	0	46.8	39	T	SLKDLAEEKGIPVVEIYETPQNTENFLDAFTKAVDDLTAAT	N	-0.3	3.76	
9	Cg3009	1	838.3709	17.4	41	48	0	54.0	34	N	FGDLADTT	G	-0.1	2.92	
9	Cg3009	1	915.4127	1.0	35	41	0	43.6	33	I	LNFFDNF	G	0.2	3.1	
9	Cg3009	1	952.4138	4.4	40	48	0	59.0	33	D	NFGDLADTT	G	-0.4	2.92	
9	Cg3009	1	956.424	-4.3	10	18	0	75.8	31	T	LGNYETFGG	N	-0.4	3.3	
9	Cg3009	1	1044.4553	5.6	37	45	0	79.0	32	N	FFDNFGDLA	D	0.3	2.92	
9	Cg3009	1	1087.4611	8.0	36	44	0	45.1	31	L	NFFDNFGDL	A	-0.2	2.92	
9	Cg3009	1	1158.4982	4.7	36	45	0	86.1	32	L	NFFDNFGDLA	D	0.0	2.92	
9	Cg3009	1	1200.5452	-2.3	35	44	0	71.4	33	I	LNFFDNFGDL	A	0.2	2.92	
9	Cg3009	1	1271.5823	3.9	35	45	0	104.0	34	I	LNFFDNFGDLA	D	0.3	2.92	
9	Cg3009	1	1314.6092	-0.2	7	18	0	56.4	34	L	KETLGNYETFGG	N	-1.0	4.26	
9	Cg3009	1	1412.6572	5.5	10	23	0	91.6	35	T	LGNYETFGGNIGTA	L	-0.1	3.3	
9	Cg3009	1	1475.6205	15.5	36	48	0	68.8	32	L	NFFDNFGDLADTT	G	-0.4	2.82	
9	Cg3009	1	1540.7773	1.6	5	18	0	71.2	36	S	LLKETLGNYETFGG	N	-0.3	4.26	
9	Cg3009	1	1588.7046	-0.7	35	48	0	96.7	33	I	LNFFDNFGDLADTT	G	-0.1	2.82	
9	Cg3009	1	1770.8424	5.3	7	23	0	90.1	36	L	KETLGNYETFGGNIGTA	L	-0.6	4.26	
9	Cg3009	1	1812.8934	20.2	30	45	0	149.5	37	T	LLDSILNFFDNFGDLA	D	0.7	2.82	
9	Cg3009	1	1925.9735	-0.6	5	22	0	135.2	37	S	LLKETLGNYETFGGNIGT	A	-0.2	4.26	
9	Cg3009	1	1997.0106	3.1	5	23	0	153.7	37	S	LLKETLGNYETFGGNIGTA	L	-0.1	4.26	
9	Cg3009	1	2130.0157	16.8	30	48	0	134.1	37	T	LLDSILNFFDNFGDLADTT	G	0.3	2.74	
9	Cg3009	1	2410.2016	-0.2	7	29	0	78.9	38	L	KETLGNYETFGGNIGTALQSIPT	L	-0.4	4.26	
9	Cg3009	1	2636.3697	10.4	5	29	0	135.8	37	S	LLKETLGNYETFGGNIGTALQSIPT	L	0.0	4.26	
9	Cg3009	1	3177.6809	3.6	5	34	0	57.7	38	S	LLKETLGNYETFGGNIGTALQSIPTLLDSI	L	0.2	3.82	
10	Cg0447	1	791.4905	-1.0	184	190	0	48.5	23	V	HLSLLPL	G	1.4	7.84	
10	Cg0447	1	1037.5757	3.2	32	40	0	69.1	32	M	SILELLDHV	N	1.0	4.06	
10	Cg0447	1	1270.667	-3.4	4	14	0	48.5	36	L	TLEIWRQAGPT	A	-0.5	6.98	
10	Cg0447	1	1280.5997	2.3	133	145	0	78.2	35	I	NAGTAPDADTLHV	N	-0.3	3.88	
10	Cg0447	1	1310.7558	1.9	186	197	0	73.0	33	L	SLLPLGKEERGL	R	-0.3	7.1	
10	Cg0447	1	1360.6596	1.0	71	83	0	88.9	36	V	NGRPHGADQNKPA	C	-2.0	10.08	
10	Cg0447	1	1450.862	-2.9	187	199	0	42.4	31	S	LLPLGKEERGLRA	R	-0.4	10.08	
10	Cg0447	1	1491.7755	-1.6	106	118	0	80.9	36	A	AYPVIKDMVVDRS	A	0.1	6.82	
10	Cg0447	1	1521.7463	-4.1	41	53	0	95.2	36	V	NNKFIEEGKEPFA	F	-1.2	4.56	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
10	Cg0447	1	1537.894	-7.1	186	199	0	48.6	33	L	SLLPLGKEERGLRA	R	-0.4	10.08	
10	Cg0447	1	1550.7763	-2.0	119	132	0	111.7	36	S	ALDRVMEQGGYVTI	N	0.2	4.08	
10	Cg0447	1	1560.8987	2.4	184	197	0	94.0	32	V	HLSLLPLGKEERGL	R	-0.2	7.82	
10	Cg0447	1	1562.8127	0.2	105	118	0	71.0	37	S	AAYPVIKDMVVDRS	A	0.3	6.82	
10	Cg0447	1	1579.7552	-0.3	18	31	0	51.4	36	G	KFETVQVDDAVAQM	S	-0.1	3.7	
10	Cg0447	1	1642.8865	-7.7	1	14	0	72.5	37	-	MKLTLEIWRQAGPT	A	-0.3	10.08	
10	Cg0447	1	1659.9672	-1.4	183	197	0	52.4	32	L	VHLSLLPLGKEERGL	R	0.1	7.82	
10	Cg0447	1	1739.8519	2.1	41	55	0	90.6	36	V	NNKFIEEGKEPFAFA	S	-0.7	4.56	
10	Cg0447	1	1836.8564	-0.8	15	31	0	132.3	35	T	AEGKFETVQVDDAVAQM	S	-0.2	3.58	
10	Cg0447	1	1872.9006	1.9	38	53	0	36.8	36	L	DHVNNKFIEEGKEPFA	F	-1.1	4.62	
10	Cg0447	1	2074.9556	-0.4	133	152	0	102.0	35	I	NAGTAPDADTLHVNHETAEL	A	-0.6	4.06	
10	Cg0447	1	2541.3115	2.0	32	53	0	96.3	38	M	SILELLDHVNNKFIEEGKEPFA	F	-0.3	4.36	
10	Cg0447	1	2759.417	-1.7	32	55	0	108.3	38	M	SILELLDHVNNKFIEEGKEPFAFA	S	-0.1	4.36	
11	Cg0583	1	1041.5971	2.7	186	194	0	42.4	35	A	LTWRGVTPI	G	0.4	11.04	
11	Cg0583	1	1080.5088	0.6	89	97	0	65.7	35	V	DFTVEVERS	L	-0.6	3.82	
11	Cg0583	1	1171.6058	2.2	635	645	0	40.7	36	I	GDVNSRRGQIA	S	-1.0	10.88	
11	Cg0583	1	1229.6517	-6.1	544	554	0	40.1	37	T	GGRVPREYIPS	V	-0.9	9.84	
11	Cg0583	1	1358.6289	-14.8	663	674	0	48.6	33	L	SQMFGYVGDLRS	K	-0.2	6.7	
11	Cg0583	1	1583.78	-0.8	456	469	0	39.6	36	G	GMGELHLDVLVDRM	K	0.3	4.3	
11	Cg0583	1	1587.7715	-2.6	663	676	0	49.7	36	L	SQMFGYVGDLRSKT	Q	-0.5	9.72	
11	Cg0583	1	1595.7692	1.1	498	512	0	92.9	36	L	SYTHKKQTGGSGQFA	K	-1.3	10.18	
11	Cg0583	1	1734.8247	-9.6	53	66	0	52.6	35	T	DWMEQEKERGITIT	S	-1.3	4.16	
11	Cg0583	1	1753.8855	-2.6	454	469	0	96.8	37	V	IGGMGELHLDVLVDRM	K	0.5	4.3	
11	Cg0583	1	1799.953	0.7	470	485	0	121.8	37	M	KREFKVEANIGDPQVA	Y	-0.8	7.1	
11	Cg0583	1	1921.0925	-0.1	269	286	0	51.4	33	N	KGIQPLLDAVVDFLPSPL	D	0.7	3.88	
11	Cg0583	1	1974.8404	18.5	223	239	0	53.3	33	V	AESDEELMEKYFGGEEL	S	-1.0	3.44	
11	Cg0583	1	2397.3308	0.3	265	286	0	100.5	35	T	AYKNKGIQPLLDAVVDFLPSPL	D	0.2	6.8	
11	Cg0583	1	2835.3531	-2.9	444	469	0	87.5	37	V	HLDDESGQTVIGGMGELHLDVLVDRM	K	-0.1	3.98	
11	Cg0583	1	2859.4477	-0.9	169	194	0	55.5	38	I	GAEDNFDGVIDLLEMKALTWRGVTPI	G	0.1	3.84	
11	Cg0583	1	2980.427	-6.5	619	645	0	86.0	37	I	MSVEITTPEEYMGEVIGDVNSRRGQIA	S	-0.3	4	
12	Cg2780	1	765.4061	3.9	274	280	0	50.5	33	L	PFFGIVS	E	1.6	6.02	
12	Cg2780	1	839.433	1.7	341	346	0	33.5	33	V	KFFNWV	G	0.3	10.1	
12	Cg2780	1	890.4651	3.1	442	449	0	39.4	35	V	GFHGTFLI	Q	1.2	7.84	
12	Cg2780	1	921.4708	12.7	500	506	0	37.1	35	S	WRYGELV	T	-0.4	6.88	
12	Cg2780	1	995.5076	2.9	382	390	0	60.6	34	A	SPPLDFHLA	D	0.2	4.94	
12	Cg2780	1	997.5022	2.9	341	348	0	44.7	34	V	KFFNWVGT	M	0.1	10.1	
12	Cg2780	1	1118.5259	0.5	416	423	0	44.8	35	V	YFWFPKMT	G	-0.1	9.72	
12	Cg2780	1	1123.5774	-3.5	250	259	0	57.1	35	A	NGGSLLWQHL	F	-0.1	7.84	
12	Cg2780	1	1185.5641	4.3	544	552	0	58.5	35	A	FELHYPHMI	E	0.0	6.02	
12	Cg2780	1	1201.559	2.1	544	552	0	44.1	35	A	FELHYPHMI	E	0.0	6.02	Oxidation (M)

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
12	Cg2780	1	1222.6387	-4.8	94	104	0	40.2	35	L	LYGTPIVWGFA	N	1.1	5.92	
12	Cg2780	1	1274.6158	3.1	414	423	0	45.9	36	A	GVYFWFPKMT	G	0.3	9.72	
12	Cg2780	1	1297.6125	3.9	163	174	0	77.1	35	I	HSPGLGSDMWIV	G	0.2	4.94	
12	Cg2780	1	1390.7609	-1.6	64	75	0	74.2	35	I	RAELFTPGLQFL	S	0.4	6.98	
12	Cg2780	1	1395.646	-9.9	140	153	0	55.4	34	T	GFLTPGGAADFGWT	M	0.3	3.1	
12	Cg2780	1	1453.7024	2.9	163	176	0	67.5	36	I	HSPGLGSDMWIVGV	G	0.5	4.94	
12	Cg2780	1	1467.7663	-0.5	119	130	0	62.2	36	A	FPRLNAFGFWIT	T	0.6	11.04	
12	Cg2780	1	1616.8311	1.6	236	249	0	87.1	37	V	LYDRKLGGHLYDPA	N	-0.7	7.68	
12	Cg2780	1	1725.8911	-4.5	5	20	0	44.4	37	V	APRVDGHVAPQRPEPT	G	-1.1	7.84	
12	Cg2780	1	1751.7937	2.9	76	90	0	92.9	34	L	SNEQFNQLFTMHGTV	M	-0.5	5.12	
12	Cg2780	1	1824.9595	-3.1	4	20	0	58.9	37	A	VAPRVDGHVAPQRPEPT	G	-0.8	7.84	
13	Cg1656	1	969.3981	-0.8	123	130	0	47.0	30	S	YFGNDHFA	E	-0.6	4.94	
13	Cg1656	1	1156.5149	3.8	196	205	0	76.9	33	L	AGEYKNFNTN	S	-1.6	6.86	
13	Cg1656	1	1269.5989	-4.4	195	205	0	70.6	34	T	LAGEYKNFNTN	S	-1.1	6.86	
13	Cg1656	1	1427.6681	0.5	195	207	0	120.3	34	T	LAGEYKNFNTNSA	K	-0.8	6.86	
13	Cg1656	1	1470.6204	2.2	123	135	0	86.1	31	S	YFGNDHFAEFAPG	M	-0.4	4.06	
13	Cg1656	1	1493.8354	-4.6	213	226	0	69.8	34	L	DGAPQVLPPFGKRL	G	-0.3	10.08	
13	Cg1656	1	1550.8569	-5.1	213	227	0	91.1	34	L	DGAPQVLPPFGKRLG	R	-0.3	10.08	
13	Cg1656	1	1606.9195	-18.9	211	225	0	38.2	34	I	LLDGAPQVLPPFGKR	L	-0.1	10.08	
13	Cg1656	1	1663.8066	-3.2	192	205	0	65.7	36	A	HRTLAGEYKNFNTN	S	-1.5	9.72	
13	Cg1656	1	1720.0036	-2.8	211	226	0	80.4	31	I	LLDGAPQVLPPFGKRL	G	0.2	10.08	
13	Cg1656	1	1777.025	-4.5	211	227	0	81.0	32	I	LLDGAPQVLPPFGKRLG	R	0.2	10.08	
13	Cg1656	1	1821.8758	-5.1	192	207	0	47.5	36	A	HRTLAGEYKNFNTNSA	K	-1.2	9.72	
13	Cg1656	1	1859.9305	-0.8	100	115	0	43.7	37	A	SLGEFTRVFEYDSLVV	G	0.4	3.82	
13	Cg1656	1	1890.1091	-6.5	210	227	0	43.0	31	I	ILLDGAPQVLPPFGKRLG	R	0.4	10.08	
13	Cg1656	1	1960.9966	-0.3	451	467	0	43.5	37	A	SSDLPIELRDNQRFSGK	-	-1.2	7.06	
13	Cg1656	1	2118.2062	-26.8	211	230	0	58.3	36	I	LLDGAPQVLPPFGKRLGRNA	Q	-0.2	11.32	
13	Cg1656	1	2448.0829	4.9	346	366	0	56.2	33	I	EAEVEGRSNTEREAFDYFDKG	S	-1.5	4.02	
13	Cg1656	1	2586.1737	0.8	123	145	0	110.2	34	S	YFGNDHFAEFAPGMKSIDDALEI	R	-0.2	3.84	
14	Cg0957	1	1034.5185	1.2	1951	1958	0	36.1	36	A	ILFDDRWA	S	0.1	3.88	
14	Cg0957	1	1045.5345	5.0	794	801	0	39.4	37	A	RWWGLDTL	W	-0.4	6.78	
14	Cg0957	1	1280.734	-1.7	1061	1071	0	36.1	32	L	LDLRIPLEELA	N	0.4	3.82	
14	Cg0957	1	1316.6361	-14.7	1427	1437	0	44.2	35	A	ATEVENWVDRV	A	-0.5	3.82	
14	Cg0957	1	1426.7932	0.2	2312	2324	0	41.9	35	I	KALPSPKHPEQPV	G	-1.2	9.88	
14	Cg0957	1	1592.7987	4.0	688	699	0	41.8	37	M	TYAEWIQRWVEL	A	-0.4	4.26	
14	Cg0957	1	1618.7628	-1.7	704	716	0	56.0	36	T	QDPTWDDRFLDLV	H	-0.8	3.42	
14	Cg0957	1	1663.8358	-0.4	688	700	0	54.4	37	M	TYAEWIQRWVELA	Y	-0.2	4.26	
14	Cg0957	1	1825.0097	-4.4	1056	1070	0	53.2	36	V	HLDHLLDLRIPLEEL	A	0.1	4.52	
14	Cg0957	1	1896.0469	-2.8	1056	1071	0	67.5	35	V	HLDHLLDLRIPLEELA	N	0.2	4.52	
14	Cg0957	1	1954.9313	-6.1	910	925	0	78.8	36	A	DSYFDDLPVEQRPYLV	Q	-0.6	3.5	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
14	Cg0957	1	1971.9731	3.0	332	348	0	94.2	37	G	FHVPTAEDWSEFAPKLV	K	-0.1	4.42	
14	Cg0957	1	1979.9265	-5.7	701	716	0	51.1	35	A	YPTQDPTWDDRFLDLV	H	-0.9	3.42	
14	Cg0957	1	1995.1153	-2.8	1055	1071	0	88.3	35	A	VHLDHLLDLRIPLEELA	N	0.4	4.52	
15	Cg2403	1	938.4749	-3.2	56	63	0	47.5	34	T	LFFDPSIT	K	0.9	3.1	
15	Cg2403	1	945.547	6.9	245	252	0	52.8	32	I	RIMPLFAV	K	1.6	11.04	
15	Cg2403	1	970.527	2.2	442	450	0	37.6	35	G	IIKQMPNGA	F	0.0	10.1	
15	Cg2403	1	985.4844	3.2	180	186	0	40.3	34	G	TWMHWLI	F	0.6	7.84	
15	Cg2403	1	1027.5484	-4.2	441	450	0	62.3	35	T	GIIKQMPNGA	F	-0.1	10.1	
15	Cg2403	1	1184.59	1.2	194	202	0	46.3	35	S	DLMLDRFYI	A	0.4	3.88	
15	Cg2403	1	1236.6754	-0.5	64	74	0	73.4	34	T	KVIYDGGYLPL	N	0.4	6.62	
15	Cg2403	1	1255.6271	-1.7	194	203	0	39.9	35	S	DLMLDRFYIA	H	0.6	3.88	
15	Cg2403	1	1305.599	-0.5	492	503	0	73.9	35	T	RGGFFGPDPEDI	R	-0.8	3.7	
15	Cg2403	1	1344.6462	-1.6	275	286	0	49.2	36	I	NAIWNLGPYNPS	Q	-0.6	5.92	
15	Cg2403	1	1535.6893	-5.6	490	503	0	35.9	33	V	ETRGGFFGPDPEDI	R	-1.0	3.58	
15	Cg2403	1	1579.8695	-4.6	353	365	0	54.2	35	A	HHNLLQRPRDVPV	R	-1.0	10.88	
15	Cg2403	1	1776.8716	2.8	476	491	0	50.8	37	A	AVPKQMNQLGYAEVET	R	-0.5	4.26	
15	Cg2403	1	2022.9469	-2.0	289	307	0	62.5	36	V	SAGSQPDVYMLWTDGAARV	M	-0.1	3.88	
15	Cg2403	1	2116.049	-0.3	455	474	0	46.9	37	V	HQPLGPVDDHGHPIPLPYAG	A	-0.6	5.72	
15	Cg2403	1	2187.0862	-1.0	455	475	0	116.5	37	V	HQPLGPVDDHGHPIPLPYAGA	A	-0.5	5.72	
15	Cg2403	1	2298.1676	-3.3	520	539	0	63.2	38	A	NTLRALNEANIERDKNEGKN	-	-1.7	7.18	
15	Cg2403	1	2476.254	3.1	451	472	0	47.4	38	A	FIEVHQPLGPVDDHGHPIPLPY	A	-0.3	5.02	
15	Cg2403	1	2675.3496	-3.6	451	475	0	78.3	38	A	FIEVHQPLGPVDDHGHPIPLPYAGA	A	-0.1	5.02	
16	Cg2843	1	1048.5342	4.9	90	98	0	42.7	36	V	FQKANPFPT	M	-0.8	10.1	
16	Cg2843	1	1197.5455	4.3	10	19	0	65.2	34	V	NIYYGDFHAV	Q	0.0	4.94	
16	Cg2843	1	1267.6197	-2.1	217	228	0	46.5	35	T	AFYSLEATGRPG	R	-0.3	6.88	
16	Cg2843	1	1538.7154	-5.8	10	22	0	35.2	35	V	NIYYGDFHAVQNV	N	-0.2	4.94	
16	Cg2843	1	1626.7049	6.5	240	252	0	83.6	33	I	FENPDQKETEDYI	S	-1.9	3.5	
16	Cg2843	1	1770.7584	-0.8	240	254	0	115.5	31	I	FENPDQKETEDYISG	R	-1.7	3.5	
16	Cg2843	1	1812.9509	-22.8	186	200	0	70.7	37	A	VEDLIHELKEEFTIV	I	0.2	4	
16	Cg2843	1	1883.988	-9.3	185	200	0	111.0	37	L	AVEDLIHELKEEFTIV	I	0.3	4	
16	Cg2843	1	1925.0007	-5.0	132	148	0	53.2	37	A	NLWEEVKDRLDKPGGGL	S	-1.1	4.56	
16	Cg2843	1	1997.0721	-2.1	184	200	0	82.1	36	T	LAVEDLIHELKEEFTIV	I	0.5	4	
16	Cg2843	1	2009.0766	7.3	138	156	0	45.5	36	V	KDRLDKPGGGLSGGQQQRL	C	-1.4	10.58	
16	Cg2843	1	2086.0834	-2.2	182	199	0	59.7	37	I	STLAVEDLIHELKEEFTI	V	0.1	4	
16	Cg2843	1	2098.1198	-6.7	183	200	0	56.6	37	S	TLAVEDLIHELKEEFTIV	I	0.4	4	
16	Cg2843	1	2130.9494	-1.3	240	257	0	150.1	33	I	FENPDQKETEDYISGRFG	-	-1.6	3.92	
16	Cg2843	1	2185.1518	-2.5	182	200	0	130.0	37	I	STLAVEDLIHELKEEFTIV	I	0.3	4	
16	Cg2843	1	2397.3043	-5.8	182	202	0	68.4	37	I	STLAVEDLIHELKEEFTIVIV	T	0.7	4	
16	Cg2843	1	2436.2437	-0.7	2	22	0	49.0	38	M	SKLKLNDVNIYYGDFHAVQNV	N	-0.3	7.66	
17	Cg2404	1	906.5651	2.3	374	381	0	52.1	24	A	RALPQLPI	T	0.3	11.04	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
17	Cg2404	1	977.6022	-5.6	373	381	0	47.4	26	A	ARALPQLPI	T	0.5	11.04	
17	Cg2404	1	1084.5553	-6.3	392	402	0	41.7	35	A	AGNFIEPLGPA	F	0.3	3.3	
17	Cg2404	1	1125.5284	1.0	76	83	0	35.4	34	I	FWPWEYKA	H	-0.9	6.86	
17	Cg2404	1	1178.656	3.2	35	43	0	34.3	33	I	AYRKERFPI	A	-1.1	10.38	
17	Cg2404	1	1284.5087	-2.5	321	330	0	67.1	26	S	FHYGDYYAYS	K	-0.9	4.94	
17	Cg2404	1	1296.6285	-1.3	187	197	0	49.3	35	I	KNPWNPKEGPM	D	-2.0	9.88	
17	Cg2404	1	1349.7819	1.8	369	381	0	64.7	31	V	FGPAARALPQLPI	T	0.5	11.04	
17	Cg2404	1	1371.6241	-1.3	282	292	0	43.9	34	A	KDVYEHQMHSV	H	-1.1	6.02	
17	Cg2404	1	1377.7908	-3.2	116	126	0	62.6	32	V	LYVKKFIPEEI	A	0.2	7	
17	Cg2404	1	1401.6757	5.9	74	83	0	48.4	36	T	YIFWPWEYKA	H	-0.4	6.8	
17	Cg2404	1	1502.7234	-0.5	73	83	0	55.6	36	A	TYIFWPWEYKA	H	-0.5	6.8	
17	Cg2404	1	1510.7238	-0.8	187	199	0	66.6	36	I	KNPWNPKEGPMDV	Q	-1.7	6.98	
17	Cg2404	1	1760.8165	-3.0	284	298	0	73.6	35	D	VYEHQMHSVHGPRNA	V	-1.1	8	
17	Cg2404	1	1868.8913	6.3	183	199	0	74.2	36	M	GGMIKNPWNPKEGPMDV	Q	-1.0	6.98	
17	Cg2404	1	2035.0375	-6.0	209	226	0	112.9	37	S	GWTLVENDVKVYLGRDTA	A	-0.3	4.3	
17	Cg2404	1	2068.1204	-5.2	373	391	0	58.2	37	A	ARALPQLPITVDEEGYLIA	A	0.3	3.82	
18	Cg2708	1	1148.605	1.0	71	80	0	42.3	35	T	HVAPRDRDIA	M	-0.9	7.84	
18	Cg2708	1	1383.6281	-9.0	83	93	0	39.8	33	V	FQNYALYPHMT	V	-0.4	7.7	
18	Cg2708	1	1457.7337	-12.3	152	163	0	36.5	36	V	RNPQVFLMDEPL	S	-0.4	4.08	
18	Cg2708	1	1482.6966	-0.2	83	94	0	86.1	35	V	FQNYALYPHMTV	G	-0.1	7.7	
18	Cg2708	1	1500.8664	-1.2	124	136	0	74.5	33	L	GLTEFLERKPKAL	S	-0.5	9.88	
18	Cg2708	1	1613.9504	-1.2	123	136	0	60.2	31	T	LGLTEFLERKPKAL	S	-0.2	9.88	
18	Cg2708	1	1714.9981	-4.0	122	136	0	39.0	32	A	TLGLTEFLERKPKAL	S	-0.2	9.88	
18	Cg2708	1	1743.8679	-3.4	281	296	0	78.3	37	I	GFRPEALEIIPEGEST	D	-0.4	3.8	
18	Cg2708	1	1771.8927	-1.6	152	166	0	42.4	37	V	RNPQVFLMDEPLSNL	D	-0.4	4.08	
18	Cg2708	1	1857.0723	-4.4	120	136	0	34.9	33	A	AATLGLTEFLERKPKAL	S	0.0	9.88	
18	Cg2708	1	2089.0878	-5.8	157	174	0	44.3	37	V	FLMDEPLSNLDAKLRVQT	R	-0.2	4.3	
18	Cg2708	1	2137.128	-7.2	62	80	0	38.3	37	A	IFIGDKDVTHVAPRDRDIA	M	-0.2	5.26	
18	Cg2708	1	2382.2318	-7.1	281	302	0	116.2	38	I	GFRPEALEIIPEGESTDLSIPI	K	0.0	3.58	
19	Cg1787	1	1085.6121	6.2	546	554	0	53.3	35	A	GILDELWKI	D	0.5	4.08	
19	Cg1787	1	1243.7289	4.7	10	20	0	76.0	32	I	RFLGQILGEVI	A	1.0	6.98	
19	Cg1787	1	1396.7714	1.4	743	754	0	67.7	35	S	SVEDLRAIPWVL	S	0.6	4.08	
19	Cg1787	1	1483.8035	1.5	742	754	0	45.8	36	T	SSVEDLRAIPWVL	S	0.5	4.08	
19	Cg1787	1	1735.79	1.3	79	92	0	81.8	35	A	NLAEDLYDEELREQ	A	-1.5	3.44	
19	Cg1787	1	1786.8261	18.6	415	429	0	44.6	36	N	SESYEDVLTELFERA	Q	-0.6	3.58	
19	Cg1787	1	1965.0894	-4.2	218	234	0	81.9	35	L	SLLEEIPRINRDVAVEL	R	0.1	4.16	
19	Cg1787	1	2089.1381	-3.6	500	518	0	53.1	36	A	SSVTDVLEPMVLLKEFGLI	A	1.0	3.82	
19	Cg1787	1	2114.1008	-5.9	10	28	0	62.6	37	I	RFLGQILGEVIAEQEGQEV	Y	0.0	3.8	
19	Cg1787	1	2260.1627	-3.7	535	554	0	97.1	38	L	FETIEDLQAGAGILDELWKI	D	0.2	3.5	
19	Cg1787	1	2881.6024	-3.7	434	457	0	36.6	35	A	NYRELSEAEKLEVLLKELRSPRPL	I	-0.8	7.2	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
19	Cg1787	1	3018.6614	-7.6	219	244	0	40.5	37	S	LLEEIPRINRDVAVELRERFGEGVPL	K	-0.2	4.5	
20	Cg1368	1	1284.6867	4.6	260	269	0	65.5	36	L	LFIDNIFRFT	Q	0.9	6.78	
20	Cg1368	1	1326.6721	-2.6	418	428	0	63.5	36	I	ERFLGQNFFVA	E	0.3	6.98	
20	Cg1368	1	1426.7456	-7.1	26	38	0	64.2	36	A	VVDVEFPRGELPA	L	0.2	3.82	
20	Cg1368	1	1524.7209	-2.8	248	259	0	65.5	35	A	EYFRDVQNQDVL	L	-1.0	3.7	
20	Cg1368	1	1540.7634	-5.8	117	129	0	79.2	36	V	SLNNNPEIERWGI	H	-1.0	4.26	
20	Cg1368	1	1554.8042	-7.8	24	38	0	44.5	36	I	GAVVDVEFPRGELPA	L	0.3	3.82	
20	Cg1368	1	1598.6956	11.3	204	216	0	33.6	33	T	REGTDLFLEMEEM	G	-0.7	3.58	
20	Cg1368	1	1637.8049	-9.4	248	260	0	45.9	36	A	EYFRDVQNQDVLL	F	-0.6	3.7	
20	Cg1368	1	1754.7855	-0.7	204	218	0	85.7	33	T	REGTDLFLEMEEMGV	L	-0.3	3.58	
20	Cg1368	1	1897.9574	-1.9	248	262	0	55.2	37	A	EYFRDVQNQDVLLFI	D	0.0	3.7	
20	Cg1368	1	2095.095	-3.1	464	483	0	77.1	37	A	FNGLGGLDDVEAAYKKLTGK	-	-0.4	6.96	
21	Cg0791	1	828.4229	26.2	908	915	0	44.8	35	Y	DIPDSVIA	F	0.7	2.92	
21	Cg0791	1	1143.64	1.5	731	739	0	43.7	35	A	LRREFDLPV	H	-0.3	7.04	
21	Cg0791	1	1433.6463	3.8	591	601	0	60.2	35	L	FEDPWDRLDEL	R	-1.3	3.42	
21	Cg0791	1	1509.7827	-4.4	638	651	0	53.5	36	A	ASSGVDIFRIFDAL	N	0.9	3.88	
21	Cg0791	1	1517.8929	-5.1	498	510	0	41.3	31	I	DKLPNIKDLPLPR	G	-0.9	9.88	
21	Cg0791	1	1592.8199	3.3	641	654	0	39.4	36	S	GVDIFRIFDALNDV	S	0.7	3.6	
21	Cg0791	1	1661.9464	-5.0	498	512	0	76.9	34	I	DKLPNIKDLPLPRGS	R	-0.9	9.88	
21	Cg0791	1	1834.9366	-3.8	916	932	0	69.1	37	A	FLRGELGNPPGGWPEPL	R	-0.6	4.26	
21	Cg0791	1	1837.921	0.4	638	654	0	52.0	37	A	ASSGVDIFRIFDALNDV	S	0.6	3.6	
21	Cg0791	1	1924.9531	0.1	638	655	0	44.3	37	A	ASSGVDIFRIFDALNDVS	Q	0.5	3.6	
21	Cg0791	1	2163.096	-3.3	459	477	0	58.7	37	P	HLLQAPPADDEQGRILDYL	A	-0.5	3.96	
21	Cg0791	1	2549.2762	-3.1	459	481	0	40.2	38	P	HLLQAPPADDEQGRILDYLADVT	V	-0.4	3.76	
22	Cg2875	1	856.4443	0.6	11	18	0	55.2	34	S	IFDGVHGL	V	1.0	4.94	
22	Cg2875	1	955.5127	3.7	11	19	0	59.1	34	S	IFDGVHGLV	G	1.3	4.94	
22	Cg2875	1	1012.5342	1.0	11	20	0	57.3	34	S	IFDGVHGLVG	S	1.2	4.94	
22	Cg2875	1	1035.5237	-3.2	27	36	0	78.2	36	A	QGVFDSIVTA	S	0.9	3.1	
22	Cg2875	1	1071.5349	2.1	9	18	0	66.7	36	I	QSIFDGVHGL	V	0.4	4.94	
22	Cg2875	1	1099.5662	-3.4	11	21	0	45.5	36	S	IFDGVHGLVGS	I	1.0	4.94	
22	Cg2875	1	1170.6033	-1.3	9	19	0	73.8	36	I	QSIFDGVHGLV	G	0.7	4.94	
22	Cg2875	1	1212.6503	-0.1	11	22	0	95.4	35	S	IFDGVHGLVGSI	F	1.3	4.94	
22	Cg2875	1	1227.6248	-2.1	9	20	0	83.8	36	I	QSIFDGVHGLVG	S	0.6	4.94	
22	Cg2875	1	1314.6568	-9.3	9	21	0	109.3	36	I	QSIFDGVHGLVGS	I	0.5	4.94	
22	Cg2875	1	1427.7409	-1.5	9	22	0	119.3	36	I	QSIFDGVHGLVGSI	F	0.8	4.94	
22	Cg2875	1	1842.9629	-0.9	11	29	0	81.0	37	S	IFDGVHGLVGSIFAGAQGV	F	1.1	4.94	
23	Cg2181	1	1238.5779	-5.7	271	281	0	38.8	35	S	SFEDELSGRSI	N	-0.6	3.82	
23	Cg2181	1	1435.6983	2.6	406	418	0	44.7	36	I	DAIGNPYPDFKSL	R	-0.6	3.88	
23	Cg2181	1	1472.6783	-2.4	269	281	0	79.4	34	A	FSSFEDELSGRSI	N	-0.4	3.82	
23	Cg2181	1	1834.8697	-2.8	271	287	0	57.2	36	S	SFEDELSGRSINQPSAV	F	-0.6	3.82	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
23	Cg2181	1	2068.9702	-2.7	269	287	0	77.3	36	A	FSSFEDELSGRSINQPSAV	F	-0.4	3.82	
23	Cg2181	1	2138.9797	21.3	288	306	0	62.4	37	V	FQSFTIPESLEHFSGEEGV	L	-0.3	3.78	
23	Cg2181	1	2252.0637	-4.2	288	307	0	68.0	36	V	FQSFTIPESLEHFSGEEGVL	R	-0.1	3.78	
23	Cg2181	1	2393.1611	-3.8	406	426	0	57.0	37	I	DAIGNPYPDFKSLRDDVTNRT	I	-1.1	4.34	
23	Cg2181	1	2876.4457	-3.0	288	312	0	81.4	38	V	FQSFTIPESLEHFSGEEGVLRRQAI	S	-0.3	4.7	
23	Cg2181	1	2963.4777	-20.7	288	313	0	45.0	37	V	FQSFTIPESLEHFSGEEGVLRRQAIS	L	-0.3	4.7	
24	Cg1081	1	909.5647	10.1	78	85	0	35.2	27	A	ILRPELGI	M	0.8	6.98	
24	Cg1081	1	1093.5741	4.5	250	258	0	43.0	34	I	RDNNHVRIA	T	-1.4	10.88	
24	Cg1081	1	1399.7824	0.3	230	242	0	86.4	35	I	SFVLRGGQVELPV	L	0.6	6.98	
24	Cg1081	1	1779.9917	-2.0	78	94	0	61.1	34	A	ILRPELGIMLQSGGLPS	Q	0.5	6.98	
24	Cg1081	1	1785.9526	-2.9	27	42	0	66.6	37	G	LNFHVQRGEVFGLLGT	N	0.3	7.84	
24	Cg1081	1	1962.0898	-3.2	116	132	0	104.9	35	I	KDVLADVDLLHRENVKV	G	-0.2	5.32	
24	Cg1081	1	2019.1113	-2.1	116	133	0	75.9	35	I	KDVLADVDLLHRENVKVG	A	-0.2	5.32	
25	Cg1111	1	977.5698	8.1	126	133	0	43.2	30	A	GLPLFRYI	G	0.9	9.84	
25	Cg1111	1	1373.7456	-19.7	126	138	0	53.7	37	A	GLPLFRYIGGPNA	H	0.2	9.84	
25	Cg1111	1	1756.957	0.6	213	228	0	96.2	36	G	STREALDLIVEAIEKA	G	0.1	4.16	
25	Cg1111	1	1919.0781	-7.3	126	143	0	46.9	35	A	GLPLFRYIGGPNAHVLPV	P	0.6	9.84	
25	Cg1111	1	2220.1902	-4.5	397	416	0	57.0	37	A	KYNQLLRIEQLLGDAGVYAG	R	-0.1	6.88	
25	Cg1111	1	2247.1535	-5.5	305	324	0	47.3	38	V	QIVGDDFFVTNPERLKEGIA	K	-0.2	4.06	
25	Cg1111	1	2855.3308	-7.5	67	92	0	133.0	35	A	VENVNEEIGDELAGLEADDQRLIDEA	M	-0.6	3.16	
26	Cg3186	1	897.5032	-2.7	302	309	0	34.2	32	A	RLQGLNPT	A	-0.8	11.04	
26	Cg3186	1	1000.5202	6.4	38	45	0	44.5	37	A	ANRDWLRA	D	-1.2	10.88	
26	Cg3186	1	1196.605	1.4	191	200	0	67.1	35	A	AKHPDQFRQA	M	-1.7	10.08	
26	Cg3186	1	1223.536	4.0	242	250	0	34.1	33	R	RFENDPFWN	M	-1.7	4.08	
26	Cg3186	1	1411.5979	-5.8	242	252	0	35.9	30	R	RFENDPFWNMG	G	-1.3	4.08	
26	Cg3186	1	1414.6841	-4.8	265	277	0	52.8	36	A	SGLWSPQDDGVRV	D	-0.6	3.88	
26	Cg3186	1	1652.7406	-5.7	242	255	0	84.8	33	R	RFENDPFWNMGGLA	N	-0.6	4.08	
26	Cg3186	1	1668.7355	-6.2	242	255	0	42.5	32	R	RFENDPFWNMGGLA	N	-0.6	4.08	Oxidation (M)
26	Cg3186	1	2333.1375	-3.6	236	255	0	77.2	37	G	SIINPRRFENDPFWNMGGLA	N	-0.5	7.04	
27	Cg0445	1	799.3501	-8.8	134	141	0	34.8	30	V	GGFNSFAT	R	0.2	6.02	
27	Cg0445	1	1037.4454	8.3	173	181	0	45.3	33	T	SFEHGEVYA	N	-0.4	4.24	
27	Cg0445	1	1061.5658	6.2	186	194	0	36.2	35	A	SFSRWPVAI	W	0.5	11.04	
27	Cg0445	1	1125.5455	-8.6	131	141	0	80.8	35	T	NLVGGFNSFAT	R	0.6	6.02	
27	Cg0445	1	1170.7012	-1.5	241	251	0	46.3	32	V	LIGNITIPFAI	A	1.8	6.02	
27	Cg0445	1	1230.7012	-0.3	154	163	0	64.0	34	A	FIIFHILDLT	M	1.9	4.94	
27	Cg0445	1	1239.6135	-0.2	75	84	0	73.2	35	V	DVYGEFLREI	G	-0.1	3.82	
27	Cg0445	1	1306.583	2.1	170	181	0	57.4	34	A	APTSFEHGEVYA	N	-0.4	4.24	
27	Cg0445	1	1368.6786	0.7	131	143	0	72.5	36	T	NLVGGFNSFATRS	M	0.1	11.04	
27	Cg0445	1	1412.8	0.1	217	228	0	52.7	35	S	DLGITGRRWRAI	L	-0.4	12.1	
27	Cg0445	1	1466.7405	0.7	73	84	0	81.4	36	A	QVDVYGEFLREI	G	-0.1	3.82	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
28	Cg0924	1	922.48	-4.0	225	232	0	35.7	34	T	YGPIFDLV	G	1.1	3.1	
28	Cg0924	1	1030.5923	-1.2	123	131	0	42.1	34	S	LIINGQRFA	Q	0.6	11.04	
28	Cg0924	1	1179.6288	-1.9	223	232	0	53.9	35	G	RTYGPIFDLV	G	0.3	6.7	
28	Cg0924	1	1206.588	4.5	182	192	0	42.7	36	I	VADFESALERA	K	0.0	3.82	
28	Cg0924	1	1737.8421	-2.0	148	162	0	40.8	36	V	ELDPRDGEPLDQELI	R	-1.1	3.38	
28	Cg0924	1	1863.8486	-1.8	163	179	0	129.0	34	I	RQAETLGEIFGEEEDAA	K	-0.8	3.5	
28	Cg0924	1	1930.9901	5.6	67	82	0	47.1	37	T	DNRAFELLDRWGVELV	A	-0.2	4.06	
28	Cg0924	1	1935.9789	-4.2	146	162	0	83.6	37	T	VVELDPRDGEPLDQELI	R	-0.5	3.38	
28	Cg0924	1	2032.0378	-4.8	66	82	0	49.8	37	A	TDNRAFELLDRWGVELV	A	-0.2	4.06	
28	Cg0924	1	2174.112	-5.1	64	82	0	79.7	38	V	AATDNRAFELLDRWGVELV	A	0.0	4.06	
29	Cg2196	1	959.3508	11.0	58	65	0	41.4	25	E	YEGDQEGY	G	-2.2	2.94	
29	Cg2196	1	1457.6899	3.1	74	85	0	39.3	35	S	RDDSGEEVPRWL	E	-1.6	4.06	
29	Cg2196	1	1544.7219	6.8	73	85	0	48.1	35	S	SRDDSGEEVPRWL	E	-1.5	4.06	
29	Cg2196	1	1687.7802	0.4	74	87	0	48.8	35	S	RDDSGEEVPRWLET	W	-1.6	3.92	
29	Cg2196	1	1774.8122	4.5	73	87	0	43.0	35	S	SRDDSGEEVPRWLET	W	-1.6	3.92	
29	Cg2196	1	1996.7235	27.6	50	65	0	146.1	22	S	SWNDYNEEYEGDQEGY	G	-2.4	2.76	
29	Cg2196	1	2007.8923	7.0	68	85	0	56.8	34	I	DGFGSSRDDSGEEVPRWL	E	-1.2	3.84	
29	Cg2196	1	2237.9825	2.3	68	87	0	33.1	32	I	DGFGSSRDDSGEEVPRWLET	W	-1.3	3.76	
29	Cg2196	1	2318.3766	2.4	99	119	0	87.7	29	T	SVLGLVVFPVVNFLKYNGLIK	-	1.3	10.18	
29	Cg2196	1	3006.4723	5.0	73	98	0	39.4	38	S	SRDDSGEEVPRWLETWGKVFDALTIT	S	-0.6	4.06	
30	Cg2405	1	1349.6472	-1.9	223	234	0	59.3	36	A	MLTGPQNMPKFS	D	-0.5	10.1	
30	Cg2405	1	1522.6899	-1.6	162	174	0	40.4	34	M	EELRGENYDGQIT	S	-1.5	3.68	
30	Cg2405	1	1653.7304	0.2	161	174	0	70.1	33	A	MEELRGENYDGQIT	S	-1.3	3.68	
30	Cg2405	1	1936.9166	1.1	206	222	0	96.2	36	G	KYAPNLDAANEQEIYQA	M	-1.0	3.82	
30	Cg2405	1	2080.9701	1.8	204	222	0	99.7	36	S	SGKYAPNLDAANEQEIYQA	M	-1.0	3.82	
30	Cg2405	1	2517.0965	2.0	153	174	0	89.7	32	V	YNEDGTLAMEELRGENYDGQIT	S	-1.2	3.44	
30	Cg2405	1	3168.4306	-5.3	145	174	0	41.1	33	A	NGGGPGLVYNEDGTLAMEELRGENYDGQIT	S	-0.8	3.44	
31	Cg1437	1	1202.5204	1.6	309	318	0	44.1	32	A	SYNNHPIEET	G	-1.7	4.24	
31	Cg1437	1	1293.6717	1.4	257	268	0	69.5	36	A	EFGGYLSGPRVI	D	0.2	6.88	
31	Cg1437	1	1296.6826	-1.1	101	113	0	53.1	35	N	AGDALLFGHGLNI	H	0.8	4.94	
31	Cg1437	1	1364.7088	-2.9	256	268	0	66.0	36	T	AEFGGYLSGPRVI	D	0.3	6.88	
31	Cg1437	1	1551.8297	-5.0	114	127	0	100.3	36	I	HFDLIKPADDIIVG	M	0.5	4.16	
31	Cg1437	1	2196.0308	-0.9	25	45	0	65.1	36	V	GYGSQGHAHSQNLRDSGVEVV	I	-0.7	6.02	
31	Cg1437	1	2370.1373	-2.3	269	289	0	104.8	37	I	DADTKSRMKDILTDIQDGTFT	K	-0.9	4.04	
31	Cg1437	1	2454.2179	4.5	91	113	0	46.7	38	I	FTNDIEPNLNAGDALLFGHGLNI	H	0.1	3.7	
31	Cg1437	1	2696.3446	-7.4	89	113	0	94.3	38	A	EIFTNDIEPNLNAGDALLFGHGLNI	H	0.1	3.58	
32	Cg3227	1	728.3051	18.1	184	189	0	34.9	31	L	MFTVDT	P	0.7	3.1	Oxidation (M)
32	Cg3227	1	1152.6233	-0.5	218	225	0	36.6	34	A	IPRPWWWI	D	-0.2	11.04	
32	Cg3227	1	1337.7033	2.8	216	225	0	53.0	35	L	NAIPRPWWWI	D	-0.3	11.04	
32	Cg3227	1	1372.6663	-0.4	72	82	0	63.5	36	A	FENIEFHPDIL	K	0.0	3.82	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
32	Cg3227	1	1450.7874	-3.7	215	225	0	49.9	35	V	LNAIPRPWWWI	D	0.1	11.04	
32	Cg3227	1	1650.9035	1.2	213	225	0	46.0	35	S	TVLNAIPRPWWWI	D	0.3	11.04	
32	Cg3227	1	1825.9668	-1.8	215	228	0	37.2	37	V	LNAIPRPWWWIDFL	T	0.3	6.78	
32	Cg3227	1	2426.2787	-0.9	213	232	0	54.0	37	S	TVLNAIPRPWWWIDFLTTPT	L	0.2	6.78	
33	Cg0756	1	982.4701	2.7	499	505	0	37.0	34	A	FWYHFAI	M	0.9	7.76	
33	Cg0756	1	1039.5743	-3.8	354	362	0	37.0	33	S	GSLFPFLFI	T	2.0	6.02	
33	Cg0756	1	1273.6489	-2.4	329	339	0	67.6	37	I	LFARPEVQMPS	V	-0.1	6.98	
33	Cg0756	1	1289.6438	-3.6	329	339	0	40.8	37	I	LFARPEVQMPS	V	-0.1	6.98	Oxidation (M)
33	Cg0756	1	1376.6183	2.1	743	754	0	64.6	34	A	MWDERYPGGAPV	S	-0.8	4.08	
33	Cg0756	1	1392.7224	1.0	414	424	0	41.2	36	A	VILDRHLYFSM	N	0.7	7.76	
33	Cg0756	1	1446.7871	0.6	303	314	0	39.8	35	V	WLLLAPRDYLST	F	0.3	6.7	
33	Cg0756	1	1463.7595	-1.4	413	424	0	43.9	36	T	AVILDRHLYFSM	N	0.8	7.76	
33	Cg0756	1	1473.765	-1.6	329	341	0	42.4	37	I	LFARPEVQMPSVT	S	0.2	6.98	
34	Cg0766	1	1121.5506	0.3	596	604	0	43.2	36	L	RWDSLGEFL	A	-0.4	4.08	
34	Cg0766	1	1192.5877	-0.6	596	605	0	64.2	36	L	RWDSLGEFLA	L	-0.1	4.08	
34	Cg0766	1	1365.6929	-5.2	542	552	0	38.1	36	V	LRDYNTDLFPI	L	-0.3	3.88	
34	Cg0766	1	1578.8042	-1.0	540	552	0	60.5	37	G	NVLRDYNTDLFPI	L	-0.2	3.88	
34	Cg0766	1	1635.8257	-3.1	539	552	0	73.4	37	T	GNVLRDYNTDLFPI	L	-0.2	3.88	
34	Cg0766	1	1922.9738	-1.7	536	552	0	60.5	37	I	SVTGNVLRDYNTDLFPI	L	0.0	3.88	
34	Cg0766	1	2271.1634	-5.3	496	515	0	104.3	38	A	SLVEKYLADHDTEGLDIQIL	S	-0.1	3.84	
35	Cg2743	1	1216.6968	0.9	2142	2152	0	49.5	33	T	LLFPFAAPRVS	G	1.1	11.04	
35	Cg2743	1	1557.794	-1.0	316	330	0	46.6	37	A	GARWFLDVGPDGGIV	K	0.4	3.88	
35	Cg2743	1	2002.0081	-3.7	1231	1248	0	58.6	37	T	MLAPVLPGEEIEFSVERS	A	0.2	3.8	
35	Cg2743	1	2497.1624	8.0	705	724	0	42.3	36	V	YFGDIGSMTYEQWLNRYLEL	S	-0.4	3.82	
36	Cg1290	1	1180.6492	0.8	188	196	0	54.0	34	A	LFEVYERLI	K	0.7	4.26	
36	Cg1290	1	1491.8297	-3.4	584	596	0	71.6	34	I	QVDEPAIRELLPL	R	0.0	3.82	
36	Cg1290	1	1589.7613	10.6	479	492	0	79.5	37	V	QYFSELLDGFLSTA	N	0.3	3	
36	Cg1290	1	1598.7576	-5.2	328	340	0	56.5	35	L	EAENIEPEVRDWL	A	-1.1	3.58	
36	Cg1290	1	1669.7947	-4.2	328	341	0	46.1	35	L	EAENIEPEVRDWLA	F	-0.9	3.58	
36	Cg1290	1	2334.1492	2.1	77	97	0	47.6	38	I	LGVLPERFDDIADHENDGLPL	W	-0.4	3.68	
36	Cg1290	1	2518.2704	-3.6	75	97	0	57.0	38	A	AILGVLPERFDDIADHENDGLPL	W	-0.1	3.68	
37	Cg1790	1	906.4058	2.4	322	329	0	35.8	34	I	FWNGPMGV	F	0.3	6.02	
37	Cg1790	1	1455.747	-5.7	369	381	0	63.3	36	V	RVLGLNEDGFSHI	S	-0.1	5.22	
37	Cg1790	1	1612.8321	0.9	63	76	0	73.4	36	A	HLGRPKGEVNEKYS	L	-1.6	9.62	
37	Cg1790	1	1776.9734	-29.5	6	21	0	96.4	37	T	LKDLLDEGVDGRHVIV	R	0.1	4.44	
37	Cg1790	1	1846.8697	-4.9	24	39	0	51.9	35	S	DFNVPLNDDREITDKG	R	-1.3	3.76	
37	Cg1790	1	1993.0745	0.4	63	80	0	73.8	36	A	HLGRPKGEVNEKYSLAPV	A	-0.8	9.62	
37	Cg1790	1	2090.0029	0.8	22	39	0	40.2	37	V	RSDFNVPLNDDREITDKG	R	-1.4	4.12	
37	Cg1790	1	2308.3042	-12.3	172	192	0	108.3	35	A	KLLPHYAGGLVETEISVLEKI	A	0.4	5.4	
37	Cg1790	1	2419.1543	-9.3	278	298	0	58.9	36	A	SEFNKDAEKQIVDLDSIPEGW	M	-0.9	3.76	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
38	Cg1366	1	1092.5757	-4.6	244	253	0	36.5	35	A	GFKWLAPFAG	A	0.6	10.1	
38	Cg1366	1	1139.5611	5.5	399	408	0	49.7	35	A	AFRDLEAFAT	F	0.3	4.08	
38	Cg1366	1	1163.6128	1.0	244	254	0	52.9	36	A	GFKWLAPFAGA	A	0.7	10.1	
38	Cg1366	1	1307.7085	-0.2	139	149	0	45.3	35	T	VLERQPVEEPL	A	-0.5	3.96	
38	Cg1366	1	1363.8048	-7.1	285	296	0	45.0	31	I	SLLLRRPPGREA	Y	-0.7	12.1	
38	Cg1366	1	1422.8347	-14.1	106	118	0	49.3	32	A	FLGRVINPLGQPI	D	0.6	11.04	
38	Cg1366	1	1477.7313	2.8	465	475	0	55.4	37	V	RRFESELHEYL	G	-1.3	5.4	
38	Cg1366	1	1704.9046	1.0	135	149	0	43.4	36	L	QAPTVLERQPVEEPL	A	-0.6	3.96	
38	Cg1366	1	2320.1812	-5.8	347	367	0	55.6	38	I	SITDGQVFLESDLFNRGVRPA	I	-0.2	4.3	
39	Cg2523	1	1833.8785	1.4	222	238	0	74.0	37	M	HAAEPLPPTEDSPYLPT	T	-0.8	3.82	
39	Cg2523	1	2475.1475	10.1	251	271	0	48.8	36	V	EDIPEFNQLEIDLRDDIAEMA	A	-0.6	3.24	
39	Cg2523	1	2481.2248	-15.0	272	292	0	37.2	37	A	AEFRERNLTSDIIERNDVYAA	K	-0.7	4.28	
39	Cg2523	1	2490.1849	-1.5	507	529	0	42.4	36	I	GEDLGTFEPWVQDALAQRGIMGT	S	-0.3	3.58	
39	Cg2523	1	2801.4058	-4.9	504	529	0	59.0	38	A	VVIGEDLGTFEPWVQDALAQRGIMGT	S	0.3	3.58	
39	Cg2523	1	2929.4644	-3.0	502	529	0	99.3	38	A	GAVVIGEDLGTFEPWVQDALAQRGIMGT	S	0.3	3.58	
40	Cg2958	1	1138.5982	6.5	220	230	0	35.1	34	A	LGRPSVPEDVA	G	-0.2	4.08	
40	Cg2958	1	1160.6666	-1.0	158	168	0	50.8	33	T	KFAVRGLTQAA	A	0.3	11.48	
40	Cg2958	1	1162.6234	-5.8	56	66	0	81.8	36	A	VFVGLDVTDKA	N	0.8	3.88	
40	Cg2958	1	1407.7722	-13.6	220	233	0	61.8	35	A	LGRPSVPEDVAGLV	S	0.4	4.08	
40	Cg2958	1	1481.715	8.2	203	215	0	41.9	36	I	NGKPIGENFKEYS	S	-1.5	7	
40	Cg2958	1	1588.9301	-7.0	124	137	0	57.7	32	A	SRKFDELGVKGKII	N	-0.4	10.32	
40	Cg2958	1	1655.7791	-6.8	203	217	0	91.8	35	I	NGKPIGENFKEYSSS	I	-1.4	7	
40	Cg2958	1	1809.9261	-1.9	201	216	0	56.0	37	S	KINGKPIGENFKEYSS	S	-1.2	9.56	
40	Cg2958	1	1896.9581	-3.0	201	217	0	75.8	37	S	KINGKPIGENFKEYSSS	I	-1.2	9.56	
41	Cg2499	1	1311.6935	5.9	250	259	0	38.5	35	L	RLYEHPQEKL	S	-1.7	7.74	
41	Cg2499	1	1727.7944	-1.4	307	319	0	82.3	34	S	FFDQETNERWIPF	V	-0.9	3.82	
41	Cg2499	1	1939.9469	-4.2	307	321	0	42.1	37	S	FFDQETNERWIPFVI	E	-0.2	3.82	
41	Cg2499	1	1998.9759	-16.3	339	356	0	42.1	36	A	YHEDEAPNSKGGVDKRVV	L	-1.3	5.38	
41	Cg2499	1	2157.0378	-25.2	147	165	0	103.3	34	T	FLGPVDDEEGLHYLRPETA	Q	-0.6	3.92	
41	Cg2499	1	2237.0793	-4.6	307	324	0	95.0	37	S	FFDQETNERWIPFVIEPA	A	-0.4	3.68	
42	Cg1429	1	906.4811	12.9	122	130	0	59.1	34	V	PPAPPTQVT	R	-0.6	6.02	
42	Cg1429	1	1457.7263	-0.5	71	83	0	54.8	36	T	AFERPDNQSAKPV	A	-1.2	7.02	
42	Cg1429	1	1461.5936	-1.6	147	159	0	57.5	28	S	YSEPYTDSDFAPA	G	-0.9	2.88	
42	Cg1429	1	1471.6579	1.2	134	146	0	35.0	33	I	SRPEEPGYQPEPS	Y	-2.2	3.96	
42	Cg1429	1	1524.6845	-2.4	277	290	0	91.1	33	V	NTHEGGWGELSEPL	M	-1.1	3.96	
42	Cg1429	1	1712.8006	-7.9	132	146	0	42.1	35	R	QISRPEEPGYQPEPS	Y	-1.8	3.96	
42	Cg1429	1	1868.9017	-0.2	131	146	0	43.1	36	T	RQISRPEEPGYQPEPS	Y	-2.0	4.56	
42	Cg1429	1	2603.1372	1.3	6	28	0	176.3	32	S	RNSNQNFDQPDLNDLDDDSAIPT	Y	-1.5	3.22	
43	Cg1791	1	1551.7603	-2.6	165	178	0	39.7	36	V	LNDKFGIENGLMTT	V	-0.2	4.08	
43	Cg1791	1	1737.8057	-4.1	54	68	0	41.5	35	G	RLGQEVEYDDDSITV	G	-0.8	3.42	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
43	Cg1791	1	2364.4144	-6.0	218	239	0	74.9	30	V	ALVLPELKGKLDGYALRVPVIT	G	0.7	9.62	
43	Cg1791	1	2463.4828	-9.2	217	239	0	77.6	29	A	VALVLPELKGKLDGYALRVPVIT	G	0.8	9.62	
43	Cg1791	1	2907.5012	0.2	34	59	0	86.4	38	V	NDLTDNKTLSTLLKFDSIMGRLGQEV	E	-0.3	4.46	
43	Cg1791	1	3077.6067	-17.5	32	59	0	96.7	38	V	AVNDLTDNKTLSTLLKFDSIMGRLGQEV	E	-0.1	4.46	
44	Cg1001	1	1008.5505	3.4	5	12	0	34.1	33	G	FRDFVLRG	N	0.1	10.88	
44	Cg1001	1	1425.8052	-7.5	125	135	0	65.2	35	I	RDLLQEQKRLQ	-	-1.7	10.08	
44	Cg1001	1	1444.7198	-2.1	45	58	0	85.4	37	A	SIGSTEVEGLGFHI	R	0.4	4.24	
44	Cg1001	1	1768.9795	-5.0	122	135	0	83.3	36	L	TEIRDLLQEQKRLQ	-	-1.3	7.14	
44	Cg1001	1	2124.1902	-3.2	119	135	0	106.8	35	A	ELLTEIRDLLQEQKRLQ	-	-0.9	4.64	
44	Cg1001	1	2524.386	-8.9	115	135	0	119.8	37	A	SIEAELLTEIRDLLQEQKRLQ	-	-0.6	4.36	
45	Cg2211	1	1152.5941	4.6	26	34	0	44.3	35	A	WGWHGLKRN	T	-1.5	11.48	
45	Cg2211	1	1416.5946	22.9	98	109	0	64.6	33	V	GHVEPDWTYDQA	T	-1.3	3.7	
45	Cg2211	1	1475.7369	-4.9	114	126	0	60.1	37	G	TWGNLTDSQLRSV	N	-0.6	6.78	
45	Cg2211	1	1532.7583	-2.9	113	126	0	97.9	37	T	GTWGNLTDSQLRSV	N	-0.6	6.78	
45	Cg2211	1	1614.8002	1.0	2	16	0	64.2	37	M	AGSSHTIEPEIYRGV	S	-0.4	5.3	
45	Cg2211	1	1847.9378	-1.6	110	126	0	116.7	37	A	TLTGTWGNLTDSQLRSV	N	-0.3	6.78	
45	Cg2211	1	2199.0345	-2.1	91	109	0	63.9	36	I	TSRNKPVGHVEPDWTYDQA	T	-1.4	5.28	
45	Cg2211	1	2486.1925	0.1	2	25	0	40.1	37	M	AGSSHTIEPEIYRGVSTLDEPSAA	W	-0.4	4.16	
46	Cg1737	1	997.6172	-25.8	43	51	0	37.8	32	S	LKVLGENLL	R	0.9	6.94	
46	Cg1737	1	1249.7255	-1.7	372	382	0	37.9	31	S	IAGPKRPQDRI	L	-1.2	11.32	
46	Cg1737	1	1254.7085	-6.5	170	181	0	49.4	34	S	NFRVVPPGTGIV	H	0.6	11.04	
46	Cg1737	1	1395.7834	-7.5	768	779	0	64.9	34	A	NIRLQNQLVDIA	G	0.1	6.78	
46	Cg1737	1	1525.6797	-1.2	780	793	0	78.0	33	A	GGYTRDFTQEGAPQ	A	-1.4	4.08	
46	Cg1737	1	1604.8021	-10.5	686	699	0	57.5	37	I	RKAPYFDGMPVEPV	A	-0.5	6.94	
47	Cg0953	1	1096.6645	-3.4	498	507	0	41.0	31	A	IFPLKNPGLV	S	0.8	10.1	
47	Cg0953	1	1234.7034	-0.8	326	338	0	38.7	33	A	ALVGPDRVIAAPG	A	0.8	6.78	
47	Cg0953	1	1386.6966	-2.2	516	528	0	63.7	36	A	GWIGTLVGKPDNM	D	-0.1	6.76	
47	Cg0953	1	1456.8514	-2.7	122	133	0	35.5	33	A	DVLSFRLRQKPV	R	-0.3	11.32	
47	Cg0953	1	1800.8716	-0.3	516	532	0	64.7	36	A	GWIGTLVGKPDNMDDLA	A	-0.1	3.6	
47	Cg0953	1	2259.1939	-7.0	442	460	0	63.3	37	A	SANLPTILYSLYWKKFNTT	G	-0.2	9.94	
48	Cg0576	1	1515.8045	-4.7	14	27	0	41.6	37	T	KSVVDIPGAPQRYS	F	-0.5	9.72	
48	Cg0576	1	1768.957	-2.3	70	85	0	63.2	36	A	RVTSGLENILEELSPI	Q	0.1	3.96	
48	Cg0576	1	2012.9844	-2.7	230	246	0	74.2	37	A	LGWTTEQITERFGFSEI	M	-0.3	3.96	
48	Cg0576	1	3125.6073	1.9	32	59	0	94.0	38	V	SAPIEVPGLLDLQLDSYSWLIGTPEWRA	R	0.1	3.58	
49	Cg0737	1	1494.7678	-4.8	275	288	0	49.7	36	T	SVPVDRPGADLQEI	L	-0.3	3.7	
49	Cg0737	1	1504.8038	-5.2	253	264	0	75.4	36	A	RLVELWHDPEVL	A	-0.1	4.42	
49	Cg0737	1	1652.8522	-6.7	84	97	0	110.4	36	A	LAQDQLDVNLFQHL	K	0.0	3.88	
49	Cg0737	1	2002.9272	9.1	123	140	0	108.7	36	L	ALFWKDHDSIDGIDGESV	A	-0.4	3.76	
49	Cg0737	1	3336.6011	4.0	123	153	0	54.7	38	L	ALFWKDHDSIDGIDGESVAIPNDPSNQGRAI	N	-0.5	3.92	
50	Cg1685	1	1262.568	-4.6	74	83	0	69.2	34	N	FEQHYQGQQV	Q	-1.5	5.12	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
50	Cg1685	1	1598.7437	1.4	84	96	0	68.2	35	V	QQPQNPQTPDYRQ	N	-2.8	6.7	
50	Cg1685	1	1671.7277	-0.1	68	81	0	69.2	32	I	EAPQPNFEQHYQGQ	Q	-2.0	4.24	
50	Cg1685	1	1898.8547	-0.2	68	83	0	92.8	34	I	EAPQPNFEQHYQGQQV	Q	-1.7	4.24	
50	Cg1685	1	2263.0465	-6.8	46	65	0	64.6	34	M	NKDGDTPEQQQQPQQQIAPN	Q	-2.3	3.7	
50	Cg1685	1	2504.1891	7.3	46	67	0	57.0	37	M	NKDGDTPEQQQQPQQQIAPNQI	E	-2.0	3.7	
50	Cg1685	1	2588.164	8.4	84	104	0	35.3	35	V	QQPQNPQTPDYRQNYEDPNRT	S	-2.8	4.3	
50	Cg1685	1	2675.196	3.1	84	105	0	38.3	34	V	QQPQNPQTPDYRQNYEDPNRTS	-	-2.7	4.3	
51	Cg2444	1	957.4781	1.5	150	158	0	51.3	35	G	DFGGPRGPR	G	-1.6	10.88	
51	Cg2444	1	1267.6534	-1.7	150	161	0	43.7	35	G	DFGGPRGPRGPR	N	-1.7	12.1	
51	Cg2444	1	1671.7794	0.2	159	175	0	66.4	35	R	GPRNDGPFGPFGPFGPG	Y	-0.8	6.78	
51	Cg2444	1	1701.7006	21.8	97	110	0	73.2	32	I	YADDLIDEDEDYRA	Q	-1.4	3.22	
51	Cg2444	1	1800.8853	5.2	115	130	0	46.0	37	S	QINDEVINEIRDGISS	F	-0.6	3.58	
51	Cg2444	1	1834.8428	0.1	159	176	0	51.5	35	R	GPRNDGPFGPFGPFGPGY	R	-0.8	6.7	
51	Cg2444	1	2138.0123	-4.6	162	181	0	63.7	36	R	NDGPFGPFGPFGPGYRGPRF	-	-0.8	9.84	
51	Cg2444	1	2332.1547	-3.0	115	135	0	48.0	37	S	QINDEVINEIRDGISSFVDGI	V	-0.1	3.42	
52	Cg0545	1	962.5338	5.8	242	249	0	38.2	34	T	YLGGWRVI	R	0.6	9.84	
52	Cg0545	1	1041.5607	-1.1	115	125	0	83.9	35	S	SHALFGGLIGA	A	1.2	7.84	
52	Cg0545	1	1426.6881	6.8	217	229	0	64.9	36	T	GHLGTDADIPFWV	K	0.2	3.88	
52	Cg0545	1	1671.8064	-0.2	411	425	0	83.4	36	A	AQAVQDLNNENEVTK	-	-1.1	3.82	
53	Cg3079	1	1317.6929	-4.0	753	763	0	41.8	37	V	IFDRLSPEQLT	S	-0.3	4.08	
53	Cg3079	1	1407.7762	-0.9	686	697	0	67.0	34	A	HPDVFDILLQVL	D	1.0	3.88	
53	Cg3079	1	1640.9461	-17.1	764	777	0	42.9	35	T	SIVDIQIKQLTDRL	A	0.1	6.9	
53	Cg3079	1	1708.8672	10.9	686	700	0	90.1	36	A	HPDVFDILLQVLDEG	R	0.3	3.5	
53	Cg3079	1	2079.1001	0.6	686	703	0	82.1	37	A	HPDVFDILLQVLDEGRLT	D	0.2	3.96	
53	Cg3079	1	2792.4457	-0.1	686	710	0	50.6	38	A	HPDVFDILLQVLDEGRLTDGQGRTV	D	-0.2	4.12	
54	Cg1880	1	1270.671	4.5	565	575	0	47.5	36	A	LFGSIERFFGV	L	1.0	6.98	
54	Cg1880	1	1496.8391	0.6	565	577	0	46.5	34	A	LFGSIERFFGVLL	E	1.5	6.98	
54	Cg1880	1	1517.7038	1.6	459	470	0	47.8	35	L	RDYGLDDFYLEL	S	-0.6	3.5	
54	Cg1880	1	1632.7995	-2.9	479	492	0	48.5	37	S	VGSDEIWERSTEIL	N	-0.4	3.68	
54	Cg1880	1	1743.8719	-0.2	457	470	0	63.3	37	S	LLRDYGLDDFYLEL	S	0.0	3.5	
54	Cg1880	1	1830.904	1.0	457	471	0	56.7	37	S	LLRDYGLDDFYLELS	T	0.0	3.5	
54	Cg1880	1	1915.8774	-3.5	535	549	0	43.5	34	V	QLDFNMPERFNLEYT	S	-0.9	3.82	
55	Cg0647	1	1196.5826	1.9	150	159	0	39.6	35	L	SADRNFFDLI	V	0.0	3.88	
55	Cg0647	1	1309.6666	0.8	149	159	0	43.5	35	V	LSADRNFFDLI	V	0.3	3.88	
55	Cg0647	1	1314.6469	2.1	299	308	0	48.7	36	S	DNWWQRNIIA	H	-1.0	6.78	
55	Cg0647	1	1330.6418	6.8	298	307	0	49.5	36	V	SDNWWQRNII	A	-1.2	6.78	
55	Cg0647	1	1401.6789	0.0	298	308	0	65.0	36	V	SDNWWQRNIIA	H	-0.9	6.78	
55	Cg0647	1	1762.9188	-2.9	345	360	0	116.8	37	A	ENMKKYGGFIPGIRPG	R	-0.7	10.18	
56	Cg2291	1	1461.7939	-8.1	171	182	0	36.5	36	A	LSEKDIRDLRFA	L	-0.6	7.06	
56	Cg2291	1	1475.7369	0.9	333	345	0	43.4	37	V	RFAETDGRVPDLT	H	-0.8	4.3	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
56	Cg2291	1	1620.8723	1.3	244	258	0	117.4	35	A	RGDLGVEVPLEEVPL	V	0.1	3.68	
56	Cg2291	1	2108.9089	-8.1	37	53	0	66.0	29	L	NFSHGDHPDHEQNYKWV	R	-1.9	5.74	
56	Cg2291	1	2557.4592	-3.6	244	266	0	45.3	34	A	RGDLGVEVPLEEVPLVQKRAIQI	A	0.0	4.64	
56	Cg2291	1	2628.4963	-3.0	244	267	0	75.4	34	A	RGDLGVEVPLEEVPLVQKRAIQIA	R	0.1	4.64	
57	Cg2840	1	896.4504	7.3	456	462	0	35.8	34	A	HPDYRPL	L	-1.7	7.76	
57	Cg2840	1	975.4814	5.4	488	495	0	52.4	36	A	FDFHINLA	K	0.7	4.94	
57	Cg2840	1	979.6178	1.1	336	343	0	45.4	24	S	IILRPQQI	S	0.5	11.04	
57	Cg2840	1	1147.5662	2.5	486	495	0	71.5	36	A	TAFDFHINLA	K	0.7	4.94	
57	Cg2840	1	1351.7684	-0.7	438	449	0	42.0	33	A	DLRGLAPRERVA	K	-0.6	10.8	
57	Cg2840	1	1664.7834	-4.1	456	468	0	49.8	35	A	HPDYRPLLEEYYA	R	-1.2	4.42	
58	Cg1169	1	1059.4873	-2.5	507	517	0	36.2	34	T	LVDGPPGSDFG	V	-0.1	2.92	
58	Cg1169	1	1320.6979	4.7	37	47	0	44.7	35	V	GLGNIWRFPYV	A	0.2	9.84	
58	Cg1169	1	1391.735	3.0	37	48	0	47.0	36	V	GLGNIWRFPYVA	Y	0.4	9.84	
58	Cg1169	1	1817.8948	-3.7	509	525	0	60.2	37	V	DGPPGSDFGVLPEFKRT	L	-0.8	4.3	
58	Cg1169	1	2030.0473	-12.4	507	525	0	94.9	37	T	LVDGPPGSDFGVLPEFKRT	L	-0.3	4.3	
58	Cg1169	1	2249.0237	-2.2	534	554	0	66.2	34	A	SNDPISPFDANEDASRFPTVA	I	-0.7	3.5	
59	Cg2845	1	927.4338	-8.6	302	310	0	43.4	33	S	LFDGGTTFA	T	0.6	3.1	
59	Cg2845	1	1120.5706	7.6	169	177	0	40.3	35	V	YGLWGWQVL	G	0.5	5.92	
59	Cg2845	1	1190.5316	1.3	317	327	0	58.4	34	A	APEFNDNTRAG	A	-1.3	4.08	
59	Cg2845	1	1318.6737	-0.6	275	287	0	43.3	37	A	MLGLGRALGETMA	L	0.7	6.98	
59	Cg2845	1	1375.6116	3.1	315	327	0	43.8	34	A	NAAPEFNDNTRAG	A	-1.3	4.08	
60	Cg2949	1	1885.9017	0.4	166	184	0	69.3	36	V	SAPVLESGVENREVGGDTA	E	-0.4	3.68	
60	Cg2949	1	2085.9814	1.0	166	186	0	67.1	36	V	SAPVLESGVENREVGGDTAEA	S	-0.4	3.58	
60	Cg2949	1	2272.0819	0.2	162	184	0	100.5	36	I	DATVSAPVLESGVENREVGGDTA	E	-0.2	3.5	
60	Cg2949	1	2383.0915	-0.5	84	105	0	78.6	35	T	SHTLESVTVDGEEVELDDAEPI	E	-0.4	3.28	
60	Cg2949	1	2472.1616	1.1	162	186	0	105.9	36	I	DATVSAPVLESGVENREVGGDTAEA	S	-0.3	3.44	
61	Cg1586	1	1623.8104	-2.8	283	296	0	40.9	36	A	HEALEDVTIERELA	R	-0.4	4	
61	Cg1586	1	1633.7988	-2.1	188	201	0	66.1	37	T	GYLEDLWNAPTKDI	Y	-0.6	3.7	
61	Cg1586	1	1910.0333	-1.0	235	252	0	88.6	36	V	SVLQAIEELNRRAGAQGV	G	-0.1	7.12	
61	Cg1586	1	1946.985	-1.4	171	187	0	41.4	37	V	KSPFSIDQNVWGRAIET	G	-0.6	7.02	
61	Cg1586	1	2544.1696	6.8	188	209	0	65.7	36	T	GYLEDLWNAPTKDIYAYTEDPA	L	-0.8	3.42	
62	Cg3365	1	1016.6383	8.9	288	296	0	33.3	25	A	VILFGVRTI	L	2.0	11.04	
62	Cg3365	1	1423.8228	-2.9	361	373	0	59.8	32	V	ALILPGLVPHFFT	G	1.5	7.84	
62	Cg3365	1	1446.7871	2.5	497	511	0	76.0	35	T	YPKIAPPAGAPTPPA	R	-0.3	9.72	
62	Cg3365	1	1696.0287	-0.9	288	303	0	33.0	29	A	VILFGVRTILGELVPA	F	1.7	6.98	
62	Cg3365	1	1836.0298	-6.4	361	379	0	56.3	34	V	ALILPGLVPHFFTGGAAGV	Y	1.4	7.84	
62	Cg3365	1	1903.0316	-3.0	492	511	0	39.6	36	T	AGARTYPKIAPPAGAPTPPA	R	-0.3	10.4	
63	Cg2120	1	984.5393	4.8	599	607	0	51.8	35	A	ADPFRVIPA	M	0.4	6.78	
63	Cg2120	1	1147.5008	-2.4	331	341	0	72.4	32	A	LGFAFGGYDMA	N	0.8	3.1	
63	Cg2120	1	1551.7417	6.1	11	24	0	64.5	36	V	RLDVDFGDSTTDVI	N	-0.1	3.42	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
64	Cg1579	1	1402.7092	-8.1	99	112	0	97.5	37	V	QEAPAPVEQAPAPV	Q	-0.3	3.12	
64	Cg1579	1	1463.6794	-2.5	118	134	0	113.9	35	A	ADAPPALPGGGGGHAGY	-	-0.2	4.94	
64	Cg1579	1	1959.9075	-2.0	113	134	0	119.9	35	V	QEAPAADAPPALPGGGGGHAGY	-	-0.4	4.06	
64	Cg1579	1	2254.1481	10.6	77	98	0	91.8	37	V	EAPVEQAPVVEQAPVEQAPAPV	Q	-0.1	2.96	
65	Cg1556	1	1164.6767	-1.7	40	48	0	39.5	30	I	RYVLPRKYA	K	-0.8	10.56	
65	Cg1556	1	1443.747	1.1	132	144	0	45.5	37	V	DTEGKPGVKWRAT	N	-1.4	9.88	
65	Cg1556	1	1629.8475	-3.8	130	144	0	81.4	37	T	SVDTEGKPGVKWRAT	N	-1.0	9.88	
65	Cg1556	1	1776.7479	1.6	172	186	0	74.8	30	A	SDWFNDTSDKVTEYA	Y	-1.2	3.5	
65	Cg1556	1	2014.9272	1.0	187	203	0	106.8	35	A	YTAQDFVGENKDDWIKS	A	-1.2	3.96	
66	Cg2137	1	1424.6895	2.9	114	127	0	36.7	35	I	AATYSINAGRSESV	N	-0.2	6.88	
66	Cg2137	1	1489.6838	-3.6	213	224	0	55.4	34	G	YSQQYEGDFRVV	E	-0.9	4.08	
66	Cg2137	1	1641.8879	-0.2	128	142	0	36.7	36	V	NFGGPYLLTHQALLV	R	0.6	7.76	
66	Cg2137	1	1921.7928	3.1	225	240	0	90.8	28	V	EMEKDGEPFTDEYYGI	G	-1.3	3.44	
67	Cg2410	1	1464.7435	-0.4	481	492	0	40.7	36	L	DLFTWMRGDILV	K	0.6	3.88	
67	Cg2410	1	2013.9697	-0.7	561	577	0	63.4	36	M	RHWLAGDELFGWAQDTI	K	-0.4	4.3	
67	Cg2410	1	2032.1357	-6.7	501	517	0	36.1	35	A	NSLELRVPFLDKEVFKV	A	0.1	7.1	
67	Cg2410	1	2348.2562	-7.0	498	517	0	41.4	37	I	NMANSLELRVPFLDKEVFKV	A	0.1	7.1	
68	Cg2195	1	1643.6812	-0.5	65	78	0	81.5	29	I	FGEEHERDNENTPA	W	-2.2	4	
68	Cg2195	1	2000.8348	-3.0	62	78	0	75.0	28	G	EDIFGEEHERDNENTPA	W	-1.9	3.74	
68	Cg2195	1	2158.9039	1.0	60	78	0	107.4	29	V	TGEDIFGEEHERDNENTPA	W	-1.8	3.74	
68	Cg2195	1	3271.345	4.4	50	78	0	152.6	26	V	GEDWDADQPVTGEDIFGEEHERDNENTPA	W	-1.7	3.42	
69	Cg0577	1	1827.0506	-1.1	113	128	0	64.9	33	S	RLGYLLDLAPKDLDLI	I	0.4	4.18	
69	Cg0577	1	2383.1921	-6.1	1030	1052	0	42.0	38	T	FHQGGVGGDITGGLPRVQELFEA	R	-0.1	4.42	
70	Cg0935	1	1104.5716	0.4	63	71	0	52.4	36	T	GYVHPYTRI	N	-0.5	9.58	
70	Cg0935	1	1362.6092	-2.6	46	57	0	71.0	33	A	SSPWGDDKEFPV	S	-1.1	3.7	
70	Cg0935	1	1561.7049	-6.7	43	57	0	76.7	33	V	AGASSPWGDDKEFPV	S	-0.7	3.7	
70	Cg0935	1	1879.8112	0.6	46	62	0	105.7	31	A	SSPWGDDKEFPVSAEET	G	-1.2	3.5	
70	Cg0935	1	2078.9069	2.2	43	62	0	77.3	32	V	AGASSPWGDDKEFPVSAEET	G	-0.9	3.5	
71	Cg1280	1	1966.9577	1.5	1203	1218	0	80.0	37	A	NQGPWPFYQEHLPELI	P	-0.8	4.24	
71	Cg1280	1	1972.8877	7.0	369	384	0	39.0	34	S	RLLTDDSFWDEIFDAM	N	-0.2	3.36	
72	Cg0703	1	1660.8824	-4.6	482	494	0	81.2	36	A	DWTRLPYEVLEKI	S	-0.5	4.44	
72	Cg0703	1	2302.2685	-4.0	366	384	0	50.8	36	V	EFKLVEPLRDLFKDEVRAV	G	-0.2	4.72	
72	Cg0703	1	2387.2961	-2.8	385	407	0	65.8	36	V	GRELGLPEEIVGRQPFPGPGLGI	R	-0.2	4.56	
73	Cg2558	1	1392.631	-1.5	210	221	0	37.5	34	V	ADIGEGEWRDFV	C	-0.6	3.58	
73	Cg2558	1	1425.7656	5.3	51	64	0	79.4	35	I	IAPWFGGLLGLDPA	H	1.0	3.1	
73	Cg2558	1	1594.7264	-6.5	157	170	0	47.3	34	T	QDGPVTFDGEFDRI	A	-0.8	3.5	
73	Cg2558	1	1635.8297	-3.8	124	136	0	68.5	37	A	FHPYFKVDDVEKI	E	-0.5	5.28	
73	Cg2558	1	1831.8701	-4.3	148	163	0	58.0	36	L	NRLNNEVETQDGPVTF	D	-1.1	3.82	
73	Cg2558	1	2722.2987	0.8	72	95	0	60.3	37	S	AWDVTEHDGQIHAEYGRDGLLLDI	R	-0.5	3.98	
74	Cg2799	1	968.4868	-5.2	147	153	0	37.0	34	T	LYWNFRA	F	-0.3	9.84	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
74	Cg2799	1	1069.5345	0.4	146	153	0	40.7	35	A	TLYWNFRA	F	-0.3	9.84	
74	Cg2799	1	1571.7005	-6.0	141	153	0	55.2	32	A	DSNDATLYWNFRA	F	-0.9	3.88	
74	Cg2799	1	1741.806	-1.1	139	153	0	71.2	35	A	VADSNDATLYWNFRA	F	-0.4	3.88	
75	Cg2704	1	782.4075	17.4	100	105	0	37.5	32	T	NFFRTV	F	0.2	11.04	
75	Cg2704	1	1211.6233	4.5	184	192	0	42.3	35	V	NKWEMLRHV	T	-1.1	10.08	
75	Cg2704	1	1295.651	-2.4	211	221	0	76.8	35	S	NSFKLFDQNLA	L	-0.3	6.76	
75	Cg2704	1	1392.682	1.1	240	251	0	46.5	36	I	NTLFNRMNVEGV	G	-0.2	6.98	
76	Cg1363	1	1231.5689	2.4	42	52	0	62.4	35	A	LEGMARQPEMA	G	-0.5	4.26	
76	Cg1363	1	1364.8391	-5.3	27	41	0	41.1	28	A	TIGPGLGIGILVGKA	L	1.3	10.1	
76	Cg1363	1	1869.9804	1.2	35	52	0	65.6	37	I	GILVGKALEGMARQPEMA	G	0.2	7.1	
76	Cg1363	1	2578.3975	-7.3	27	52	0	124.2	37	A	TIGPGLGIGILVGKALEGMARQPEMA	G	0.5	7.1	
76	Cg1363	1	2649.4346	-11.3	26	52	0	97.0	37	I	ATIGPGLGIGILVGKALEGMARQPEMA	G	0.6	7.1	
77	Cg2900	1	1942.0047	-5.4	304	320	0	106.9	37	A	PYLLSPENLDDLIARDV	-	-0.1	3.5	
77	Cg2900	1	2453.3053	-3.9	299	320	0	48.6	37	T	VLEVAPYLLSPENLDDLIARDV	-	0.4	3.42	
77	Cg2900	1	2701.4214	4.9	297	320	0	50.8	37	A	FTVLEVAPYLLSPENLDDLIARDV	-	0.5	3.42	
78	Cg2192	1	1368.6867	1.2	321	332	0	37.2	36	L	FGPYGGWTPKFL	K	-0.2	9.72	
78	Cg2192	1	1594.8548	-2.6	319	332	0	102.3	36	G	LLFGPYGGWTPKFL	K	0.4	9.72	
78	Cg2192	1	1863.973	-1.9	336	351	0	66.6	37	G	SYLDLFKSIRPDNIPS	Y	-0.4	6.82	
78	Cg2192	1	2095.0779	-2.3	314	332	0	39.5	37	I	EGEKGLLFGPYGGWTPKFL	K	-0.3	7	
79	Cg2695	1	1298.7055	-3.3	443	454	0	47.2	36	V	LSGGERNRLNLA	L	-0.7	10.88	
79	Cg2695	1	1610.8304	-5.8	305	318	0	63.5	36	L	DFEEIQIPTPPRLG	N	-0.6	3.82	
79	Cg2695	1	1841.0775	-4.0	336	352	0	61.8	32	V	LIKDLSFTLPRNGIVGV	I	0.7	10.08	
79	Cg2695	1	1902.9799	-0.6	86	101	0	65.8	37	V	RQNVEEGLGEIFEKKQ	R	-1.4	4.72	
80	Cg3149	1	1292.5476	3.9	401	410	0	49.3	32	T	GFNWPHHDHF	R	-1.4	6.3	
80	Cg3149	1	1680.8763	-25.5	365	378	0	47.8	36	A	LYAFPKLDPNVYEI	H	0.1	4.08	
80	Cg3149	1	1889.8949	-1.9	116	131	0	43.1	36	T	RYEVVPGFPHFDVDDV	F	-0.3	3.96	
80	Cg3149	1	2477.2016	-2.5	116	137	0	61.3	37	T	RYEVVPGFPHFDVDDVFLGNGV	S	0.1	3.96	
81	Cg0834	1	1110.571	2.3	326	334	0	35.4	35	A	TARDFIEFI	I	0.5	4.08	
81	Cg0834	1	1850.8758	1.1	308	325	0	109.1	36	V	STLGGYNNGINVNSENKA	T	-0.9	6.86	
81	Cg0834	1	1881.9948	-4.9	159	175	0	80.3	37	T	NGQLLFRNTEIIPEAPA	N	-0.2	4.26	
81	Cg0834	1	1938.9323	-6.4	326	341	0	50.4	36	A	TARDFIEFIINEENQT	W	-0.6	3.68	
82	Cg1451	1	1406.7405	1.1	373	385	0	66.0	36	V	RGLFSGIIEESVT	F	0.4	4.26	
82	Cg1451	1	1639.9118	-13.4	443	457	0	42.3	36	I	TRINGRGLDLRAEGL	N	-0.5	10.8	
83	Cg2963	1	1075.5815	-12.6	612	621	0	41.5	36	S	RLFGAPPGYV	G	0.3	9.84	
83	Cg2963	1	1361.7303	-9.2	187	198	0	41.1	36	T	SLVLDQFGRNLT	Q	0.1	6.78	
83	Cg2963	1	1669.8271	-4.8	60	74	0	36.5	36	V	RQEVEEIIGQGSQPT	T	-1.1	3.96	
83	Cg2963	1	2626.3966	-4.9	365	387	0	67.7	38	V	QVPEPSVDLTVEILKGLRDRYEA	H	-0.4	4.28	
84	Cg0414	1	1405.7201	-3.3	131	143	0	56.0	37	A	NAVGESFKNVIQT	E	-0.2	6.94	
84	Cg0414	1	1632.9086	-9.1	221	235	0	53.4	35	G	GIIADSEVEKHPLII	K	0.5	4.42	
84	Cg0414	1	1684.7369	10.3	441	456	0	72.3	33	V	AGYGYGNYGYGDTSKI	N	-0.8	6.54	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
85	Cg1203	1	1464.8313	-8.1	164	176	0	34.6	34	I	HYGLIPRANRGIV	A	0.0	11.14	
85	Cg1203	1	1708.758	-7.8	342	355	0	44.5	32	I	EFESGEEGREWEIL	D	-1.2	3.58	
85	Cg1203	1	2063.98	-0.8	338	355	0	37.3	36	L	GGKIEFESGEEGREWEIL	D	-1.0	3.96	
85	Cg1203	1	2896.4243	0.6	338	362	0	62.8	38	L	GGKIEFESGEEGREWEILDYLLRTA	T	-0.7	4.08	
86	Cg1813	1	1501.7412	-5.3	486	498	0	75.9	36	V	DAPFLNEDLLREA	K	-0.4	3.58	
86	Cg1813	1	1699.7995	1.4	413	426	0	37.2	35	G	FWTKPDEFFAGERA	T	-0.8	4.44	
86	Cg1813	1	1756.8209	-11.7	412	426	0	39.8	34	Q	GFWTKPDEFFAGERA	T	-0.7	4.44	
88	Cg1603	1	2013.0643	-5.2	245	264	0	38.9	37	S	GANVILPADPDGHAVGLERI	Q	0.2	4.3	
88	Cg1603	1	2286.0764	-1.3	298	319	0	59.5	36	I	VNVGGPVTLDGVFENREDSDPA	A	-0.4	3.42	
89	Cg2157	1	1336.7391	-0.3	249	259	0	44.4	34	M	YFLLDGLLDRL	V	0.8	3.88	
89	Cg2157	1	1665.8111	-0.1	282	296	0	117.4	36	A	LHENNLPFINGGENV	S	-0.5	4.24	
89	Cg2157	1	1685.7533	1.4	153	166	0	55.7	33	L	LWDEVRDTPETDPN	D	-1.6	3.42	
89	Cg2157	1	2305.0573	-3.9	153	171	0	53.8	34	L	LWDEVRDTPETDPNDMFII	K	-0.7	3.32	
90	Cg2984	1	2155.977	3.3	731	751	0	74.7	35	A	QAPEQSPDSSGGRPNPYATPT	A	-1.5	4.08	
91	Cg0896	1	1018.5733	7.8	295	304	0	37.1	33	L	MLLSSVIIGA	A	2.3	6.02	Oxidation (M)
91	Cg0896	1	1312.6452	4.3	231	240	0	36.8	36	A	GYWLDRYDLL	T	-0.4	3.88	
91	Cg0896	1	1415.7561	2.8	703	713	0	52.5	36	A	HLRYPEDLFKV	Q	-0.6	7.74	
92	Cg1362	1	1354.7285	6.3	232	242	0	64.4	35	I	EFFSTFILRPV	T	0.9	6.98	
92	Cg1362	1	1647.7569	2.2	56	69	0	93.6	35	G	EFHAPDLDKEFFPG	H	-0.8	4.06	
92	Cg1362	1	1963.9138	-1.4	53	69	0	63.8	35	S	MKGEFHAPDLDKEFFPG	H	-0.8	4.54	
92	Cg1362	1	2887.3487	4.8	53	78	0	53.6	36	S	MKGEFHAPDLDKEFFPGHVTDSGEVV	N	-0.5	4.36	
94	Cg3008	1	802.3902	-3.4	22	27	0	43.6	36	G	YVFDFL	G	1.5	3.1	
94	Cg3008	1	859.4116	-5.4	21	27	0	51.5	35	I	GYVFDFL	G	1.2	3.1	
94	Cg3008	1	1142.6012	20.6	18	27	0	50.9	36	S	GLIGYVFDFL	G	1.6	3.1	
94	Cg3008	1	1373.6867	3.7	15	27	0	93.9	37	L	SGSGLIGYVFDFL	G	1.1	3.1	
94	Cg3008	1	1501.7453	14.7	15	29	0	75.1	37	L	SGSGLIGYVFDFLGA	S	1.0	3.1	
95	Cg1525	1	1941.9758	-5.0	244	260	0	49.1	37	V	KDLELPLGPDDFEMKPV	Q	-0.6	3.84	
95	Cg1525	1	2127.1827	0.2	77	95	0	55.8	35	A	TPPEFKGQVEILKEVLSTL	G	0.0	4.56	
95	Cg1525	1	2360.1913	-2.9	742	760	0	55.6	38	S	YFERFGGVQRYLREIVEEA	R	-0.5	4.72	
96	Cg0610	1	1241.7357	0.4	113	122	0	33.7	32	A	LPRIRDFRGL	S	-0.4	12.1	
96	Cg0610	1	1338.6456	-4.6	20	30	0	38.5	35	T	KLQGEFEFENV	M	-0.7	3.96	
96	Cg0610	1	1387.7646	-11.2	79	90	0	46.8	36	S	IANFKLREGMPI	G	0.2	10.08	
98	Cg2466	1	946.4297	-2.3	160	168	0	35.5	34	I	FFQGHASPG	M	-0.3	7.84	
98	Cg2466	1	1325.6405	3.5	552	562	0	49.1	35	A	RTFGLDSWFPT	L	-0.3	6.78	
98	Cg2466	1	1871.0516	-5.2	437	452	0	43.6	35	L	TLDDLKLFRDKQGIPI	T	-0.4	6.96	
98	Cg2466	1	2090.9579	-6.1	251	269	0	42.3	34	A	FLGDGEMDEPESRGLIQQA	A	-0.7	3.5	
99	Cg1121	1	1853.8081	-4.3	29	45	0	31.6	31	T	QRPQGQNPYGGYDNFGG	V	-1.8	6.64	
99	Cg1121	1	1952.8766	-0.1	29	46	0	58.6	34	T	QRPQGQNPYGGYDNFGGV	Y	-1.5	6.64	
99	Cg1121	1	2372.057	-1.2	29	49	0	74.5	33	T	QRPQGQNPYGGYDNFGGVYQQ	N	-1.6	6.58	
99	Cg1121	1	2486.1	-5.5	29	50	0	51.3	32	T	QRPQGQNPYGGYDNFGGVYQQN	V	-1.7	6.58	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
99	Cg1121	1	2881.3168	4.0	29	54	0	52.0	35	T	QRPQGQNPYGGYDNFGGVYQQNVAPQ	K	-1.4	6.58	
100	Cg0238	1	1865.0564	-4.1	125	141	0	69.2	34	A	ALPYGLWVPVLPGTRQV	T	0.5	9.84	
100	Cg0238	1	1904.9666	-5.7	369	384	0	44.8	37	T	EAVEPFKDIIRDMQKS	G	-0.8	4.56	
100	Cg0238	1	2257.1565	-4.5	426	444	0	41.7	38	A	FLDDLDKRVMEFGGRLYLA	K	0.0	4.46	
102	Cg2166	1	1752.9887	-3.3	673	688	0	41.0	34	A	NPQLPKVGERFLGTVV	K	0.0	10.08	
102	Cg2166	1	1812.824	-1.5	537	553	0	38.0	34	T	DILGAEDAFGDMDFKVA	G	0.2	3.36	
102	Cg2166	1	2122.1899	-5.3	669	688	0	47.5	35	I	NALANPQLPKVGERFLGTVV	K	0.2	10.08	
103	Cg1314	1	1657.6969	-2.1	220	235	0	113.3	29	A	NSNDYGPHTDGIGNPT	Y	-1.5	3.88	
104	Cg3219	1	1441.7089	-3.1	174	186	0	56.8	36	A	YIIGEHGDTELPV	L	-0.1	3.82	
104	Cg3219	1	1829.9134	-1.1	155	169	0	44.6	37	A	RFRYMLGELYEVAPS	S	-0.2	6.98	
104	Cg3219	1	1875.889	2.2	260	276	0	97.9	36	A	LLHGEYGEEDIYIGTPA	V	-0.3	3.68	
104	Cg3219	1	1941.0353	0.3	199	214	0	57.9	37	S	RMLDKDPELEGRLEKI	F	-1.2	4.72	
105	Cg2496	1	2103.8897	3.5	655	682	0	99.6	30	G	GFGGGGGFGGGGGGFSGGGGGGGGFRGG	R	-0.1	11.04	
105	Cg2496	1	2618.2249	-7.5	121	144	0	64.8	35	A	LAPEERQYGIQGGTQWTDAELDAA	N	-0.8	3.5	
107	Cg0656	1	1793.91	-6.0	78	92	0	93.7	37	A	YLFNELAPKFENRPG	G	-0.8	7.02	
108	Cg1463	1	1713.7482	4.6	132	145	0	43.0	33	G	YDNFDRDLTEEQVA	A	-1.3	3.42	
108	Cg1463	1	2561.3489	-3.3	89	110	0	94.1	38	S	QRKDIYQDVLKQLIDAGEVYPA	Y	-0.6	4.46	
109	Cg0835	1	1409.6688	-11.5	321	332	0	39.6	35	A	HHFDLESGERIA	-	-0.8	5.18	
110	Cg2492	1	1616.8443	-3.6	444	457	0	47.8	37	V	SSILDSLREMPEKI	Q	-0.3	4.44	
110	Cg2492	1	1898.9486	-4.2	108	124	0	46.3	37	V	HNGIIENFAELRSELSA	K	-0.2	4.54	
113	Cg3195	1	1682.794	1.8	35	47	0	51.3	36	V	QLFEDEGYWRDLL	A	-0.8	3.58	
113	Cg3195	1	2080.9836	1.1	221	236	0	47.0	36	V	WYDHLPYIPFPDHWPV	F	-0.6	4.94	
113	Cg3195	1	2490.2543	-5.5	436	457	0	57.2	38	A	GFLLDFGDDDSGLFLKYLRRGS	G	-0.2	4.34	
114	Cg0047	1	1525.8001	0.5	124	135	0	62.2	36	A	TEKKESHWVRNL	S	-1.7	9.88	
114	Cg0047	1	2258.0927	-2.4	54	73	0	86.2	37	T	ARESAKEFYTESRDKAGNVT	K	-1.3	7.1	
115	Cg0303	1	1514.7001	-6.7	545	557	0	62.7	34	L	GIDVEIQEYNQHA	R	-0.8	3.82	
115	Cg0303	1	1771.8489	0.3	545	559	0	37.8	36	L	GIDVEIQEYNQHART	S	-1.1	4.42	
116	Cg0654	1	1478.8609	-3.5	165	176	0	38.1	32	A	WLQVVPENLRIL	V	0.6	6.98	
116	Cg0654	1	2409.3645	-3.5	165	184	0	39.1	34	A	WLQVVPENLRILVHQLPERA	Q	0.0	7.86	
117	Cg2096	1	1430.5811	5.5	11	24	0	73.0	29	E	PNNNGGNSNDPFNA	N	-1.8	3.1	
117	Cg2096	1	1765.8271	1.9	56	72	0	53.4	36	S	GYTGGFENSPLNAPKNT	A	-1.0	6.86	
117	Cg2096	1	2313.9774	9.6	25	47	0	108.6	31	A	NQGEPYGAPYGESFGPSSGAQQS	G	-1.2	3.12	
117	Cg2096	1	2633.167	8.1	48	72	0	39.2	34	S	GYQDPYGSGYTGGFENSPLNAPKNT	A	-1.2	4.08	
118	Cg1643	1	1321.6779	-5.1	456	467	0	39.1	36	A	ALIQGQRDFFGA	H	0.1	6.78	
118	Cg1643	1	1701.7231	17.0	360	374	0	43.6	33	A	GSDENNWDVDPRDLA	T	-1.5	3.36	
118	Cg1643	1	1770.9628	-9.0	413	427	0	37.9	37	S	ELGDLIDSWRRVIVT	A	0.2	4.3	
119	Cg0235	1	1702.8467	2.0	404	417	0	52.8	37	A	FWLPYNNGTRPEPI	I	-0.9	6.88	
120	Cg2703	1	970.531	-4.4	213	220	0	49.1	35	V	VWPMLKPT	A	0.2	10.1	
120	Cg2703	1	1526.6606	0.1	259	273	0	48.9	32	S	FVGSNGNRDTGAMMA	M	-0.2	6.78	
120	Cg2703	1	1539.6736	2.2	257	271	0	39.8	33	I	QSFVGSNGNRDTGAM	M	-0.8	6.78	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
120	Cg2703	1	1595.8096	-0.1	285	297	0	53.6	36	I	FYFSTQRHIIEGV	A	0.1	7.76	
120	Cg2703	1	1741.7512	0.5	257	273	0	42.9	32	I	QSFVGSNGNRDTGAMMA	M	-0.4	6.78	
121	Cg3100	1	1774.7758	0.7	194	209	0	95.7	32	T	SGDNELGGDDWDQRIV	D	-1.2	3.36	
121	Cg3100	1	2461.3693	-5.3	425	448	0	56.1	35	A	NKLLGSFELGGIAPAPRGVPQIEV	T	0.2	7.1	
122	Cg2333	1	2193.0127	-16.1	73	91	0	82.7	33	V	SDDSYLWGDQQWTGRILPG	S	-1.0	3.6	
122	Cg2333	1	2657.3225	-4.6	101	124	0	65.0	38	G	TFSEDGTFEGVVDKLPYLRDLGVT	A	-0.1	3.84	
123	Cg3154	1	2220.2154	-4.9	99	117	0	52.3	36	T	YVRQVVEDLVPLLEGEHII	F	0.5	4.16	
123	Cg3154	1	3035.6696	-3.6	99	125	0	61.9	36	T	YVRQVVEDLVPLLEGEHIIFGKSTVPV	G	0.5	4.62	
124	Cg1238	1	1112.5655	1.6	255	263	0	52.5	35	L	GWELPYHLV	H	0.1	5.12	
124	Cg1238	1	1283.7172	-0.2	59	68	0	38.4	35	A	RELPMIWRIA	K	0.2	10.88	
124	Cg1238	1	1641.8039	-2.9	250	263	0	104.6	36	V	GTEELGWELPYHLV	H	-0.2	3.96	
125	Cg0161	1	1925.9595	-6.0	214	230	0	57.2	37	T	GTDAPPTRPQDFERQIV	L	-1.2	4.3	
127	Cg2406	1	913.4803	2.4	18	25	0	46.0	35	A	ALNRPNMV	S	-0.2	11.04	
127	Cg2406	1	984.5175	3.7	17	25	0	44.6	35	V	AALNRPNMV	S	0.0	11.04	
127	Cg2406	1	1394.7711	2.8	97	107	0	49.6	34	G	DVYGLRKWFLV	T	0.4	9.72	
134	Cg1725	1	1836.8928	-1.7	140	155	0	65.2	37	I	DSILDMRQLFDGIDLS	S	0.1	3.42	
134	Cg1725	1	2021.0139	-3.7	138	155	0	44.0	37	V	AIDSILDMRQLFDGIDLS	S	0.4	3.42	
137	Cg2678	1	1199.5975	-12.8	54	62	0	52.5	35	T	YLEPQFFRT	L	-0.6	6.88	
137	Cg2678	1	1956.9693	-7.6	305	320	0	37.3	37	V	NNSFNFRFKNELLSDI	R	-0.7	7.02	
138	Cg1364	1	1434.7355	0.1	171	183	0	77.1	36	S	GTIDRFLADLDTV	A	0.3	3.6	
138	Cg1364	1	1901.9847	-5.3	171	188	0	79.0	37	S	GTIDRFLADLDTVAPNGK	-	-0.2	4.18	
143	Cg2586	1	1583.8784	-10.0	419	432	0	60.8	36	T	STKWILQGTGQIRP	-	-0.6	11.48	
144	Cg2292	1	2279.1393	-2.1	294	316	0	101.7	37	V	ASPDGKPLPKAGEGIDGETPSTR	-	-1.1	4.56	
148	Cg3182	1	1544.7623	4.8	132	144	0	38.4	37	Y	SSPNREFPEIWAL	D	-0.6	4.26	
149	Cg2811	1	1527.7205	1.1	200	213	0	38.6	35	A	GYLERYTDGATVPS	V	-0.6	4.08	
150	Cg0658	1	1396.8078	-0.6	110	121	0	38.2	33	G	AWLIIDRAVDLL	L	1.3	3.88	
151	Cg0472	1	1701.9301	-4.1	137	151	0	78.8	36	T	SQGFAEQLIQELIKV	T	0.2	4.26	
151	Cg0472	1	1802.9778	-3.4	137	152	0	67.9	36	T	SQGFAEQLIQELIKVT	D	0.1	4.26	
151	Cg0472	1	2219.1434	-3.6	132	152	0	43.2	37	T	GGNSTSQGFAEQLIQELIKVT	D	-0.2	4.26	
153	Cg0683	1	1140.5564	-4.4	508	517	0	35.6	35	A	NRGYATVYPT	A	-0.8	9.58	
153	Cg0683	1	1193.6153	-1.0	342	351	0	47.4	35	V	RRFLGDSEKS	L	-1.5	10.08	
155	Cg2571	1	1610.8953	-1.4	182	196	0	59.2	35	T	GMGVPELLDKVVELI	P	0.9	3.82	
155	Cg2571	1	1977.0856	14.5	182	200	0	64.6	34	T	GMGVPELLDKVVELIPAPT	S	0.6	3.82	
156	Cg3237	1	1144.5045	4.0	158	166	0	44.2	33	V	LMLDMWEHA	F	0.2	4.06	
156	Cg3237	1	2291.0997	-1.0	2	21	0	98.0	37	M	AVYELPELDYAYDALEPHIA	A	0.0	3.5	
157	Cg0007	1	1249.6893	1.8	556	565	0	39.5	34	T	LLFRFMPDLV	A	1.4	6.78	
157	Cg0007	1	1350.737	-0.1	555	565	0	55.5	35	L	TLLFRFMPDLV	A	1.2	6.78	
157	Cg0007	1	1510.7092	-8.5	168	179	0	44.1	35	I	RFWPDAEIFETT	E	-0.6	3.82	
161	Cg1234	1	2001.1034	-7.3	711	728	0	49.3	36	T	LLDLFDQLVDDGKSVIVI	E	0.9	3.42	
164	Cg1133	1	1542.7678	-5.8	11	23	0	38.1	36	V	RYQPLNELDPEVA	A	-1.0	3.82	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
164	Cg1133	1	2022.9588	-1.2	181	197	0	68.4	36	A	GWSAYPRHLDFEAFQSI	A	-0.4	5.22	
165	Cg0062	1	1354.7245	-8.6	171	182	0	45.7	36	T	LEQFPALPGDRL	L	-0.2	4.08	
168	Cg2833	1	2084.1518	-1.2	227	244	0	60.9	35	A	NFIPEVLDRKVLDDVLTV	S	0.4	3.96	
173	Cg2262	1	2709.2756	7.5	126	149	0	108.4	37	A	TPEPETSDDVVEEPEVKEPEVKEV	V	-1.3	3.56	
175	Cg3018	1	1968.0833	-29.8	908	923	0	68.7	37	I	VFDSLLPPIEKQWRQI	T	-0.2	7.02	
176	Cg3191	1	2173.1783	-9.1	498	517	0	103.5	37	D	FLAGPDQLFSILDTSLPRIA	A	0.6	3.88	
181	Cg2925	1	878.4399	11.7	101	107	0	41.3	35	A	NWFSRAV	K	-0.1	11.04	
181	Cg2925	1	974.5008	2.4	285	292	0	36.6	36	A	MRWVGDVL	A	0.6	6.78	
182	Cg1082	1	1109.587	1.9	197	206	0	53.5	34	I	RFVFGDSIVA	D	1.1	6.78	
186	Cg3220	1	828.4705	-28.4	29	37	0	38.5	36	L	ASLGAQVIA	E	1.5	6.02	
189	Cg0336	1	2409.1673	-7.1	775	795	0	43.6	37	S	TNNRGTTIEDAINDAINQFFR	-	-0.8	4.3	
193	Cg0326	1	1231.7441	0.8	520	528	0	36.8	28	V	LFRKELWKI	A	-0.2	10.58	
193	Cg0326	1	1252.675	-0.4	551	561	0	34.4	34	A	NLLGKFFGRMA	D	0.4	11.48	
196	Cg1836	1	1684.8519	-9.3	68	82	0	49.5	37	S	SISELGPELEERDIV	A	-0.3	3.58	
196	Cg1836	1	1856.9367	-0.3	68	84	0	41.7	37	S	SISELGPELEERDIVAT	N	-0.2	3.58	
199	Cg1861	1	1466.7154	1.5	280	291	0	40.9	36	V	RGRDFDDIFDLV	G	-0.4	3.88	
200	Cg1841	1	2191.2041	-4.9	190	208	0	56.4	36	G	TFYALPQSPQLFKQLLQVA	G	0.2	9.72	
202	Cg0854	1	2062.1098	-9.1	159	175	0	48.9	37	A	YAEYLNELVDLKNIRPL	K	-0.3	4.44	
203	Cg0410	1	1860.0145	-4.2	286	301	0	61.4	36	V	LLLKEFLEGGRDFQPV	F	0.0	4.44	
204	Cg1195	1	1435.7249	-0.6	208	219	0	42.8	37	V	GFFHLDRFGLEV	I	0.4	5.22	
207	Cg2657	1	2145.0127	-0.1	165	185	0	122.2	36	V	ATDETPNYYPGGNVAGRPVPA	G	-0.8	4.08	
212	Cg1345	1	1765.81	-1.4	346	359	0	50.0	35	S	RAETPDDFWPFLWS	M	-0.7	3.7	
215	Cg0783	1	1848.941	-0.7	260	275	0	43.6	37	V	FLGKFGEIFTFNSQKS	L	-0.1	9.88	
218	Cg2470	1	1796.854	-3.2	308	323	0	51.7	36	I	NEDAAERQGVEIPQEI	L	-1.1	3.58	
218	Cg2470	1	2172.0698	-1.7	305	323	0	51.2	37	T	YVINEDAAERQGVEIPQEI	L	-0.5	3.58	
220	Cg2613	1	1701.9123	0.9	59	73	0	36.5	36	V	AMELLDSAFPLLRNI	T	0.7	4.08	
220	Cg2613	1	1774.8315	2.5	215	228	0	51.3	36	V	DHDWYVEEFIPRVA	N	-0.6	4.06	
220	Cg2613	1	2102.0109	-6.5	212	228	0	51.3	36	T	DLVDHDWYVEEFIPRVA	N	-0.2	3.84	
223	Cg1502	1	1419.7048	-6.7	97	107	0	47.5	37	V	FQNFNLFPHRT	V	-0.8	11.04	
224	Cg3161	1	791.4905	-1.0	336	342	0	26.7	23	S	HISLPLL	G	1.5	7.84	
227	Cg0602	1	1693.9515	-11.2	67	81	0	42.9	35	I	NIFPDRPLTQKPLGV	R	-0.4	10.08	
228	Cg3244	1	1133.7536	2.5	94	103	0	44.2	16	A	RVLTPLLLPI	I	1.6	11.04	
228	Cg3244	1	1845.9221	-2.4	159	174	0	77.9	37	A	GFVRDVEERLNELEAA	A	-0.5	4	
229	Cg0523	1	2292.0182	-5.4	266	284	0	50.1	32	A	VGDDIQNDPETWEDYELRV	N	-1.3	3.28	
232	Cg2437	1	1399.7136	3.3	324	334	0	57.7	36	A	SNFERFIFDLL	G	0.4	4.08	
232	Cg2437	1	1598.7213	3.0	287	299	0	48.0	34	A	TNENDVLDEFFRT	G	-1.0	3.58	
235	Cg3429	1	944.5484	0.4	111	118	0	57.8	34	V	FLGLFHVL	R	2.2	7.84	
236	Cg1365	1	1975.0011	-2.1	114	130	0	53.1	37	A	EKQGQLGQVEDELFRLS	R	-0.9	4.16	
236	Cg1365	1	2046.0382	-8.9	113	130	0	74.3	37	S	AEKQGQLGQVEDELFRLS	R	-0.8	4.16	
237	Cg2800	1	2496.257	-3.4	405	426	0	58.5	38	A	SFLRMDGTTWSTDKDGLILDLL	A	0.0	3.88	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
238	Cg2176	1	1709.8234	-0.2	206	222	0	50.6	36	A	NNPFSTGGGERPAPRPG	G	-1.4	10.88	
239	Cg1227	1	1260.6575	8.6	190	201	0	46.1	36	T	GALDRFAAGREV	-	-0.1	7.04	
239	Cg1227	1	1427.7925	-0.4	120	130	0	45.3	35	A	LFLYRRYSLPT	T	0.0	10.2	
239	Cg1227	1	1645.898	-2.2	118	130	0	46.7	36	I	FALFLYRRYSLPT	T	0.3	10.2	
240	Cg0952	1	1020.4876	2.0	24	32	0	43.7	36	A	SPEFGELRS	K	-0.9	4.26	
240	Cg0952	1	1129.5743	5.7	33	41	0	55.8	37	S	KFRSFAFPM	T	0.1	11.48	
240	Cg0952	1	1145.5692	3.2	33	41	0	43.6	36	S	KFRSFAFPM	T	0.1	11.48	Oxidation (M)
240	Cg0952	1	1611.6987	-0.9	15	28	0	51.3	32	T	AQEFRDMQASPEFG	E	-1.0	3.82	
243	Cg0559	1	2251.0719	5.6	232	250	0	45.0	37	G	MIFQIVDDIIDIFSETHES	G	0.4	3.42	
243	Cg0559	1	2632.3596	-5.7	280	302	0	61.9	38	A	ELRDILTGPLEDDETVNHVLELL	S	-0.1	3.68	
244	Cg3323	1	1524.7249	6.3	43	55	0	49.4	36	V	KFGDYHVGDIEFV	A	-0.1	4.3	
244	Cg3323	1	2095.9601	0.5	216	233	0	39.1	35	T	MQLNVGGNMDFKNMLDRN	R	-0.7	6.9	
246	Cg1229	1	757.4163	3.4	244	249	0	36.7	36	T	GFFKFL	G	1.3	10.1	
246	Cg1229	1	1917.0036	-4.6	73	88	0	50.4	37	A	LYGRPDGKEYFSFLLI	H	0.0	6.88	
247	Cg1435	1	2140.1357	-8.7	191	208	0	78.2	37	A	ELDFVWPPKIDLPGYRPV	S	-0.3	4.3	
249	Cg0928	1	2029.9633	-8.1	121	136	0	65.5	35	I	DFFNLTELEDRYLDQL	S	-0.6	3.42	
251	Cg1456	1	2477.2478	-4.0	6	27	0	59.9	38	M	SVELEEIRDFLAGFEPFAQLPA	E	0.2	3.58	
252	Cg2527	1	1362.6833	2.5	454	465	0	49.4	37	I	FHEFGHGLHGLL	S	0.2	6.3	
260	Cg2675	1	1844.9376	-6.4	194	209	0	68.5	37	I	ILDLLEDMQRELGMGI	L	0.3	3.58	
263	Cg3011	1	1917.9908	-19.8	6	22	0	42.4	37	I	AFDEEARRGLEKGLNTL	A	-0.8	4.64	
264	Cg2092	1	2689.381	-4.9	418	441	0	105.4	38	V	SFTLLQDQLQDVLETLSEREAGVV	K	0.0	3.5	
269	Cg2846	1	1163.6492	-1.8	133	142	0	36.9	34	A	WHLPFVIGPV	A	1.2	7.84	
269	Cg2846	1	1885.9058	-0.9	327	342	0	61.3	36	A	GYDETTRDQVKDFLTV	A	-0.9	3.96	
270	Cg1562	1	1739.8155	1.3	365	378	0	35.4	35	I	ALEEYWRSFETNPV	S	-0.8	3.96	
273	Cg3405	1	1775.9168	4.4	130	144	0	61.3	37	I	SLLDFLDMKPGEWLI	Q	0.4	3.7	
275	Cg2372	1	1150.5447	0.6	356	364	0	44.9	35	V	FYSDWLHLA	E	0.3	4.94	
278	Cg0508	1	1634.7649	-2.7	231	247	0	48.0	35	A	QSNGPTSQEIAGGGHPV	G	-0.8	5.12	
278	Cg0508	1	1781.8294	3.4	76	90	0	66.0	35	A	FMEANPDIEVEVYRA	G	-0.2	3.68	
280	Cg2261	1	1545.706	-0.6	406	418	0	45.3	34	A	TVGWRVDDDVEQQ	G	-1.1	3.5	
283	Cg2151	1	2551.4016	-4.3	52	72	0	56.0	36	V	IGNQRQLEMQLNRRLAEIEKL	Q	-0.9	10.08	
284	Cg0153	1	1698.8537	27.5	146	164	0	38.9	36	R	VAIGGDSAGGNIAAVTAQQ	L	0.5	3.1	
284	Cg0153	1	1715.8802	17.7	143	161	0	39.4	37	D	TSRVAIGGDSAGGNIAAVT	A	0.4	6.78	
287	Cg3189	1	1945.9381	-0.3	285	304	0	112.4	37	I	AILRYAAGVDTGDGGAPDEV	A	0.0	3.5	
291	Cg0249	1	1501.7816	0.0	244	255	0	82.6	37	A	ELNPLYHYLEIV	R	0.2	4.24	
292	Cg3255	1	2185.0976	-1.0	52	70	0	67.3	38	G	MVPPQELFDDLQAEALEKI	N	-0.2	3.5	
295	Cg0915	1	2086.0178	-14.0	154	172	0	36.3	36	S	NVIDQVDDLRGATENLDSI	R	-0.4	3.36	
303	Cg4005	1	1499.762	1.1	69	81	0	72.9	37	A	ELQLEDTPVPRFG	F	-0.6	3.82	
303	Cg4005	1	1991.9476	-14.3	69	85	0	41.1	35	A	ELQLEDTPVPRFGFDET	Q	-0.8	3.5	
303	Cg4005	1	2320.1223	-1.3	69	88	0	52.3	37	A	ELQLEDTPVPRFGFDETQSI	L	-0.6	3.5	
310	Cg2968	1	915.4913	27.9	301	309	0	51.4	36	A	IIDVTLDGA	K	1.2	2.92	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
311	Cg1911	1	1260.5451	-0.9	168	176	0	35.5	32	M	SFRFDYYYT	V	-0.9	6.58	
311	Cg1911	1	1579.8318	-4.2	123	137	0	38.4	36	I	DANNSLIQPRSIVPG	S	-0.3	6.78	
311	Cg1911	1	2487.203	-5.7	88	108	0	68.5	37	Q	KHPVDIEDFENEQGKGTIERF	A	-1.3	4.42	
314	Cg1794	1	1914.0305	-0.2	210	224	0	41.7	37	V	RFLPNPFWVPELRPF	R	-0.2	10.88	
321	Cg0250	1	1691.8883	-0.4	296	310	0	93.2	36	G	LFEHLVESLEGLHAV	H	0.7	4.52	
323	Cg1582	1	1385.8031	-0.5	106	118	0	63.4	33	V	LFGQVGRDLVGLI	N	1.1	6.78	
326	Cg0949	1	1618.7701	-22.3	15	28	0	63.0	34	A	VLHYPGGEFEMDII	E	0.3	3.82	
328	Cg0134	1	2166.1896	-7.7	302	321	0	39.5	36	S	LLPEALKDISKRVDDVLDGA	A	0.0	4.12	
335	Cg0327	1	986.6164	19.4	364	373	0	24.9	24	L	FGALGILLLA	T	2.5	6.02	
343	Cg1109	1	1860.9217	-2.3	59	75	0	56.3	37	A	AGVLEEGQYNRELAEAI	A	-0.3	3.8	
344	Cg0464	1	1279.6138	-7.8	154	164	0	53.4	35	I	FFWGGSPFHKA	T	-0.1	10.1	
348	Cg2361	1	2217.0801	-3.5	39	56	0	59.8	37	A	LVQFQEENEDLKQQVEEL	E	-1.1	3.5	
349	Cg1829	1	1274.7234	-1.5	162	172	0	41.8	34	S	FLRETLGVEVL	S	0.9	4.26	
349	Cg1829	1	1637.8083	16.7	389	401	0	37.6	36	S	NIDTYLKNIEERM	K	-1.0	4.44	
350	Cg1268	1	1638.8366	-10.7	172	185	0	37.8	36	V	LNGIDTELWQPRPT	F	-0.9	4.08	
351	Cg0040	1	2032.945	-0.7	269	288	0	35.5	35	V	QAPDSYGRIGNQSGSDVSPV	V	-0.8	3.88	
351	Cg0040	1	2216.1437	-6.7	289	307	0	56.2	38	V	VLGDYKVDKDADLERPERV	S	-1.0	4.3	
353	Cg1164	1	902.5113	-5.4	160	167	0	40.1	35	G	IATLPEFL	N	1.4	3.3	
353	Cg1164	1	1550.9032	-8.7	282	295	0	33.7	32	A	SVPEILVQGVIERL	A	0.8	4.26	
353	Cg1164	1	1621.9403	-1.7	282	296	0	35.3	32	A	SVPEILVQGVIERLA	E	0.9	4.26	
357	Cg0451	1	1290.7601	0.7	85	94	0	32.4	30	A	LFRHPLWLPI	P	0.7	11.04	
357	Cg0451	1	1705.9151	-1.5	188	203	0	53.4	36	T	WGPPAGRLLEQLLAEG	K	-0.1	4.26	
359	Cg2300	1	2033.9193	-7.3	130	146	0	34.8	33	T	NSPMFEGISPDERFYFV	H	-0.4	3.82	
360	Cg1128	1	829.397	3.6	29	37	0	34.7	34	Q	GGPLGPEFG	K	-0.2	3.3	
360	Cg1128	1	1677.7999	-10.6	74	88	0	51.8	36	I	FAERNGLDPFDIEGV	R	-0.3	3.58	
366	Cg1629	1	1727.9669	-28.0	342	358	0	37.8	37	L	AVSEGGKILDTITLQAL	I	0.6	4.08	
370	Cg1594	1	1649.6958	3.0	382	394	0	59.1	31	V	NNERIESDDWEPF	A	-1.9	3.5	
372	Cg1005	1	1318.7649	-6.3	313	323	0	47.4	32	S	LVIFETFVRPV	V	1.5	6.98	
372	Cg1005	1	2436.2683	-5.7	392	413	0	44.7	38	A	NGMIRIPEDVTEIRPGDVVDVI	F	0.1	3.84	
376	Cg1333	1	2541.2136	5.1	106	128	0	38.6	37	I	LAQGETFGNSDHLSHLDVNLEFV	S	-0.1	4.06	
388	Cg1855	1	1933.9462	8.3	46	62	0	90.0	37	A	GFEHIELPIFEDTGLFA	R	0.4	3.68	
392	Cg0528	1	1947.885	14.2	42	57	0	92.0	36	V	KGPDDDEEFLWNIEKN	R	-1.7	3.76	
399	Cg0085	1	915.5025	15.6	312	319	0	51.4	36	N	IIDEALSR	G	0.3	4.08	
403	Cg1418	1	1878.9839	-1.5	322	338	0	55.8	37	T	RFALDALVPLLEEHAGE	-	0.2	4.16	
412	Cg2862	1	1810.8697	-1.9	396	411	0	55.5	36	V	ARPENQDELQLEGEIA	R	-1.2	3.58	
413	Cg2474	1	2979.5263	-7.5	6	32	0	43.0	38	I	SYLTDMDGVLIKEGEIIPGADRFLQSL	T	0.1	3.84	
414	Cg3049	1	2176.0874	-2.4	27	45	0	50.1	37	S	DTDVQIDLFERMPAPFGLI	R	0.2	3.5	
416	Cg2052	1	1138.6175	-1.8	200	209	0	34.2	34	A	FPNIPWVGPI	S	0.6	6.02	
416	Cg2052	1	1209.6546	0.9	199	209	0	37.2	34	V	AFPNIPWVGPI	S	0.7	6.02	
419	Cg0291	1	1764.7955	-1.9	205	219	0	44.3	34	I	HFEVFPDRDSITDST	N	-0.8	3.96	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
421	Cg3069	1	2395.1188	-0.9	175	195	0	47.7	36	I	TDWIFDNLIDGDGLVMDGLRM	R	0.1	3.3	
422	Cg0237	1	990.5651	1.2	240	247	0	34.9	33	A	FQFIPRAI	F	0.9	11.04	
426	Cg0413	1	1699.7492	-0.2	339	352	0	42.5	32	T	GTHSWGWWQDDLRG	S	-1.4	5.1	
428	Cg1796	1	1491.7432	5.2	153	164	0	75.1	37	A	RLELPDFEFVPM	W	0.1	3.82	
430	Cg2510	1	3103.4444	12.3	202	228	0	68.1	37	V	MTDLLPEGPKFYPDDHITDEDTNTRIA	E	-1.0	3.84	
435	Cg0867	1	1924.9755	-7.6	17	33	0	49.7	37	V	SITGRNVEVPDHFAERV	N	-0.5	5.34	
437	Cg2408	1	1456.6834	0.1	66	77	0	66.2	35	V	RVDVLPEDWEEA	E	-0.9	3.5	
438	Cg2235	1	964.4978	-0.6	64	72	0	48.6	35	V	SFGIGVERT	F	0.1	6.98	
441	Cg0936	1	1206.5418	7.8	58	69	0	62.1	35	T	GNGYHGGLQFSA	S	-0.5	7.76	
441	Cg0936	1	1421.6324	1.1	56	69	0	54.0	34	I	NTGNGYHGGLQFSA	S	-0.7	7.76	
443	Cg1859	1	1763.8577	2.2	79	95	0	90.3	37	V	KVIAGEAESFTSDNLPS	G	-0.2	3.82	
454	Cg3107	1	1263.6976	-8.9	306	316	0	54.1	35	L	DFFARGLIKPT	V	0.1	10.08	
457	Cg1228	1	1557.7998	-0.9	346	358	0	46.3	37	V	DASERIEELLDRL	R	-0.7	3.92	
469	Cg1789	1	1440.7653	-7.0	28	39	0	59.0	36	L	AFALPKEYFEKV	D	0.0	7	
472	Cg0628	1	2316.1921	-15.6	105	127	0	65.6	38	I	STSQGLLTDRQATEKGVGGEVLA	Y	-0.3	4.44	
475	Cg2325	1	981.4742	5.5	24	31	0	36.5	34	A	DFFRPMGI	N	0.3	6.78	
475	Cg2325	1	985.5022	0.9	13	20	0	40.5	35	A	DFLHVWGL	T	0.8	4.94	
475	Cg2325	1	1086.5499	3.0	13	21	0	56.3	36	A	DFLHVWGLT	V	0.7	4.94	
477	Cg0779	1	1234.6386	5.4	49	58	0	40.1	36	A	FYFIPDLHAI	T	1.1	4.94	
488	Cg0680	1	2657.2802	9.6	260	282	0	41.3	38	V	VSYFGQELQEHAFPKDTSPFAFL	N	-0.2	4.42	
489	Cg2199	1	1011.5825	-5.8	258	266	0	33.7	33	A	PDIVSRVAR	I	0.0	10.88	
490	Cg1574	1	1177.6496	5.9	334	343	0	49.3	33	G	DIRFTLPFGI	Q	0.8	6.78	
493	Cg2368	1	3121.5549	2.3	201	227	0	57.3	38	L	DFFKTPEAYFQVFDDFAGRITPNGKLV	V	-0.2	4.46	
512	Cg1436	1	2293.2529	-5.8	57	76	0	83.7	36	V	DADELNIEQITKQLNKLIPV	L	-0.4	4.06	
517	Cg1337	1	1066.6611	-9.0	152	161	0	30.7	29	P	VVGPLRRSLA	G	0.6	12.4	
537	Cg3096	1	1092.5604	-1.1	399	407	0	52.0	35	I	FREEIFGPV	L	0.1	4.26	
539	Cg2841	1	1333.5431	-28.2	101	112	0	30.7	23	L	ADHIDMNFGCPV	P	0.2	3.88	Oxidation (M)
543	Cg2876	1	1778.9389	-4.1	360	373	0	58.2	36	A	MIERELERYLPFLA	T	0.0	4.56	
557	Cg2154	1	1500.83	-3.3	87	100	0	71.5	36	A	RGLVTDFGKIADPI	A	0.2	6.9	
559	Cg1604	1	2475.3221	1.3	66	88	0	51.6	37	A	DSIIDHIVEDVVAGTLTDRPVLV	M	0.6	3.76	
564	Cg2100	1	997.6171	-25.8	79	88	0	34.4	32	K	LAALLGEALK	T	1.3	6.94	
565	Cg1247	1	1881.8704	-0.6	87	105	0	49.1	35	T	GDGSEGGDIEIPDNAPRIA	Q	-0.7	3.42	
568	Cg2440	1	1187.6855	0.2	135	143	0	34.6	33	M	RILPFWFPL	K	1.0	11.04	
570	Cg1665	1	1181.4989	1.9	189	199	0	47.0	32	I	SWLDDGSGQFA	A	-0.5	2.92	
570	Cg1665	1	1252.536	-1.0	189	200	0	51.9	32	I	SWLDDGSGQFAA	S	-0.3	2.92	
571	Cg3068	1	1717.8345	3.5	2	16	0	57.8	37	M	PIATPEVYNEMLDRA	K	-0.4	3.82	
590	Cg0939	1	1669.6896	-0.2	105	118	0	87.4	28	T	IYDDPAANDEFYHT	S	-1.1	3.5	
592	Cg0655	1	1793.9352	-2.2	20	35	0	57.8	37	S	RFVIEPLEPGFGYTLG	N	0.3	4.26	
595	Cg3325	1	2002.1099	-6.8	463	481	0	43.3	36	T	TILGSVDEGIFRNLGVLVT	S	0.9	4.08	
597	Cg0565	1	798.4123	15.0	479	485	0	33.5	33	E	IDLNDPL	T	0.0	2.92	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
610	Cg0873	1	862.4913	6.8	227	234	0	32.1	32	W	VVHPGEIL	G	1.0	5.12	
616	Cg2418	1	1051.5888	3.8	153	160	0	50.6	32	S	LYLRPFMI	S	1.2	9.84	
625	Cg0489	1	1939.9123	-6.4	88	105	0	56.2	35	A	SVEGDVDKQETPERPAPS	N	-1.5	3.92	
631	Cg0933	1	1035.5601	26.0	15	23	0	37.1	32	K	TVLLEIDHP	Q	0.4	4.06	
642	Cg0564	1	1901.0258	-5.7	186	202	0	99.1	37	L	AENYGALLDEIIRIKPS	S	-0.1	4.44	
644	Cg0442	1	2055.1113	-5.6	227	245	0	40.7	37	A	IFDALRRIEPGAGGELQLT	D	0.0	4.44	
648	Cg1641	1	1915.0666	-4.0	2	17	0	40.1	35	M	TTFLELKLPDEIVREL	R	0.1	4.16	
656	Cg1432	1	2013.8817	14.0	354	370	0	61.6	34	V	HSNDLEGWLDDWDIRSG	K	-1.2	3.76	
662	Cg2342	1	1055.54	-0.7	161	169	0	55.8	35	V	NLYGSFRVT	K	0.0	9.84	
667	Cg2994	1	1559.7256	-0.1	171	183	0	41.3	35	L	SFERYGKDSPFEV	S	-1.1	4.44	
671	Cg2924	1	1444.6524	0.2	80	90	0	36.0	34	A	SENGRPWWEWV	S	-1.5	4.26	
674	Cg3343	1	1087.6389	-4.4	99	107	0	43.3	33	A	GIKLEIPRY	-	-0.3	9.72	
674	Cg3343	1	1226.5204	-1.2	45	54	0	31.9	31	A	SDYERDIWGS	S	-1.5	3.7	
692	Cg1129	1	2479.2383	-15.0	110	131	0	44.0	37	I	VGWKGLINDPHLNETYDIPEGL	R	-0.5	4.06	
694	Cg2460	1	2131.0069	-1.8	149	168	0	47.6	36	V	NRGYESSEGTIVPEIEPAPS	T	-0.9	3.8	
698	Cg1730	1	1471.8399	-2.6	44	57	0	51.6	34	V	SGGLTLLVPFVDRV	R	1.1	6.78	
703	Cg1069	1	1758.9186	-2.2	68	83	0	78.3	37	S	SLDILRELVDMNLGTA	S	0.5	3.7	
704	Cg1764	1	1330.6915	0.2	470	481	0	51.5	37	N	RLIELQMEGSVG	-	0.1	4.26	
706	Cg1675	1	2036.9538	-5.1	170	187	0	52.5	35	S	DLKPEDFTKGKDESDGEK	-	-2.1	4.16	
709	Cg2890	1	950.5113	-26.5	75	82	0	52.6	35	T	DIFIAYPL	Y	1.4	3.1	
710	Cg2676	1	1081.5669	8.0	29	38	0	44.8	34	K	ALGNPWTRPA	A	-0.6	11.04	
714	Cg0594	1	1988.0401	-4.1	13	29	0	63.7	37	T	KLGMTQIFDEENRVIPV	T	-0.2	4.44	
735	Cg3387	1	862.5164	-25.9	367	374	0	48.7	32	T	FIIGLSLT	T	2.2	6.02	
755	Cg1458	1	798.4123	15.0	184	190	0	33.5	33	I	DLDNLPI	K	0.0	2.92	
756	Cg1874	1	1007.4461	3.5	97	105	0	36.3	34	A	GGWRFSDPS	E	-1.1	6.78	
756	Cg1874	1	1444.7714	-0.2	106	117	0	38.7	36	S	EKPHTFFDKILA	Q	-0.4	7.8	
788	Cg2467	1	1431.8085	0.1	238	249	0	63.4	34	S	KLTVRDLLQEFA	N	0.1	7.02	
820	Cg1623	1	986.6164	15.8	83	92	0	26.0	25	F	FGGIALIAII	D	2.7	6.02	
824	Cg1646	1	828.4593	-17.7	126	133	0	36.4	35	E	VLDIADLA	Q	1.6	2.92	
830	Cg3240	1	1133.7787	-19.7	108	118	0	18.4	16	T	LAIIVGLILPL	V	3.0	6.02	
834	Cg3304	1	2106.0885	-1.8	96	113	0	65.6	37	T	TVIDILDILTPEDFYRPS	H	0.2	3.5	
841	Cg1740	1	1749.8461	-2.5	63	77	0	41.2	36	L	SVEDWADLLKDFDVV	V	0.1	3.36	
850	Cg0396	1	3107.5353	11.6	89	114	0	48.0	38	L	FFLNPDTVIDDPTLFNSLRRVDEQWA	A	-0.3	3.76	
857	Cg3257	1	876.5069	8.1	27	33	0	31.4	31	S	RTLFDLL	F	0.8	6.78	
857	Cg3257	1	1207.6601	4.2	27	36	0	50.6	33	S	RTLFDLLFPS	N	0.6	6.78	
870	Cg2362	1	1059.6917	3.0	60	68	0	25.0	18	L	RRVIPPLPL	G	0.3	12.4	
884	Cg0914	1	1256.6554	0.4	83	92	0	47.0	36	I	GYVFQDFRLL	K	0.4	6.7	
887	Cg3160	1	1728.9444	6.0	22	40	0	42.6	35	V	VGIAVGAVAVVGVSMISGQ	D	1.8	6.02	Oxidation (M)
893	Cg2619	1	1262.6507	2.9	208	220	0	36.6	36	M	SFGASLPSTNVLA	S	0.7	6.02	
899	Cg2561	1	1773.8322	-4.1	170	185	0	45.7	35	V	FGDHTEGFRDVAEVPV	T	-0.3	4.06	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
958	Cg3215	1	2678.3479	5.9	85	106	0	51.7	38	V	LTLNNLLDIFEDYPDKHLYIET	K	-0.3	3.84	
967	Cg0620	1	1771.0648	-2.4	194	209	0	76.9	29	A	LYQGLITIPGLVLPKF	-	1.1	9.72	
977	Cg1904	1	862.5164	-18.4	50	57	0	39.3	32	I	FIIGLSTL	V	2.2	6.02	
977	Cg1904	1	1018.5851	-3.9	218	226	0	33.1	33	F	FLLWSILGA	D	2.0	6.02	
979	Cg0475	1	2419.1907	3.0	146	167	0	49.4	38	A	DALGELFANEGALTEKWISENL	-	-0.2	3.58	
988	Cg0573	1	1616.761	-1.7	23	35	0	62.0	35	S	EFVKEFEEVFDVT	A	-0.1	3.58	
989	Cg1341	1	1011.5865	-9.8	163	170	0	53.6	33	T	ISPWLRQL	L	0.1	11.04	
990	Cg1505	1	1607.6892	-4.6	220	232	0	40.5	31	V	SFGSWEEYGERYV	R	-1.1	3.96	
1002	Cg3407	1	978.5135	5.3	33	41	0	36.8	34	A	RGVFGTTEI	D	0.1	6.98	
1010	Cg2954	1	1031.5764	-6.7	17	25	0	43.9	35	A	LLAGNERFI	S	0.5	6.98	
1020	Cg2604	1	2475.2605	-5.6	62	82	0	55.4	38	V	VFTQEQIDQLKELKSRDQEAA	A	-1.1	4.28	
1052	Cg0674	1	1459.7671	-3.2	105	116	0	40.9	37	L	VLLDRENQFDIV	A	0.1	3.7	
1057	Cg0359	1	1133.608	3.4	68	77	0	50.7	35	S	SLFRAEVELA	K	0.6	4.26	
1058	Cg1731	1	1030.5997	3.1	58	66	0	33.9	33	A	ALLMFIRPA	I	1.6	11.04	
1080	Cg0556	1	1999.0601	-7.1	156	172	0	52.7	37	V	FGTVYKEYLMRLLPQAA	R	0.2	9.52	
1117	Cg1635	1	1615.7002	18.5	27	40	0	57.9	34	A	DGYLDIDEFDTRTG	A	-1.0	3.36	
1121	Cg1092	1	862.4834	15.9	12	19	0	36.3	32	L	IISMGLIT	A	2.2	6.02	Oxidation (M)
1132	Cg1312	1	1166.5244	1.0	125	133	0	65.6	34	T	YEIENWDKA	K	-1.5	3.82	
1139	Cg0653	1	1347.6783	-1.9	88	100	0	44.7	37	V	DVFVKGPGSGRET	A	-0.7	7.02	
1145	Cg3254	1	997.5961	-4.6	41	50	0	64.8	32	I	IGGLLGGWLL	G	1.7	6.02	
1148	Cg3361	1	1828.0499	-1.3	173	189	0	38.9	33	A	LKFPTIFNTLGPLLSPA	R	0.7	10.1	
1195	Cg1811	1	1124.5502	1.0	98	106	0	43.9	35	A	LLERFGFED	-	-0.2	3.82	
1215	Cg2033	1	935.4713	15.3	82	90	0	36.6	35	A	VGKGFDKAD	A	-0.8	6.88	
1220	Cg0726	1	2621.3489	-3.8	53	74	0	55.9	38	L	ALPEIENSIDLERYKGKWYQVA	A	-0.7	4.64	
1231	Cg1072	1	1121.5869	-1.2	87	95	0	56.1	35	T	FHIDHLDLL	A	0.6	4.94	
1236	Cg0609	1	1311.6571	-0.1	84	94	0	45.0	35	V	GYRFDENGKKV	R	-1.6	9.62	
1276	Cg1672	1	1609.7889	-4.6	82	94	0	41.9	36	A	GFQWGLERDYQVL	C	-0.5	4.08	
1319	Cg2535	1	1989.9167	3.6	100	117	0	64.5	35	A	DAIDPPTLDIEDYNGNKT	N	-1.1	3.36	
1345	Cg3367	1	1282.7245	3.3	267	278	0	39.1	34	L	RIIIDAGGQDII	S	0.7	3.88	
1346	Cg3353	1	909.5396	6.9	375	383	0	28.4	28	G	RIGAVVAPQ	L	0.7	11.04	
1413	Cg1694	1	1066.6247	26.0	13	22	0	36.0	29	P	RPLALSPSRA	G	-0.3	12.4	
1414	Cg1568	1	915.5099	7.5	106	113	0	39.7	36	L	LLAMLLDQ	K	1.5	3.1	
1426	Cg0412	1	862.48	16.3	332	339	0	32.6	32	W	PIYGSLLT	S	0.9	5.92	
1433	Cg3139	1	1488.8525	-4.7	45	58	0	48.1	33	A	GRLPKNIGDIPRPG	R	-0.9	11.32	
1436	Cg1810	1	1654.9083	-1.3	126	139	0	52.8	36	I	FLAPPSWEVLVERL	T	0.6	4.26	
1481	Cg1085	1	1004.4141	1.2	8	14	0	35.0	30	V	NHWFEWS	T	-1.4	5.12	
1483	Cg0600	1	1459.7055	-6.0	62	74	0	40.2	36	A	NAENNFGLDPRTL	V	-1.0	4.08	
1506	Cg1751	1	862.5164	-22.4	90	97	0	36.5	32	V	IFLGLSTI	V	2.2	6.02	
1525	Cg0561	1	1160.6441	-2.1	98	108	0	56.9	35	V	DFLAGLGVEKI	L	0.8	4.08	
1526	Cg0524	1	1417.703	2.5	118	128	0	37.4	37	S	RFPFGNLYEYI	L	-0.2	6.82	

hit	**accession**	**z**	**mass**	**ppm**	**start**	**end**	**mc**	**score**	**id**	**-**	**sequence**	**+**	**gravy**	**pI**	**modification**
1529	Cg2737	1	1837.925	2.0	86	100	0	45.5	37	A	LQWPDILDEFIEHLA	R	0.1	3.58	
1543	Cg1259	1	1875.9155	-6.7	32	46	0	37.2	37	Q	IFNPDQWAERYPLEV	G	-0.7	3.82	
1559	Cg0652	1	1856.9116	-6.8	38	54	0	41.1	36	T	GISPDLRTDNLTDEQIA	A	-0.7	3.5	
1582	Cg2773	1	1811.8802	3.8	128	143	0	41.1	36	A	NADTIVDRFLNSPDHV	K	-0.4	4.16	
1698	Cg0966	1	1206.6033	4.2	38	47	0	38.6	36	I	RFDLNEGFPL	L	-0.4	4.08	
1748	Cg2735	1	1612.8896	1.2	79	91	0	45.7	35	A	NDLKEIQRLLSER	-	-1.2	7.14	

END OF LIST III

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
IV. Purple membrane; elastase digest, nLC-MALDI MS/MS; no search specificity															
1	P02945|BACR	1	713.4799	27.2	234	239	0	28.4	18	G	LILLRS	R	1.8	11.04	
1	P02945|BACR	1	731.4582	-4.6	231	237	0	57.7	26	V	GFGLILL	R	2.6	6.02	
1	P02945|BACR	1	741.4061	-24.8	54	59	0	40.5	32	K	KFYAIT	T	0.5	9.72	
1	P02945|BACR	1	762.4024	19.3	240	246	0	50.5	32	S	RAIFGEA	E	0.4	6.98	
1	P02945|BACR	1	781.4738	-18.2	38	43	0	30.0	28	T	LYFLVK	G	1.6	9.72	
1	P02945|BACR	1	799.4916	6.8	187	193	0	38.5	30	V	LRNVTVV	L	1.1	11.04	
1	P02945|BACR	1	829.4182	-6.0	112	119	0	54.7	35	A	LLVDADQG	T	0.3	2.92	
1	P02945|BACR	1	849.4344	2.1	239	246	0	41.5	34	R	SRAIFGEA	E	0.2	6.98	
1	P02945|BACR	1	866.5477	3.7	104	111	0	68.0	22	T	PLLLLDLA	L	2.0	3.1	
1	P02945|BACR	1	876.4745	-14.6	99	105	0	39.0	33	D	WLFTTPL	L	0.9	6.02	
1	P02945|BACR	1	887.4786	-25.8	124	132	0	60.2	36	A	LVGADGIMI	G	1.8	3.1	
1	P02945|BACR	1	887.5593	4.4	231	238	0	62.2	23	V	GFGLILLR	S	1.7	11.04	
1	P02945|BACR	1	914.4174	-16.7	96	102	0	33.9	31	R	YADWLFT	T	0.3	3.1	
1	P02945|BACR	1	917.4276	0.1	174	181	0	37.9	35	A	ESMRPEVA	S	-0.8	4.26	
1	P02945|BACR	1	930.4811	-6.2	201	209	0	68.7	36	V	VWLIGSEGA	G	0.9	3.3	
1	P02945|BACR	1	957.4556	9.9	83	91	0	73.4	34	V	PFGGEQNPI	Y	-0.8	3.3	
1	P02945|BACR	1	958.6215	-6.1	229	237	0	44.1	18	A	KVGFGLILL	R	2.0	10.1	
1	P02945|BACR	1	967.5954	-5.5	103	111	0	64.7	27	T	TPLLLLDLA	L	1.7	3.1	
1	P02945|BACR	1	974.5913	-6.1	231	239	0	63.7	27	V	GFGLILLRS	R	1.4	11.04	
1	P02945|BACR	1	986.6277	-3.4	230	238	0	74.8	23	K	VGFGLILLR	S	2.0	11.04	
1	P02945|BACR	1	999.4736	-21.8	76	84	0	63.1	32	L	GYGLTMVPF	G	0.9	5.92	Oxidation (M)
1	P02945|BACR	1	1005.5356	-1.8	238	246	0	37.5	33	L	RSRAIFGEA	E	-0.3	10.88	
1	P02945|BACR	1	1015.4651	-23.0	96	103	0	39.3	31	R	YADWLFTT	P	0.2	3.1	
1	P02945|BACR	1	1032.44	-18.0	243	252	0	80.2	30	I	FGEAEAPEPS	A	-0.9	3.02	
1	P02945|BACR	1	1043.5499	-2.0	112	121	0	72.5	35	A	LLVDADQGTI	L	0.7	2.92	
1	P02945|BACR	1	1055.5552	-11.0	19	26	0	38.6	33	T	GRPEWIWL	A	-0.4	6.98	
1	P02945|BACR	1	1062.6186	-2.5	182	190	0	56.9	28	A	STFKVLRNV	T	0.2	11.48	
1	P02945|BACR	1	1069.5709	-4.5	20	27	0	45.9	33	G	RPEWIWLA	L	-0.2	6.98	
1	P02945|BACR	1	1070.5185	24.5	95	102	0	61.3	34	A	RYADWLFT	T	-0.3	6.7	
1	P02945|BACR	1	1081.5556	1.9	16	24	0	61.4	33	A	QITGRPEWI	W	-0.7	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1098.5822	2.5	16	24	0	50.6	34	A	QITGRPEWI	W	-0.7	6.98	
1	P02945|BACR	1	1109.6485	-12.8	34	43	0	84.1	30	M	GLGTLYFLVK	G	1.2	9.72	
1	P02945|BACR	1	1116.6907	4.9	227	237	0	53.5	22	V	SAKVGFGLILL	R	1.7	10.1	
1	P02945|BACR	1	1126.5923	16.7	19	27	0	51.6	33	T	GRPEWIWLA	L	-0.2	6.98	
1	P02945|BACR	1	1130.6924	-1.5	231	240	0	44.1	25	V	GFGLILLRSR	A	0.8	12.4	
1	P02945|BACR	1	1133.5142	-25.1	85	94	0	69.3	32	F	GGEQNPIYWA	R	-0.9	3.3	
1	P02945|BACR	1	1145.524	-25.4	242	252	0	79.0	32	A	IFGEAEAPEPS	A	-0.4	3.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	1	1156.6029	6.2	18	26	0	56.0	34	I	TGRPEWIWL	A	-0.5	6.98	
1	P02945|BACR	1	1156.634	0.3	112	122	0	106.5	34	A	LLVDADQGTIL	A	0.9	2.92	
1	P02945|BACR	1	1159.6635	-8.5	131	142	0	84.1	32	I	MIGTGLVGALTK	V	1.1	10.1	
1	P02945|BACR	1	1171.5662	-1.7	95	103	0	63.2	34	A	RYADWLFTT	P	-0.4	6.7	
1	P02945|BACR	1	1187.5645	-21.1	81	91	0	93.9	33	T	MVPFGGEQNPI	Y	-0.1	3.3	
1	P02945|BACR	1	1203.5594	-19.2	81	91	0	81.4	33	T	MVPFGGEQNPI	Y	-0.1	3.3	Oxidation (M)
1	P02945|BACR	1	1215.7115	-8.0	101	111	0	62.7	30	L	FTTPLLLLDLA	L	1.6	3.1	
1	P02945|BACR	1	1216.5612	-20.9	241	252	0	114.2	32	R	AIFGEAEAPEPS	A	-0.2	3.02	
1	P02945|BACR	1	1225.6019	-17.6	96	105	0	73.1	33	R	YADWLFTTPL	L	0.4	3.1	
1	P02945|BACR	1	1227.64	22.3	18	27	0	56.7	34	I	TGRPEWIWLA	L	-0.2	6.98	
1	P02945|BACR	1	1227.6711	-24.1	112	123	0	113.1	34	A	LLVDADQGTILA	L	1.0	2.92	
1	P02945|BACR	1	1239.6764	-2.6	19	28	0	37.1	32	T	GRPEWIWLAL	G	0.2	6.98	
1	P02945|BACR	1	1242.5822	-3.0	92	100	0	36.3	33	I	YWARYADWL	F	-0.6	6.64	
1	P02945|BACR	1	1253.6292	-0.8	48	58	0	66.4	34	V	SDPDAKKFYAI	T	-0.7	6.8	
1	P02945|BACR	1	1274.7711	3.0	183	193	0	61.6	24	S	TFKVLRNVTVV	L	0.9	11.48	
1	P02945|BACR	1	1280.6513	3.6	14	24	0	72.7	33	S	QAQITGRPEWI	W	-0.7	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1289.6153	-0.4	85	95	0	87.9	35	F	GGEQNPIYWAR	Y	-1.2	6.88	
1	P02945|BACR	1	1296.6979	-7.1	19	29	0	43.9	33	T	GRPEWIWLALG	T	0.2	6.98	
1	P02945|BACR	1	1296.7152	-14.7	31	42	0	35.0	33	T	ALMGLGTLYFLV	K	1.9	5.92	
1	P02945|BACR	1	1306.5982	-4.2	83	93	0	47.0	34	V	PFGGEQNPIYW	A	-0.9	3.3	
1	P02945|BACR	1	1314.8136	-2.6	231	242	0	70.3	24	V	GFGLILLRSRAI	F	1.2	12.4	
1	P02945|BACR	1	1354.6769	5.9	48	59	0	75.7	34	V	SDPDAKKFYAIT	T	-0.7	6.8	
1	P02945|BACR	1	1361.8031	1.8	182	193	0	76.5	27	A	STFKVLRNVTVV	L	0.8	11.48	
1	P02945|BACR	1	1372.6623	5.1	240	252	0	109.7	35	S	RAIFGEAEAPEPS	A	-0.5	3.96	
1	P02945|BACR	1	1377.6353	5.2	83	94	0	93.1	35	V	PFGGEQNPIYWA	R	-0.6	3.3	
1	P02945|BACR	1	1380.719	-3.1	16	26	0	71.8	34	A	QITGRPEWIWL	A	-0.3	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1381.703	16.1	95	105	0	74.5	33	A	RYADWLFTTPL	L	-0.1	6.7	
1	P02945|BACR	1	1397.7456	-0.4	18	29	0	55.3	34	I	TGRPEWIWLALG	T	0.1	6.98	
1	P02945|BACR	1	1409.7919	-15.3	201	214	0	111.2	32	V	VWLIGSEGAGIVPL	N	1.3	3.3	
1	P02945|BACR	1	1424.8101	-3.3	31	43	0	43.6	31	T	ALMGLGTLYFLVK	G	1.5	9.72	
1	P02945|BACR	1	1443.6994	0.1	240	253	0	83.6	35	S	RAIFGEAEAPEPSA	G	-0.4	3.96	
1	P02945|BACR	1	1451.7561	1.0	16	27	0	88.0	34	A	QITGRPEWIWLA	L	-0.1	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1459.6943	1.3	239	252	0	126.7	35	R	SRAIFGEAEAPEPS	A	-0.5	3.96	
1	P02945|BACR	1	1468.7827	11.0	16	27	0	61.8	33	A	QITGRPEWIWLA	L	-0.1	6.98	
1	P02945|BACR	1	1469.7952	-13.4	34	47	0	95.7	34	M	GLGTLYFLVKGMGV	S	1.2	9.72	Oxidation (M)
1	P02945|BACR	1	1490.6983	2.3	92	102	0	53.0	35	I	YWARYADWLFT	T	-0.3	6.64	
1	P02945|BACR	1	1498.7932	0.3	18	30	0	89.2	34	I	TGRPEWIWLALGT	A	0.0	6.98	
1	P02945|BACR	1	1510.7668	-0.5	46	59	0	99.5	34	M	GVSDPDAKKFYAIT	T	-0.3	6.8	
1	P02945|BACR	1	1514.8748	0.3	99	111	0	48.1	30	D	WLFTTPLLLLDLA	L	1.5	3.1	
1	P02945|BACR	1	1523.7157	9.3	85	97	0	42.6	35	F	GGEQNPIYWARYA	D	-1.0	6.82	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	1	1530.7314	-0.5	239	253	0	74.9	35	R	SRAIFGEAEAPEPSA	G	-0.4	3.96	
1	P02945|BACR	1	1533.7365	2.9	83	95	0	122.7	35	V	PFGGEQNPIYWAR	Y	-0.9	6.88	
1	P02945|BACR	1	1540.7596	-4.7	45	58	0	61.1	35	G	MGVSDPDAKKFYAI	T	-0.1	6.8	
1	P02945|BACR	1	1572.8545	-7.2	126	142	0	38.0	34	V	GADGIMIGTGLVGALTK	V	0.9	6.76	
1	P02945|BACR	1	1579.8147	0.2	14	26	0	81.9	34	S	QAQITGRPEWIWL	A	-0.4	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1597.781	1.3	44	58	0	49.2	35	K	GMGVSDPDAKKFYAI	T	-0.2	6.8	
1	P02945|BACR	1	1607.7442	3.4	81	94	0	64.3	35	T	MVPFGGEQNPIYWA	R	-0.1	3.3	
1	P02945|BACR	1	1607.8712	4.1	95	107	0	77.8	32	A	RYADWLFTTPLLL	L	0.5	6.7	
1	P02945|BACR	1	1615.7954	1.2	238	252	0	108.0	35	L	RSRAIFGEAEAPEPS	A	-0.8	4.56	
1	P02945|BACR	1	1629.9018	4.5	98	111	0	64.6	32	A	DWLFTTPLLLLDLA	L	1.2	2.92	
1	P02945|BACR	1	1641.8072	-6.3	45	59	0	95.7	35	G	MGVSDPDAKKFYAIT	T	-0.2	6.8	
1	P02945|BACR	1	1650.8518	10.8	14	27	0	106.1	34	S	QAQITGRPEWIWLA	L	-0.2	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1671.923	-12.1	126	143	0	91.6	34	V	GADGIMIGTGLVGALTKV	Y	1.1	6.76	
1	P02945|BACR	1	1678.8025	-3.5	76	91	0	123.4	35	L	GYGLTMVPFGGEQNPI	Y	0.0	3.3	
1	P02945|BACR	1	1686.8325	-4.8	238	253	0	82.3	35	L	RSRAIFGEAEAPEPSA	G	-0.6	4.56	
1	P02945|BACR	1	1694.7974	-7.2	76	91	0	115.0	34	L	GYGLTMVPFGGEQNPI	Y	0.0	3.3	Oxidation (M)
1	P02945|BACR	1	1698.8287	-10.5	44	59	0	60.3	35	K	GMGVSDPDAKKFYAIT	T	-0.2	6.8	
1	P02945|BACR	1	1718.9832	0.8	231	246	0	57.5	29	V	GFGLILLRSRAIFGEA	E	0.9	10.88	
1	P02945|BACR	1	1720.9552	-1.7	95	108	0	101.0	32	A	RYADWLFTTPLLLL	D	0.7	6.7	
1	P02945|BACR	1	1722.9093	8.1	16	30	0	98.0	33	A	QITGRPEWIWLALGT	A	0.1	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1739.9359	3.7	16	30	0	70.5	34	A	QITGRPEWIWLALGT	A	0.1	6.98	
1	P02945|BACR	1	1743.8064	-2.3	240	257	0	54.0	34	S	RAIFGEAEAPEPSAGDGA	A	-0.4	3.68	
1	P02945|BACR	1	1763.8454	2.8	81	95	0	102.9	35	T	MVPFGGEQNPIYWAR	Y	-0.4	6.88	
1	P02945|BACR	1	1767.8369	1.1	83	97	0	79.9	35	V	PFGGEQNPIYWARYA	D	-0.8	6.82	
1	P02945|BACR	1	1779.8403	2.3	81	95	0	59.9	35	T	MVPFGGEQNPIYWAR	Y	-0.4	6.88	Oxidation (M)
1	P02945|BACR	1	1785.007	-4.6	124	142	0	161.0	32	A	LVGADGIMIGTGLVGALTK	V	1.2	6.76	
1	P02945|BACR	1	1801.8828	1.1	92	105	0	76.1	36	I	YWARYADWLFTTPL	L	-0.1	6.64	
1	P02945|BACR	1	1820.9574	-22.7	14	29	0	49.8	35	S	QAQITGRPEWIWLALG	T	0.0	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1826.9237	12.0	43	59	0	39.8	35	V	KGMGVSDPDAKKFYAIT	T	-0.4	9.56	
1	P02945|BACR	1	1835.9669	-4.5	48	64	0	95.0	34	V	SDPDAKKFYAITTLVPA	I	0.0	6.8	
1	P02945|BACR	1	1841.9635	-11.6	236	252	0	64.1	35	I	LLRSRAIFGEAEAPEPS	A	-0.3	4.56	
1	P02945|BACR	1	1864.0022	14.8	96	111	0	81.3	32	R	YADWLFTTPLLLLDLA	L	1.1	2.92	
1	P02945|BACR	1	1884.0754	0.5	124	143	0	110.6	30	A	LVGADGIMIGTGLVGALTKV	Y	1.4	6.76	
1	P02945|BACR	1	1922.005	-2.2	14	30	0	101.8	34	S	QAQITGRPEWIWLALGT	A	0.0	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1955.0476	-3.5	235	252	0	58.1	34	L	ILLRSRAIFGEAEAPEPS	A	0.0	4.56	
1	P02945|BACR	1	2020.1033	-2.5	95	111	0	127.6	33	A	RYADWLFTTPLLLLDLA	L	0.7	3.88	
1	P02945|BACR	1	2073.9603	-0.5	240	261	0	57.1	35	S	RAIFGEAEAPEPSAGDGAAATS	D	-0.2	3.68	
1	P02945|BACR	1	2160.9923	-4.1	239	261	0	48.2	34	R	SRAIFGEAEAPEPSAGDGAAATS	D	-0.3	3.68	
1	P02945|BACR	1	2210.1484	-3.7	8	27	0	44.2	35	T	AVEGVSQAQITGRPEWIWLA	L	0.1	4.26	
1	P02945|BACR	1	2329.243	-4.9	231	252	0	119.5	35	V	GFGLILLRSRAIFGEAEAPEPS	A	0.3	4.56	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	1	2382.2327	7.4	31	53	0	62.1	35	T	ALMGLGTLYFLVKGMGVSDPDAK	K	0.6	6.8	
1	P02945|BACR	1	2440.2831	-0.2	92	111	0	75.3	35	I	YWARYADWLFTTPLLLLDLA	L	0.6	3.88	
1	P02945|BACR	1	2497.2066	4.0	85	105	0	37.9	36	F	GGEQNPIYWARYADWLFTTPL	L	-0.5	4.08	
2	P00772|ELA1	1	789.4133	-5.8	156	162	0	45.1	35	I	TGWGLTR	T	-0.5	11.04	
2	P00772|ELA1	1	800.3851	9.2	54	61	0	46.1	33	A	HTCGGTLI	R	0.7	7.16	
2	P00772|ELA1	1	882.5287	0.6	138	146	0	30.3	29	L	GVLPRAGTI	L	0.7	11.04	
2	P00772|ELA1	1	890.461	15.9	156	163	0	49.8	33	I	TGWGLTRT	N	-0.6	11.04	
2	P00772|ELA1	1	909.5396	-9.1	136	144	0	42.3	27	V	QLGVLPRAG	T	0.4	11.04	
2	P00772|ELA1	1	913.4446	2.0	104	110	0	37.0	32	I	VVHPYWN	T	-0.3	7.76	
2	P00772|ELA1	1	933.4491	0.3	62	68	0	40.3	35	I	RQNWVMT	A	-1.0	11.04	
2	P00772|ELA1	1	943.4512	-7.2	223	231	0	49.9	33	V	NGQYAVHGV	T	-0.2	7.76	
2	P00772|ELA1	1	1004.4862	-2.5	62	69	0	45.1	35	I	RQNWVMTA	A	-0.7	11.04	
2	P00772|ELA1	1	1008.608	-5.3	135	144	0	35.4	25	Y	VQLGVLPRAG	T	0.7	11.04	
2	P00772|ELA1	1	1009.6284	-7.9	139	148	0	31.2	26	G	VLPRAGTILA	N	1.3	11.04	
2	P00772|ELA1	1	1013.4818	-5.7	187	195	0	38.9	33	S	SSYWGSTVK	N	-0.6	9.72	
2	P00772|ELA1	1	1014.4923	7.2	104	111	0	55.5	34	I	VVHPYWNT	D	-0.4	7.76	
2	P00772|ELA1	1	1043.6128	-7.7	134	142	0	32.1	31	S	YVQLGVLPR	A	0.5	9.84	
2	P00772|ELA1	1	1066.6499	0.0	138	148	0	54.4	26	L	GVLPRAGTILA	N	1.1	11.04	
2	P00772|ELA1	1	1097.5254	3.6	34	42	0	71.2	34	A	QRNSWPSQI	S	-1.6	11.04	Gln->pyro-Glu (N-term Q)
2	P00772|ELA1	1	1114.5519	10.2	34	42	0	55.5	35	A	QRNSWPSQI	S	-1.6	11.04	
2	P00772|ELA1	1	1123.6713	-5.1	136	146	0	39.4	28	V	QLGVLPRAGTI	L	0.6	11.04	
2	P00772|ELA1	1	1130.6448	-3.4	133	142	0	82.6	31	N	SYVQLGVLPR	A	0.4	9.84	
2	P00772|ELA1	1	1171.6713	-6.4	134	144	0	53.1	32	S	YVQLGVLPRAG	T	0.6	9.84	
2	P00772|ELA1	1	1214.5568	-8.9	187	197	0	66.1	33	S	SSYWGSTVKNS	M	-0.9	9.72	
2	P00772|ELA1	1	1240.5836	-0.2	43	53	0	63.8	34	I	SLQYRSGSSWA	H	-0.7	9.84	
2	P00772|ELA1	1	1244.5462	6.2	105	114	0	72.6	33	V	VHPYWNTDDV	A	-1.0	3.88	
2	P00772|ELA1	1	1258.7034	3.5	133	144	0	98.1	32	N	SYVQLGVLPRAG	T	0.4	9.84	
2	P00772|ELA1	1	1262.6659	-15.8	254	264	0	41.0	34	S	AYISWINNVIA	S	1.0	5.92	
2	P00772|ELA1	1	1315.5833	10.9	105	115	0	62.6	34	V	VHPYWNTDDVA	A	-0.7	3.88	
2	P00772|ELA1	1	1321.6813	-8.2	239	250	0	42.9	34	L	GCNVTRKPTVFT	R	-0.2	10.1	
2	P00772|ELA1	1	1343.6146	-2.2	104	114	0	75.6	33	I	VVHPYWNTDDV	A	-0.5	3.88	
2	P00772|ELA1	1	1385.8031	-2.6	134	146	0	51.3	30	S	YVQLGVLPRAGTI	L	0.8	9.84	
2	P00772|ELA1	1	1386.6204	4.4	105	116	0	96.9	33	V	VHPYWNTDDVAA	G	-0.5	3.88	
2	P00772|ELA1	1	1414.6517	1.6	104	115	0	81.2	34	I	VVHPYWNTDDVA	A	-0.3	3.88	
2	P00772|ELA1	1	1427.7481	-3.9	162	174	0	56.8	35	T	RTNGQLAQTLQQA	Y	-1.0	11.04	
2	P00772|ELA1	1	1443.6419	4.8	105	117	0	81.7	33	V	VHPYWNTDDVAAG	Y	-0.5	3.88	
2	P00772|ELA1	1	1445.7449	-5.5	57	69	0	36.2	35	C	GGTLIRQNWVMTA	A	0.1	11.04	
2	P00772|ELA1	1	1456.6987	-6.9	103	114	0	53.1	34	K	IVVHPYWNTDDV	A	-0.1	3.88	
2	P00772|ELA1	1	1458.8195	0.9	130	142	0	119.6	31	V	TLNSYVQLGVLPR	A	0.3	9.84	
2	P00772|ELA1	1	1472.8351	0.3	133	146	0	60.0	31	N	SYVQLGVLPRAGTI	L	0.7	9.84	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	P00772|ELA1	1	1485.6889	-1.8	104	116	0	89.6	34	I	VVHPYWNTDDVAA	G	-0.2	3.88	
2	P00772|ELA1	1	1486.7165	1.3	27	40	0	66.5	35	R	VVGGTEAQRNSWPS	Q	-0.7	6.98	
2	P00772|ELA1	1	1529.7223	-0.3	29	42	0	71.0	35	V	GGTEAQRNSWPSQI	S	-1.3	6.98	
2	P00772|ELA1	1	1542.7103	6.3	104	117	0	103.0	34	I	VVHPYWNTDDVAAG	Y	-0.2	3.88	
2	P00772|ELA1	1	1586.878	2.0	130	144	0	127.6	32	V	TLNSYVQLGVLPRAG	T	0.3	9.84	
2	P00772|ELA1	1	1656.9563	-1.0	133	148	0	53.3	30	N	SYVQLGVLPRAGTILA	N	0.9	9.84	
2	P00772|ELA1	1	1698.9013	3.9	159	174	0	122.2	34	W	GLTRTNGQLAQTLQQA	Y	-0.6	11.04	
2	P00772|ELA1	1	1705.7737	-2.6	104	118	0	91.8	34	I	VVHPYWNTDDVAAGY	D	-0.2	3.88	
2	P00772|ELA1	1	1712.8522	-17.2	101	114	0	92.1	35	V	QKIVVHPYWNTDDV	A	-0.6	5.1	
2	P00772|ELA1	1	1715.8955	0.2	156	171	0	67.9	35	I	TGWGLTRTNGQLAQTL	Q	-0.4	11.04	
2	P00772|ELA1	1	1716.7339	1.3	83	97	0	121.7	31	V	VGEHNLNQNDGTEQY	V	-1.7	3.82	
2	P00772|ELA1	1	1727.8591	-0.1	27	42	0	99.4	36	R	VVGGTEAQRNSWPSQI	S	-0.6	6.98	
2	P00772|ELA1	1	1770.9992	0.3	132	148	0	37.3	31	L	NSYVQLGVLPRAGTILA	N	0.7	9.84	
2	P00772|ELA1	1	1772.9785	-1.7	127	142	0	44.5	32	A	QSVTLNSYVQLGVLPR	A	0.2	9.84	
2	P00772|ELA1	1	1801.0098	-0.6	130	146	0	127.3	31	V	TLNSYVQLGVLPRAGTI	L	0.5	9.84	
2	P00772|ELA1	1	1815.8024	-2.5	83	98	0	130.9	32	V	VGEHNLNQNDGTEQYV	G	-1.4	3.82	
2	P00772|ELA1	1	1815.8024	5.0	82	97	0	102.5	33	V	VVGEHNLNQNDGTEQY	V	-1.4	3.82	
2	P00772|ELA1	1	1901.0371	0.0	127	144	0	55.1	33	A	QSVTLNSYVQLGVLPRAG	T	0.3	9.84	
2	P00772|ELA1	1	1905.8533	-0.6	105	121	0	119.4	34	V	VHPYWNTDDVAAGYDIA	L	-0.3	3.6	
2	P00772|ELA1	1	1914.8708	1.0	82	98	0	132.9	34	V	VVGEHNLNQNDGTEQYV	G	-1.0	3.82	
2	P00772|ELA1	1	1933.8847	9.8	104	120	0	65.5	35	I	VVHPYWNTDDVAAGYDI	A	-0.2	3.6	
2	P00772|ELA1	1	1971.8923	2.7	83	100	0	147.5	34	V	VGEHNLNQNDGTEQYVGV	Q	-1.0	3.82	
2	P00772|ELA1	1	1985.131	-3.7	130	148	0	109.7	30	V	TLNSYVQLGVLPRAGTILA	N	0.8	9.84	
2	P00772|ELA1	1	2004.9218	-0.4	104	121	0	144.5	35	I	VVHPYWNTDDVAAGYDIA	L	-0.1	3.6	
2	P00772|ELA1	1	2013.9392	-3.2	81	98	0	125.2	35	R	VVVGEHNLNQNDGTEQYV	G	-0.7	3.82	
2	P00772|ELA1	1	2043.0498	3.2	156	174	0	103.5	35	I	TGWGLTRTNGQLAQTLQQA	Y	-0.6	11.04	
2	P00772|ELA1	1	2070.9607	-2.5	82	100	0	154.5	34	V	VVGEHNLNQNDGTEQYVGV	Q	-0.7	3.82	
2	P00772|ELA1	1	2099.9508	-2.6	83	101	0	154.4	34	V	VGEHNLNQNDGTEQYVGVQ	K	-1.1	3.82	
2	P00772|ELA1	1	2118.0058	1.8	103	121	0	103.9	36	K	IVVHPYWNTDDVAAGYDIA	L	0.2	3.6	
2	P00772|ELA1	1	2199.0193	-1.2	82	101	0	142.3	35	V	VVGEHNLNQNDGTEQYVGVQ	K	-0.9	3.82	
2	P00772|ELA1	1	2231.0899	-4.3	104	123	0	137.8	36	I	VVHPYWNTDDVAAGYDIALL	R	0.3	3.6	
2	P00772|ELA1	1	2341.1299	-5.7	83	103	0	96.7	36	V	VGEHNLNQNDGTEQYVGVQKI	V	-1.0	4.42	
2	P00772|ELA1	1	2374.1594	-0.3	101	121	0	130.5	36	V	QKIVVHPYWNTDDVAAGYDIA	L	-0.2	4.16	
2	P00772|ELA1	1	2440.1983	4.2	82	103	0	110.4	36	V	VVGEHNLNQNDGTEQYVGVQKI	V	-0.8	4.42	
2	P00772|ELA1	1	2885.4712	8.9	104	129	0	66.9	36	I	VVHPYWNTDDVAAGYDIALLRLAQSV	T	0.3	4.16	
3	Q9HMW9|Q9HMW9	1	978.5287	8.2	636	643	0	55.1	31	A	FHLQPPQL	F	-0.4	7.84	
3	Q9HMW9|Q9HMW9	1	1125.5971	3.1	636	644	0	55.3	32	A	FHLQPPQLF	S	0.0	7.84	
3	Q9HMW9|Q9HMW9	1	1166.6084	-23.3	616	624	0	48.3	34	A	YVINREQFV	S	-0.1	6.88	
3	Q9HMW9|Q9HMW9	1	1212.6292	3.9	636	645	0	70.1	34	A	FHLQPPQLFS	D	-0.1	7.84	
3	Q9HMW9|Q9HMW9	1	1215.6149	-2.3	182	191	0	36.3	35	L	GWVADYPRPR	N	-1.2	9.84	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
3	Q9HMW9|Q9HMW9	1	1253.6404	-2.8	616	625	0	49.8	34	A	YVINREQFVS	D	-0.1	6.88	
3	Q9HMW9|Q9HMW9	1	1269.6176	5.3	614	623	0	44.8	34	A	MAYVINREQF	V	-0.1	6.88	
3	Q9HMW9|Q9HMW9	1	1286.5455	-7.5	92	101	0	56.4	29	T	DYQPDFDKYP	Y	-2.1	3.6	
3	Q9HMW9|Q9HMW9	1	1296.5809	-9.9	133	142	0	75.6	32	L	QYQSPTWKEM	A	-1.8	6.86	
3	Q9HMW9|Q9HMW9	1	1329.6578	-1.5	182	192	0	36.7	35	L	GWVADYPRPRN	F	-1.4	9.84	
3	Q9HMW9|Q9HMW9	1	1367.618	-8.8	133	143	0	37.8	33	L	QYQSPTWKEMA	N	-1.5	6.86	
3	Q9HMW9|Q9HMW9	1	1368.686	-1.2	614	624	0	41.0	34	A	MAYVINREQFV	S	0.3	6.88	
3	Q9HMW9|Q9HMW9	1	1391.6034	-10.1	93	103	0	45.1	31	D	YQPDFDKYPYG	I	-1.7	3.88	
3	Q9HMW9|Q9HMW9	1	1411.6884	2.0	275	285	0	48.1	34	H	NLAQSFWYDRL	D	-0.5	6.7	
3	Q9HMW9|Q9HMW9	1	1441.7049	-3.6	166	178	0	93.1	35	S	SLLETTKQGEHEA	F	-1.1	4.54	
3	Q9HMW9|Q9HMW9	1	1455.718	-2.1	614	625	0	39.1	35	A	MAYVINREQFVS	D	0.2	6.88	
3	Q9HMW9|Q9HMW9	1	1467.7358	-1.0	616	627	0	38.3	34	A	YVINREQFVSDV	F	-0.1	4.08	
3	Q9HMW9|Q9HMW9	1	1476.7262	2.2	182	193	0	39.7	35	L	GWVADYPRPRNF	M	-1.1	9.84	
3	Q9HMW9|Q9HMW9	1	1506.6303	-3.8	92	103	0	81.4	30	T	DYQPDFDKYPYG	I	-1.9	3.6	
3	Q9HMW9|Q9HMW9	1	1619.7144	-5.0	92	104	0	85.3	32	T	DYQPDFDKYPYGI	D	-1.4	3.6	
3	Q9HMW9|Q9HMW9	1	1638.7678	-1.3	119	132	0	54.3	34	E	AGYGPDNKYELNWL	Q	-1.0	4.08	
3	Q9HMW9|Q9HMW9	1	1660.6893	7.2	88	101	0	49.3	30	T	GESTDYQPDFDKYP	Y	-1.9	3.5	
3	Q9HMW9|Q9HMW9	1	1695.7926	-3.9	133	146	0	89.6	34	L	QYQSPTWKEMANTI	R	-1.1	6.86	
3	Q9HMW9|Q9HMW9	1	1728.7301	-3.1	116	130	0	78.6	30	V	MEEAGYGPDNKYELN	W	-1.5	3.68	
3	Q9HMW9|Q9HMW9	1	1734.7413	-4.3	92	105	0	85.6	31	T	DYQPDFDKYPYGID	E	-1.5	3.42	
3	Q9HMW9|Q9HMW9	1	1736.8958	0.9	619	633	0	89.0	34	I	NREQFVSDVFKGRGV	G	-0.7	10.08	
3	Q9HMW9|Q9HMW9	1	1767.8104	5.8	118	132	0	46.3	34	E	EAGYGPDNKYELNWL	Q	-1.2	3.82	
3	Q9HMW9|Q9HMW9	1	1802.905	-1.4	166	181	0	124.4	36	S	SLLETTKQGEHEAFTL	G	-0.5	4.54	
3	Q9HMW9|Q9HMW9	1	1822.8712	0.3	129	142	0	45.1	35	E	LNWLQYQSPTWKEM	A	-1.0	6.86	
3	Q9HMW9|Q9HMW9	1	1823.7526	-1.9	88	102	0	78.7	29	T	GESTDYQPDFDKYPY	G	-1.8	3.5	
3	Q9HMW9|Q9HMW9	1	1849.8047	4.7	93	107	0	97.6	33	D	YQPDFDKYPYGIDET	K	-1.5	3.5	
3	Q9HMW9|Q9HMW9	1	1857.9335	-0.5	595	610	0	105.2	36	I	DTYYVGFNMTKVPKPV	R	-0.3	9.46	
3	Q9HMW9|Q9HMW9	1	1864.9544	0.1	619	635	0	92.1	35	I	NREQFVSDVFKGRGVGA	F	-0.5	10.08	
3	Q9HMW9|Q9HMW9	1	1880.7741	-0.5	88	103	0	78.6	29	T	GESTDYQPDFDKYPYG	I	-1.8	3.5	
3	Q9HMW9|Q9HMW9	1	1893.9083	-20.8	129	143	0	80.1	34	E	LNWLQYQSPTWKEMA	N	-0.9	6.86	
3	Q9HMW9|Q9HMW9	1	1954.8908	2.5	339	355	0	73.1	34	M	DLFDAPTNYENGRTEIT	N	-1.1	3.58	
3	Q9HMW9|Q9HMW9	1	1964.8316	-1.5	92	107	0	120.4	30	T	DYQPDFDKYPYGIDET	K	-1.6	3.36	
3	Q9HMW9|Q9HMW9	1	1971.0176	-5.5	594	610	0	53.8	36	T	IDTYYVGFNMTKVPKPV	R	0.0	9.46	
3	Q9HMW9|Q9HMW9	1	1987.9421	-0.4	149	165	0	40.2	35	A	RLEQAHIEMTINDANFS	S	-0.5	4.42	
3	Q9HMW9|Q9HMW9	1	1993.8582	1.5	88	104	0	90.4	32	T	GESTDYQPDFDKYPYGI	D	-1.4	3.5	
3	Q9HMW9|Q9HMW9	1	2072.0653	-8.3	593	610	0	36.7	36	S	TIDTYYVGFNMTKVPKPV	R	-0.1	9.46	
3	Q9HMW9|Q9HMW9	1	2092.9266	-27.5	92	108	0	45.8	29	T	DYQPDFDKYPYGIDETK	V	-1.7	3.76	
3	Q9HMW9|Q9HMW9	1	2108.8851	-1.4	88	105	0	83.2	30	T	GESTDYQPDFDKYPYGID	E	-1.5	3.36	
3	Q9HMW9|Q9HMW9	1	2112.1116	2.3	616	633	0	95.5	35	A	YVINREQFVSDVFKGRGV	G	-0.2	9.72	
3	Q9HMW9|Q9HMW9	1	2159.0973	0.5	592	610	0	39.7	36	V	STIDTYYVGFNMTKVPKPV	R	-0.1	9.46	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
3	Q9HMW9|Q9HMW9	1	2222.083	-1.6	129	146	0	72.7	36	E	LNWLQYQSPTWKEMANTI	R	-0.7	6.86	
3	Q9HMW9|Q9HMW9	1	2240.1702	-3.3	616	635	0	56.5	35	A	YVINREQFVSDVFKGRGVGA	F	-0.1	9.72	
3	Q9HMW9|Q9HMW9	1	2263.0321	3.4	92	110	0	35.0	35	T	DYQPDFDKYPYGIDETKVA	E	-1.2	3.76	
3	Q9HMW9|Q9HMW9	1	2314.1892	-0.5	614	633	0	97.4	36	A	MAYVINREQFVSDVFKGRGV	G	0.0	9.72	
3	Q9HMW9|Q9HMW9	1	2338.9754	7.7	88	107	0	98.9	30	T	GESTDYQPDFDKYPYGIDET	K	-1.6	3.32	
3	Q9HMW9|Q9HMW9	1	2442.2478	1.7	614	635	0	52.0	36	A	MAYVINREQFVSDVFKGRGVGA	F	0.1	9.72	
3	Q9HMW9|Q9HMW9	1	2467.0703	-20.7	88	108	0	40.7	28	T	GESTDYQPDFDKYPYGIDETK	V	-1.7	3.68	
3	Q9HMW9|Q9HMW9	1	2637.1759	0.4	88	110	0	42.8	33	T	GESTDYQPDFDKYPYGIDETKVA	E	-1.3	3.68	
3	Q9HMW9|Q9HMW9	1	2766.2184	8.0	88	111	0	49.2	34	T	GESTDYQPDFDKYPYGIDETKVAE	A	-1.4	3.62	
4	Q9HR99|Q9HR99	1	1419.6154	-3.6	122	134	0	65.3	32	V	DAGETLEHTFETA	G	-0.7	3.68	
4	Q9HR99|Q9HR99	1	1473.6195	-5.4	106	119	0	75.8	30	A	SGFGTMDKDGNQFA	V	-0.8	3.88	
4	Q9HR99|Q9HR99	1	1491.7246	-7.0	57	70	0	84.6	35	A	VAPDGGFKFEPSEL	T	-0.3	3.82	
4	Q9HR99|Q9HR99	1	1562.7617	-5.1	56	70	0	78.5	35	I	AVAPDGGFKFEPSEL	T	-0.1	3.82	
4	Q9HR99|Q9HR99	1	1651.7664	7.1	91	105	0	55.8	35	S	AWPDMHDKISIPDGA	S	-0.6	4.16	
4	Q9HR99|Q9HR99	1	1671.7563	-1.6	106	121	0	133.1	33	A	SGFGTMDKDGNQFAVV	D	-0.2	3.88	
4	Q9HR99|Q9HR99	1	1687.7512	-4.7	106	121	0	54.8	32	A	SGFGTMDKDGNQFAVV	D	-0.2	3.88	Oxidation (M)
4	Q9HR99|Q9HR99	1	1691.8407	0.9	57	72	0	105.2	35	A	VAPDGGFKFEPSELTV	S	0.0	3.82	
4	Q9HR99|Q9HR99	1	1762.8778	-3.5	56	72	0	119.1	36	I	AVAPDGGFKFEPSELTV	S	0.1	3.82	
4	Q9HR99|Q9HR99	1	1869.7905	-0.4	122	138	0	149.6	31	V	DAGETLEHTFETAGEYT	Y	-0.9	3.58	
4	Q9HR99|Q9HR99	1	2016.8953	3.4	123	140	0	37.0	34	D	AGETLEHTFETAGEYTYV	C	-0.5	3.78	
4	Q9HR99|Q9HR99	1	2064.9753	2.8	48	68	0	47.1	35	A	SQSGGNTIAVAPDGGFKFEPS	E	-0.4	4.08	
4	Q9HR99|Q9HR99	1	2092.0113	4.0	50	70	0	44.7	36	Q	SGGNTIAVAPDGGFKFEPSEL	T	-0.2	3.82	
4	Q9HR99|Q9HR99	1	2131.9222	7.6	122	140	0	152.5	33	V	DAGETLEHTFETAGEYTYV	C	-0.7	3.58	
4	Q9HR99|Q9HR99	1	2176.0007	11.1	86	105	0	118.8	35	S	SHNVSAWPDMHDKISIPDGA	S	-0.6	5.02	
4	Q9HR99|Q9HR99	1	2205.0954	5.3	51	72	0	45.8	36	S	GGNTIAVAPDGGFKFEPSELTV	S	0.0	3.82	
4	Q9HR99|Q9HR99	1	2212.0107	4.0	100	121	0	56.4	35	I	SIPDGASGFGTMDKDGNQFAVV	D	-0.1	3.6	
4	Q9HR99|Q9HR99	1	2292.1274	0.6	50	72	0	86.5	36	Q	SGGNTIAVAPDGGFKFEPSELTV	S	0.0	3.82	
4	Q9HR99|Q9HR99	1	2307.1019	5.5	48	70	0	104.2	36	A	SQSGGNTIAVAPDGGFKFEPSEL	T	-0.3	3.82	
4	Q9HR99|Q9HR99	1	2507.218	5.4	48	72	0	128.2	36	A	SQSGGNTIAVAPDGGFKFEPSELTV	S	-0.2	3.82	
4	Q9HR99|Q9HR99	1	2594.25	9.1	48	73	0	66.2	36	A	SQSGGNTIAVAPDGGFKFEPSELTVS	V	-0.2	3.82	
4	Q9HR99|Q9HR99	1	3073.3611	0.4	106	134	0	91.2	33	A	SGFGTMDKDGNQFAVVDAGETLEHTFETA	G	-0.4	3.74	
5	Q9HN93|Q9HN93	1	1239.5156	-6.1	118	128	0	77.7	30	A	DWGGHDPIENT	G	-1.5	3.7	
5	Q9HN93|Q9HN93	1	1326.5517	-4.5	38	49	0	62.2	29	A	QAYDGWFSGDAK	G	-1.0	3.88	Gln->pyro-Glu (N-term Q)
5	Q9HN93|Q9HN93	1	1332.6099	-2.1	98	108	0	38.4	34	V	SFEWVSNTHNI	L	-0.5	5.12	
5	Q9HN93|Q9HN93	1	1398.6528	-0.8	206	217	0	39.5	34	V	SYYRRTPAPDSS	G	-1.6	9.58	
5	Q9HN93|Q9HN93	1	1440.5946	-5.5	38	51	0	95.0	28	A	QAYDGWFSGDAKGG	A	-0.9	3.88	Gln->pyro-Glu (N-term Q)
5	Q9HN93|Q9HN93	1	1564.7481	-6.4	103	117	0	51.3	35	V	SNTHNILIDAQPDGA	D	-0.5	3.88	
5	Q9HN93|Q9HN93	1	1610.7002	1.7	38	53	0	96.9	32	A	QAYDGWFSGDAKGGAV	G	-0.4	3.88	Gln->pyro-Glu (N-term Q)
5	Q9HN93|Q9HN93	1	1667.7216	0.1	38	54	0	106.3	32	A	QAYDGWFSGDAKGGAVG	N	-0.4	3.88	Gln->pyro-Glu (N-term Q)
5	Q9HN93|Q9HN93	1	1711.7479	-2.3	129	143	0	73.1	32	T	GFTHTHTFDTEGVYT	Y	-0.6	5.04	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
5	Q9HN93|Q9HN93	1	1755.7853	-2.0	37	54	0	90.3	33	A	AQAYDGWFSGDAKGGAVG	N	-0.3	3.88	
5	Q9HN93|Q9HN93	1	1761.737	6.6	240	254	0	54.0	31	A	FEPDTELGHDEYDPV	G	-1.3	3.38	
5	Q9HN93|Q9HN93	1	1832.7741	-2.8	239	254	0	68.9	30	D	AFEPDTELGHDEYDPV	G	-1.1	3.38	
5	Q9HN93|Q9HN93	1	1990.8432	-25.8	239	256	0	56.6	26	D	AFEPDTELGHDEYDPVGT	L	-1.0	3.38	
5	Q9HN93|Q9HN93	1	2018.8382	11.0	237	254	0	39.6	31	E	ADAFEPDTELGHDEYDPV	G	-1.1	3.28	
5	Q9HN93|Q9HN93	1	2213.0389	4.4	98	117	0	147.7	35	V	SFEWVSNTHNILIDAQPDGA	D	-0.3	3.7	
5	Q9HN93|Q9HN93	1	2418.0401	5.8	38	61	0	176.6	32	A	QAYDGWFSGDAKGGAVGNYDGTTV	D	-0.5	3.6	Gln->pyro-Glu (N-term Q)
5	Q9HN93|Q9HN93	1	2583.1726	4.9	62	87	0	52.4	34	V	DRTGTDEVTIDVGVDANGGTYGFGPA	A	-0.4	3.36	
5	Q9HN93|Q9HN93	1	2790.2158	2.1	38	64	0	199.1	32	A	QAYDGWFSGDAKGGAVGNYDGTTVDRT	G	-0.8	3.88	Gln->pyro-Glu (N-term Q)
5	Q9HN93|Q9HN93	1	2804.2049	-5.6	210	236	0	39.1	30	R	RTPAPDSSGAFDYEPGGDTDDQPAIPE	A	-1.2	3.22	
5	Q9HN93|Q9HN93	1	3291.4229	0.9	38	69	0	83.0	31	A	QAYDGWFSGDAKGGAVGNYDGTTVDRTGTDEV	T	-0.8	3.64	Gln->pyro-Glu (N-term Q)
5	Q9HN93|Q9HN93	1	3444.5018	-2.8	206	237	0	41.2	31	V	SYYRRTPAPDSSGAFDYEPGGDTDDQPAIPEA	D	-1.2	3.58	
5	Q9HN93|Q9HN93	1	3505.5547	15.3	38	71	0	63.8	35	A	QAYDGWFSGDAKGGAVGNYDGTTVDRTGTDEVTI	D	-0.6	3.64	Gln->pyro-Glu (N-term Q)
6	Q9HMI3|Q9HMI3	1	1172.619	-5.7	556	566	0	53.9	35	V	GGPFLDRVELA	-	0.2	4.08	
6	Q9HMI3|Q9HMI3	1	1319.6986	-2.2	181	191	0	36.9	34	T	QQYAPFLRNLA	I	-0.4	9.84	
6	Q9HMI3|Q9HMI3	1	1358.7194	-4.9	554	566	0	64.0	35	T	SVGGPFLDRVELA	-	0.5	4.08	
6	Q9HMI3|Q9HMI3	1	1475.7157	-0.9	390	402	0	61.1	35	A	TFSNPRGYNPNPI	Q	-1.2	9.84	
6	Q9HMI3|Q9HMI3	1	1554.7103	1.4	237	250	0	45.1	34	V	RLTAFDDYWGGAPS	V	-0.5	3.88	
6	Q9HMI3|Q9HMI3	1	1577.8202	-2.9	178	190	0	59.0	35	I	DLTQQYAPFLRNL	A	-0.5	6.7	
6	Q9HMI3|Q9HMI3	1	1648.8573	-5.1	178	191	0	50.7	35	I	DLTQQYAPFLRNLA	I	-0.3	6.7	
6	Q9HMI3|Q9HMI3	1	1793.8221	3.7	222	236	0	102.8	34	T	GPFEFDQLDNETQRV	R	-1.2	3.58	
6	Q9HMI3|Q9HMI3	1	1808.9309	17.6	78	93	0	102.9	34	V	TNQIFDTLIQFKPGTS	G	-0.3	6.76	
6	Q9HMI3|Q9HMI3	1	1852.8228	2.4	220	235	0	107.9	33	V	GTGPFEFDQLDNETQR	V	-1.5	3.58	
6	Q9HMI3|Q9HMI3	1	1881.8745	1.1	460	476	0	110.0	35	V	LLHPGTDIDDVPADQNY	I	-0.7	3.42	
6	Q9HMI3|Q9HMI3	1	1951.8912	1.1	220	236	0	140.2	34	V	GTGPFEFDQLDNETQRV	R	-1.1	3.58	
6	Q9HMI3|Q9HMI3	1	1994.9585	-4.4	460	477	0	89.1	35	V	LLHPGTDIDDVPADQNYI	A	-0.4	3.42	
6	Q9HMI3|Q9HMI3	1	2016.929	0.9	53	69	0	38.7	35	E	LVYSRGDHPQNYDPQQT	T	-1.7	5.1	
6	Q9HMI3|Q9HMI3	1	2209.1267	-2.9	78	97	0	94.8	36	V	TNQIFDTLIQFKPGTSGELT	S	-0.3	4.08	
6	Q9HMI3|Q9HMI3	1	2296.1587	-6.4	78	98	0	111.5	36	V	TNQIFDTLIQFKPGTSGELTS	G	-0.3	4.08	
6	Q9HMI3|Q9HMI3	1	2310.1339	1.6	198	219	0	64.2	36	I	LSRDQIESLGADAQPELGTDPV	G	-0.5	3.42	
6	Q9HMI3|Q9HMI3	1	2494.2551	2.2	196	219	0	98.1	36	A	AILSRDQIESLGADAQPELGTDPV	G	-0.2	3.42	
6	Q9HMI3|Q9HMI3	1	2565.2922	2.0	195	219	0	44.2	36	A	AAILSRDQIESLGADAQPELGTDPV	G	-0.1	3.42	
6	Q9HMI3|Q9HMI3	1	3202.4691	5.2	207	236	0	72.6	35	L	GADAQPELGTDPVGTGPFEFDQLDNETQRV	R	-0.9	3.28	
7	Q48302|Q48302	1	904.5059	-11.4	82	89	0	33.8	32	V	VFVVPTPF	-	1.8	6.02	
7	Q48302|Q48302	1	979.4723	-5.6	40	49	0	47.4	33	A	GYAERGIGSA	A	-0.3	6.88	
7	Q48302|Q48302	1	1012.5375	-0.3	18	27	0	45.6	33	S	NMPAITPKAA	A	0.1	10.1	
7	Q48302|Q48302	1	1050.5094	1.8	39	49	0	50.1	34	A	AGYAERGIGSA	A	-0.1	6.88	
7	Q48302|Q48302	1	1099.5695	-3.4	17	27	0	54.8	35	G	SNMPAITPKAA	A	0.0	10.1	
7	Q48302|Q48302	1	1149.5778	-2.2	40	51	0	63.8	34	A	GYAERGIGSAAV	G	0.2	6.88	
7	Q48302|Q48302	1	1156.591	-1.7	16	27	0	54.2	34	T	GSNMPAITPKAA	A	-0.1	10.1	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
7	Q48302|Q48302	1	1206.5993	0.7	40	52	0	38.1	35	A	GYAERGIGSAAVG	A	0.2	6.88	
7	Q48302|Q48302	1	1220.6149	-4.8	39	51	0	54.4	34	A	AGYAERGIGSAAV	G	0.4	6.88	
7	Q48302|Q48302	1	1234.6306	-0.8	36	48	0	60.9	34	A	ALAAGYAERGIGS	A	0.3	6.88	
7	Q48302|Q48302	1	1234.6306	-2.8	37	49	0	68.2	35	A	LAAGYAERGIGSA	A	0.3	6.88	
7	Q48302|Q48302	1	1277.6364	-0.9	40	53	0	103.4	35	A	GYAERGIGSAAVGA	I	0.3	6.88	
7	Q48302|Q48302	1	1305.6677	2.4	36	49	0	72.1	34	A	ALAAGYAERGIGSA	A	0.4	6.88	
7	Q48302|Q48302	1	1348.6735	-0.3	39	53	0	95.6	35	A	AGYAERGIGSAAVGA	I	0.4	6.88	
7	Q48302|Q48302	1	1386.6813	-1.9	14	27	0	47.5	35	A	ETGSNMPAITPKAA	A	-0.4	6.94	
7	Q48302|Q48302	1	1457.7184	-10.2	13	27	0	101.0	35	L	AETGSNMPAITPKAA	A	-0.2	6.94	
7	Q48302|Q48302	1	1473.7133	-1.8	13	27	0	38.4	35	L	AETGSNMPAITPKAA	A	-0.2	6.94	Oxidation (M)
7	Q48302|Q48302	1	1475.7732	-4.6	36	51	0	49.2	35	A	ALAAGYAERGIGSAAV	G	0.8	6.88	
7	Q48302|Q48302	1	1603.8318	0.6	36	53	0	83.8	35	A	ALAAGYAERGIGSAAVGA	I	0.7	6.88	
7	Q48302|Q48302	1	1683.8865	-3.9	11	27	0	110.4	35	T	ILAETGSNMPAITPKAA	A	0.3	6.94	
7	Q48302|Q48302	1	1901.037	3.6	28	48	0	90.6	33	A	AALAVGLAALAAGYAERGIGS	A	1.1	6.88	
7	Q48302|Q48302	1	1972.0741	-2.0	28	49	0	71.7	33	A	AALAVGLAALAAGYAERGIGSA	A	1.1	6.88	
8	Q9HHN1|Q9HHN1	1	939.4563	0.3	195	201	0	47.6	33	V	DLWDHVR	G	-1.1	5.1	
8	Q9HHN1|Q9HHN1	1	1534.6949	3.6	421	434	0	95.8	34	S	EPMIPWNSGGVFMA	S	0.3	3.3	
8	Q9HHN1|Q9HHN1	1	1571.674	-1.9	395	407	0	37.0	31	T	FRDLNDEYDLDGT	S	-1.3	3.36	
8	Q9HHN1|Q9HHN1	1	1585.7049	6.9	9	21	0	53.6	33	S	YEDFDPEKRPSFG	Q	-1.7	4.06	
8	Q9HHN1|Q9HHN1	1	1672.7369	13.0	8	21	0	86.5	34	R	SYEDFDPEKRPSFG	Q	-1.7	4.06	
8	Q9HHN1|Q9HHN1	1	1803.7621	0.2	393	407	0	88.1	30	G	MTFRDLNDEYDLDGT	S	-1.1	3.36	
8	Q9HHN1|Q9HHN1	1	2038.9881	-2.9	166	185	0	40.6	35	A	GAILSGVYMGDKQSPLSDTT	L	-0.1	3.88	
8	Q9HHN1|Q9HHN1	1	2045.9728	5.2	411	428	0	81.0	36	S	RTLEETGTVSEPMIPWNS	G	-0.7	3.96	
8	Q9HHN1|Q9HHN1	1	2054.9334	8.8	5	21	0	94.9	35	F	EPRSYEDFDPEKRPSFG	Q	-1.9	4.28	
8	Q9HHN1|Q9HHN1	1	2090.9103	8.8	393	410	0	33.4	33	G	MTFRDLNDEYDLDGTSLS	R	-0.8	3.36	
8	Q9HHN1|Q9HHN1	1	2169.9889	9.9	389	407	0	49.3	35	I	VIPGMTFRDLNDEYDLDGT	S	-0.5	3.36	
8	Q9HHN1|Q9HHN1	1	2283.0729	-4.8	388	407	0	59.9	35	S	IVIPGMTFRDLNDEYDLDGT	S	-0.3	3.36	
8	Q9HHN1|Q9HHN1	1	2336.1934	1.3	166	188	0	49.8	36	A	GAILSGVYMGDKQSPLSDTTLLA	S	0.3	3.88	
8	Q9HHN1|Q9HHN1	1	2430.1128	1.3	2	21	0	44.0	35	M	VEFEPRSYEDFDPEKRPSFG	Q	-1.5	4.12	
8	Q9HHN1|Q9HHN1	1	2608.2302	0.7	411	434	0	152.4	36	S	RTLEETGTVSEPMIPWNSGGVFMA	S	-0.1	3.96	
8	Q9HHN1|Q9HHN1	1	2624.2251	1.6	411	434	0	56.4	35	S	RTLEETGTVSEPMIPWNSGGVFMA	S	-0.1	3.96	Oxidation (M)
8	Q9HHN1|Q9HHN1	1	2895.3783	0.7	408	434	0	36.1	36	T	SLSRTLEETGTVSEPMIPWNSGGVFMA	S	0.0	3.96	
8	Q9HHN1|Q9HHN1	1	2907.2943	2.9	383	407	0	68.0	34	A	DQYMSIVIPGMTFRDLNDEYDLDGT	S	-0.5	3.26	
10	Q9HM69|CSG	1	1133.6445	-2.6	677	686	0	35.2	31	Q	FRLVDGLTTI	E	0.9	6.78	
10	Q9HM69|CSG	1	1227.6459	-6.9	764	773	0	34.3	34	D	RQNVEIVEEL	E	-0.5	3.96	
10	Q9HM69|CSG	1	1244.6765	-3.1	676	686	0	82.9	34	Q	QFRLVDGLTTI	E	0.5	6.78	Gln->pyro-Glu (N-term Q)
10	Q9HM69|CSG	1	1261.703	-5.8	676	686	0	74.0	32	Q	QFRLVDGLTTI	E	0.5	6.78	
10	Q9HM69|CSG	1	1308.7877	4.2	840	852	0	54.4	26	V	AVLGAALLALRQN	-	1.1	11.04	
10	Q9HM69|CSG	1	1315.6045	-23.0	733	744	0	70.0	32	W	NSDGQWSVDVPL	S	-0.5	2.92	
10	Q9HM69|CSG	1	1664.7529	2.9	598	611	0	65.0	34	T	FDEEDIDISELRQG	S	-1.0	3.38	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
10	Q9HM69|CSG	1	1909.8541	9.4	598	614	0	43.8	34	T	FDEEDIDISELRQGSAS	A	-0.8	3.38	
10	Q9HM69|CSG	1	2093.8774	2.3	747	765	0	74.1	30	N	VEPGNYTVEADDGDNTDRQ	N	-1.6	3.32	
10	Q9HM69|CSG	1	2207.9203	0.4	746	765	0	81.8	29	S	NVEPGNYTVEADDGDNTDRQ	N	-1.7	3.32	
10	Q9HM69|CSG	1	2265.9986	2.5	751	770	0	57.3	33	G	NYTVEADDGDNTDRQNVEIV	E	-1.2	3.32	
10	Q9HM69|CSG	1	2294.9523	1.9	745	765	0	108.4	29	L	SNVEPGNYTVEADDGDNTDRQ	N	-1.7	3.32	
10	Q9HM69|CSG	1	2384.0139	2.4	591	611	0	92.1	31	I	SVDSDDTFDEEDIDISELRQG	S	-1.1	3.12	
10	Q9HM69|CSG	1	2542.0831	12.0	591	613	0	73.9	32	I	SVDSDDTFDEEDIDISELRQGSA	S	-1.0	3.12	
10	Q9HM69|CSG	1	2629.1151	5.8	591	614	0	115.6	31	I	SVDSDDTFDEEDIDISELRQGSAS	A	-1.0	3.12	
12	Q9HMG3|Q9HMG3	1	1037.5254	8.9	35	43	0	48.2	33	I	AQDVLEHRA	S	-0.7	5.22	
12	Q9HMG3|Q9HMG3	1	1494.6515	0.5	44	56	0	33.1	32	A	STVPETDFPEPYN	R	-1.2	2.94	
12	Q9HMG3|Q9HMG3	1	1650.7526	-0.8	44	57	0	97.1	34	A	STVPETDFPEPYNR	S	-1.4	3.82	
12	Q9HMG3|Q9HMG3	1	1737.7846	-1.0	44	58	0	117.7	34	A	STVPETDFPEPYNRS	I	-1.4	3.82	
12	Q9HMG3|Q9HMG3	1	2207.0131	1.1	44	65	0	85.0	35	A	STVPETDFPEPYNRSIGGGGGA	G	-0.7	3.82	
12	Q9HMG3|Q9HMG3	1	2264.0346	5.2	44	66	0	135.3	35	A	STVPETDFPEPYNRSIGGGGGAG	A	-0.7	3.82	
12	Q9HMG3|Q9HMG3	1	2335.0717	-1.4	44	67	0	107.0	34	A	STVPETDFPEPYNRSIGGGGGAGA	V	-0.6	3.82	
12	Q9HMG3|Q9HMG3	1	2434.1401	4.2	44	68	0	63.2	36	A	STVPETDFPEPYNRSIGGGGGAGAV	A	-0.4	3.82	
12	Q9HMG3|Q9HMG3	1	2505.1772	3.0	44	69	0	107.0	36	A	STVPETDFPEPYNRSIGGGGGAGAVA	G	-0.3	3.82	
12	Q9HMG3|Q9HMG3	1	2514.1663	-1.3	35	56	0	37.4	35	I	AQDVLEHRASTVPETDFPEPYN	R	-1.0	3.92	
12	Q9HMG3|Q9HMG3	1	2562.1987	4.0	44	70	0	47.1	36	A	STVPETDFPEPYNRSIGGGGGAGAVAG	G	-0.3	3.82	
12	Q9HMG3|Q9HMG3	1	2690.2573	1.8	44	72	0	60.5	36	A	STVPETDFPEPYNRSIGGGGGAGAVAGGA	E	-0.3	3.82	
12	Q9HMG3|Q9HMG3	1	2757.2994	-6.9	35	58	0	46.0	35	I	AQDVLEHRASTVPETDFPEPYNRS	I	-1.1	4.28	
12	Q9HMG3|Q9HMG3	1	2906.3319	-4.2	44	74	0	36.7	34	A	STVPETDFPEPYNRSIGGGGGAGAVAGGAES	E	-0.4	3.68	
13	Q9HRQ9|Q9HRQ9	1	1164.5597	1.5	183	193	0	83.9	35	R	SPHEMGVPIQA	H	-0.2	5.12	
13	Q9HRQ9|Q9HRQ9	1	1398.6681	-6.8	102	113	0	57.9	34	V	KWVWEGSTGHNV	H	-0.8	7.82	
13	Q9HRQ9|Q9HRQ9	1	1497.7576	-3.5	78	91	0	50.7	35	T	VKVGPNNQNVFDPA	E	-0.6	6.76	
13	Q9HRQ9|Q9HRQ9	1	1626.8002	-1.5	79	93	0	90.2	35	V	KVGPNNQNVFDPAEV	Y	-0.8	4.08	
13	Q9HRQ9|Q9HRQ9	1	1674.8148	0.5	175	191	0	100.5	36	S	GGGGPVERSPHEMGVPI	Q	-0.4	5.3	
13	Q9HRQ9|Q9HRQ9	1	1707.8118	4.3	102	116	0	104.8	35	V	KWVWEGSTGHNVHAT	S	-0.8	7.96	
13	Q9HRQ9|Q9HRQ9	1	1725.8686	-0.6	78	93	0	84.3	35	T	VKVGPNNQNVFDPAEV	Y	-0.4	4.08	
13	Q9HRQ9|Q9HRQ9	1	1873.9105	-1.0	175	193	0	88.5	36	S	GGGGPVERSPHEMGVPIQA	H	-0.5	5.3	
13	Q9HRQ9|Q9HRQ9	1	1955.0112	2.0	76	93	0	73.2	35	T	KTVKVGPNNQNVFDPAEV	Y	-0.7	6.98	
13	Q9HRQ9|Q9HRQ9	1	2306.0716	-13.4	102	122	0	96.1	34	V	KWVWEGSTGHNVHATSVPDEA	G	-0.7	5.18	
13	Q9HRQ9|Q9HRQ9	1	2445.1812	8.3	79	101	0	87.2	36	V	KVGPNNQNVFDPAEVYVSPGDTV	K	-0.5	3.7	
13	Q9HRQ9|Q9HRQ9	1	2544.2497	-4.2	78	101	0	47.9	36	T	VKVGPNNQNVFDPAEVYVSPGDTV	K	-0.3	3.7	
14	Q9HSA8|Q9HSA8	1	927.445	2.6	59	66	0	41.1	33	L	TVFGEYRG	L	-0.5	6.88	
14	Q9HSA8|Q9HSA8	1	953.4971	9.1	61	68	0	37.6	32	V	FGEYRGLL	E	0.0	6.88	
14	Q9HSA8|Q9HSA8	1	1236.6139	2.3	61	71	0	69.8	34	V	FGEYRGLLEPG	I	-0.5	4.26	
14	Q9HSA8|Q9HSA8	1	1274.5965	0.0	83	92	0	41.6	35	T	YTFDMRTQTI	D	-0.6	6.7	
14	Q9HSA8|Q9HSA8	1	1463.7409	-1.3	61	73	0	70.2	35	V	FGEYRGLLEPGIN	V	-0.3	4.26	
14	Q9HSA8|Q9HSA8	1	1672.7944	2.0	165	178	0	43.0	35	R	IRTELDEPTDEWGI	R	-1.0	3.5	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
14	Q9HSA8|Q9HSA8	1	1706.9719	-4.3	66	81	0	46.7	30	R	GLLEPGINVIPPFVSR	T	0.6	6.98	
14	Q9HSA8|Q9HSA8	1	2017.0673	0.2	61	78	0	120.2	34	V	FGEYRGLLEPGINVIPPF	V	0.2	4.26	
14	Q9HSA8|Q9HSA8	1	2203.1677	2.0	61	80	0	119.1	34	V	FGEYRGLLEPGINVIPPFVS	R	0.4	4.26	
14	Q9HSA8|Q9HSA8	1	2359.2688	3.9	61	81	0	45.9	33	V	FGEYRGLLEPGINVIPPFVSR	T	0.1	7.04	
15	Q9HRS0|Q9HRS0	1	1286.6156	-0.9	119	129	0	52.0	35	V	RFVWESGGHNV	H	-0.5	7.84	
15	Q9HRS0|Q9HRS0	1	1327.6408	-4.9	145	156	0	85.7	34	T	DIAGPPKEYTHT	F	-1.2	5.22	
15	Q9HRS0|Q9HRS0	1	1475.6067	-1.2	219	230	0	64.6	29	A	YFFMKYGGDYGE	-	-0.7	4.08	
15	Q9HRS0|Q9HRS0	1	1478.7592	-4.3	103	115	0	49.6	34	S	NVFKPAEMYVKPG	T	-0.4	9.62	
15	Q9HRS0|Q9HRS0	1	1595.7593	0.1	119	132	0	58.1	35	V	RFVWESGGHNVHAT	E	-0.6	8	
15	Q9HRS0|Q9HRS0	1	1917.8956	-1.5	183	200	0	84.7	35	V	TDSPPENKGYQTIVPDSA	K	-1.1	3.7	
15	Q9HRS0|Q9HRS0	1	2344.1798	8.0	179	200	0	96.7	36	G	TIIVTDSPPENKGYQTIVPDSA	K	-0.4	3.7	
15	Q9HRS0|Q9HRS0	1	2541.166	1.4	133	156	0	45.0	35	T	EVPGDADWGVSTDIAGPPKEYTHT	F	-0.8	3.84	
15	Q9HRS0|Q9HRS0	1	2570.1602	-12.0	145	167	0	70.5	32	T	DIAGPPKEYTHTFDGPTGEYNYV	C	-1.0	4.06	
15	Q9HRS0|Q9HRS0	1	2809.2845	3.0	119	144	0	61.0	35	V	RFVWESGGHNVHATEVPGDADWGVST	D	-0.5	4.52	
16	Q9HSS1|Q9HSS1	1	940.4866	-2.6	249	258	0	35.7	32	A	LAGALEDGPV	S	0.6	3	
16	Q9HSS1|Q9HSS1	1	1051.5451	-7.0	153	162	0	48.7	33	V	GFVGFGEIAR	G	0.7	6.98	
16	Q9HSS1|Q9HSS1	1	1207.635	-3.4	153	164	0	75.4	33	V	GFVGFGEIARGV	A	0.9	6.98	
16	Q9HSS1|Q9HSS1	1	1232.6401	-6.0	210	220	0	42.6	35	V	FAPLTEETRGL	V	-0.2	4.26	
16	Q9HSS1|Q9HSS1	1	1253.5829	-12.8	134	145	0	73.9	33	R	GGWAWNDAPAPL	R	-0.3	3.1	
16	Q9HSS1|Q9HSS1	1	1409.684	-2.3	133	145	0	61.3	34	R	RGGWAWNDAPAPL	R	-0.6	6.78	
16	Q9HSS1|Q9HSS1	1	1593.8151	-0.8	149	164	0	57.8	34	A	DATVGFVGFGEIARGV	A	0.8	4.08	
16	Q9HSS1|Q9HSS1	1	1646.8152	-2.7	210	224	0	37.1	35	V	FAPLTEETRGLVDEA	A	-0.2	3.68	
16	Q9HSS1|Q9HSS1	1	1888.0306	0.1	262	279	0	102.3	33	A	ALDVLPTEPPVESPLVGR	S	0.1	3.82	
16	Q9HSS1|Q9HSS1	1	1959.0677	4.3	261	279	0	87.4	33	A	AALDVLPTEPPVESPLVGR	S	0.2	3.82	
16	Q9HSS1|Q9HSS1	1	2736.4698	8.0	262	287	0	44.1	33	A	ALDVLPTEPPVESPLVGRSDVLVTPH	C	0.2	4.06	
16	Q9HSS1|Q9HSS1	1	2807.5069	-0.3	261	287	0	65.3	34	A	AALDVLPTEPPVESPLVGRSDVLVTPH	C	0.2	4.06	
17	Q9HN95|Q9HN95	1	940.5018	5.1	454	463	0	65.8	32	V	LAPGSPGFPV	-	0.6	6.02	
17	Q9HN95|Q9HN95	1	1064.5403	-6.4	224	233	0	66.5	34	R	GGSGYIGWLR	A	-0.1	9.84	
17	Q9HN95|Q9HN95	1	1139.5764	-7.2	31	40	0	75.7	33	T	FYPPLQAHPA	F	-0.3	7.76	
17	Q9HN95|Q9HN95	1	1240.6241	2.4	30	40	0	39.1	34	Y	TFYPPLQAHPA	F	-0.3	7.76	
17	Q9HN95|Q9HN95	1	1296.631	0.9	69	79	0	39.9	34	A	DNPDERIPLQT	F	-1.6	3.7	
17	Q9HN95|Q9HN95	1	1403.6874	-2.0	29	40	0	42.0	35	L	YTFYPPLQAHPA	F	-0.4	7.7	
17	Q9HN95|Q9HN95	1	1450.8224	-0.3	140	151	0	44.5	30	A	YLAWYTILPKLA	G	0.8	9.52	
17	Q9HN95|Q9HN95	1	1516.7714	-4.5	28	40	0	87.6	36	V	LYTFYPPLQAHPA	F	-0.1	7.7	
17	Q9HN95|Q9HN95	1	1729.8828	-3.6	26	40	0	58.0	36	A	NVLYTFYPPLQAHPA	F	0.0	7.7	
17	Q9HN95|Q9HN95	1	2062.9901	1.4	176	193	0	62.7	36	V	GFHHQYTDPGIAEGFKFI	A	-0.4	6.02	
18	Q9HN94|Q9HN94	1	1209.5415	6.2	18	27	0	51.0	33	A	DNFRDPGVYQ	A	-1.5	3.88	
18	Q9HN94|Q9HN94	1	1516.6318	-2.7	28	40	0	99.8	30	Q	ADDDSYDVYVEAR	Q	-1.0	3.36	
18	Q9HN94|Q9HN94	1	1791.7588	2.2	28	42	0	87.0	31	Q	ADDDSYDVYVEARQF	A	-0.9	3.36	
18	Q9HN94|Q9HN94	1	2161.9335	-3.7	1	21	0	210.1	31	-	MVGDDGGTVNPDNPTAADNFR	D	-0.9	3.42	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
18	Q9HN94|Q9HN94	1	2821.225	-2.4	1	27	0	126.3	31	-	MVGDDGGTVNPDNPTAADNFRDPGVYQ	A	-0.9	3.3	
19	Q9HRL3|Q9HRL3	1	1103.5651	-7.9	586	595	0	62.8	35	A	WLLYSGPAPT	K	0.2	5.92	
19	Q9HRL3|Q9HRL3	1	1311.6169	2.4	274	285	0	77.5	34	T	WLPDAMEGPTPV	S	-0.2	3	
19	Q9HRL3|Q9HRL3	1	1876.9472	-3.7	524	540	0	87.9	36	T	GLHIEFLHTWLAGPEGT	A	0.1	5.12	
19	Q9HRL3|Q9HRL3	1	1916.9592	-2.6	630	648	0	58.8	36	L	ARGADTFDQGVIDGIVNAV	S	0.3	3.6	
19	Q9HRL3|Q9HRL3	1	1977.9949	-19.5	523	540	0	105.1	36	A	TGLHIEFLHTWLAGPEGT	A	0.1	5.12	
19	Q9HRL3|Q9HRL3	1	2106.0245	-4.6	267	285	0	41.3	36	S	AQFPLHTWLPDAMEGPTPV	S	-0.1	4.06	
20	Q9HMF1|Q9HMF1	1	1198.5982	-7.7	160	169	0	71.4	34	V	RLEGELPEWA	T	-0.9	3.96	
20	Q9HMF1|Q9HMF1	1	1411.7095	-0.6	158	169	0	70.8	34	V	NVRLEGELPEWA	T	-0.7	3.96	
20	Q9HMF1|Q9HMF1	1	1931.984	0.1	191	208	0	82.6	36	K	VLEYTGPGVESLSVPERT	T	-0.2	3.96	
20	Q9HMF1|Q9HMF1	1	2193.0073	1.6	581	599	0	52.7	35	L	NIDEETYARIEQGDDVEVV	D	-0.8	3.32	
20	Q9HMF1|Q9HMF1	1	2948.3775	7.6	434	462	0	110.0	36	Y	SGGYGAGDTDIITPEESIDDDLIKGPNIS	S	-0.5	3.22	
20	Q9HMF1|Q9HMF1	1	3198.4728	-1.6	432	462	0	40.8	35	T	SYSGGYGAGDTDIITPEESIDDDLIKGPNIS	S	-0.5	3.22	
21	Q9HMT7|Q9HMT7	1	1497.6736	-9.3	148	161	0	69.8	32	S	ATDYDASGPFEGIR	A	-0.7	3.7	
21	Q9HMT7|Q9HMT7	1	1559.6892	4.8	150	163	0	40.1	33	T	DYDASGPFEGIRAY	R	-0.7	3.7	
21	Q9HMT7|Q9HMT7	1	1702.7322	-0.9	44	59	0	127.6	31	V	DVDTEAYEESHAPGAI	G	-0.7	3.5	
21	Q9HMT7|Q9HMT7	1	1731.774	6.4	148	163	0	67.8	34	S	ATDYDASGPFEGIRAY	R	-0.6	3.7	
21	Q9HMT7|Q9HMT7	1	2369.1751	4.1	178	199	0	64.7	36	L	VDVRSPEEFSGEILAPPGLQET	A	-0.4	3.58	
21	Q9HMT7|Q9HMT7	1	2564.0074	4.8	126	147	0	66.1	25	L	DGGRDYWMDNDYPTSEEPPSFS	A	-1.7	3.32	
22	Q9HND8|VATI	1	1332.631	-3.1	364	374	0	44.7	35	I	NRPQYTEIDPT	V	-1.8	4.08	
22	Q9HND8|VATI	1	1445.715	-3.9	363	374	0	52.3	35	V	INRPQYTEIDPT	V	-1.3	4.08	
22	Q9HND8|VATI	1	1530.7678	-4.5	364	376	0	44.1	36	I	NRPQYTEIDPTVV	L	-0.9	4.08	
22	Q9HND8|VATI	1	1544.7835	-0.6	362	374	0	38.4	35	E	VINRPQYTEIDPT	V	-0.9	4.08	
22	Q9HND8|VATI	1	1673.826	-1.1	361	374	0	73.3	36	T	EVINRPQYTEIDPT	V	-1.1	3.82	
22	Q9HND8|VATI	1	1871.9629	-2.7	361	376	0	82.0	36	T	EVINRPQYTEIDPTVV	L	-0.4	3.82	
22	Q9HND8|VATI	1	2086.0946	-5.8	359	376	0	48.6	35	S	LTEVINRPQYTEIDPTVV	L	-0.2	3.82	
23	Q9HRR1|Q9HRR1	1	713.4799	27.2	189	194	0	30.0	18	P	ILIIRS	P	2.0	11.04	
23	Q9HRR1|Q9HRR1	1	2366.0986	29.8	26	51	0	172.2	36	A	GAGTAGTAVLESVTNPTGSGGGQTNY	F	-0.3	3.3	
23	Q9HRR1|Q9HRR1	1	2719.1198	13.6	151	174	0	124.0	30	V	NIDEFDDYDTWENDYGDAGIGKPA	K	-1.3	3.16	
24	Q9HRR0|Q9HRR0	1	1333.6051	3.3	7	17	0	55.2	34	S	NYGDIHRYEPA	S	-1.5	5.22	
24	Q9HRR0|Q9HRR0	1	1420.6371	0.4	6	17	0	72.0	33	G	SNYGDIHRYEPA	S	-1.4	5.22	
24	Q9HRR0|Q9HRR0	1	1459.6653	1.0	109	120	0	64.1	34	T	SMFENTVEQFKT	A	-0.7	4.26	
24	Q9HRR0|Q9HRR0	1	1477.6586	2.5	5	17	0	46.5	34	K	GSNYGDIHRYEPA	S	-1.4	5.22	
24	Q9HRR0|Q9HRR0	1	1530.7024	3.9	109	121	0	78.9	35	T	SMFENTVEQFKTA	L	-0.5	4.26	
24	Q9HRR0|Q9HRR0	1	1592.7834	-3.2	94	105	0	36.1	35	R	KWEDLYIREDQV	D	-1.3	4.06	
25	Q9HSQ7|Q9HSQ7	1	2034.8039	2.8	7	24	0	40.6	26	D	NEGDDDPFEEQRADVDNA	M	-1.9	3.2	
25	Q9HSQ7|Q9HSQ7	1	2039.9283	8.3	358	375	0	63.1	35	M	NEPSRIEENPDADELVVD	D	-1.2	3.32	
25	Q9HSQ7|Q9HSQ7	1	2040.9124	5.0	359	376	0	58.8	34	N	EPSRIEENPDADELVVDD	G	-1.2	3.24	
25	Q9HSQ7|Q9HSQ7	1	2154.9553	3.1	358	376	0	109.1	33	M	NEPSRIEENPDADELVVDD	G	-1.3	3.24	
26	Q9HRL1|Q9HRL1	1	1517.7878	-0.8	335	347	0	52.8	35	I	NSALSLFYYSRVV	K	0.6	9.58	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
26	Q9HRL1|Q9HRL1	1	1940.948	-0.6	350	366	0	58.2	35	A	LWIEDPRDDLSLSGQPT	G	-0.8	3.5	
26	Q9HRL1|Q9HRL1	1	2070.984	-2.2	131	149	0	52.4	35	A	SVPFHFWAPEAYEGAPAPV	S	0.1	4.24	
26	Q9HRL1|Q9HRL1	1	2142.0211	-0.8	130	149	0	134.1	35	T	ASVPFHFWAPEAYEGAPAPV	S	0.2	4.24	
27	Q9HNB9|Q9HNB9	1	1631.6587	1.3	26	38	0	77.7	28	Q	SDDQYEETRDVEF	D	-1.9	3.38	
27	Q9HNB9|Q9HNB9	1	1746.6857	-3.6	26	39	0	79.1	25	Q	SDDQYEETRDVEFD	L	-2.0	3.28	
27	Q9HNB9|Q9HNB9	1	2444.0139	-0.8	26	46	0	91.2	28	Q	SDDQYEETRDVEFDLPAEDTA	V	-1.4	3.16	
28	Q9HQP2|Q9HQP2	1	1263.6976	-0.5	162	172	0	38.8	31	L	GLLPGYFLQRT	L	0.2	9.84	
28	Q9HQP2|Q9HQP2	1	1269.5778	-19.5	208	217	0	32.1	32	V	FEQFRAWDAT	G	-0.7	4.08	
29	Q9HHP3|Q9HHP3	1	1600.7594	-3.8	228	241	0	50.5	35	A	AVDPESGDQVWRRS	L	-1.2	4.3	
29	Q9HHP3|Q9HHP3	1	1615.7519	-0.1	39	53	0	54.4	35	I	QDAPVGEVTGPWPTY	Q	-0.6	3	
29	Q9HHP3|Q9HHP3	1	1671.7965	-2.1	227	241	0	38.2	35	V	AAVDPESGDQVWRRS	L	-1.0	4.3	
29	Q9HHP3|Q9HHP3	1	1911.8599	3.6	111	126	0	85.4	34	T	SFDINENTRSWNVETT	G	-1.2	3.82	
31	Q9HQA6|Q9HQA6	1	925.4869	-5.8	300	307	0	37.4	32	S	VSPEELRP	S	-0.9	4.26	
31	Q9HQA6|Q9HQA6	1	1176.5411	7.1	96	105	0	77.1	35	D	FEDATDINPR	K	-1.2	3.7	
31	Q9HQA6|Q9HQA6	1	1291.5681	1.1	95	105	0	77.5	33	D	DFEDATDINPR	K	-1.4	3.5	
32	Q9HMW4|Q9HMW4	1	1411.6884	1.0	348	359	0	53.2	34	K	NPYRSWSGYLGI	N	-0.6	9.58	
32	Q9HMW4|Q9HMW4	1	1578.7467	-1.8	402	415	0	47.1	35	T	LHPTWGPYAPENPT	T	-1.1	5.12	
32	Q9HMW4|Q9HMW4	1	2202.097	-6.2	252	270	0	37.0	36	A	AFNGNLGPWDLKRWSQQSV	M	-0.8	10.08	
32	Q9HMW4|Q9HMW4	1	2393.0692	-0.8	231	251	0	72.2	33	A	KPYVEAEDADGLEQDEEVMRA	A	-1.1	3.62	
32	Q9HMW4|Q9HMW4	1	2577.1904	-5.4	229	251	0	35.5	35	A	LAKPYVEAEDADGLEQDEEVMRA	A	-0.8	3.62	
33	Q9HQF4|Q9HQF4	1	1538.7577	-1.6	102	116	0	93.5	35	A	TEDGDPSVPGPIVRT	E	-0.7	3.7	
33	Q9HQF4|Q9HQF4	1	2539.1926	0.4	102	125	0	57.1	35	A	TEDGDPSVPGPIVRTEEGQDIEVT	L	-0.8	3.32	
33	Q9HQF4|Q9HQF4	1	2610.2297	-1.5	101	125	0	64.8	36	F	ATEDGDPSVPGPIVRTEEGQDIEVT	L	-0.7	3.32	
34	Q9HRL8|Q9HRL8	1	1243.5833	2.0	198	208	0	51.5	34	G	RNPFDTPEAPT	E	-1.5	4.08	
34	Q9HRL8|Q9HRL8	1	1826.8799	-5.1	192	208	0	64.0	35	A	NLAEVGRNPFDTPEAPT	E	-0.8	3.82	
34	Q9HRL8|Q9HRL8	1	1955.9225	0.9	192	209	0	74.6	35	A	NLAEVGRNPFDTPEAPTE	I	-1.0	3.68	
35	Q9HMX1|Q9HMX1	1	1760.8329	-1.8	111	126	0	53.3	35	L	SRDVIPNQGYNDPSTV	R	-1.0	3.88	
35	Q9HMX1|Q9HMX1	1	1987.0011	1.2	109	126	0	61.7	36	T	LLSRDVIPNQGYNDPSTV	R	-0.5	3.88	
35	Q9HMX1|Q9HMX1	1	2330.0146	0.6	497	519	0	43.6	32	A	NALGDGIRDAIDPESEGGSEEEA	A	-1.0	3.28	
36	Q9HM89|EF1A	1	1440.7937	-6.2	235	249	0	34.7	33	I	SGIGTVPVGRIETGV	M	0.5	6.98	
36	Q9HM89|EF1A	1	1443.7106	-1.3	280	293	0	67.1	35	N	AEPGDNVGFNVRGI	G	-0.3	4.08	
36	Q9HM89|EF1A	1	1521.71	-5.7	165	178	0	50.6	34	V	KDLFGQVGFNPDDA	K	-0.6	3.6	
36	Q9HM89|EF1A	1	1764.8319	2.8	162	178	0	87.0	35	V	SGVKDLFGQVGFNPDDA	K	-0.3	3.6	
37	Q9HR04|Q9HR04	1	1863.8024	1.0	94	108	0	66.5	32	I	NQYYDDFSATQQTQR	S	-1.9	3.88	
37	Q9HR04|Q9HR04	1	1950.8344	-1.3	94	109	0	60.9	31	I	NQYYDDFSATQQTQRS	S	-1.9	3.88	
37	Q9HR04|Q9HR04	1	2491.2442	6.1	52	75	0	52.7	36	A	IVQERPAPGGESIADLPDLEGELS	I	-0.4	3.44	
38	Q9HSM4|DHE42	1	1255.6925	-3.7	241	251	0	57.3	34	A	LLLDDWGARVV	A	0.8	3.88	
38	Q9HSM4|DHE42	1	2482.1282	5.8	142	165	0	93.3	35	F	AAELRDEVGPSQDIPAPDMGTDAQ	T	-0.8	3.32	
39	Q9HMB6|Q9HMB6	1	1825.9098	-5.0	5	21	0	69.8	35	A	VYQGPGEIAVEEVPKPD	I	-0.6	3.68	
39	Q9HMB6|Q9HMB6	1	2171.0747	2.9	65	85	0	129.2	36	I	VEEVGDDVTSVAPGDRVIAPF	A	0.2	3.42	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
40	Q9HMB7|Q9HMB7	1	1423.662	3.4	123	134	0	74.1	34	A	REEDDFSIFAPV	L	-0.4	3.58	
40	Q9HMB7|Q9HMB7	1	2308.0648	8.6	380	398	0	121.1	35	A	DVPEAWNDKYEEYLGVRPE	T	-1.4	3.82	
40	Q9HMB7|Q9HMB7	1	2511.1402	5.6	189	211	0	37.2	35	A	DIRDSDVTLADPFAGSQFDVDTQ	E	-0.5	3.22	
41	Q9HNL7|Q9HNL7	1	1405.7354	-3.8	12	23	0	35.7	34	F	GVPYNFERPKLS	A	-0.9	9.72	
41	Q9HNL7|Q9HNL7	1	1752.9199	-8.0	9	23	0	48.7	35	G	SLFGVPYNFERPKLS	A	-0.3	9.72	
41	Q9HNL7|Q9HNL7	1	1920.9444	0.0	28	44	0	84.2	36	S	AYWQPGEGMLVEKPFGI	G	-0.1	4.26	
41	Q9HNL7|Q9HNL7	1	2451.2798	2.9	2	23	0	101.7	35	M	VEKPTSGSLFGVPYNFERPKLS	A	-0.5	9.62	
42	Q9HP76|Q9HP76	1	1741.8886	-5.5	38	52	0	43.7	35	E	YIEELAELQDRVPPA	D	-0.4	3.68	
42	Q9HP76|Q9HP76	1	2314.1117	3.8	38	57	0	43.4	36	E	YIEELAELQDRVPPADWAEA	Q	-0.5	3.44	
45	Q9HRL9|Q9HRL9	1	1336.7139	-6.9	344	355	0	62.1	33	R	LGGVVWDIPEPR	A	0.0	4.08	
45	Q9HRL9|Q9HRL9	1	1556.841	-0.2	548	562	0	68.5	34	V	ATLGSLDVILGEVDR	-	0.6	3.7	
47	Q9HPB1|SECY	1	1086.4883	-8.8	55	63	0	42.4	32	A	GNDFFGQFR	S	-0.8	6.78	
47	Q9HPB1|SECY	1	1135.5696	-0.9	421	429	0	47.3	34	V	MERYIPQVT	V	-0.5	6.88	
48	Q9HM85|EF2	1	1379.8024	-3.0	614	625	0	38.8	29	A	LIDADIRLLEPI	Q	0.8	3.7	
48	Q9HM85|EF2	1	1786.8407	18.2	155	169	0	67.9	36	I	SELQEGPEEMQERLL	S	-1.2	3.68	
49	Q9HMU9|Q9HMU9	1	1069.4393	-3.3	37	45	0	35.1	29	A	GYGYFFDTT	T	-0.3	3.1	
49	Q9HMU9|Q9HMU9	1	1269.6254	-3.9	257	265	0	37.7	34	G	YWRFNTRDL	-	-1.4	9.84	
49	Q9HMU9|Q9HMU9	1	1731.8904	-0.1	193	207	0	42.8	35	T	SEDSILNLTPGRRQF	L	-0.8	7.04	
49	Q9HMU9|Q9HMU9	1	2168.0862	2.3	189	207	0	78.6	36	V	AYTTSEDSILNLTPGRRQF	L	-0.7	6.96	
50	Q9HNH3|Q9HNH3	1	1156.6088	22.0	390	400	0	36.1	34	G	PETTVRAGDVL	L	-0.1	4.08	
51	Q9HMH4|Q9HMH4	1	1344.5358	5.1	56	67	0	53.9	28	A	SFSYDDPDADTL	G	-0.9	2.74	
51	Q9HMH4|Q9HMH4	1	1773.7006	5.0	56	71	0	101.6	26	A	SFSYDDPDADTLGWEG	G	-1.0	2.72	
54	Q9HP84|HTR4	1	731.4582	-4.6	324	330	0	29.2	26	T	GILGFIL	V	2.7	6.02	
57	Q9HSC3|LONH	1	1309.7241	-7.3	403	414	0	62.5	32	F	APDAIRELILEA	K	0.5	3.82	
58	Q9HMX0|Q9HMX0	1	1880.9785	2.3	188	205	0	36.1	35	S	NALQHLFSGIDPFAGVPV	L	0.6	4.94	
58	Q9HMX0|Q9HMX0	1	1968.0105	2.3	187	205	0	78.8	35	T	SNALQHLFSGIDPFAGVPV	L	0.5	4.94	
61	Q9HQ23|Q9HQ23	1	866.5225	24.8	286	294	0	26.1	24	G	LPLLNGGAI	A	1.3	6.02	
62	Q9HNN6|Q9HNN6	1	2021.8926	-4.7	163	181	0	39.0	32	G	AFVEPDQDSQADADRGSKS	R	-1.3	3.76	
63	Q9HT00|GLMS	1	930.4658	10.2	537	546	0	51.2	36	G	ADVIGLASDA	G	1.0	2.92	
64	Q9HP88|Q9HP88	1	1498.7126	0.7	171	183	0	77.5	34	T	AFRDYASTDMLPL	A	0.0	3.88	
64	Q9HP88|Q9HP88	1	1689.9301	-2.5	397	412	0	55.1	32	I	LLPIAPGLDDTPEIRA	Q	0.2	3.7	
66	Q9HNY9|Q9HNY9	1	1156.5975	26.6	218	229	0	35.6	34	R	AVDLLDGAALAE	A	1.0	2.88	
66	Q9HNY9|Q9HNY9	1	1227.6347	12.9	218	230	0	40.9	34	R	AVDLLDGAALAEA	S	1.1	2.88	
74	Q9HPA6|Q9HPA6	1	1637.7719	-4.2	164	176	0	72.2	35	S	KYQEQAQELQDKM	S	-2.0	4.44	
75	Q9HNR0|Q9HNR0	1	1097.4989	27.8	38	48	0	40.0	34	G	QQAATGDPTNL	N	-0.9	3.1	Gln->pyro-Glu (N-term Q)
77	Q9HNS6|Q9HNS6	1	1361.7456	-5.9	68	81	0	98.4	33	T	NAIGFGPIVGPHIA	F	0.9	7.84	
78	Q9HS12|Q9HS12	1	731.4694	-15.4	23	28	0	32.0	25	V	FRALLL	A	1.9	11.04	
78	Q9HS12|Q9HS12	1	876.4263	24.2	511	518	0	48.2	34	S	ETVTAMPL	Q	0.7	3.3	Oxidation (M)
78	Q9HS12|Q9HS12	1	974.5913	5.0	23	31	0	35.6	25	V	FRALLLAAT	L	1.6	11.04	
80	Q9HMK0|Q9HMK0	1	1573.6718	1.8	179	191	0	31.7	31	A	SDVEAQEYFAERM	D	-0.9	3.68	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
80	Q9HMK0|Q9HMK0	1	1807.7723	4.1	177	191	0	56.5	32	D	YASDVEAQEYFAERM	D	-0.7	3.68	
80	Q9HMK0|Q9HMK0	1	2619.1071	3.0	170	191	0	82.4	30	E	LTTDHEDYASDVEAQEYFAERM	D	-1.0	3.68	
81	Q9HQQ9|Q9HQQ9	1	1694.8839	-1.5	334	349	0	68.2	35	R	AVPVIDGLQDREADVV	A	0.3	3.5	
85	Q9HRL2|Q9HRL2	1	1401.7041	-7.1	244	256	0	78.2	35	T	WLPDAHVQAPTPA	S	-0.2	4.94	
91	Q9HR92|HTR6	1	887.548	24.2	27	35	0	29.5	23	K	FGVALLAVV	V	2.9	6.02	
92	Q9HSQ2|HTPX	1	1422.5721	-0.8	57	68	0	75.8	28	V	GAEDMDEQEFPR	I	-1.8	3.5	
92	Q9HSQ2|HTPX	1	1521.6406	-0.2	56	68	0	93.3	30	S	VGAEDMDEQEFPR	I	-1.3	3.5	
94	Q9HS26|Q9HS26	1	1711.7577	2.6	16	31	0	55.7	33	A	GDDSEPEIDFYGGKLA	S	-0.8	3.42	
95	P57684|ATKA	1	731.4582	0.1	548	554	0	25.7	25	P	AFVGLLI	G	2.9	6.02	
96	Q9HMB4|Q9HMB4	1	1621.8141	1.0	448	461	0	57.5	35	A	EFIRDYVPFVPGPS	A	0.0	4.08	
97	Q9HR32|TOP6A	1	2300.0419	2.5	20	39	0	44.0	34	I	AEQFYDQFADGDIPRMSLPT	R	-0.6	3.5	
100	Q9HPQ2|Q9HPQ2	1	1402.6517	-0.1	332	343	0	71.1	34	A	YVVDNYGYSRPA	T	-0.7	6.58	
104	Q9HR98|Q9HR98	1	2059.9698	5.3	134	153	0	70.0	35	V	SFVDATDPDAVADAIRPETA	F	-0.1	3.36	
105	Q9HMQ2|ASSY	1	1365.6564	-2.7	146	156	0	44.5	35	L	GLTREWEIEYA	A	-0.7	3.96	
105	Q9HMQ2|ASSY	1	2114.9433	-11.2	181	199	0	50.8	32	R	SVEGGHLEEPDYQPPADIY	A	-1.0	3.5	
109	Q9HMQ8|Q9HMQ8	1	1972.0856	-7.8	269	288	0	33.5	33	A	AVGAVVVFAAGLLAFPPVMQ	S	1.9	6.02	Oxidation (M)
110	Q9HS00|Q9HS00	1	799.4804	13.9	492	500	0	32.1	30	T	AAVVAATVV	R	2.6	6.02	
112	Q9HHI3|Q9HHI3	1	1145.5088	-12.1	69	79	0	32.6	32	V	SLPDSVETDPS	I	-0.8	2.88	
115	Q9HQU8|Q9HQU8	1	2107.9698	-0.5	13	30	0	41.1	35	A	RLTDQDEFTPPESFVEQA	N	-1.1	3.5	
117	Q9HT01|Q9HT01	1	731.4582	-0.1	552	558	0	25.7	25	R	IGVAFLL	V	2.9	6.02	
119	Q9HP48|Q9HP48	1	1821.7694	6.5	204	220	0	74.7	31	V	FESGVDHFEVDDDGALA	A	-0.3	3.32	
119	Q9HP48|Q9HP48	1	1892.8065	2.0	204	221	0	53.6	31	V	FESGVDHFEVDDDGALAA	A	-0.1	3.32	
122	Q9HPG8|Q9HPG8	1	1317.6241	0.8	661	670	0	67.9	35	V	EFDDYFLRTL	E	-0.4	3.7	
126	P25964|BACS1	1	1355.5816	-0.8	219	230	0	36.0	31	V	FMHSESPPAPEQ	A	-1.1	4.24	
128	Q9HN02|Q9HN02	1	1096.5917	-0.8	163	171	0	52.0	32	V	LFDYLTRAV	N	0.7	6.7	
131	Q9HHP2|Q9HHP2	1	762.4024	19.3	502	508	0	35.6	32	P	ARLFADA	P	0.6	6.78	
139	Q9HMZ3|Q9HMZ3	1	2517.1237	3.8	413	432	0	53.9	34	V	EYLWYVGDYPSYDERNQHIA	R	-1.2	4.06	
141	Q9HRR3|Q9HRR3	1	1128.5716	0.2	176	184	0	43.2	35	R	RPVEQPFWA	S	-0.8	6.98	
141	Q9HRR3|Q9HRR3	1	1900.86	-2.8	235	248	0	39.4	33	T	MREGYMYDLNKRYY	K	-1.5	9.3	
144	Q9HN43|CAPPA	1	1267.6561	11.5	308	319	0	45.9	33	L	RDADLGAPPFPI	D	-0.2	3.88	
146	Q9HRJ5|Q9HRJ5	1	1243.6561	-15.1	96	106	0	36.8	35	A	TTPLSRAEWLA	A	-0.1	6.98	
148	Q9HNI3|Q9HNI3	1	731.4582	0.1	114	120	0	30.6	25	G	FGLAVIL	A	2.9	6.02	
149	Q9HS86|Q9HS86	1	1261.5939	-0.5	95	106	0	42.6	35	I	AAGEFERADIPS	S	-0.4	3.82	
160	Q9HN22|Q9HN22	1	1719.8104	2.4	149	165	0	48.7	35	A	AAFLADIDHSAYGTTPA	Q	0.3	3.88	
160	Q9HN22|Q9HN22	1	1875.8487	-4.1	121	139	0	86.6	33	R	HPDTLPDTPGDPTDGAVAT	D	-0.8	3.42	
166	Q9HNP7|Q9HNP7	1	1784.9632	19.9	270	288	0	43.2	32	V	RLGTVSGEEVGLVGASALA	D	0.7	4.26	
173	Q9HRT0|Q9HRT0	1	731.4582	-6.0	73	79	0	30.5	26	M	GLIFGLI	G	2.7	6.02	
174	Q9HP01|Q9HP01	1	887.5328	29.2	79	87	0	41.8	24	F	VTSLLLSVG	I	1.9	6.02	
175	Q9HQ43|Q9HQ43	1	2524.1242	-1.7	141	163	0	60.6	33	A	FLDTGSDDTVAPRDDDDLAVQPY	T	-0.7	3.14	
176	Q9HPT9|Q9HPT9	1	2263.0128	2.7	61	82	0	56.9	34	A	ALDLPGHGDSDDIETDPGPETL	D	-0.8	3.22	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
184	Q48294|Q48294	1	1551.7569	-6.6	376	388	0	48.1	35	Y	TLERPDVNFGEYL	R	-0.6	3.82	
187	Q9HR74|Q9HR74	1	2213.0753	-14.6	540	558	0	53.5	35	P	TTRQADIILPAAHWFETED	L	-0.5	4.06	
195	Q9HQU4|Q9HQU4	1	1972.0378	16.4	260	278	0	36.8	33	R	LRVGVAVGPFDTERATAVD	E	0.3	4.3	
200	Q9HR22|Q9HR22	1	1658.8304	2.2	72	86	0	36.5	35	V	YSELFLGAIGHPEQV	L	0.2	4.24	
207	Q9HP66|Q9HP66	1	830.5266	9.9	117	124	0	25.1	23	V	FLGLLAVV	L	3.0	6.02	
211	Q9HRZ2|Q9HRZ2	1	2117.0211	3.3	257	277	0	77.8	36	A	ATNPSIDGGEYIGPGGVLNMR	G	-0.3	4.08	
217	Q9HNS4|Q9HNS4	1	2258.9492	8.6	321	339	0	55.7	31	L	YEPPDVDSDDPTDITRDYF	L	-1.4	3.18	
222	Q9HSW2|Q9HSW2	1	713.4799	27.2	22	27	0	25.1	18	S	IRSLLI	I	1.9	11.04	
239	Q9HPY6|Q9HPY6	1	731.4694	-20.0	390	395	0	34.3	26	A	FARLLL	A	1.9	11.04	
246	Q9HQN2|Q9HQN2	1	1311.6605	-28.9	156	168	0	34.1	34	A	VDSLPAMQAAGPR	P	0.0	6.78	
255	Q9HRS9|Q9HRS9	1	1311.6533	-25.4	184	195	0	51.5	34	S	WLPDAMVAPTPV	S	0.7	3.1	Oxidation (M)
258	Q9HMU8|Q9HMU8	1	1186.671	-7.0	47	56	0	79.6	33	I	NILLDFVRPT	T	0.5	6.78	
264	Q9HN37|Q9HN37	1	1314.8275	-13.2	539	550	0	25.2	24	A	LVFQVKLSVVIA	A	2.1	10.1	
266	Q9HN92|Q9HN92	1	955.5273	-2.9	1	8	0	42.7	33	-	MNVRPQVI	A	0.2	11.04	
266	Q9HN92|Q9HN92	1	1026.5644	0.6	1	9	0	55.2	33	-	MNVRPQVIA	T	0.4	11.04	
282	Q9HR54|Q9HR54	1	958.5964	20.2	335	343	0	24.0	18	V	LFRAGGLLL	V	1.6	11.04	
290	Q9HSZ8|Q9HSZ8	1	763.3422	18.1	14	20	0	40.9	34	R	MGPLTET	R	-0.2	3.3	Oxidation (M)
301	Q9HNU9|COFG	1	1901.0339	-4.4	257	273	0	34.8	34	E	TMRRVVAMARAVLPAEV	G	0.7	12.1	2 Oxidation (M)
317	Q9HQU3|Q9HQU3	1	731.4582	-6.0	143	149	0	36.3	26	V	IIGLGFL	A	2.7	6.02	
318	Q9HMU6|Q9HMU6	1	1231.6098	-6.7	114	124	0	46.9	35	V	GDSPPRWHAPL	L	-1.1	7.84	
320	Q9HNW7|Q9HNW7	1	1582.7086	1.7	235	248	0	59.8	33	L	MFQGLEGYDDVRPG	S	-0.7	3.7	
323	Q9HQ64|Q9HQ64	1	1716.8907	-1.9	79	94	0	71.3	35	V	YNALVNQGIEGNAKRA	A	-0.6	9.72	
325	Q9HN54|Q9HN54	1	1366.6299	0.0	8	18	0	45.8	34	R	MDEYDQRALRA	S	-1.4	4.3	
339	Q9HMJ2|Q9HMJ2	1	876.4263	24.2	149	156	0	36.3	34	A	EVSMLADI	D	1.1	3	
362	Q9HST4|MOAA	1	3508.5649	-19.5	232	267	0	31.1	30	V	SSRDAGSTADDAAQSVTPDGGAHPDQGMVEIVDPVG	N	-0.5	3.52	
374	Q9HPI6|Q9HPI6	1	882.5175	26.2	15	24	0	33.2	28	T	LPAAIGGITA	Y	1.5	6.02	
391	P57697|PSMA	1	731.4582	-4.6	134	140	0	46.7	26	P	FGVALLI	A	2.9	6.02	
402	Q9HNQ9|Q9HNQ9	1	1122.5094	7.9	209	218	0	44.0	34	S	GGFWESVDRA	M	-0.5	4.08	
412	Q9HQ52|THYX	1	2507.2292	5.6	111	134	0	65.1	36	A	AVAEGELVVTPPSATDPDWVGRNQ	D	-0.3	3.58	
449	Q9HPW3|Q9HPW3	1	1900.9968	15.1	29	48	0	36.3	34	L	ALAVAAGLFAALPDVDMVAA	L	1.7	2.92	Oxidation (M)
453	Q9HSW6|CDC61	1	1098.6172	-23.7	145	154	0	36.6	33	I	LIVLDEVDAI	G	1.6	2.88	
462	Q9HN08|Q9HN08	1	1727.8625	11.9	1	16	0	39.1	35	-	MPTQDGERRDVVIVGG	G	-0.5	4.3	
474	Q9HRL4|Q9HRL4	1	1369.6514	2.0	83	93	0	56.1	34	T	LYRNFDDIDVT	N	-0.5	3.6	
476	Q9HM88|Q9HM88	1	1187.567	-5.2	56	68	0	37.0	35	A	SEIGTGAPSDALA	A	0.2	3	
479	Q9HRS4|Q9HRS4	1	2054.809	6.7	16	35	0	81.0	26	A	AADQGIDPWTADDHEGGDGE	-	-1.3	3.22	
493	Q9HN36|Q9HN36	1	731.4581	-4.6	259	264	0	39.6	26	T	FNLLLL	V	2.4	6.02	
519	Q9HNC8|Q9HNC8	1	789.3981	13.4	107	114	0	36.0	35	Y	TGITGGRE	N	-0.8	6.98	
542	Q9HMC9|Q9HMC9	1	1137.6758	0.7	533	543	0	27.1	27	S	NNASVVLLIPV	A	1.6	6.02	
558	Q9HQU7|Q9HQU7	1	1071.5461	-3.5	166	174	0	48.9	35	A	STLQPNAWR	I	-1.1	11.04	
559	Q9HRK1|Q9HRK1	1	1651.7995	-1.9	14	28	0	49.1	35	H	HLPAVEDWPKGFGEA	S	-0.5	4.42	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
560	Q9HRS8|Q9HRS8	1	887.5844	-24.0	98	105	0	23.6	23	L	IVVGLFIK	V	2.5	10.1	
564	Q9HPK2|Y1595	1	974.5648	29.6	69	77	0	38.2	26	G	STTLLQLIS	D	1.0	6.02	
585	Q9HQ34|Q9HQ34	1	1008.5968	8.5	139	149	0	34.8	25	A	GLAGVVIVANP	G	1.7	6.02	
599	Q9HQI3|Q9HQI3	1	1208.7353	-22.2	44	54	0	29.4	28	Y	ILEAGGKRLRP	A	-0.4	11.32	
603	Q9HPQ1|Q9HPQ1	1	731.4582	-6.0	376	382	0	28.3	26	A	GLIGFLL	F	2.6	6.02	
615	Q9HSF1|Q9HSF1	1	1882.9313	-10.2	218	233	0	53.2	35	A	TFLEEFVDQGTIDTLR	A	-0.2	3.58	
618	Q9HQV6|Q9HQV6	1	731.4582	-4.6	27	33	0	55.8	26	L	FGGLLLI	P	2.6	6.02	
618	Q9HQV6|Q9HQV6	1	731.4582	-6.0	26	32	0	32.5	26	V	LFGGLLL	I	2.5	6.02	
650	Q9HNE5|Q9HNE5	1	1727.9319	-29.6	27	43	0	36.8	35	R	PTAGFSPTRRDAVLGAL	A	0.1	10.88	
684	O52037|O52037	1	1008.6304	-27.5	20	28	0	34.7	25	R	ARLRLAGPR	S	-0.5	12.7	
704	O51975|O51975	1	713.4799	27.2	189	194	0	23.0	18	R	LRSLLI	I	1.8	11.04	
717	Q9HML4|Q9HML4	1	745.4222	17.8	275	281	0	29.4	29	D	LVDVSLT	P	1.6	3.1	
732	Q9HSA0|Q9HSA0	1	1260.6251	-2.2	39	50	0	52.5	35	A	FEHGLPSGPHLA	D	-0.2	6.02	
791	Q9HNB8|Q9HNB8	1	1293.6717	-8.5	12	24	0	34.3	34	A	SGHLAPLFDAAPV	R	0.7	4.94	
808	Q9HS40|Q9HS40	1	1544.6995	3.3	151	163	0	40.4	34	A	DSFVDLSERTETF	L	-0.6	3.58	
830	Q9HQE2|Q9HQE2	1	1498.8104	-11.5	114	127	0	36.3	34	L	DRLRDAGLDVAVVT	N	0.2	4.18	
861	Q9HP98|Q9HP98	1	930.5022	-21.7	23	32	0	40.6	36	G	SVVLLSGEAG	A	1.2	3.3	
864	Q9HPF2|RADB	1	866.5225	24.8	146	153	0	28.2	24	Q	ITHLLSLA	R	1.6	7.84	
880	Q9HRW7|Q9HRW7	1	1618.7012	8.1	2	15	0	47.8	33	M	SDALDAFDHDAWRT	A	-0.9	3.86	
894	Q9HRN0|Q9HRN0	1	1159.6601	-5.5	57	69	0	32.0	32	T	AFAALVAAGSLAV	T	2.2	6.02	
899	Q9HME2|Q9HME2	1	1988.0078	0.6	2	18	0	42.4	35	M	VWIIDNLVTMVEHFTTA	A	0.9	4.06	
928	Q9HMK6|Q9HMK6	1	1727.9166	-19.4	184	199	0	36.0	35	T	EKDVSEARRDAVLAGI	T	-0.4	4.56	
939	Q9HNI4|Q9HNI4	1	1216.5208	12.3	19	29	0	34.1	32	E	SDEETRAPPSE	A	-2.0	3.68	
1035	Q9HSP8|Q9HSP8	1	1972.0517	9.4	108	128	0	33.6	33	R	VALAGVLEAYAADIADGAAVL	A	1.4	2.88	
1041	Q9HR01|Q9HR01	1	830.5266	9.9	184	191	0	25.1	23	H	LVFVLVAA	T	3.3	6.02	
1095	Q9HRH6|Q9HRH6	1	1480.731	2.6	143	156	0	38.8	35	A	SYTGLRWLAGGAET	-	-0.2	6.88	
1125	Q9HQ91|Q9HQ91	1	731.4582	-6.0	14	20	0	30.5	26	P	GLLFGLL	L	2.5	6.02	
1161	Q9HMB0|Q9HMB0	1	896.4127	-0.6	10	17	0	35.0	32	L	LYTTPTDS	D	-0.7	3.1	
1189	Q9HRR5|Q9HRR5	1	1313.5863	4.4	22	32	0	38.7	33	I	MAGWYRTPEFG	H	-0.6	6.88	
1204	Q9HSJ4|Q9HSJ4	1	830.5266	9.9	21	28	0	25.1	23	G	VFVILAVA	A	3.4	6.02	
1247	Q9HRR2|Q9HRR2	1	1688.8661	-1.7	42	54	0	47.2	35	V	DYLELLETLYYRV	N	0.0	3.82	
1287	Q9HNI2|GLNA	1	866.5226	24.8	120	127	0	24.6	24	R	QVLKNVLA	R	0.9	10.1	Gln->pyro-Glu (N-term Q)
1414	Q9HQB1|Q9HQB1	1	958.6328	-17.7	70	77	0	19.6	18	V	KAVFRLLI	E	1.6	11.48	
1581	Q9HRK3|Q9HRK3	1	974.5589	27.2	47	54	0	29.8	27	I	IQFVLIGW	I	1.9	6.02	
1657	Q9HP64|Q9HP64	1	830.5266	9.9	13	20	0	25.1	23	C	FVVLLGLA	V	3.0	6.02	
1659	Q9HNA9|Q9HNA9	1	887.544	18.7	75	82	0	25.0	24	Q	IVTSLSLR	A	1.2	11.04	

END OF LIST IV

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
V. Purple membrane; elastase digest; nLC-MALDI MS/MS; AVLISTG search specificity															
1	P02945|BACR	1	713.4799	27.2	234	239	4	28.4	14	G	LILLRS	R	1.8	11.04	
1	P02945|BACR	1	731.4582	-4.6	231	237	5	57.7	22	V	GFGLILL	R	2.6	6.02	
1	P02945|BACR	1	734.4401	-13.3	219	224	3	25.4	20	T	LLFMVL	D	3.4	6.02	
1	P02945|BACR	1	756.3919	-5.4	19	24	1	27.5	27	T	GRPEWI	W	-1.1	6.98	
1	P02945|BACR	1	762.4024	19.3	240	246	3	50.5	28	S	RAIFGEA	E	0.4	6.98	
1	P02945|BACR	1	799.4916	6.8	187	193	4	38.5	27	V	LRNVTVV	L	1.1	11.04	
1	P02945|BACR	1	817.4011	-8.0	165	171	3	33.5	30	V	LFFGFTS	K	1.5	6.02	
1	P02945|BACR	1	828.3918	23.3	92	97	1	30.7	27	I	YWARYA	D	-0.7	9.58	
1	P02945|BACR	1	829.4182	-6.0	112	119	4	54.7	29	A	LLVDADQG	T	0.3	2.92	
1	P02945|BACR	1	834.4276	-5.5	194	200	3	30.7	28	V	LWSAYPV	V	0.7	5.92	
1	P02945|BACR	1	835.4514	-12.2	220	226	3	28.5	27	L	LFMVLDV	S	2.5	3.1	
1	P02945|BACR	1	857.4395	-4.1	18	24	2	32.2	30	I	TGRPEWI	W	-1.0	6.98	
1	P02945|BACR	1	869.4391	-6.7	69	75	3	26.9	26	T	MYLSMLL	G	1.9	5.92	
1	P02945|BACR	1	887.4786	-25.8	124	132	6	60.2	30	A	LVGADGIMI	G	1.8	3.1	
1	P02945|BACR	1	917.4276	0.1	174	181	2	37.9	29	A	ESMRPEVA	S	-0.8	4.26	
1	P02945|BACR	1	930.4811	-6.2	201	209	6	68.7	30	V	VWLIGSEGA	G	0.9	3.3	
1	P02945|BACR	1	958.6215	-6.1	229	237	6	44.1	14	A	KVGFGLILL	R	2.0	10.1	
1	P02945|BACR	1	967.5954	-5.5	103	111	5	64.7	22	T	TPLLLLDLA	L	1.7	3.1	
1	P02945|BACR	1	974.5913	-6.1	231	239	6	63.7	23	V	GFGLILLRS	R	1.4	11.04	
1	P02945|BACR	1	991.5015	-7.5	98	105	2	29.0	29	A	DWLFTTPL	L	0.4	3.1	
1	P02945|BACR	1	1005.5356	-1.8	238	246	4	37.5	28	L	RSRAIFGEA	E	-0.3	10.88	
1	P02945|BACR	1	1032.44	-18.0	243	252	2	80.2	23	I	FGEAEAPEPS	A	-0.9	3.02	
1	P02945|BACR	1	1043.5499	-2.0	112	121	6	72.5	30	A	LLVDADQGTI	L	0.7	2.92	
1	P02945|BACR	1	1055.5552	-11.0	19	26	2	38.6	28	T	GRPEWIWL	A	-0.4	6.98	
1	P02945|BACR	1	1062.6186	-2.5	182	190	4	56.9	23	A	STFKVLRNV	T	0.2	11.48	
1	P02945|BACR	1	1069.5709	-4.5	20	27	2	45.9	27	G	RPEWIWLA	L	-0.2	6.98	
1	P02945|BACR	1	1070.5185	24.5	95	102	2	61.3	29	A	RYADWLFT	T	-0.3	6.7	
1	P02945|BACR	1	1081.5556	1.9	16	24	3	61.4	28	A	QITGRPEWI	W	-0.7	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1098.5822	2.5	16	24	3	50.6	28	A	QITGRPEWI	W	-0.7	6.98	
1	P02945|BACR	1	1116.6907	4.9	227	237	8	53.5	18	V	SAKVGFGLILL	R	1.7	10.1	
1	P02945|BACR	1	1126.5923	16.7	19	27	3	51.6	27	T	GRPEWIWLA	L	-0.2	6.98	
1	P02945|BACR	1	1145.524	-25.4	242	252	3	79.0	25	A	IFGEAEAPEPS	A	-0.4	3.02	
1	P02945|BACR	1	1156.6029	6.2	18	26	3	56.0	29	I	TGRPEWIWL	A	-0.5	6.98	
1	P02945|BACR	1	1156.634	0.3	112	122	7	106.5	28	A	LLVDADQGTIL	A	0.9	2.92	
1	P02945|BACR	1	1173.7234	2.8	184	193	5	18.7	18	T	FKVLRNVTVV	L	1.1	11.48	
1	P02945|BACR	1	1187.5645	-21.1	81	91	2	93.9	27	T	MVPFGGEQNPI	Y	-0.1	3.3	
1	P02945|BACR	1	1203.5594	-19.2	81	91	2	81.4	27	T	MVPFGGEQNPI	Y	-0.1	3.3	Oxidation (M)

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	1	1215.7115	-8.0	101	111	6	62.7	25	L	FTTPLLLLDLA	L	1.6	3.1	
1	P02945|BACR	1	1227.64	22.3	18	27	4	56.7	29	I	TGRPEWIWLA	L	-0.2	6.98	
1	P02945|BACR	1	1227.6711	-24.1	112	123	8	113.1	28	A	LLVDADQGTILA	L	1.0	2.92	
1	P02945|BACR	1	1239.6764	-2.6	19	28	4	37.1	26	T	GRPEWIWLAL	G	0.2	6.98	
1	P02945|BACR	1	1242.5822	-3.0	92	100	2	36.3	27	I	YWARYADWL	F	-0.6	6.64	
1	P02945|BACR	1	1253.6292	-0.8	48	58	3	66.4	28	V	SDPDAKKFYAI	T	-0.7	6.8	
1	P02945|BACR	1	1274.7711	3.0	183	193	6	61.6	20	S	TFKVLRNVTVV	L	0.9	11.48	
1	P02945|BACR	1	1280.6513	3.6	14	24	4	72.7	28	S	QAQITGRPEWI	W	-0.7	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1296.6979	-7.1	19	29	5	43.9	27	T	GRPEWIWLALG	T	0.2	6.98	
1	P02945|BACR	1	1296.7152	-14.7	31	42	8	35.0	27	T	ALMGLGTLYFLV	K	1.9	5.92	
1	P02945|BACR	1	1314.8136	-2.6	231	242	8	70.3	17	V	GFGLILLRSRAI	F	1.2	12.4	
1	P02945|BACR	1	1340.7241	-0.5	18	28	5	28.5	27	I	TGRPEWIWLAL	G	0.1	6.98	
1	P02945|BACR	1	1354.6769	5.9	48	59	4	75.7	28	V	SDPDAKKFYAIT	T	-0.7	6.8	
1	P02945|BACR	1	1361.8031	1.8	182	193	7	76.5	21	A	STFKVLRNVTVV	L	0.8	11.48	
1	P02945|BACR	1	1372.6623	5.1	240	252	4	109.7	29	S	RAIFGEAEAPEPS	A	-0.5	3.96	
1	P02945|BACR	1	1380.719	-3.1	16	26	4	71.8	28	A	QITGRPEWIWL	A	-0.3	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1381.703	16.1	95	105	3	74.5	27	A	RYADWLFTTPL	L	-0.1	6.7	
1	P02945|BACR	1	1397.7456	-0.4	18	29	6	55.3	28	I	TGRPEWIWLALG	T	0.1	6.98	
1	P02945|BACR	1	1409.7919	-15.3	201	214	9	111.2	26	V	VWLIGSEGAGIVPL	N	1.3	3.3	
1	P02945|BACR	1	1443.6994	0.1	240	253	5	83.6	29	S	RAIFGEAEAPEPSA	G	-0.4	3.96	
1	P02945|BACR	1	1451.7561	1.0	16	27	5	88.0	28	A	QITGRPEWIWLA	L	-0.1	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1468.7827	11.0	16	27	5	61.8	27	A	QITGRPEWIWLA	L	-0.1	6.98	
1	P02945|BACR	1	1490.6983	2.3	92	102	3	53.0	29	I	YWARYADWLFT	T	-0.3	6.64	
1	P02945|BACR	1	1498.7932	0.3	18	30	7	89.2	28	I	TGRPEWIWLALGT	A	0.0	6.98	
1	P02945|BACR	1	1540.7596	-4.7	45	58	5	61.1	28	G	MGVSDPDAKKFYAI	T	-0.1	6.8	
1	P02945|BACR	1	1579.8147	0.2	14	26	5	81.9	28	S	QAQITGRPEWIWL	A	-0.4	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1607.7442	3.4	81	94	3	64.3	28	T	MVPFGGEQNPIYWA	R	-0.1	3.3	
1	P02945|BACR	1	1607.8712	4.1	95	107	5	77.8	26	A	RYADWLFTTPLLL	L	0.5	6.7	
1	P02945|BACR	1	1615.7954	1.2	238	252	5	108.0	29	L	RSRAIFGEAEAPEPS	A	-0.8	4.56	
1	P02945|BACR	1	1629.9018	4.5	98	111	7	64.6	25	A	DWLFTTPLLLLDLA	L	1.2	2.92	
1	P02945|BACR	1	1641.8072	-6.3	45	59	6	95.7	28	G	MGVSDPDAKKFYAIT	T	-0.2	6.8	
1	P02945|BACR	1	1650.8518	10.8	14	27	6	106.1	27	S	QAQITGRPEWIWLA	L	-0.2	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1678.8025	-3.5	76	91	6	123.4	28	L	GYGLTMVPFGGEQNPI	Y	0.0	3.3	
1	P02945|BACR	1	1686.8325	-4.8	238	253	6	82.3	29	L	RSRAIFGEAEAPEPSA	G	-0.6	4.56	
1	P02945|BACR	1	1694.7974	-7.2	76	91	6	115.0	27	L	GYGLTMVPFGGEQNPI	Y	0.0	3.3	Oxidation (M)
1	P02945|BACR	1	1720.9552	-1.7	95	108	6	101.0	24	A	RYADWLFTTPLLLL	D	0.7	6.7	
1	P02945|BACR	1	1722.9093	8.1	16	30	8	98.0	26	A	QITGRPEWIWLALGT	A	0.1	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1739.9359	3.7	16	30	8	70.5	26	A	QITGRPEWIWLALGT	A	0.1	6.98	
1	P02945|BACR	1	1743.8064	-2.3	240	257	8	54.0	27	S	RAIFGEAEAPEPSAGDGA	A	-0.4	3.68	
1	P02945|BACR	1	1754.9104	-2.2	13	27	7	33.0	27	V	SQAQITGRPEWIWLA	L	-0.3	6.98	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	1	1801.8828	1.1	92	105	4	76.1	28	I	YWARYADWLFTTPL	L	-0.1	6.64	
1	P02945|BACR	1	1820.9574	-22.7	14	29	8	49.8	28	S	QAQITGRPEWIWLALG	T	0.0	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1826.9237	12.0	43	59	7	39.8	27	V	KGMGVSDPDAKKFYAIT	T	-0.4	9.56	
1	P02945|BACR	1	1835.9669	-4.5	48	64	7	95.0	27	V	SDPDAKKFYAITTLVPA	I	0.0	6.8	
1	P02945|BACR	1	1841.9635	-11.6	236	252	7	64.1	28	I	LLRSRAIFGEAEAPEPS	A	-0.3	4.56	
1	P02945|BACR	1	1922.005	-2.2	14	30	9	101.8	26	S	QAQITGRPEWIWLALGT	A	0.0	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1955.0476	-3.5	235	252	8	58.1	25	L	ILLRSRAIFGEAEAPEPS	A	0.0	4.56	
1	P02945|BACR	1	2020.1033	-2.5	95	111	8	127.6	24	A	RYADWLFTTPLLLLDLA	L	0.7	3.88	
1	P02945|BACR	1	2440.2831	-0.2	92	111	9	75.3	22	I	YWARYADWLFTTPLLLLDLA	L	0.6	3.88	
2	P00772|ELA1	1	800.3851	9.2	54	61	5	46.1	27	A	HTCGGTLI	R	0.7	7.16	
2	P00772|ELA1	1	873.4093	0.5	34	40	1	28.8	28	A	QRNSWPS	Q	-2.2	11.04	
2	P00772|ELA1	1	882.5287	0.6	138	146	5	30.3	24	L	GVLPRAGTI	L	0.7	11.04	
2	P00772|ELA1	1	890.461	15.9	156	163	5	49.8	28	I	TGWGLTRT	N	-0.6	11.04	
2	P00772|ELA1	1	909.5396	-9.1	136	144	4	42.3	21	V	QLGVLPRAG	T	0.4	11.04	
2	P00772|ELA1	1	915.4239	-1.4	105	111	1	29.8	27	V	VHPYWNT	D	-1.0	7.76	
2	P00772|ELA1	1	933.4491	0.3	62	68	1	40.3	29	I	RQNWVMT	A	-1.0	11.04	
2	P00772|ELA1	1	943.4512	-7.2	223	231	4	49.9	27	V	NGQYAVHGV	T	-0.2	7.76	
2	P00772|ELA1	1	1004.4862	-2.5	62	69	2	45.1	29	I	RQNWVMTA	A	-0.7	11.04	
2	P00772|ELA1	1	1009.6284	-7.9	139	148	6	31.2	21	G	VLPRAGTILA	N	1.3	11.04	
2	P00772|ELA1	1	1014.4923	7.2	104	111	2	55.5	28	I	VVHPYWNT	D	-0.4	7.76	
2	P00772|ELA1	1	1066.6499	0.0	138	148	7	54.4	21	L	GVLPRAGTILA	N	1.1	11.04	
2	P00772|ELA1	1	1097.5254	3.6	34	42	2	71.2	28	A	QRNSWPSQI	S	-1.6	11.04	Gln->pyro-Glu (N-term Q)
2	P00772|ELA1	1	1114.5519	10.2	34	42	2	55.5	29	A	QRNSWPSQI	S	-1.6	11.04	
2	P00772|ELA1	1	1123.6713	-5.1	136	146	6	39.4	23	V	QLGVLPRAGTI	L	0.6	11.04	
2	P00772|ELA1	1	1171.6713	-6.4	134	144	5	53.1	27	S	YVQLGVLPRAG	T	0.6	9.84	
2	P00772|ELA1	1	1214.5568	-8.9	187	197	6	66.1	26	S	SSYWGSTVKNS	M	-0.9	9.72	
2	P00772|ELA1	1	1240.5836	-0.2	43	53	6	63.8	28	I	SLQYRSGSSWA	H	-0.7	9.84	
2	P00772|ELA1	1	1244.5462	6.2	105	114	2	72.6	27	V	VHPYWNTDDV	A	-1.0	3.88	
2	P00772|ELA1	1	1262.6659	-15.8	254	264	6	41.0	29	S	AYISWINNVIA	S	1.0	5.92	
2	P00772|ELA1	1	1307.7925	-5.4	136	148	8	22.4	20	V	QLGVLPRAGTILA	N	1.0	11.04	
2	P00772|ELA1	1	1315.5833	10.9	105	115	3	62.6	27	V	VHPYWNTDDVA	A	-0.7	3.88	
2	P00772|ELA1	1	1321.6813	-8.2	239	250	5	42.9	28	L	GCNVTRKPTVFT	R	-0.2	10.1	
2	P00772|ELA1	1	1343.6146	-2.2	104	114	3	75.6	27	I	VVHPYWNTDDV	A	-0.5	3.88	
2	P00772|ELA1	1	1385.8031	-2.6	134	146	7	51.3	24	S	YVQLGVLPRAGTI	L	0.8	9.84	
2	P00772|ELA1	1	1386.6204	4.4	105	116	4	96.9	27	V	VHPYWNTDDVAA	G	-0.5	3.88	
2	P00772|ELA1	1	1414.6517	1.6	104	115	4	81.2	28	I	VVHPYWNTDDVA	A	-0.3	3.88	
2	P00772|ELA1	1	1427.7481	-3.9	162	174	6	56.8	29	T	RTNGQLAQTLQQA	Y	-1.0	11.04	
2	P00772|ELA1	1	1443.6419	4.8	105	117	5	81.7	27	V	VHPYWNTDDVAAG	Y	-0.5	3.88	
2	P00772|ELA1	1	1485.6889	-1.8	104	116	5	89.6	27	I	VVHPYWNTDDVAA	G	-0.2	3.88	
2	P00772|ELA1	1	1529.7223	-0.3	29	42	6	71.0	28	V	GGTEAQRNSWPSQI	S	-1.3	6.98	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	P00772|ELA1	1	1542.7103	6.3	104	117	6	103.0	28	I	VVHPYWNTDDVAAG	Y	-0.2	3.88	
2	P00772|ELA1	1	1586.878	2.0	130	144	8	127.6	25	V	TLNSYVQLGVLPRAG	T	0.3	9.84	
2	P00772|ELA1	1	1590.8729	-1.2	124	137	8	31.5	25	L	RLAQSVTLNSYVQL	G	0.2	9.84	
2	P00772|ELA1	1	1712.8522	-17.2	101	114	4	92.1	28	V	QKIVVHPYWNTDDV	A	-0.6	5.1	
2	P00772|ELA1	1	1815.8024	-2.5	83	98	5	130.9	25	V	VGEHNLNQNDGTEQYV	G	-1.4	3.82	
2	P00772|ELA1	1	1905.8533	-0.6	105	121	7	119.4	26	V	VHPYWNTDDVAAGYDIA	L	-0.3	3.6	
2	P00772|ELA1	1	1914.8708	1.0	82	98	6	132.9	26	V	VVGEHNLNQNDGTEQYV	G	-1.0	3.82	
2	P00772|ELA1	1	1933.8847	9.8	104	120	7	65.5	27	I	VVHPYWNTDDVAAGYDI	A	-0.2	3.6	
2	P00772|ELA1	1	1971.8923	2.7	83	100	7	147.5	26	V	VGEHNLNQNDGTEQYVGV	Q	-1.0	3.82	
2	P00772|ELA1	1	2004.9218	-0.4	104	121	8	144.5	26	I	VVHPYWNTDDVAAGYDIA	L	-0.1	3.6	
2	P00772|ELA1	1	2070.9607	-2.5	82	100	8	154.5	26	V	VVGEHNLNQNDGTEQYVGV	Q	-0.7	3.82	
2	P00772|ELA1	1	2118.0058	2.6	104	122	9	34.4	26	I	VVHPYWNTDDVAAGYDIAL	L	0.2	3.6	
2	P00772|ELA1	1	2317.1087	3.5	79	98	7	35.5	26	T	FRVVVGEHNLNQNDGTEQYV	G	-0.8	4.42	
2	P00772|ELA1	1	2341.1299	-5.7	83	103	8	96.7	25	V	VGEHNLNQNDGTEQYVGVQKI	V	-1.0	4.42	
2	P00772|ELA1	1	2374.1594	-0.3	101	121	9	130.5	26	V	QKIVVHPYWNTDDVAAGYDIA	L	-0.2	4.16	
2	P00772|ELA1	1	2440.1983	4.2	82	103	9	110.4	24	V	VVGEHNLNQNDGTEQYVGVQKI	V	-0.8	4.42	
2	P00772|ELA1	1	2473.1986	-6.8	79	100	9	27.3	24	T	FRVVVGEHNLNQNDGTEQYVGV	Q	-0.5	4.42	
3	Q9HMW9|Q9HMW9	1	978.5287	8.2	636	643	1	55.1	27	A	FHLQPPQL	F	-0.4	7.84	
3	Q9HMW9|Q9HMW9	1	1166.6084	-23.3	616	624	2	48.3	28	A	YVINREQFV	S	-0.1	6.88	
3	Q9HMW9|Q9HMW9	1	1212.6292	3.9	636	645	2	70.1	28	A	FHLQPPQLFS	D	-0.1	7.84	
3	Q9HMW9|Q9HMW9	1	1253.6404	-2.8	616	625	3	49.8	28	A	YVINREQFVS	D	-0.1	6.88	
3	Q9HMW9|Q9HMW9	1	1367.618	-8.8	133	143	1	37.8	26	L	QYQSPTWKEMA	N	-1.5	6.86	
3	Q9HMW9|Q9HMW9	1	1368.686	-1.2	614	624	3	41.0	28	A	MAYVINREQFV	S	0.3	6.88	
3	Q9HMW9|Q9HMW9	1	1441.7049	-3.6	166	178	6	93.1	28	S	SLLETTKQGEHEA	F	-1.1	4.54	
3	Q9HMW9|Q9HMW9	1	1455.718	-2.1	614	625	4	39.1	28	A	MAYVINREQFVS	D	0.2	6.88	
3	Q9HMW9|Q9HMW9	1	1467.7358	-1.0	616	627	4	38.3	28	A	YVINREQFVSDV	F	-0.1	4.08	
3	Q9HMW9|Q9HMW9	1	1506.6303	-3.8	92	103	0	81.4	23	T	DYQPDFDKYPYG	I	-1.9	3.6	
3	Q9HMW9|Q9HMW9	1	1567.7307	-7.4	120	132	2	33.7	27	A	GYGPDNKYELNWL	Q	-1.2	4.08	
3	Q9HMW9|Q9HMW9	1	1619.7144	-5.0	92	104	1	85.3	26	T	DYQPDFDKYPYGI	D	-1.4	3.6	
3	Q9HMW9|Q9HMW9	1	1695.7926	-3.9	133	146	3	89.6	27	L	QYQSPTWKEMANTI	R	-1.1	6.86	
3	Q9HMW9|Q9HMW9	1	1736.8958	0.9	619	633	5	89.0	27	I	NREQFVSDVFKGRGV	G	-0.7	10.08	
3	Q9HMW9|Q9HMW9	1	1802.905	-1.4	166	181	8	124.4	28	S	SLLETTKQGEHEAFTL	G	-0.5	4.54	
3	Q9HMW9|Q9HMW9	1	1857.9335	-0.5	595	610	4	105.2	27	I	DTYYVGFNMTKVPKPV	R	-0.3	9.46	
3	Q9HMW9|Q9HMW9	1	1864.9544	0.1	619	635	7	92.1	27	I	NREQFVSDVFKGRGVGA	F	-0.5	10.08	
3	Q9HMW9|Q9HMW9	1	1880.7741	-0.5	88	103	3	78.6	20	T	GESTDYQPDFDKYPYG	I	-1.8	3.5	
3	Q9HMW9|Q9HMW9	1	1964.8316	-1.5	92	107	2	120.4	22	T	DYQPDFDKYPYGIDET	K	-1.6	3.36	
3	Q9HMW9|Q9HMW9	1	1971.0176	-5.5	594	610	5	53.8	27	T	IDTYYVGFNMTKVPKPV	R	0.0	9.46	
3	Q9HMW9|Q9HMW9	1	1987.9421	-0.4	149	165	6	40.2	27	A	RLEQAHIEMTINDANFS	S	-0.5	4.42	
3	Q9HMW9|Q9HMW9	1	1993.8582	1.5	88	104	4	90.4	23	T	GESTDYQPDFDKYPYGI	D	-1.4	3.5	
3	Q9HMW9|Q9HMW9	1	2072.0653	-8.3	593	610	6	36.7	26	S	TIDTYYVGFNMTKVPKPV	R	-0.1	9.46	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
3	Q9HMW9|Q9HMW9	1	2112.1116	2.3	616	633	7	95.5	24	A	YVINREQFVSDVFKGRGV	G	-0.2	9.72	
3	Q9HMW9|Q9HMW9	1	2159.0973	0.5	592	610	7	39.7	26	V	STIDTYYVGFNMTKVPKPV	R	-0.1	9.46	
3	Q9HMW9|Q9HMW9	1	2240.1702	-3.3	616	635	9	56.5	25	A	YVINREQFVSDVFKGRGVGA	F	-0.1	9.72	
3	Q9HMW9|Q9HMW9	1	2263.0321	3.4	92	110	4	35.0	26	T	DYQPDFDKYPYGIDETKVA	E	-1.2	3.76	
3	Q9HMW9|Q9HMW9	1	2314.1892	-0.5	614	633	8	97.4	24	A	MAYVINREQFVSDVFKGRGV	G	0.0	9.72	
3	Q9HMW9|Q9HMW9	1	2338.9754	7.7	88	107	5	98.9	20	T	GESTDYQPDFDKYPYGIDET	K	-1.6	3.32	
3	Q9HMW9|Q9HMW9	1	2637.1759	0.4	88	110	7	42.8	23	T	GESTDYQPDFDKYPYGIDETKVA	E	-1.3	3.68	
4	Q9HR99|Q9HR99	1	1419.6154	-3.6	122	134	6	65.3	25	V	DAGETLEHTFETA	G	-0.7	3.68	
4	Q9HR99|Q9HR99	1	1473.6195	-5.4	106	119	5	75.8	23	A	SGFGTMDKDGNQFA	V	-0.8	3.88	
4	Q9HR99|Q9HR99	1	1491.7246	-7.0	57	70	4	84.6	29	A	VAPDGGFKFEPSEL	T	-0.3	3.82	
4	Q9HR99|Q9HR99	1	1562.7617	-5.1	56	70	5	78.5	29	I	AVAPDGGFKFEPSEL	T	-0.1	3.82	
4	Q9HR99|Q9HR99	1	1651.7664	7.1	91	105	4	55.8	28	S	AWPDMHDKISIPDGA	S	-0.6	4.16	
4	Q9HR99|Q9HR99	1	1671.7563	-1.6	106	121	7	133.1	26	A	SGFGTMDKDGNQFAVV	D	-0.2	3.88	
4	Q9HR99|Q9HR99	1	1687.7512	-4.7	106	121	7	54.8	25	A	SGFGTMDKDGNQFAVV	D	-0.2	3.88	Oxidation (M)
4	Q9HR99|Q9HR99	1	1691.8407	0.9	57	72	6	105.2	28	A	VAPDGGFKFEPSELTV	S	0.0	3.82	
4	Q9HR99|Q9HR99	1	1762.8778	-3.5	56	72	7	119.1	28	I	AVAPDGGFKFEPSELTV	S	0.1	3.82	
4	Q9HR99|Q9HR99	1	1849.9098	-1.5	56	73	8	31.7	28	I	AVAPDGGFKFEPSELTVS	V	0.0	3.82	
4	Q9HR99|Q9HR99	1	1869.7905	-0.4	122	138	8	149.6	23	V	DAGETLEHTFETAGEYT	Y	-0.9	3.58	
4	Q9HR99|Q9HR99	1	2131.9222	7.6	122	140	9	152.5	24	V	DAGETLEHTFETAGEYTYV	C	-0.7	3.58	
4	Q9HR99|Q9HR99	1	2176.0007	11.1	86	105	7	118.8	26	S	SHNVSAWPDMHDKISIPDGA	S	-0.6	5.02	
5	Q9HMI3|Q9HMI3	1	1172.619	-5.7	556	566	4	53.9	29	V	GGPFLDRVELA	-	0.2	4.08	
5	Q9HMI3|Q9HMI3	1	1248.6615	-3.7	181	190	1	32.1	28	T	QQYAPFLRNL	A	-0.6	9.84	
5	Q9HMI3|Q9HMI3	1	1319.6986	-2.2	181	191	2	36.9	28	T	QQYAPFLRNLA	I	-0.4	9.84	
5	Q9HMI3|Q9HMI3	1	1358.7194	-4.9	554	566	6	64.0	29	T	SVGGPFLDRVELA	-	0.5	4.08	
5	Q9HMI3|Q9HMI3	1	1475.7157	-0.9	390	402	3	61.1	29	A	TFSNPRGYNPNPI	Q	-1.2	9.84	
5	Q9HMI3|Q9HMI3	1	1554.7103	1.4	237	250	5	45.1	27	V	RLTAFDDYWGGAPS	V	-0.5	3.88	
5	Q9HMI3|Q9HMI3	1	1577.8202	-2.9	178	190	3	59.0	28	I	DLTQQYAPFLRNL	A	-0.5	6.7	
5	Q9HMI3|Q9HMI3	1	1648.8573	-5.1	178	191	4	50.7	28	I	DLTQQYAPFLRNLA	I	-0.3	6.7	
5	Q9HMI3|Q9HMI3	1	1696.8056	-0.3	331	345	6	30.1	28	I	NRDEIVDSIYQGFAA	S	-0.3	3.7	
5	Q9HMI3|Q9HMI3	1	1793.8221	3.7	222	236	2	102.8	27	T	GPFEFDQLDNETQRV	R	-1.2	3.58	
5	Q9HMI3|Q9HMI3	1	1808.9309	17.6	78	93	7	102.9	26	V	TNQIFDTLIQFKPGTS	G	-0.3	6.76	
5	Q9HMI3|Q9HMI3	1	1951.8912	1.1	220	236	4	140.2	26	V	GTGPFEFDQLDNETQRV	R	-1.1	3.58	
5	Q9HMI3|Q9HMI3	1	1994.9585	-4.4	460	477	6	89.1	27	V	LLHPGTDIDDVPADQNYI	A	-0.4	3.42	
6	Q48302|Q48302	1	904.5059	-11.4	82	89	2	33.8	28	V	VFVVPTPF	-	1.8	6.02	
6	Q48302|Q48302	1	908.4352	-10.1	40	48	5	30.6	28	A	GYAERGIGS	A	-0.6	6.88	
6	Q48302|Q48302	1	979.4723	-5.6	40	49	6	47.4	28	A	GYAERGIGSA	A	-0.3	6.88	
6	Q48302|Q48302	1	1012.5375	-0.3	18	27	3	45.6	27	S	NMPAITPKAA	A	0.1	10.1	
6	Q48302|Q48302	1	1050.5094	1.8	39	49	7	50.1	28	A	AGYAERGIGSA	A	-0.1	6.88	
6	Q48302|Q48302	1	1099.5695	-3.4	17	27	4	54.8	29	G	SNMPAITPKAA	A	0.0	10.1	
6	Q48302|Q48302	1	1149.5778	-2.2	40	51	8	63.8	29	A	GYAERGIGSAAV	G	0.2	6.88	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
6	Q48302|Q48302	1	1156.591	-1.7	16	27	5	54.2	29	T	GSNMPAITPKAA	A	-0.1	10.1	
6	Q48302|Q48302	1	1163.5935	2.1	37	48	8	30.4	29	A	LAAGYAERGIGS	A	0.2	6.88	
6	Q48302|Q48302	1	1172.5859	-0.9	16	27	5	31.8	29	T	GSNMPAITPKAA	A	-0.1	10.1	Oxidation (M)
6	Q48302|Q48302	1	1206.5993	0.7	40	52	9	38.1	29	A	GYAERGIGSAAVG	A	0.2	6.88	
6	Q48302|Q48302	1	1220.6149	-4.8	39	51	9	54.4	29	A	AGYAERGIGSAAV	G	0.4	6.88	
6	Q48302|Q48302	1	1234.6306	-0.8	36	48	9	60.9	29	A	ALAAGYAERGIGS	A	0.3	6.88	
6	Q48302|Q48302	1	1234.6306	-2.8	37	49	9	68.2	29	A	LAAGYAERGIGSA	A	0.3	6.88	
6	Q48302|Q48302	1	1386.6813	-1.9	14	27	6	47.5	29	A	ETGSNMPAITPKAA	A	-0.4	6.94	
6	Q48302|Q48302	1	1457.7184	-10.2	13	27	7	101.0	29	L	AETGSNMPAITPKAA	A	-0.2	6.94	
6	Q48302|Q48302	1	1473.7133	-1.8	13	27	7	38.4	29	L	AETGSNMPAITPKAA	A	-0.2	6.94	Oxidation (M)
6	Q48302|Q48302	1	1683.8865	-3.9	11	27	9	110.4	27	T	ILAETGSNMPAITPKAA	A	0.3	6.94	
6	Q48302|Q48302	1	1699.8814	1.6	11	27	9	33.7	28	T	ILAETGSNMPAITPKAA	A	0.3	6.94	Oxidation (M)
7	Q9HRQ9|Q9HRQ9	1	1398.6681	-6.8	102	113	5	57.9	27	V	KWVWEGSTGHNV	H	-0.8	7.82	
7	Q9HRQ9|Q9HRQ9	1	1497.7576	-3.5	78	91	3	50.7	28	T	VKVGPNNQNVFDPA	E	-0.6	6.76	
7	Q9HRQ9|Q9HRQ9	1	1626.8002	-1.5	79	93	3	90.2	28	V	KVGPNNQNVFDPAEV	Y	-0.8	4.08	
7	Q9HRQ9|Q9HRQ9	1	1674.8148	0.5	175	191	5	100.5	29	S	GGGGPVERSPHEMGVPI	Q	-0.4	5.3	
7	Q9HRQ9|Q9HRQ9	1	1707.8118	4.3	102	116	7	104.8	28	V	KWVWEGSTGHNVHAT	S	-0.8	7.96	
7	Q9HRQ9|Q9HRQ9	1	1725.8686	-0.6	78	93	4	84.3	28	T	VKVGPNNQNVFDPAEV	Y	-0.4	4.08	
7	Q9HRQ9|Q9HRQ9	1	1873.9105	-1.0	175	193	6	88.5	28	S	GGGGPVERSPHEMGVPIQA	H	-0.5	5.3	
7	Q9HRQ9|Q9HRQ9	1	1955.0112	2.0	76	93	5	73.2	26	T	KTVKVGPNNQNVFDPAEV	Y	-0.7	6.98	
7	Q9HRQ9|Q9HRQ9	1	2306.0716	-13.4	102	122	9	96.1	24	V	KWVWEGSTGHNVHATSVPDEA	G	-0.7	5.18	
7	Q9HRQ9|Q9HRQ9	1	2445.1812	8.3	79	101	7	87.2	25	V	KVGPNNQNVFDPAEVYVSPGDTV	K	-0.5	3.7	
7	Q9HRQ9|Q9HRQ9	1	2544.2497	-4.2	78	101	8	47.9	24	T	VKVGPNNQNVFDPAEVYVSPGDTV	K	-0.3	3.7	
8	Q9HN93|Q9HN93	1	1239.5156	-6.1	118	128	3	77.7	23	A	DWGGHDPIENT	G	-1.5	3.7	
8	Q9HN93|Q9HN93	1	1332.6099	-2.1	98	108	4	38.4	28	V	SFEWVSNTHNI	L	-0.5	5.12	
8	Q9HN93|Q9HN93	1	1398.6528	-0.8	206	217	2	39.5	27	V	SYYRRTPAPDSS	G	-1.6	9.58	
8	Q9HN93|Q9HN93	1	1440.5946	-5.5	38	51	6	95.0	22	A	QAYDGWFSGDAKGG	A	-0.9	3.88	Gln->pyro-Glu (N-term Q)
8	Q9HN93|Q9HN93	1	1564.7481	-6.4	103	117	7	51.3	28	V	SNTHNILIDAQPDGA	D	-0.5	3.88	
8	Q9HN93|Q9HN93	1	1610.7002	1.7	38	53	8	96.9	26	A	QAYDGWFSGDAKGGAV	G	-0.4	3.88	Gln->pyro-Glu (N-term Q)
8	Q9HN93|Q9HN93	1	1667.7216	0.1	38	54	9	106.3	25	A	QAYDGWFSGDAKGGAVG	N	-0.4	3.88	Gln->pyro-Glu (N-term Q)
8	Q9HN93|Q9HN93	1	1711.7479	-2.3	129	143	7	73.1	25	T	GFTHTHTFDTEGVYT	Y	-0.6	5.04	
8	Q9HN93|Q9HN93	1	1761.737	6.6	240	254	3	54.0	24	A	FEPDTELGHDEYDPV	G	-1.3	3.38	
8	Q9HN93|Q9HN93	1	2213.0389	4.4	98	117	9	147.7	26	V	SFEWVSNTHNILIDAQPDGA	D	-0.3	3.7	
8	Q9HN93|Q9HN93	1	3444.5018	-2.8	206	237	9	41.2	15	V	SYYRRTPAPDSSGAFDYEPGGDTDDQPAIPEA	D	-1.2	3.58	
9	Q9HHN1|Q9HHN1	1	1534.6949	3.6	421	434	4	95.8	28	S	EPMIPWNSGGVFMA	S	0.3	3.3	
9	Q9HHN1|Q9HHN1	1	1571.674	-1.9	395	407	3	37.0	24	T	FRDLNDEYDLDGT	S	-1.3	3.36	
9	Q9HHN1|Q9HHN1	1	1585.7049	6.9	9	21	1	53.6	27	S	YEDFDPEKRPSFG	Q	-1.7	4.06	
9	Q9HHN1|Q9HHN1	1	1803.7621	0.2	393	407	4	88.1	23	G	MTFRDLNDEYDLDGT	S	-1.1	3.36	
9	Q9HHN1|Q9HHN1	1	2045.9728	5.2	411	428	7	81.0	27	S	RTLEETGTVSEPMIPWNS	G	-0.7	3.96	
9	Q9HHN1|Q9HHN1	1	2090.9103	8.8	393	410	7	33.4	25	G	MTFRDLNDEYDLDGTSLS	R	-0.8	3.36	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
9	Q9HHN1|Q9HHN1	1	2169.9889	9.9	389	407	6	49.3	26	I	VIPGMTFRDLNDEYDLDGT	S	-0.5	3.36	
9	Q9HHN1|Q9HHN1	1	2283.0729	-4.8	388	407	7	59.9	25	S	IVIPGMTFRDLNDEYDLDGT	S	-0.3	3.36	
9	Q9HHN1|Q9HHN1	1	2430.1128	1.3	2	21	3	44.0	24	M	VEFEPRSYEDFDPEKRPSFG	Q	-1.5	4.12	
9	Q9HHN1|Q9HHN1	1	2907.2943	2.9	383	407	8	68.0	21	A	DQYMSIVIPGMTFRDLNDEYDLDGT	S	-0.5	3.26	
10	Q9HRS0|Q9HRS0	1	1286.6156	-0.9	119	129	4	52.0	29	V	RFVWESGGHNV	H	-0.5	7.84	
10	Q9HRS0|Q9HRS0	1	1327.6408	-4.9	145	156	3	85.7	28	T	DIAGPPKEYTHT	F	-1.2	5.22	
10	Q9HRS0|Q9HRS0	1	1475.6067	-1.2	219	230	3	64.6	22	A	YFFMKYGGDYGE	-	-0.7	4.08	
10	Q9HRS0|Q9HRS0	1	1478.7592	-4.3	103	115	3	49.6	28	S	NVFKPAEMYVKPG	T	-0.4	9.62	
10	Q9HRS0|Q9HRS0	1	1595.7593	0.1	119	132	6	58.1	28	V	RFVWESGGHNVHAT	E	-0.6	8	
10	Q9HRS0|Q9HRS0	1	1917.8956	-1.5	183	200	5	84.7	27	V	TDSPPENKGYQTIVPDSA	K	-1.1	3.7	
10	Q9HRS0|Q9HRS0	1	2147.0382	-2.2	183	202	6	30.2	27	V	TDSPPENKGYQTIVPDSAKT	M	-1.3	4.3	
10	Q9HRS0|Q9HRS0	1	2344.1798	8.0	179	200	9	96.7	24	G	TIIVTDSPPENKGYQTIVPDSA	K	-0.4	3.7	
10	Q9HRS0|Q9HRS0	1	2541.166	1.4	133	156	9	45.0	23	T	EVPGDADWGVSTDIAGPPKEYTHT	F	-0.8	3.84	
10	Q9HRS0|Q9HRS0	1	2570.1602	-12.0	145	167	6	70.5	21	T	DIAGPPKEYTHTFDGPTGEYNYV	C	-1.0	4.06	
11	Q9HN95|Q9HN95	1	940.5018	5.1	454	463	3	65.8	27	V	LAPGSPGFPV	-	0.6	6.02	
11	Q9HN95|Q9HN95	1	1139.5764	-7.2	31	40	2	75.7	28	T	FYPPLQAHPA	F	-0.3	7.76	
11	Q9HN95|Q9HN95	1	1296.631	0.9	69	79	1	39.9	28	A	DNPDERIPLQT	F	-1.6	3.7	
11	Q9HN95|Q9HN95	1	1403.6874	-2.0	29	40	3	42.0	29	L	YTFYPPLQAHPA	F	-0.4	7.7	
11	Q9HN95|Q9HN95	1	1450.8224	-0.3	140	151	5	44.5	24	A	YLAWYTILPKLA	G	0.8	9.52	
11	Q9HN95|Q9HN95	1	1516.7714	-4.5	28	40	4	87.6	29	V	LYTFYPPLQAHPA	F	-0.1	7.7	
11	Q9HN95|Q9HN95	1	1729.8828	-3.6	26	40	5	58.0	28	A	NVLYTFYPPLQAHPA	F	0.0	7.7	
11	Q9HN95|Q9HN95	1	2062.9901	1.4	176	193	6	62.7	27	V	GFHHQYTDPGIAEGFKFI	A	-0.4	6.02	
12	Q9HSA8|Q9HSA8	1	727.3289	-10.0	61	66	1	30.7	25	V	FGEYRG	L	-1.2	6.88	
12	Q9HSA8|Q9HSA8	1	927.445	2.6	59	66	3	41.1	27	L	TVFGEYRG	L	-0.5	6.88	
12	Q9HSA8|Q9HSA8	1	953.4971	9.1	61	68	3	37.6	27	V	FGEYRGLL	E	0.0	6.88	
12	Q9HSA8|Q9HSA8	1	1236.6139	2.3	61	71	4	69.8	28	V	FGEYRGLLEPG	I	-0.5	4.26	
12	Q9HSA8|Q9HSA8	1	1274.5965	0.0	83	92	3	41.6	29	T	YTFDMRTQTI	D	-0.6	6.7	
12	Q9HSA8|Q9HSA8	1	1335.6823	-7.0	60	71	5	32.8	29	T	VFGEYRGLLEPG	I	-0.1	4.26	
12	Q9HSA8|Q9HSA8	1	2203.1677	2.0	61	80	8	119.1	23	V	FGEYRGLLEPGINVIPPFVS	R	0.4	4.26	
13	Q9HM69|CSG	1	1664.7529	2.9	598	611	4	65.0	27	T	FDEEDIDISELRQG	S	-1.0	3.38	
13	Q9HM69|CSG	1	1909.8541	9.4	598	614	7	43.8	27	T	FDEEDIDISELRQGSAS	A	-0.8	3.38	
13	Q9HM69|CSG	1	2265.9986	2.5	751	770	7	57.3	24	G	NYTVEADDGDNTDRQNVEIV	E	-1.2	3.32	
13	Q9HM69|CSG	1	2384.0139	2.4	591	611	8	92.1	21	I	SVDSDDTFDEEDIDISELRQG	S	-1.1	3.12	
13	Q9HM69|CSG	1	2637.1678	2.3	751	773	8	27.0	22	G	NYTVEADDGDNTDRQNVEIVEEL	E	-1.2	3.24	
13	Q9HM69|CSG	1	2762.2267	6.9	746	770	9	24.5	21	S	NVEPGNYTVEADDGDNTDRQNVEIV	E	-1.1	3.28	
14	Q9HRL3|Q9HRL3	1	1103.5651	-7.9	586	595	3	62.8	30	A	WLLYSGPAPT	K	0.2	5.92	
14	Q9HRL3|Q9HRL3	1	1311.6169	2.4	274	285	1	77.5	28	T	WLPDAMEGPTPV	S	-0.2	3	
14	Q9HRL3|Q9HRL3	1	1749.7707	-1.9	478	493	5	29.3	25	T	FHGEPRSDTAEDPHGV	R	-1.4	4.52	
14	Q9HRL3|Q9HRL3	1	1876.9472	-3.7	524	540	8	87.9	28	T	GLHIEFLHTWLAGPEGT	A	0.1	5.12	
14	Q9HRL3|Q9HRL3	1	1977.9949	-19.5	523	540	9	105.1	27	A	TGLHIEFLHTWLAGPEGT	A	0.1	5.12	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
14	Q9HRL3|Q9HRL3	1	2106.0245	-4.6	267	285	4	41.3	27	S	AQFPLHTWLPDAMEGPTPV	S	-0.1	4.06	
15	Q9HND8|VATI	1	1332.631	-3.1	364	374	2	44.7	28	I	NRPQYTEIDPT	V	-1.8	4.08	
15	Q9HND8|VATI	1	1445.715	-3.9	363	374	3	52.3	29	V	INRPQYTEIDPT	V	-1.3	4.08	
15	Q9HND8|VATI	1	1530.7678	-4.5	364	376	4	44.1	29	I	NRPQYTEIDPTVV	L	-0.9	4.08	
15	Q9HND8|VATI	1	1673.826	-1.1	361	374	4	73.3	28	T	EVINRPQYTEIDPT	V	-1.1	3.82	
15	Q9HND8|VATI	1	1871.9629	-2.7	361	376	6	82.0	28	T	EVINRPQYTEIDPTVV	L	-0.4	3.82	
15	Q9HND8|VATI	1	2086.0946	-5.8	359	376	8	48.6	26	S	LTEVINRPQYTEIDPTVV	L	-0.2	3.82	
16	Q9HRL1|Q9HRL1	1	1517.7878	-0.8	335	347	7	52.8	28	I	NSALSLFYYSRVV	K	0.6	9.58	
16	Q9HRL1|Q9HRL1	1	1557.7675	-1.6	350	362	5	33.1	29	A	LWIEDPRDDLSLS	G	-0.5	3.5	
16	Q9HRL1|Q9HRL1	1	1940.948	-0.6	350	366	7	58.2	27	A	LWIEDPRDDLSLSGQPT	G	-0.8	3.5	
16	Q9HRL1|Q9HRL1	1	2070.984	-2.2	131	149	3	52.4	27	A	SVPFHFWAPEAYEGAPAPV	S	0.1	4.24	
16	Q9HRL1|Q9HRL1	1	2142.0211	-0.8	130	149	4	134.1	26	T	ASVPFHFWAPEAYEGAPAPV	S	0.2	4.24	
17	Q9HMF1|Q9HMF1	1	1198.5982	-7.7	160	169	2	71.4	28	V	RLEGELPEWA	T	-0.9	3.96	
17	Q9HMF1|Q9HMF1	1	1411.7095	-0.6	158	169	3	70.8	28	V	NVRLEGELPEWA	T	-0.7	3.96	
17	Q9HMF1|Q9HMF1	1	1664.7682	-3.6	222	235	5	27.2	27	S	SIFPTDDRTEDWLA	R	-0.7	3.5	
17	Q9HMF1|Q9HMF1	1	1832.9156	1.6	192	208	7	30.5	28	V	LEYTGPGVESLSVPERT	T	-0.4	3.96	
17	Q9HMF1|Q9HMF1	1	2193.0073	1.6	581	599	7	52.7	26	L	NIDEETYARIEQGDDVEVV	D	-0.8	3.32	
18	Q9HRR0|Q9HRR0	1	1333.6051	3.3	7	17	2	55.2	28	S	NYGDIHRYEPA	S	-1.5	5.22	
18	Q9HRR0|Q9HRR0	1	1420.6371	0.4	6	17	3	72.0	27	G	SNYGDIHRYEPA	S	-1.4	5.22	
18	Q9HRR0|Q9HRR0	1	1459.6653	1.0	109	120	3	64.1	28	T	SMFENTVEQFKT	A	-0.7	4.26	
18	Q9HRR0|Q9HRR0	1	1530.7024	3.9	109	121	4	78.9	28	T	SMFENTVEQFKTA	L	-0.5	4.26	
19	Q9HMW4|Q9HMW4	1	1578.7467	-1.8	402	415	2	47.1	28	T	LHPTWGPYAPENPT	T	-1.1	5.12	
19	Q9HMW4|Q9HMW4	1	2202.097	-6.2	252	270	6	37.0	26	A	AFNGNLGPWDLKRWSQQSV	M	-0.8	10.08	
19	Q9HMW4|Q9HMW4	1	2393.0692	-0.8	231	251	6	72.2	23	A	KPYVEAEDADGLEQDEEVMRA	A	-1.1	3.62	
19	Q9HMW4|Q9HMW4	1	2577.1904	-5.4	229	251	8	35.5	23	A	LAKPYVEAEDADGLEQDEEVMRA	A	-0.8	3.62	
20	Q9HMT7|Q9HMT7	1	1702.7322	-0.9	44	59	6	127.6	24	V	DVDTEAYEESHAPGAI	G	-0.7	3.5	
20	Q9HMT7|Q9HMT7	1	2369.1751	4.1	178	199	8	64.7	25	L	VDVRSPEEFSGEILAPPGLQET	A	-0.4	3.58	
20	Q9HMT7|Q9HMT7	1	2564.0074	4.8	126	147	5	66.1	16	L	DGGRDYWMDNDYPTSEEPPSFS	A	-1.7	3.32	
21	Q9HMG3|Q9HMG3	1	1037.5254	8.9	35	43	3	48.2	27	I	AQDVLEHRA	S	-0.7	5.22	
21	Q9HMG3|Q9HMG3	1	1737.7846	-1.0	44	58	3	117.7	26	A	STVPETDFPEPYNRS	I	-1.4	3.82	
21	Q9HMG3|Q9HMG3	1	1874.9486	-9.3	27	43	6	28.8	28	S	SKPPAEDIAQDVLEHRA	S	-0.9	4.54	
21	Q9HMG3|Q9HMG3	1	2757.2994	-6.9	35	58	7	46.0	22	I	AQDVLEHRASTVPETDFPEPYNRS	I	-1.1	4.28	
22	Q9HNL7|Q9HNL7	1	1752.9199	-8.0	9	23	4	48.7	27	G	SLFGVPYNFERPKLS	A	-0.3	9.72	
22	Q9HNL7|Q9HNL7	1	1920.9444	0.0	28	44	6	84.2	28	S	AYWQPGEGMLVEKPFGI	G	-0.1	4.26	
22	Q9HNL7|Q9HNL7	1	2451.2798	2.9	2	23	8	101.7	22	M	VEKPTSGSLFGVPYNFERPKLS	A	-0.5	9.62	
23	Q9HHP3|Q9HHP3	1	1600.7594	-3.8	228	241	5	50.5	28	A	AVDPESGDQVWRRS	L	-1.2	4.3	
23	Q9HHP3|Q9HHP3	1	1671.7965	-2.1	227	241	6	38.2	28	V	AAVDPESGDQVWRRS	L	-1.0	4.3	
23	Q9HHP3|Q9HHP3	1	1911.8599	3.6	111	126	6	85.4	26	T	SFDINENTRSWNVETT	G	-1.2	3.82	
24	Q9HSS1|Q9HSS1	1	940.4866	-2.6	249	258	5	35.7	26	A	LAGALEDGPV	S	0.6	3	
24	Q9HSS1|Q9HSS1	1	1207.635	-3.4	153	164	7	75.4	28	V	GFVGFGEIARGV	A	0.9	6.98	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
24	Q9HSS1|Q9HSS1	1	1232.6401	-6.0	210	220	4	42.6	29	V	FAPLTEETRGL	V	-0.2	4.26	
24	Q9HSS1|Q9HSS1	1	1646.8152	-2.7	210	224	6	37.1	29	V	FAPLTEETRGLVDEA	A	-0.2	3.68	
25	Q9HQP2|Q9HQP2	1	731.4582	-6.0	155	161	5	24.0	22	G	LFGAVIL	G	2.9	6.02	
25	Q9HQP2|Q9HQP2	1	1263.6976	-0.5	162	172	4	38.8	26	L	GLLPGYFLQRT	L	0.2	9.84	
25	Q9HQP2|Q9HQP2	1	1269.5778	-19.5	208	217	2	32.1	25	V	FEQFRAWDAT	G	-0.7	4.08	
25	Q9HQP2|Q9HQP2	1	2104.9491	0.6	746	763	4	27.0	25	V	VFYDGPRDLSQGDFYQQA	Y	-0.9	3.6	
26	Q9HQF4|Q9HQF4	1	1538.7577	-1.6	102	116	5	93.5	28	A	TEDGDPSVPGPIVRT	E	-0.7	3.7	
26	Q9HQF4|Q9HQF4	1	2168.9797	0.8	226	244	5	33.1	25	S	MAGEDVDYSPRTRNPDVFT	V	-1.0	3.96	
26	Q9HQF4|Q9HQF4	1	2539.1926	0.4	102	125	9	57.1	24	A	TEDGDPSVPGPIVRTEEGQDIEVT	L	-0.8	3.32	
27	Q9HRL8|Q9HRL8	1	1015.5603	2.3	170	178	3	32.2	29	A	GVRIPAWFA	F	0.9	11.04	
27	Q9HRL8|Q9HRL8	1	1243.5833	2.0	198	208	0	51.5	28	G	RNPFDTPEAPT	E	-1.5	4.08	
27	Q9HRL8|Q9HRL8	1	1826.8799	-5.1	192	208	4	64.0	28	A	NLAEVGRNPFDTPEAPT	E	-0.8	3.82	
28	Q9HMX1|Q9HMX1	1	1760.8329	-1.8	111	126	5	53.3	28	L	SRDVIPNQGYNDPSTV	R	-1.0	3.88	
28	Q9HMX1|Q9HMX1	1	1972.9023	-1.1	285	302	7	31.0	26	G	TLPNGRDLFTYMMGGAET	T	-0.3	4.08	
28	Q9HMX1|Q9HMX1	1	1987.0011	1.2	109	126	7	61.7	27	T	LLSRDVIPNQGYNDPSTV	R	-0.5	3.88	
29	Q9HS12|Q9HS12	1	731.4694	-15.4	23	28	3	32.0	22	V	FRALLL	A	1.9	11.04	
29	Q9HS12|Q9HS12	1	876.4263	24.2	511	518	4	48.2	29	S	ETVTAMPL	Q	0.7	3.3	Oxidation (M)
29	Q9HS12|Q9HS12	1	974.5913	5.0	23	31	6	35.6	22	V	FRALLLAAT	L	1.6	11.04	
30	Q9HMX0|Q9HMX0	1	1880.9785	2.3	188	205	8	36.1	27	S	NALQHLFSGIDPFAGVPV	L	0.6	4.94	
30	Q9HMX0|Q9HMX0	1	1968.0105	2.3	187	205	9	78.8	26	T	SNALQHLFSGIDPFAGVPV	L	0.5	4.94	
31	Q9HR04|Q9HR04	1	1239.6248	-3.4	76	87	7	29.9	28	S	IYLGGGEGGRYV	A	0.0	6.82	
31	Q9HR04|Q9HR04	1	1950.8344	-1.3	94	109	4	60.9	23	I	NQYYDDFSATQQTQRS	S	-1.9	3.88	
32	Q9HP48|Q9HP48	1	1821.7694	6.5	204	220	7	74.7	24	V	FESGVDHFEVDDDGALA	A	-0.3	3.32	
32	Q9HP48|Q9HP48	1	1892.8065	2.0	204	221	8	53.6	24	V	FESGVDHFEVDDDGALAA	A	-0.1	3.32	
33	Q9HMH4|Q9HMH4	1	1344.5358	5.1	56	67	4	53.9	22	A	SFSYDDPDADTL	G	-0.9	2.74	
33	Q9HMH4|Q9HMH4	1	1773.7006	5.0	56	71	6	101.6	19	A	SFSYDDPDADTLGWEG	G	-1.0	2.72	
34	Q9HRR1|Q9HRR1	1	1544.7583	-5.9	177	189	4	30.5	29	A	TWRSQNTDNTIPI	L	-1.1	6.78	
34	Q9HRR1|Q9HRR1	1	2719.1198	13.6	151	174	7	124.0	19	V	NIDEFDDYDTWENDYGDAGIGKPA	K	-1.3	3.16	
35	Q9HNY2|Q9HNY2	1	1026.5458	18.7	233	243	6	29.1	27	T	VPGADASALRA	G	0.4	6.78	
35	Q9HNY2|Q9HNY2	1	1126.6234	-16.4	230	241	8	29.2	27	A	LITVPGADASAL	R	1.2	3.1	
36	Q9HPG8|Q9HPG8	1	1317.6241	0.8	661	670	2	67.9	29	V	EFDDYFLRTL	E	-0.4	3.7	
37	Q9HM85|EF2	1	1379.8024	-3.0	614	625	6	38.8	23	A	LIDADIRLLEPI	Q	0.8	3.7	
37	Q9HM85|EF2	1	1786.8407	18.2	155	169	3	67.9	28	I	SELQEGPEEMQERLL	S	-1.2	3.68	
38	Q9HM89|EF1A	1	1521.71	-5.7	165	178	4	50.6	28	V	KDLFGQVGFNPDDA	K	-0.6	3.6	
38	Q9HM89|EF1A	1	1764.8319	2.8	162	178	7	87.0	28	V	SGVKDLFGQVGFNPDDA	K	-0.3	3.6	
39	Q9HNS6|Q9HNS6	1	1063.5815	10.7	71	81	4	30.2	26	I	GFGPIVGPHIA	F	0.9	7.84	
39	Q9HNS6|Q9HNS6	1	1361.7456	-5.9	68	81	6	98.4	27	T	NAIGFGPIVGPHIA	F	0.9	7.84	
40	Q9HP84|HTR4	1	731.4582	-4.6	324	330	5	29.2	22	T	GILGFIL	V	2.7	6.02	
41	Q9HMS7|Q9HMS7	1	1167.5924	-8.2	363	372	3	29.3	28	S	AFTPERFSLT	V	-0.1	6.98	
43	Q9HT00|GLMS	1	930.4658	10.2	537	546	7	51.2	30	G	ADVIGLASDA	G	1.0	2.92	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
45	Q9HP88|Q9HP88	1	1498.7126	0.7	171	183	4	77.5	28	T	AFRDYASTDMLPL	A	0.0	3.88	
45	Q9HP88|Q9HP88	1	1689.9301	-2.5	397	412	5	55.1	25	I	LLPIAPGLDDTPEIRA	Q	0.2	3.7	
47	Q9HRL2|Q9HRL2	1	1401.7041	-7.1	244	256	2	78.2	29	T	WLPDAHVQAPTPA	S	-0.2	4.94	
48	Q9HMB4|Q9HMB4	1	1621.8141	1.0	448	461	1	57.5	28	A	EFIRDYVPFVPGPS	A	0.0	4.08	
49	Q9HNN6|Q9HNN6	1	2021.8926	-4.7	163	181	7	39.0	24	G	AFVEPDQDSQADADRGSKS	R	-1.3	3.76	
50	Q9HPB1|SECY	1	1135.5696	-0.9	421	429	1	47.3	29	V	MERYIPQVT	V	-0.5	6.88	
52	Q9HPQ2|Q9HPQ2	1	1402.6517	-0.1	332	343	4	71.1	28	A	YVVDNYGYSRPA	T	-0.7	6.58	
54	Q9HS26|Q9HS26	1	1711.7577	2.6	16	31	6	55.7	26	A	GDDSEPEIDFYGGKLA	S	-0.8	3.42	
56	Q9HMU6|Q9HMU6	1	1231.6098	-6.7	114	124	1	46.9	30	V	GDSPPRWHAPL	L	-1.1	7.84	
57	Q9HRJ5|Q9HRJ5	1	1243.6561	-15.1	96	106	5	36.8	30	A	TTPLSRAEWLA	A	-0.1	6.98	
58	Q9HR32|TOP6A	1	1459.7154	9.7	7	19	6	34.2	29	T	SDETEARDQLLAI	A	-0.6	3.58	
58	Q9HR32|TOP6A	1	2300.0419	2.5	20	39	4	44.0	24	I	AEQFYDQFADGDIPRMSLPT	R	-0.6	3.5	
59	Q9HQQ9|Q9HQQ9	1	2003.9622	-1.7	350	367	6	32.8	27	V	AYDPVAAEKMAEQRPEVT	Y	-0.8	4.16	
60	Q9HSM2|MUTS1	1	1156.6088	1.1	328	338	6	29.4	29	A	RDALGDVLGEI	Y	0.2	3.7	
61	Q9HMU8|Q9HMU8	1	1186.671	-7.0	47	56	4	79.6	27	I	NILLDFVRPT	T	0.5	6.78	
62	Q9HMZ3|Q9HMZ3	1	2517.1237	3.8	413	432	5	53.9	23	V	EYLWYVGDYPSYDERNQHIA	R	-1.2	4.06	
63	Q9HSM4|DHE42	1	1255.6925	-3.7	241	251	6	57.3	28	A	LLLDDWGARVV	A	0.8	3.88	
66	Q9HHR4|Q9HHR4	1	1340.818	-0.9	235	247	8	24.3	20	A	LIGVGYIIGPRIA	A	1.5	9.84	
68	Q9HN92|Q9HN92	1	955.5273	-2.9	1	8	2	42.7	28	-	MNVRPQVI	A	0.2	11.04	
68	Q9HN92|Q9HN92	1	971.5222	-5.1	1	8	2	30.3	30	-	MNVRPQVI	A	0.2	11.04	Oxidation (M)
68	Q9HN92|Q9HN92	1	1026.5644	0.6	1	9	3	55.2	27	-	MNVRPQVIA	T	0.4	11.04	
69	Q9HNW7|Q9HNW7	1	1582.7086	1.7	235	248	4	59.8	27	L	MFQGLEGYDDVRPG	S	-0.7	3.7	
70	Q9HSJ6|Q9HSJ6	1	986.6165	8.4	160	169	8	20.8	20	G	IVGAFVLIVG	G	2.9	6.02	
72	P16102|BACH	1	962.5338	4.1	156	163	4	29.4	27	T	SALLFRWA	F	1.0	11.04	
72	P16102|BACH	1	1220.6401	-1.6	191	201	6	33.8	28	A	GTAEIFDTLRV	L	0.3	4.08	
74	Q9HHI2|Q9HHI2	1	731.4582	-6.0	40	46	5	24.0	22	L	IVFGAIL	L	3.0	6.02	
74	Q9HHI2|Q9HHI2	1	731.4582	-4.6	41	47	5	24.1	22	I	VFGAILL	M	2.9	6.02	
76	Q9HRS4|Q9HRS4	1	2054.809	6.7	16	35	9	81.0	18	A	AADQGIDPWTADDHEGGDGE	-	-1.3	3.22	
77	Q9HRS9|Q9HRS9	1	1311.6533	-25.4	184	195	2	51.5	28	S	WLPDAMVAPTPV	S	0.7	3.1	Oxidation (M)
80	Q9HS72|SECE	1	1605.8436	-1.7	1	14	6	33.3	27	-	MDVPLELSAYTRVL	R	0.5	4.08	
81	Q9HNR0|Q9HNR0	1	1097.4989	27.8	38	48	5	40.0	28	G	QQAATGDPTNL	N	-0.9	3.1	Gln->pyro-Glu (N-term Q)
84	Q9HQ64|Q9HQ64	1	1716.8907	-1.9	79	94	7	71.3	28	V	YNALVNQGIEGNAKRA	A	-0.6	9.72	
85	Q9HS86|Q9HS86	1	1261.5939	-0.5	95	106	4	42.6	29	I	AAGEFERADIPS	S	-0.4	3.82	
87	Q9HPA9|Q9HPA9	1	930.4771	-2.6	509	518	7	31.6	30	A	QGNVGLSSGI	T	0.3	6.02	
93	Q9HNQ9|Q9HNQ9	1	1122.5094	7.9	209	218	4	44.0	28	S	GGFWESVDRA	M	-0.5	4.08	
96	Q9HNK1|Q9HNK1	1	762.4276	-28.7	116	123	6	32.9	29	A	AIALFGTA	I	1.9	6.02	
97	Q9HN02|Q9HN02	1	1096.5917	-0.8	163	171	4	52.0	26	V	LFDYLTRAV	N	0.7	6.7	
99	Q9HQ23|Q9HQ23	1	866.5225	24.8	286	294	5	26.1	19	G	LPLLNGGAI	A	1.3	6.02	
99	Q9HQ23|Q9HQ23	1	1222.7074	22.2	104	115	7	20.4	20	V	NLAVWGPALALV	G	1.6	6.02	
100	Q9HSA0|Q9HSA0	1	1260.6251	-2.2	39	50	3	52.5	30	A	FEHGLPSGPHLA	D	-0.2	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
103	Q9HN43|CAPPA	1	930.4771	-1.8	326	334	5	31.5	30	L	AVIDRTADA	Y	0.2	3.88	
103	Q9HN43|CAPPA	1	1267.6561	11.5	308	319	3	45.9	27	L	RDADLGAPPFPI	D	-0.2	3.88	
105	Q9HHI3|Q9HHI3	1	1145.5088	-12.1	69	79	4	32.6	25	V	SLPDSVETDPS	I	-0.8	2.88	
110	Q9HQE2|Q9HQE2	1	1498.8104	-11.5	114	127	8	36.3	28	L	DRLRDAGLDVAVVT	N	0.2	4.18	
116	O54610|O54610	1	745.4222	1.7	427	433	5	26.3	26	T	EATLTLV	G	1.2	3.3	
118	Q9HMU9|Q9HMU9	1	1069.4393	-3.3	37	45	3	35.1	22	A	GYGYFFDTT	T	-0.3	3.1	
118	Q9HMU9|Q9HMU9	1	1269.6254	-3.9	257	265	1	37.7	28	G	YWRFNTRDL	-	-1.4	9.84	
119	Q9HPT9|Q9HPT9	1	2263.0128	2.7	61	82	8	56.9	25	A	ALDLPGHGDSDDIETDPGPETL	D	-0.8	3.22	
123	Q9HPG5|TRPE1	1	940.4866	8.2	11	20	5	27.3	26	T	ALADDGPAIV	R	0.9	2.92	
126	Q9HS00|Q9HS00	1	799.4804	13.9	492	500	8	32.1	27	T	AAVVAATVV	R	2.6	6.02	
126	Q9HS00|Q9HS00	1	1449.8919	-24.6	192	205	9	25.0	21	S	NVLTQLKPVLGVGI	G	1.0	10.1	
127	Q9HRU7|Q9HRU7	1	2158.1827	-1.2	186	204	9	25.4	22	T	VWLGYLDVIRPVFDALSPV	L	1.0	3.88	
128	Q9HN22|Q9HN22	1	1719.8104	2.4	149	165	9	48.7	28	A	AAFLADIDHSAYGTTPA	Q	0.3	3.88	
132	Q9HN79|Q9HN79	1	1037.6485	-14.6	51	61	8	21.6	21	A	VSAVGLVAPLI	G	2.3	6.02	
140	Q9HMV1|Q9HMV1	1	763.3752	-13.6	48	54	3	28.2	28	A	TFLEPGT	T	0.0	3.3	
142	Q9HPM1|Q9HPM1	1	1026.5458	18.7	164	174	7	30.5	27	I	ADGTRPAVAVA	T	0.4	6.78	
145	Q9HMB7|Q9HMB7	1	1423.662	3.4	123	134	2	74.1	28	A	REEDDFSIFAPV	L	-0.4	3.58	
150	Q9HPY6|Q9HPY6	1	731.4694	-20.0	390	395	3	34.3	22	A	FARLLL	A	1.9	11.04	
151	Q9HMY7|Q9HMY7	1	731.4582	-6.0	104	110	5	24.0	22	L	LAFVGII	V	3.0	6.02	
152	Q9HRL4|Q9HRL4	1	1369.6514	2.0	83	93	3	56.1	28	T	LYRNFDDIDVT	N	-0.5	3.6	
155	Q9HQU8|Q9HQU8	1	2107.9698	-0.5	13	30	4	41.1	26	A	RLTDQDEFTPPESFVEQA	N	-1.1	3.5	
156	Q9HSW2|Q9HSW2	1	713.4799	27.2	22	27	4	25.1	14	S	IRSLLI	I	1.9	11.04	
158	Q9HR62|Q9HR62	1	958.5964	20.2	21	29	6	14.1	14	A	FRVGLAVVV	L	2.3	11.04	
161	Q9HMQ8|Q9HMQ8	1	731.4218	6.7	196	202	3	26.9	26	A	IAAFLPT	F	1.8	6.02	
162	Q9HRA8|Q9HRA8	1	799.4803	8.0	319	326	5	31.5	28	T	ALKAVGEI	G	1.0	6.94	
164	Q9HP98|Q9HP98	1	930.5022	-21.7	23	32	8	40.6	30	G	SVVLLSGEAG	A	1.2	3.3	
165	Q9HRJ0|Q9HRJ0	1	1122.5227	-3.9	141	152	9	28.4	28	A	MAAADTSVSALA	L	1.1	3.1	Oxidation (M)
175	P25964|BACS1	1	1426.6187	-1.9	219	231	1	29.5	25	V	FMHSESPPAPEQA	T	-0.9	4.24	
177	Q9HP66|Q9HP66	1	830.5266	9.9	117	124	6	25.1	19	V	FLGLLAVV	L	3.0	6.02	
182	P33518|COX1	1	1447.6765	8.2	143	155	4	29.3	29	I	DADDMAFPRINAI	A	-0.1	3.6	
183	Q9HR22|Q9HR22	1	1658.8304	2.2	72	86	7	36.5	29	V	YSELFLGAIGHPEQV	L	0.2	4.24	
185	Q9HN36|Q9HN36	1	731.4581	-4.6	259	264	3	39.6	22	T	FNLLLL	V	2.4	6.02	
186	Q9HPK2|Y1595	1	974.5648	29.6	69	77	7	38.2	22	G	STTLLQLIS	D	1.0	6.02	
188	Q9HS30|Q9HS30	1	1222.7173	-1.5	59	70	7	24.5	22	A	LLADLPVEAGIL	V	1.5	3	
189	Q9HNY9|Q9HNY9	1	745.4446	-18.0	121	127	4	27.1	25	A	IAGTRKT	T	-0.6	11.48	
205	Q9HN37|Q9HN37	1	1314.8275	-13.2	539	550	8	25.2	17	A	LVFQVKLSVVIA	A	2.1	10.1	
221	Q9HSQ7|Q9HSQ7	1	944.512	-11.1	208	214	2	32.3	30	A	LFTYRFV	N	1.0	9.84	
234	Q9HP76|Q9HP76	1	968.5807	-8.2	119	126	3	25.9	24	I	RWSIPIVV	R	1.2	11.04	
236	Q9HPQ6|Q9HPQ6	1	997.4393	14.3	25	32	3	26.5	26	A	LVDWYTDS	H	-0.3	2.92	
239	Q9HMQ2|ASSY	1	1365.6564	-2.7	146	156	4	44.5	29	L	GLTREWEIEYA	A	-0.7	3.96	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
248	Q9HSJ4|Q9HSJ4	1	830.5266	9.9	21	28	6	25.1	19	G	VFVILAVA	A	3.4	6.02	
258	Q9HQE1|Q9HQE1	1	930.477	-1.8	226	234	5	33.0	30	T	ADLLSERGA	N	-0.2	4.08	
260	Q9HPQ1|Q9HPQ1	1	731.4582	-4.6	376	382	5	29.2	22	A	GLIGFLL	F	2.6	6.02	
266	Q9HQU3|Q9HQU3	1	731.4582	-6.0	143	149	5	36.3	22	V	IIGLGFL	A	2.7	6.02	
270	Q9HMC9|Q9HMC9	1	1137.6758	0.7	533	543	6	27.1	22	S	NNASVVLLIPV	A	1.6	6.02	
288	Q9HST9|Q9HST9	1	896.395	15.6	7	14	2	30.7	26	G	MTYADAPL	R	0.3	3.1	Oxidation (M)
289	O51975|O51975	1	713.4799	27.2	190	195	4	21.2	14	L	RSLLII	F	1.9	11.04	
289	O51975|O51975	1	1314.8169	-5.2	184	194	6	21.6	17	S	LCKTRLRSLLI	I	0.7	11.32	
294	Q9HNI3|Q9HNI3	1	731.4582	0.1	114	120	5	30.6	22	G	FGLAVIL	A	2.9	6.02	
299	Q9HQ90|Q9HQ90	1	1066.5771	27.4	239	249	7	28.8	24	A	QAALRAGADLV	R	0.6	6.78	Gln->pyro-Glu (N-term Q)
303	Q9HQ63|DHSD	1	1038.5386	-1.6	121	130	6	27.0	26	A	SVPTFLTGAF	-	1.1	6.02	
309	Q9HMC7|THI4	1	1241.6252	-8.2	83	94	5	28.4	28	V	RSPAEAVLDDLG	V	-0.2	3.7	
325	Q9HQZ3|Q9HQZ3	1	930.477	-22.9	36	44	5	30.2	30	G	ERLAAVDSA	G	0.1	4.08	
343	Q9HMB0|Q9HMB0	1	896.4127	-0.6	10	17	3	35.0	26	L	LYTTPTDS	D	-0.7	3.1	
345	Q48325|TBPB	1	1409.7514	13.3	87	99	6	28.0	26	I	RELGIDVTSNPPI	E	-0.2	4.08	
348	Q9HRW7|Q9HRW7	1	1618.7012	8.1	2	15	5	47.8	26	M	SDALDAFDHDAWRT	A	-0.9	3.86	
361	Q9HSW6|CDC61	1	1098.6172	-23.7	145	154	6	36.6	28	I	LIVLDEVDAI	G	1.6	2.88	
363	Q9HMJ2|Q9HMJ2	1	876.4263	24.2	149	156	4	36.3	29	A	EVSMLADI	D	1.1	3	
371	Q9HQH2|Q9HQH2	1	1441.6838	-2.0	152	163	4	30.7	28	V	NTRLQTFDGEYV	M	-0.9	4.08	
392	Q9HNB8|Q9HNB8	1	1293.6717	-8.5	12	24	5	34.3	28	A	SGHLAPLFDAAPV	R	0.7	4.94	
395	Q9HRR3|Q9HRR3	1	1093.4716	7.5	42	49	1	31.5	27	L	TYEYFERS	R	-1.6	4.26	
398	Q9HRR2|Q9HRR2	1	1688.8661	-1.7	42	54	5	47.2	28	V	DYLELLETLYYRV	N	0.0	3.82	
408	Q9HNJ2|Q9HNJ2	1	745.4222	0.3	116	122	5	31.9	27	S	LVTETAL	F	1.2	3.3	
411	Q9HM88|Q9HM88	1	1187.567	-5.2	56	68	8	37.0	29	A	SEIGTGAPSDALA	A	0.2	3	
433	Q9HME2|Q9HME2	1	1988.0078	0.6	2	18	9	42.4	27	M	VWIIDNLVTMVEHFTTA	A	0.9	4.06	
460	Q9HMY1|Q9HMY1	1	955.5199	4.8	286	295	6	28.5	28	A	NAAAQRVIGG	T	0.2	11.04	
488	Q9HN08|Q9HN08	1	1727.8625	11.9	1	16	7	39.1	28	-	MPTQDGERRDVVIVGG	G	-0.5	4.3	
493	Q9HRH6|Q9HRH6	1	1480.731	2.6	143	156	9	38.8	28	A	SYTGLRWLAGGAET	-	-0.2	6.88	
495	Q9HRR5|Q9HRR5	1	1313.5863	4.4	22	32	2	38.7	27	I	MAGWYRTPEFG	H	-0.6	6.88	
499	Q9HS52|SYP	1	1698.861	27.7	449	465	9	29.3	27	I	AAEIVMVPLGEDSAARA	A	0.6	3.82	
512	Q9HRK3|Q9HRK3	1	731.4582	-6.0	47	52	3	24.0	22	I	IQFVLI	G	2.7	6.02	
520	Q9HSE5|Q9HSE5	1	799.4804	20.8	81	89	8	27.2	27	S	AAAAVVTVV	L	2.6	6.02	
525	Q9HQV6|Q9HQV6	1	731.4582	-4.6	26	32	5	36.8	22	V	LFGGLLL	I	2.5	6.02	
537	Q9HMK6|Q9HMK6	1	1727.9166	-19.4	184	199	8	36.0	28	T	EKDVSEARRDAVLAGI	T	-0.4	4.56	
545	Q9HR54|Q9HR54	1	958.5964	20.2	335	343	6	24.0	14	V	LFRAGGLLL	V	1.6	11.04	
558	Q9HQW3|Q9HQW3	1	986.6277	-3.0	124	132	6	20.3	20	L	LAFRIVIVG	C	2.3	11.04	
587	Q9HPI6|Q9HPI6	1	882.5175	26.2	15	24	7	33.2	25	T	LPAAIGGITA	Y	1.5	6.02	
632	Q9HRR7|Q9HRR7	1	1289.6364	-27.7	41	55	8	32.6	28	A	ADAGGPHLAPGVSAA	A	0.3	4.94	
633	Q9HQB1|Q9HQB1	1	958.6328	-17.7	70	77	4	19.6	14	V	KAVFRLLI	E	1.6	11.48	
651	Q9HRR6|Q9HRR6	1	1286.6295	-1.0	95	104	1	30.2	29	A	DFFEFEARKV	E	-0.5	4.44	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
668	Q9HN96|Q9HN96	1	1005.5495	-16.0	41	50	6	29.3	28	G	LLKSGLFGDG	D	0.5	6.76	
689	Q9HRP9|Q9HRP9	1	1255.6633	-1.4	86	98	7	28.4	28	V	GPDAVTGAVRRAS	E	-0.2	10.88	
721	Q9HRE8|RTCA	1	1227.6711	-16.9	95	107	9	29.2	29	T	SVEVGTAGSIPLV	F	1.1	3.3	
737	Q9HRP5|Q9HRP5	1	745.4222	0.3	84	90	5	28.3	27	V	TIETAVL	Y	1.3	3.3	
743	Q9HPV1|Q9HPV1	1	958.5964	20.2	33	41	6	14.3	14	A	IAAFGLVRI	S	2.1	11.04	
755	Q9HS03|Q9HS03	1	1409.7337	26.0	60	73	8	26.1	26	G	MPAEVVSAVKATHA	V	0.6	7.82	
981	Q9HHQ7|Q9HHQ7	1	731.4581	-6.0	125	130	3	24.0	22	I	LLNFIL	H	2.5	6.02	
1081	Q9HNX9|Q9HNX9	1	713.48	27.2	126	131	4	15.6	14	G	VTRILL	G	1.9	11.04	
1082	Q9HRF3|Q9HRF3	1	713.4799	27.2	85	90	4	15.6	14	T	RLSLLL	D	1.7	11.04	

END OF LIST V

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
VI. Purple membrane; elastase digest; nLC-MALDI MS/MS; AVLIST search specificity															
1	P02945|BACR	1	731.4582	-4.6	231	237	3	57.7	21	V	GFGLILL	R	2.6	6.02	
1	P02945|BACR	1	734.4401	-13.3	219	224	3	25.4	18	T	LLFMVL	D	3.4	6.02	
1	P02945|BACR	1	756.3919	-5.4	19	24	0	27.5	25	T	GRPEWI	W	-1.1	6.98	
1	P02945|BACR	1	762.4024	19.3	240	246	2	50.5	26	S	RAIFGEA	E	0.4	6.98	
1	P02945|BACR	1	799.4916	6.8	187	193	4	38.5	25	V	LRNVTVV	L	1.1	11.04	
1	P02945|BACR	1	817.4011	-8.0	165	171	2	33.5	29	V	LFFGFTS	K	1.5	6.02	
1	P02945|BACR	1	828.3918	23.3	92	97	1	30.7	26	I	YWARYA	D	-0.7	9.58	
1	P02945|BACR	1	834.4276	-5.5	194	200	3	30.7	26	V	LWSAYPV	V	0.7	5.92	
1	P02945|BACR	1	835.4514	-12.2	220	226	3	28.5	26	L	LFMVLDV	S	2.5	3.1	
1	P02945|BACR	1	857.4395	-4.1	18	24	1	32.2	28	I	TGRPEWI	W	-1.0	6.98	
1	P02945|BACR	1	869.4391	-6.7	69	75	3	26.9	25	T	MYLSMLL	G	1.9	5.92	
1	P02945|BACR	1	887.4786	-25.8	124	132	4	60.2	29	A	LVGADGIMI	G	1.8	3.1	
1	P02945|BACR	1	917.4276	0.1	174	181	2	37.9	27	A	ESMRPEVA	S	-0.8	4.26	
1	P02945|BACR	1	930.4811	-6.2	201	209	4	68.7	29	V	VWLIGSEGA	G	0.9	3.3	
1	P02945|BACR	1	958.6215	-6.1	229	237	4	44.1	14	A	KVGFGLILL	R	2.0	10.1	
1	P02945|BACR	1	967.5954	-5.5	103	111	5	64.7	22	T	TPLLLLDLA	L	1.7	3.1	
1	P02945|BACR	1	974.5913	-6.1	231	239	4	63.7	22	V	GFGLILLRS	R	1.4	11.04	
1	P02945|BACR	1	991.5015	-7.5	98	105	2	29.0	28	A	DWLFTTPL	L	0.4	3.1	
1	P02945|BACR	1	1005.5356	-1.8	238	246	3	37.5	27	L	RSRAIFGEA	E	-0.3	10.88	
1	P02945|BACR	1	1016.5331	20.5	165	173	3	27.3	27	V	LFFGFTSKA	E	0.9	10.1	
1	P02945|BACR	1	1032.44	-18.0	243	252	1	80.2	21	I	FGEAEAPEPS	A	-0.9	3.02	
1	P02945|BACR	1	1043.5499	-2.0	112	121	5	72.5	29	A	LLVDADQGTI	L	0.7	2.92	
1	P02945|BACR	1	1055.5552	-11.0	19	26	1	38.6	26	T	GRPEWIWL	A	-0.4	6.98	
1	P02945|BACR	1	1062.6186	-2.5	182	190	4	56.9	22	A	STFKVLRNV	T	0.2	11.48	
1	P02945|BACR	1	1070.5185	24.5	95	102	2	61.3	27	A	RYADWLFT	T	-0.3	6.7	
1	P02945|BACR	1	1081.5556	1.9	16	24	2	61.4	26	A	QITGRPEWI	W	-0.7	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1098.5822	2.5	16	24	2	50.6	27	A	QITGRPEWI	W	-0.7	6.98	
1	P02945|BACR	1	1116.6907	4.9	227	237	6	53.5	17	V	SAKVGFGLILL	R	1.7	10.1	
1	P02945|BACR	1	1126.5923	16.7	19	27	2	51.6	26	T	GRPEWIWLA	L	-0.2	6.98	
1	P02945|BACR	1	1145.524	-25.4	242	252	2	79.0	23	A	IFGEAEAPEPS	A	-0.4	3.02	
1	P02945|BACR	1	1156.6029	6.2	18	26	2	56.0	28	I	TGRPEWIWL	A	-0.5	6.98	
1	P02945|BACR	1	1156.634	0.3	112	122	6	106.5	27	A	LLVDADQGTIL	A	0.9	2.92	
1	P02945|BACR	1	1173.7234	2.8	184	193	5	18.7	17	T	FKVLRNVTVV	L	1.1	11.48	
1	P02945|BACR	1	1187.5645	-21.1	81	91	0	93.9	26	T	MVPFGGEQNPI	Y	-0.1	3.3	
1	P02945|BACR	1	1203.5594	-19.2	81	91	0	81.4	26	T	MVPFGGEQNPI	Y	-0.1	3.3	Oxidation (M)
1	P02945|BACR	1	1215.7115	-8.0	101	111	6	62.7	25	L	FTTPLLLLDLA	L	1.6	3.1	
1	P02945|BACR	1	1227.64	22.3	18	27	3	56.7	28	I	TGRPEWIWLA	L	-0.2	6.98	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	1	1227.6711	-24.1	112	123	7	113.1	27	A	LLVDADQGTILA	L	1.0	2.92	
1	P02945|BACR	1	1239.6764	-2.6	19	28	3	37.1	25	T	GRPEWIWLAL	G	0.2	6.98	
1	P02945|BACR	1	1242.5822	-3.0	92	100	2	36.3	26	I	YWARYADWL	F	-0.6	6.64	
1	P02945|BACR	1	1253.6292	-0.8	48	58	3	66.4	27	V	SDPDAKKFYAI	T	-0.7	6.8	
1	P02945|BACR	1	1274.7711	3.0	183	193	6	61.6	19	S	TFKVLRNVTVV	L	0.9	11.48	
1	P02945|BACR	1	1280.6513	3.6	14	24	3	72.7	27	S	QAQITGRPEWI	W	-0.7	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1296.7152	-14.7	31	42	6	35.0	26	T	ALMGLGTLYFLV	K	1.9	5.92	
1	P02945|BACR	1	1314.8136	-2.6	231	242	6	70.3	17	V	GFGLILLRSRAI	F	1.2	12.4	
1	P02945|BACR	1	1340.7241	-0.5	18	28	4	28.5	26	I	TGRPEWIWLAL	G	0.1	6.98	
1	P02945|BACR	1	1354.6769	5.9	48	59	4	75.7	27	V	SDPDAKKFYAIT	T	-0.7	6.8	
1	P02945|BACR	1	1361.8031	1.8	182	193	7	76.5	21	A	STFKVLRNVTVV	L	0.8	11.48	
1	P02945|BACR	1	1372.6623	5.1	240	252	3	109.7	28	S	RAIFGEAEAPEPS	A	-0.5	3.96	
1	P02945|BACR	1	1380.719	-3.1	16	26	3	71.8	27	A	QITGRPEWIWL	A	-0.3	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1381.703	16.1	95	105	3	74.5	26	A	RYADWLFTTPL	L	-0.1	6.7	
1	P02945|BACR	1	1397.7456	-0.4	19	30	4	49.0	27	T	GRPEWIWLALGT	A	0.1	6.98	
1	P02945|BACR	1	1409.7919	-15.3	201	214	6	111.2	25	V	VWLIGSEGAGIVPL	N	1.3	3.3	
1	P02945|BACR	1	1443.6994	0.1	240	253	4	83.6	28	S	RAIFGEAEAPEPSA	G	-0.4	3.96	
1	P02945|BACR	1	1451.7561	1.0	16	27	4	88.0	27	A	QITGRPEWIWLA	L	-0.1	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1468.7827	11.0	16	27	4	61.8	26	A	QITGRPEWIWLA	L	-0.1	6.98	
1	P02945|BACR	1	1490.6983	2.3	92	102	3	53.0	28	I	YWARYADWLFT	T	-0.3	6.64	
1	P02945|BACR	1	1498.7932	0.3	18	30	5	89.2	28	I	TGRPEWIWLALGT	A	0.0	6.98	
1	P02945|BACR	1	1579.8147	0.2	14	26	4	81.9	27	S	QAQITGRPEWIWL	A	-0.4	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1607.7442	3.4	81	94	1	64.3	28	T	MVPFGGEQNPIYWA	R	-0.1	3.3	
1	P02945|BACR	1	1607.8712	4.1	95	107	5	77.8	25	A	RYADWLFTTPLLL	L	0.5	6.7	
1	P02945|BACR	1	1615.7954	1.2	238	252	4	108.0	28	L	RSRAIFGEAEAPEPS	A	-0.8	4.56	
1	P02945|BACR	1	1629.9018	4.5	98	111	7	64.6	25	A	DWLFTTPLLLLDLA	L	1.2	2.92	
1	P02945|BACR	1	1650.8518	10.8	14	27	5	106.1	27	S	QAQITGRPEWIWLA	L	-0.2	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1671.923	-12.1	126	143	9	91.6	26	V	GADGIMIGTGLVGALTKV	Y	1.1	6.76	
1	P02945|BACR	1	1678.8025	-3.5	76	91	2	123.4	27	L	GYGLTMVPFGGEQNPI	Y	0.0	3.3	
1	P02945|BACR	1	1686.8325	-4.8	238	253	5	82.3	28	L	RSRAIFGEAEAPEPSA	G	-0.6	4.56	
1	P02945|BACR	1	1694.7974	-7.2	76	91	2	115.0	26	L	GYGLTMVPFGGEQNPI	Y	0.0	3.3	Oxidation (M)
1	P02945|BACR	1	1718.9832	0.8	231	246	7	57.5	22	V	GFGLILLRSRAIFGEA	E	0.9	10.88	
1	P02945|BACR	1	1720.9552	-1.7	95	108	6	101.0	24	A	RYADWLFTTPLLLL	D	0.7	6.7	
1	P02945|BACR	1	1722.9093	8.1	16	30	6	98.0	26	A	QITGRPEWIWLALGT	A	0.1	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1739.9359	3.7	16	30	6	70.5	26	A	QITGRPEWIWLALGT	A	0.1	6.98	
1	P02945|BACR	1	1743.8064	-2.3	240	257	5	54.0	27	S	RAIFGEAEAPEPSAGDGA	A	-0.4	3.68	
1	P02945|BACR	1	1754.9104	-2.2	13	27	6	33.0	27	V	SQAQITGRPEWIWLA	L	-0.3	6.98	
1	P02945|BACR	1	1801.8828	1.1	92	105	4	76.1	28	I	YWARYADWLFTTPL	L	-0.1	6.64	
1	P02945|BACR	1	1826.9237	12.0	43	59	5	39.8	27	V	KGMGVSDPDAKKFYAIT	T	-0.4	9.56	
1	P02945|BACR	1	1835.9669	-4.5	48	64	7	95.0	27	V	SDPDAKKFYAITTLVPA	I	0.0	6.8	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	1	1841.9635	-11.6	236	252	6	64.1	28	I	LLRSRAIFGEAEAPEPS	A	-0.3	4.56	
1	P02945|BACR	1	1885.8806	-5.0	240	259	7	28.5	26	S	RAIFGEAEAPEPSAGDGAAA	T	-0.2	3.68	
1	P02945|BACR	1	1922.005	-2.2	14	30	7	101.8	26	S	QAQITGRPEWIWLALGT	A	0.0	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1955.0476	-3.5	235	252	7	58.1	26	L	ILLRSRAIFGEAEAPEPS	A	0.0	4.56	
1	P02945|BACR	1	2020.1033	-2.5	95	111	8	127.6	24	A	RYADWLFTTPLLLLDLA	L	0.7	3.88	
1	P02945|BACR	1	2073.9603	-0.5	240	261	9	57.1	26	S	RAIFGEAEAPEPSAGDGAAATS	D	-0.2	3.68	
1	P02945|BACR	1	2210.1484	-3.7	8	27	9	44.2	26	T	AVEGVSQAQITGRPEWIWLA	L	0.1	4.26	
1	P02945|BACR	1	2329.243	-4.9	231	252	8	119.5	24	V	GFGLILLRSRAIFGEAEAPEPS	A	0.3	4.56	
1	P02945|BACR	1	2440.2831	-0.2	92	111	9	75.3	23	I	YWARYADWLFTTPLLLLDLA	L	0.6	3.88	
2	P00772|ELA1	1	800.3851	9.2	54	61	3	46.1	25	A	HTCGGTLI	R	0.7	7.16	
2	P00772|ELA1	1	873.4093	0.5	34	40	1	28.8	27	A	QRNSWPS	Q	-2.2	11.04	
2	P00772|ELA1	1	882.5287	0.6	138	146	3	30.3	23	L	GVLPRAGTI	L	0.7	11.04	
2	P00772|ELA1	1	890.461	15.9	156	163	3	49.8	27	I	TGWGLTRT	N	-0.6	11.04	
2	P00772|ELA1	1	915.4239	-1.4	105	111	1	29.8	25	V	VHPYWNT	D	-1.0	7.76	
2	P00772|ELA1	1	933.4491	0.3	62	68	1	40.3	28	I	RQNWVMT	A	-1.0	11.04	
2	P00772|ELA1	1	943.4512	-7.2	223	231	2	49.9	26	V	NGQYAVHGV	T	-0.2	7.76	
2	P00772|ELA1	1	1004.4862	-2.5	62	69	2	45.1	28	I	RQNWVMTA	A	-0.7	11.04	
2	P00772|ELA1	1	1014.4923	7.2	104	111	2	55.5	27	I	VVHPYWNT	D	-0.4	7.76	
2	P00772|ELA1	1	1040.4675	2.4	45	53	3	25.3	25	L	QYRSGSSWA	H	-1.2	9.84	
2	P00772|ELA1	1	1066.6499	0.0	138	148	5	54.4	20	L	GVLPRAGTILA	N	1.1	11.04	
2	P00772|ELA1	1	1097.5254	3.6	34	42	2	71.2	26	A	QRNSWPSQI	S	-1.6	11.04	Gln->pyro-Glu (N-term Q)
2	P00772|ELA1	1	1114.5519	10.2	34	42	2	55.5	28	A	QRNSWPSQI	S	-1.6	11.04	
2	P00772|ELA1	1	1123.6713	-5.1	136	146	4	39.4	22	V	QLGVLPRAGTI	L	0.6	11.04	
2	P00772|ELA1	1	1214.5568	-8.9	187	197	5	66.1	25	S	SSYWGSTVKNS	M	-0.9	9.72	
2	P00772|ELA1	1	1240.5836	-0.2	43	53	5	63.8	26	I	SLQYRSGSSWA	H	-0.7	9.84	
2	P00772|ELA1	1	1244.5462	6.2	105	114	2	72.6	25	V	VHPYWNTDDV	A	-1.0	3.88	
2	P00772|ELA1	1	1262.6659	-15.8	254	264	6	41.0	28	S	AYISWINNVIA	S	1.0	5.92	
2	P00772|ELA1	1	1307.7925	-5.4	136	148	6	22.4	20	V	QLGVLPRAGTILA	N	1.0	11.04	
2	P00772|ELA1	1	1315.5833	10.9	105	115	3	62.6	26	V	VHPYWNTDDVA	A	-0.7	3.88	
2	P00772|ELA1	1	1321.6813	-8.2	239	250	4	42.9	27	L	GCNVTRKPTVFT	R	-0.2	10.1	
2	P00772|ELA1	1	1343.6146	-2.2	104	114	3	75.6	26	I	VVHPYWNTDDV	A	-0.5	3.88	
2	P00772|ELA1	1	1385.8031	-2.6	134	146	5	51.3	24	S	YVQLGVLPRAGTI	L	0.8	9.84	
2	P00772|ELA1	1	1386.6204	4.4	105	116	4	96.9	26	V	VHPYWNTDDVAA	G	-0.5	3.88	
2	P00772|ELA1	1	1414.6517	1.6	104	115	4	81.2	27	I	VVHPYWNTDDVA	A	-0.3	3.88	
2	P00772|ELA1	1	1427.7481	-3.9	162	174	5	56.8	28	T	RTNGQLAQTLQQA	Y	-1.0	11.04	
2	P00772|ELA1	1	1485.6889	-1.8	104	116	5	89.6	26	I	VVHPYWNTDDVAA	G	-0.2	3.88	
2	P00772|ELA1	1	1529.7223	-0.3	29	42	4	71.0	27	V	GGTEAQRNSWPSQI	S	-1.3	6.98	
2	P00772|ELA1	1	1590.8729	-1.2	124	137	8	31.5	25	L	RLAQSVTLNSYVQL	G	0.2	9.84	
2	P00772|ELA1	1	1712.8522	-17.2	101	114	4	92.1	27	V	QKIVVHPYWNTDDV	A	-0.6	5.1	
2	P00772|ELA1	1	1715.8955	0.2	156	171	7	67.9	27	I	TGWGLTRTNGQLAQTL	Q	-0.4	11.04	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	P00772|ELA1	1	1770.9992	0.3	132	148	8	37.3	23	L	NSYVQLGVLPRAGTILA	N	0.7	9.84	
2	P00772|ELA1	1	1801.0098	-0.6	130	146	8	127.3	23	V	TLNSYVQLGVLPRAGTI	L	0.5	9.84	
2	P00772|ELA1	1	1815.8024	-2.5	83	98	3	130.9	24	V	VGEHNLNQNDGTEQYV	G	-1.4	3.82	
2	P00772|ELA1	1	1905.8533	-0.6	105	121	6	119.4	26	V	VHPYWNTDDVAAGYDIA	L	-0.3	3.6	
2	P00772|ELA1	1	1914.8708	1.0	82	98	4	132.9	26	V	VVGEHNLNQNDGTEQYV	G	-1.0	3.82	
2	P00772|ELA1	1	1933.8847	9.8	104	120	6	65.5	27	I	VVHPYWNTDDVAAGYDI	A	-0.2	3.6	
2	P00772|ELA1	1	1971.8923	2.7	83	100	4	147.5	26	V	VGEHNLNQNDGTEQYVGV	Q	-1.0	3.82	
2	P00772|ELA1	1	2004.9218	-0.4	104	121	7	144.5	26	I	VVHPYWNTDDVAAGYDIA	L	-0.1	3.6	
2	P00772|ELA1	1	2043.0498	3.2	156	174	8	103.5	27	I	TGWGLTRTNGQLAQTLQQA	Y	-0.6	11.04	
2	P00772|ELA1	1	2070.9607	-2.5	82	100	5	154.5	26	V	VVGEHNLNQNDGTEQYVGV	Q	-0.7	3.82	
2	P00772|ELA1	1	2118.0058	2.6	104	122	8	34.4	27	I	VVHPYWNTDDVAAGYDIAL	L	0.2	3.6	
2	P00772|ELA1	1	2231.0899	-4.3	104	123	9	137.8	26	I	VVHPYWNTDDVAAGYDIALL	R	0.3	3.6	
2	P00772|ELA1	1	2317.1087	3.5	79	98	5	35.5	27	T	FRVVVGEHNLNQNDGTEQYV	G	-0.8	4.42	
2	P00772|ELA1	1	2341.1299	-5.7	83	103	5	96.7	26	V	VGEHNLNQNDGTEQYVGVQKI	V	-1.0	4.42	
2	P00772|ELA1	1	2374.1594	-0.3	101	121	8	130.5	27	V	QKIVVHPYWNTDDVAAGYDIA	L	-0.2	4.16	
2	P00772|ELA1	1	2440.1983	4.2	82	103	6	110.4	26	V	VVGEHNLNQNDGTEQYVGVQKI	V	-0.8	4.42	
2	P00772|ELA1	1	2473.1986	-6.8	79	100	6	27.3	26	T	FRVVVGEHNLNQNDGTEQYVGV	Q	-0.5	4.42	
3	Q9HMW9|Q9HMW9	1	978.5287	8.2	636	643	1	55.1	25	A	FHLQPPQL	F	-0.4	7.84	
3	Q9HMW9|Q9HMW9	1	1166.6084	-23.3	616	624	2	48.3	27	A	YVINREQFV	S	-0.1	6.88	
3	Q9HMW9|Q9HMW9	1	1212.6292	3.9	636	645	2	70.1	27	A	FHLQPPQLFS	D	-0.1	7.84	
3	Q9HMW9|Q9HMW9	1	1253.6404	-2.8	616	625	3	49.8	27	A	YVINREQFVS	D	-0.1	6.88	
3	Q9HMW9|Q9HMW9	1	1367.618	-8.8	133	143	1	37.8	25	L	QYQSPTWKEMA	N	-1.5	6.86	
3	Q9HMW9|Q9HMW9	1	1368.686	-1.2	614	624	3	41.0	27	A	MAYVINREQFV	S	0.3	6.88	
3	Q9HMW9|Q9HMW9	1	1441.7049	-3.6	166	178	5	93.1	27	S	SLLETTKQGEHEA	F	-1.1	4.54	
3	Q9HMW9|Q9HMW9	1	1455.718	-2.1	614	625	4	39.1	27	A	MAYVINREQFVS	D	0.2	6.88	
3	Q9HMW9|Q9HMW9	1	1467.7358	-1.0	616	627	4	38.3	27	A	YVINREQFVSDV	F	-0.1	4.08	
3	Q9HMW9|Q9HMW9	1	1567.7307	-7.4	120	132	1	33.7	26	A	GYGPDNKYELNWL	Q	-1.2	4.08	
3	Q9HMW9|Q9HMW9	1	1619.7144	-5.0	92	104	0	85.3	25	T	DYQPDFDKYPYGI	D	-1.4	3.6	
3	Q9HMW9|Q9HMW9	1	1695.7926	-3.9	133	146	3	89.6	26	L	QYQSPTWKEMANTI	R	-1.1	6.86	
3	Q9HMW9|Q9HMW9	1	1736.8958	0.9	619	633	3	89.0	27	I	NREQFVSDVFKGRGV	G	-0.7	10.08	
3	Q9HMW9|Q9HMW9	1	1802.905	-1.4	166	181	7	124.4	28	S	SLLETTKQGEHEAFTL	G	-0.5	4.54	
3	Q9HMW9|Q9HMW9	1	1857.9335	-0.5	595	610	3	105.2	28	I	DTYYVGFNMTKVPKPV	R	-0.3	9.46	
3	Q9HMW9|Q9HMW9	1	1864.9544	0.1	619	635	4	92.1	27	I	NREQFVSDVFKGRGVGA	F	-0.5	10.08	
3	Q9HMW9|Q9HMW9	1	1964.8316	-1.5	92	107	1	120.4	22	T	DYQPDFDKYPYGIDET	K	-1.6	3.36	
3	Q9HMW9|Q9HMW9	1	1971.0176	-5.5	594	610	4	53.8	27	T	IDTYYVGFNMTKVPKPV	R	0.0	9.46	
3	Q9HMW9|Q9HMW9	1	1987.9421	-0.4	149	165	6	40.2	27	A	RLEQAHIEMTINDANFS	S	-0.5	4.42	
3	Q9HMW9|Q9HMW9	1	1993.8582	1.5	88	104	2	90.4	23	T	GESTDYQPDFDKYPYGI	D	-1.4	3.5	
3	Q9HMW9|Q9HMW9	1	2072.0653	-8.3	593	610	5	36.7	27	S	TIDTYYVGFNMTKVPKPV	R	-0.1	9.46	
3	Q9HMW9|Q9HMW9	1	2112.1116	2.3	616	633	5	95.5	25	A	YVINREQFVSDVFKGRGV	G	-0.2	9.72	
3	Q9HMW9|Q9HMW9	1	2159.0973	0.5	592	610	6	39.7	27	V	STIDTYYVGFNMTKVPKPV	R	-0.1	9.46	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
3	Q9HMW9|Q9HMW9	1	2240.1702	-3.3	616	635	6	56.5	26	A	YVINREQFVSDVFKGRGVGA	F	-0.1	9.72	
3	Q9HMW9|Q9HMW9	1	2263.0321	3.4	92	110	3	35.0	26	T	DYQPDFDKYPYGIDETKVA	E	-1.2	3.76	
3	Q9HMW9|Q9HMW9	1	2314.1892	-0.5	614	633	6	97.4	25	A	MAYVINREQFVSDVFKGRGV	G	0.0	9.72	
3	Q9HMW9|Q9HMW9	1	2338.9754	7.7	88	107	3	98.9	21	T	GESTDYQPDFDKYPYGIDET	K	-1.6	3.32	
3	Q9HMW9|Q9HMW9	1	2442.2478	1.7	614	635	7	52.0	25	A	MAYVINREQFVSDVFKGRGVGA	F	0.1	9.72	
3	Q9HMW9|Q9HMW9	1	2637.1759	0.4	88	110	5	42.8	23	T	GESTDYQPDFDKYPYGIDETKVA	E	-1.3	3.68	
4	Q9HR99|Q9HR99	1	1419.6154	-3.6	122	134	5	65.3	24	V	DAGETLEHTFETA	G	-0.7	3.68	
4	Q9HR99|Q9HR99	1	1473.6195	-5.4	106	119	2	75.8	21	A	SGFGTMDKDGNQFA	V	-0.8	3.88	
4	Q9HR99|Q9HR99	1	1491.7246	-7.0	57	70	2	84.6	28	A	VAPDGGFKFEPSEL	T	-0.3	3.82	
4	Q9HR99|Q9HR99	1	1562.7617	-5.1	56	70	3	78.5	28	I	AVAPDGGFKFEPSEL	T	-0.1	3.82	
4	Q9HR99|Q9HR99	1	1651.7664	7.1	91	105	3	55.8	27	S	AWPDMHDKISIPDGA	S	-0.6	4.16	
4	Q9HR99|Q9HR99	1	1671.7563	-1.6	106	121	4	133.1	26	A	SGFGTMDKDGNQFAVV	D	-0.2	3.88	
4	Q9HR99|Q9HR99	1	1687.7512	-4.7	106	121	4	54.8	24	A	SGFGTMDKDGNQFAVV	D	-0.2	3.88	Oxidation (M)
4	Q9HR99|Q9HR99	1	1691.8407	0.9	57	72	4	105.2	28	A	VAPDGGFKFEPSELTV	S	0.0	3.82	
4	Q9HR99|Q9HR99	1	1762.8778	-3.5	56	72	5	119.1	28	I	AVAPDGGFKFEPSELTV	S	0.1	3.82	
4	Q9HR99|Q9HR99	1	1849.9098	-1.5	56	73	6	31.7	28	I	AVAPDGGFKFEPSELTVS	V	0.0	3.82	
4	Q9HR99|Q9HR99	1	1869.7905	-0.4	122	138	6	149.6	22	V	DAGETLEHTFETAGEYT	Y	-0.9	3.58	
4	Q9HR99|Q9HR99	1	2064.9753	2.8	48	68	6	47.1	26	A	SQSGGNTIAVAPDGGFKFEPS	E	-0.4	4.08	
4	Q9HR99|Q9HR99	1	2131.9222	7.6	122	140	7	152.5	24	V	DAGETLEHTFETAGEYTYV	C	-0.7	3.58	
4	Q9HR99|Q9HR99	1	2176.0007	11.1	86	105	6	118.8	26	S	SHNVSAWPDMHDKISIPDGA	S	-0.6	5.02	
4	Q9HR99|Q9HR99	1	2205.0954	5.3	51	72	7	45.8	27	S	GGNTIAVAPDGGFKFEPSELTV	S	0.0	3.82	
4	Q9HR99|Q9HR99	1	2212.0107	4.0	100	121	6	56.4	26	I	SIPDGASGFGTMDKDGNQFAVV	D	-0.1	3.6	
4	Q9HR99|Q9HR99	1	2307.1019	5.5	48	70	7	104.2	26	A	SQSGGNTIAVAPDGGFKFEPSEL	T	-0.3	3.82	
4	Q9HR99|Q9HR99	1	2507.218	5.4	48	72	9	128.2	25	A	SQSGGNTIAVAPDGGFKFEPSELTV	S	-0.2	3.82	
5	Q9HMI3|Q9HMI3	1	1172.619	-5.7	556	566	3	53.9	28	V	GGPFLDRVELA	-	0.2	4.08	
5	Q9HMI3|Q9HMI3	1	1248.6615	-3.7	181	190	1	32.1	27	T	QQYAPFLRNL	A	-0.6	9.84	
5	Q9HMI3|Q9HMI3	1	1319.6986	-2.2	181	191	2	36.9	27	T	QQYAPFLRNLA	I	-0.4	9.84	
5	Q9HMI3|Q9HMI3	1	1358.7194	-4.9	554	566	5	64.0	28	T	SVGGPFLDRVELA	-	0.5	4.08	
5	Q9HMI3|Q9HMI3	1	1475.7157	-0.9	390	402	2	61.1	28	A	TFSNPRGYNPNPI	Q	-1.2	9.84	
5	Q9HMI3|Q9HMI3	1	1554.7103	1.4	237	250	3	45.1	26	V	RLTAFDDYWGGAPS	V	-0.5	3.88	
5	Q9HMI3|Q9HMI3	1	1577.8202	-2.9	178	190	3	59.0	27	I	DLTQQYAPFLRNL	A	-0.5	6.7	
5	Q9HMI3|Q9HMI3	1	1648.8573	-5.1	178	191	4	50.7	27	I	DLTQQYAPFLRNLA	I	-0.3	6.7	
5	Q9HMI3|Q9HMI3	1	1696.8056	-0.3	331	345	5	30.1	27	I	NRDEIVDSIYQGFAA	S	-0.3	3.7	
5	Q9HMI3|Q9HMI3	1	1793.8221	3.7	222	236	2	102.8	26	T	GPFEFDQLDNETQRV	R	-1.2	3.58	
5	Q9HMI3|Q9HMI3	1	1808.9309	17.6	78	93	6	102.9	26	V	TNQIFDTLIQFKPGTS	G	-0.3	6.76	
5	Q9HMI3|Q9HMI3	1	1951.8912	1.1	220	236	3	140.2	26	V	GTGPFEFDQLDNETQRV	R	-1.1	3.58	
5	Q9HMI3|Q9HMI3	1	1994.9585	-4.4	460	477	5	89.1	27	V	LLHPGTDIDDVPADQNYI	A	-0.4	3.42	
5	Q9HMI3|Q9HMI3	1	2209.1267	-2.9	78	97	8	94.8	26	V	TNQIFDTLIQFKPGTSGELT	S	-0.3	4.08	
5	Q9HMI3|Q9HMI3	1	2296.1587	-6.4	78	98	9	111.5	26	V	TNQIFDTLIQFKPGTSGELTS	G	-0.3	4.08	
5	Q9HMI3|Q9HMI3	1	2310.1339	1.6	198	219	9	64.2	26	I	LSRDQIESLGADAQPELGTDPV	G	-0.5	3.42	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
5	Q9HMI3|Q9HMI3	1	3202.4691	5.2	207	236	8	72.6	21	L	GADAQPELGTDPVGTGPFEFDQLDNETQRV	R	-0.9	3.28	
6	Q48302|Q48302	1	904.5059	-11.4	82	89	2	33.8	26	V	VFVVPTPF	-	1.8	6.02	
6	Q48302|Q48302	1	908.4352	-10.1	40	48	2	30.6	26	A	GYAERGIGS	A	-0.6	6.88	
6	Q48302|Q48302	1	979.4723	-5.6	40	49	3	47.4	26	A	GYAERGIGSA	A	-0.3	6.88	
6	Q48302|Q48302	1	1012.5375	-0.3	18	27	3	45.6	26	S	NMPAITPKAA	A	0.1	10.1	
6	Q48302|Q48302	1	1050.5094	1.8	39	49	4	50.1	27	A	AGYAERGIGSA	A	-0.1	6.88	
6	Q48302|Q48302	1	1149.5778	-2.2	40	51	5	63.8	28	A	GYAERGIGSAAV	G	0.2	6.88	
6	Q48302|Q48302	1	1156.591	-1.7	16	27	4	54.2	27	T	GSNMPAITPKAA	A	-0.1	10.1	
6	Q48302|Q48302	1	1163.5935	2.1	37	48	5	30.4	27	A	LAAGYAERGIGS	A	0.2	6.88	
6	Q48302|Q48302	1	1172.5859	-0.9	16	27	4	31.8	28	T	GSNMPAITPKAA	A	-0.1	10.1	Oxidation (M)
6	Q48302|Q48302	1	1220.6149	-4.8	39	51	6	54.4	28	A	AGYAERGIGSAAV	G	0.4	6.88	
6	Q48302|Q48302	1	1234.6306	-0.8	36	48	6	60.9	28	A	ALAAGYAERGIGS	A	0.3	6.88	
6	Q48302|Q48302	1	1234.6306	-2.8	37	49	6	68.2	28	A	LAAGYAERGIGSA	A	0.3	6.88	
6	Q48302|Q48302	1	1277.6364	-0.9	40	53	6	103.4	28	A	GYAERGIGSAAVGA	I	0.3	6.88	
6	Q48302|Q48302	1	1305.6677	2.4	36	49	7	72.1	28	A	ALAAGYAERGIGSA	A	0.4	6.88	
6	Q48302|Q48302	1	1348.6735	-0.3	39	53	7	95.6	28	A	AGYAERGIGSAAVGA	I	0.4	6.88	
6	Q48302|Q48302	1	1359.6922	-0.2	54	66	5	29.3	29	A	IAEDPDLFGTGLI	L	0.6	2.88	
6	Q48302|Q48302	1	1386.6813	-1.9	14	27	5	47.5	28	A	ETGSNMPAITPKAA	A	-0.4	6.94	
6	Q48302|Q48302	1	1457.7184	-10.2	13	27	6	101.0	28	L	AETGSNMPAITPKAA	A	-0.2	6.94	
6	Q48302|Q48302	1	1473.7133	-1.8	13	27	6	38.4	28	L	AETGSNMPAITPKAA	A	-0.2	6.94	Oxidation (M)
6	Q48302|Q48302	1	1475.7732	-4.6	36	51	9	49.2	28	A	ALAAGYAERGIGSAAV	G	0.8	6.88	
6	Q48302|Q48302	1	1683.8865	-3.9	11	27	8	110.4	27	T	ILAETGSNMPAITPKAA	A	0.3	6.94	
6	Q48302|Q48302	1	1699.8814	1.6	11	27	8	33.7	28	T	ILAETGSNMPAITPKAA	A	0.3	6.94	Oxidation (M)
7	Q9HN93|Q9HN93	1	1239.5156	-6.1	118	128	1	77.7	21	A	DWGGHDPIENT	G	-1.5	3.7	
7	Q9HN93|Q9HN93	1	1332.6099	-2.1	98	108	4	38.4	27	V	SFEWVSNTHNI	L	-0.5	5.12	
7	Q9HN93|Q9HN93	1	1398.6528	-0.8	206	217	2	39.5	26	V	SYYRRTPAPDSS	G	-1.6	9.58	
7	Q9HN93|Q9HN93	1	1564.7481	-6.4	103	117	6	51.3	28	V	SNTHNILIDAQPDGA	D	-0.5	3.88	
7	Q9HN93|Q9HN93	1	1610.7002	1.7	38	53	4	96.9	25	A	QAYDGWFSGDAKGGAV	G	-0.4	3.88	Gln->pyro-Glu (N-term Q)
7	Q9HN93|Q9HN93	1	1711.7479	-2.3	129	143	5	73.1	25	T	GFTHTHTFDTEGVYT	Y	-0.6	5.04	
7	Q9HN93|Q9HN93	1	1761.737	6.6	240	254	2	54.0	23	A	FEPDTELGHDEYDPV	G	-1.3	3.38	
7	Q9HN93|Q9HN93	1	2213.0389	4.4	98	117	8	147.7	26	V	SFEWVSNTHNILIDAQPDGA	D	-0.3	3.7	
7	Q9HN93|Q9HN93	1	2418.0401	5.8	38	61	7	176.6	23	A	QAYDGWFSGDAKGGAVGNYDGTTV	D	-0.5	3.6	Gln->pyro-Glu (N-term Q)
7	Q9HN93|Q9HN93	1	2583.1726	4.9	62	87	9	52.4	24	V	DRTGTDEVTIDVGVDANGGTYGFGPA	A	-0.4	3.36	
7	Q9HN93|Q9HN93	1	2790.2158	2.1	38	64	8	199.1	21	A	QAYDGWFSGDAKGGAVGNYDGTTVDRT	G	-0.8	3.88	Gln->pyro-Glu (N-term Q)
7	Q9HN93|Q9HN93	1	3444.5018	-2.8	206	237	6	41.2	18	V	SYYRRTPAPDSSGAFDYEPGGDTDDQPAIPEA	D	-1.2	3.58	
8	Q9HRQ9|Q9HRQ9	1	1398.6681	-6.8	102	113	3	57.9	26	V	KWVWEGSTGHNV	H	-0.8	7.82	
8	Q9HRQ9|Q9HRQ9	1	1497.7576	-3.5	78	91	3	50.7	28	T	VKVGPNNQNVFDPA	E	-0.6	6.76	
8	Q9HRQ9|Q9HRQ9	1	1626.8002	-1.5	79	93	3	90.2	27	V	KVGPNNQNVFDPAEV	Y	-0.8	4.08	
8	Q9HRQ9|Q9HRQ9	1	1674.8148	0.5	175	191	1	100.5	28	S	GGGGPVERSPHEMGVPI	Q	-0.4	5.3	
8	Q9HRQ9|Q9HRQ9	1	1707.8118	4.3	102	116	5	104.8	28	V	KWVWEGSTGHNVHAT	S	-0.8	7.96	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
8	Q9HRQ9|Q9HRQ9	1	1725.8686	-0.6	78	93	4	84.3	27	T	VKVGPNNQNVFDPAEV	Y	-0.4	4.08	
8	Q9HRQ9|Q9HRQ9	1	1873.9105	-1.0	175	193	2	88.5	28	S	GGGGPVERSPHEMGVPIQA	H	-0.5	5.3	
8	Q9HRQ9|Q9HRQ9	1	1955.0112	2.0	76	93	5	73.2	27	T	KTVKVGPNNQNVFDPAEV	Y	-0.7	6.98	
8	Q9HRQ9|Q9HRQ9	1	2306.0716	-13.4	102	122	7	96.1	25	V	KWVWEGSTGHNVHATSVPDEA	G	-0.7	5.18	
8	Q9HRQ9|Q9HRQ9	1	2445.1812	8.3	79	101	6	87.2	26	V	KVGPNNQNVFDPAEVYVSPGDTV	K	-0.5	3.7	
8	Q9HRQ9|Q9HRQ9	1	2526.1928	-3.8	94	116	8	33.5	25	V	YVSPGDTVKWVWEGSTGHNVHAT	S	-0.5	6.02	
8	Q9HRQ9|Q9HRQ9	1	2544.2497	-4.2	78	101	7	47.9	26	T	VKVGPNNQNVFDPAEVYVSPGDTV	K	-0.3	3.7	
10	Q9HHN1|Q9HHN1	1	1534.6949	3.6	421	434	2	95.8	27	S	EPMIPWNSGGVFMA	S	0.3	3.3	
10	Q9HHN1|Q9HHN1	1	1571.674	-1.9	395	407	2	37.0	23	T	FRDLNDEYDLDGT	S	-1.3	3.36	
10	Q9HHN1|Q9HHN1	1	2038.9881	-2.9	166	185	8	40.6	27	A	GAILSGVYMGDKQSPLSDTT	L	-0.1	3.88	
10	Q9HHN1|Q9HHN1	1	2045.9728	5.2	411	428	6	81.0	27	S	RTLEETGTVSEPMIPWNS	G	-0.7	3.96	
10	Q9HHN1|Q9HHN1	1	2169.9889	9.9	389	407	4	49.3	26	I	VIPGMTFRDLNDEYDLDGT	S	-0.5	3.36	
10	Q9HHN1|Q9HHN1	1	2283.0729	-4.8	388	407	5	59.9	26	S	IVIPGMTFRDLNDEYDLDGT	S	-0.3	3.36	
10	Q9HHN1|Q9HHN1	1	2608.2302	0.7	411	434	8	152.4	25	S	RTLEETGTVSEPMIPWNSGGVFMA	S	-0.1	3.96	
10	Q9HHN1|Q9HHN1	1	2624.2251	1.6	411	434	8	56.4	24	S	RTLEETGTVSEPMIPWNSGGVFMA	S	-0.1	3.96	Oxidation (M)
10	Q9HHN1|Q9HHN1	1	2907.2943	2.9	383	407	6	68.0	22	A	DQYMSIVIPGMTFRDLNDEYDLDGT	S	-0.5	3.26	
11	Q9HMG3|Q9HMG3	1	1037.5254	8.9	35	43	3	48.2	26	I	AQDVLEHRA	S	-0.7	5.22	
11	Q9HMG3|Q9HMG3	1	1737.7846	-1.0	44	58	3	117.7	25	A	STVPETDFPEPYNRS	I	-1.4	3.82	
11	Q9HMG3|Q9HMG3	1	1874.9486	-9.3	27	43	6	28.8	28	S	SKPPAEDIAQDVLEHRA	S	-0.9	4.54	
11	Q9HMG3|Q9HMG3	1	2207.0131	1.1	44	65	5	85.0	26	A	STVPETDFPEPYNRSIGGGGGA	G	-0.7	3.82	
11	Q9HMG3|Q9HMG3	1	2335.0717	-1.4	44	67	6	107.0	25	A	STVPETDFPEPYNRSIGGGGGAGA	V	-0.6	3.82	
11	Q9HMG3|Q9HMG3	1	2434.1401	4.2	44	68	7	63.2	25	A	STVPETDFPEPYNRSIGGGGGAGAV	A	-0.4	3.82	
11	Q9HMG3|Q9HMG3	1	2505.1772	3.0	44	69	8	107.0	25	A	STVPETDFPEPYNRSIGGGGGAGAVA	G	-0.3	3.82	
11	Q9HMG3|Q9HMG3	1	2690.2573	1.8	44	72	9	60.5	25	A	STVPETDFPEPYNRSIGGGGGAGAVAGGA	E	-0.3	3.82	
11	Q9HMG3|Q9HMG3	1	2757.2994	-6.9	35	58	7	46.0	24	I	AQDVLEHRASTVPETDFPEPYNRS	I	-1.1	4.28	
12	Q9HRS0|Q9HRS0	1	1286.6156	-0.9	119	129	2	52.0	28	V	RFVWESGGHNV	H	-0.5	7.84	
12	Q9HRS0|Q9HRS0	1	1327.6408	-4.9	145	156	3	85.7	27	T	DIAGPPKEYTHT	F	-1.2	5.22	
12	Q9HRS0|Q9HRS0	1	1475.6067	-1.2	219	230	0	64.6	20	A	YFFMKYGGDYGE	-	-0.7	4.08	
12	Q9HRS0|Q9HRS0	1	1595.7593	0.1	119	132	4	58.1	27	V	RFVWESGGHNVHAT	E	-0.6	8	
12	Q9HRS0|Q9HRS0	1	1917.8956	-1.5	183	200	4	84.7	26	V	TDSPPENKGYQTIVPDSA	K	-1.1	3.7	
12	Q9HRS0|Q9HRS0	1	2147.0382	-2.2	183	202	5	30.2	27	V	TDSPPENKGYQTIVPDSAKT	M	-1.3	4.3	
12	Q9HRS0|Q9HRS0	1	2541.166	1.4	133	156	7	45.0	24	T	EVPGDADWGVSTDIAGPPKEYTHT	F	-0.8	3.84	
12	Q9HRS0|Q9HRS0	1	2570.1602	-12.0	145	167	5	70.5	22	T	DIAGPPKEYTHTFDGPTGEYNYV	C	-1.0	4.06	
12	Q9HRS0|Q9HRS0	1	2809.2845	3.0	119	144	8	61.0	24	V	RFVWESGGHNVHATEVPGDADWGVST	D	-0.5	4.52	
13	Q9HRL3|Q9HRL3	1	1103.5651	-7.9	586	595	3	62.8	29	A	WLLYSGPAPT	K	0.2	5.92	
13	Q9HRL3|Q9HRL3	1	1311.6169	2.4	274	285	1	77.5	26	T	WLPDAMEGPTPV	S	-0.2	3	
13	Q9HRL3|Q9HRL3	1	1749.7707	-1.9	478	493	3	29.3	25	T	FHGEPRSDTAEDPHGV	R	-1.4	4.52	
13	Q9HRL3|Q9HRL3	1	1845.9221	-3.5	631	648	7	28.9	28	A	RGADTFDQGVIDGIVNAV	S	0.2	3.6	
13	Q9HRL3|Q9HRL3	1	1876.9472	-3.7	524	540	6	87.9	28	T	GLHIEFLHTWLAGPEGT	A	0.1	5.12	
13	Q9HRL3|Q9HRL3	1	1916.9592	-2.6	630	648	8	58.8	28	L	ARGADTFDQGVIDGIVNAV	S	0.3	3.6	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
13	Q9HRL3|Q9HRL3	1	1977.9949	-19.5	523	540	7	105.1	27	A	TGLHIEFLHTWLAGPEGT	A	0.1	5.12	
13	Q9HRL3|Q9HRL3	1	2106.0245	-4.6	267	285	4	41.3	27	S	AQFPLHTWLPDAMEGPTPV	S	-0.1	4.06	
14	Q9HN95|Q9HN95	1	940.5018	5.1	454	463	1	65.8	25	V	LAPGSPGFPV	-	0.6	6.02	
14	Q9HN95|Q9HN95	1	1139.5764	-7.2	31	40	2	75.7	27	T	FYPPLQAHPA	F	-0.3	7.76	
14	Q9HN95|Q9HN95	1	1296.631	0.9	69	79	1	39.9	27	A	DNPDERIPLQT	F	-1.6	3.7	
14	Q9HN95|Q9HN95	1	1403.6874	-2.0	29	40	3	42.0	28	L	YTFYPPLQAHPA	F	-0.4	7.7	
14	Q9HN95|Q9HN95	1	1450.8224	-0.3	140	151	5	44.5	24	A	YLAWYTILPKLA	G	0.8	9.52	
14	Q9HN95|Q9HN95	1	1516.7714	-4.5	28	40	4	87.6	28	V	LYTFYPPLQAHPA	F	-0.1	7.7	
14	Q9HN95|Q9HN95	1	1729.8828	-3.6	26	40	5	58.0	28	A	NVLYTFYPPLQAHPA	F	0.0	7.7	
14	Q9HN95|Q9HN95	1	2062.9901	1.4	176	193	3	62.7	27	V	GFHHQYTDPGIAEGFKFI	A	-0.4	6.02	
15	Q9HND8|VATI	1	1332.631	-3.1	364	374	2	44.7	27	I	NRPQYTEIDPT	V	-1.8	4.08	
15	Q9HND8|VATI	1	1445.715	-3.9	363	374	3	52.3	28	V	INRPQYTEIDPT	V	-1.3	4.08	
15	Q9HND8|VATI	1	1530.7678	-4.5	364	376	4	44.1	28	I	NRPQYTEIDPTVV	L	-0.9	4.08	
15	Q9HND8|VATI	1	1673.826	-1.1	361	374	4	73.3	28	T	EVINRPQYTEIDPT	V	-1.1	3.82	
15	Q9HND8|VATI	1	1871.9629	-2.7	361	376	6	82.0	28	T	EVINRPQYTEIDPTVV	L	-0.4	3.82	
15	Q9HND8|VATI	1	2086.0946	-5.8	359	376	8	48.6	27	S	LTEVINRPQYTEIDPTVV	L	-0.2	3.82	
16	Q9HRL1|Q9HRL1	1	1517.7878	-0.8	335	347	7	52.8	28	I	NSALSLFYYSRVV	K	0.6	9.58	
16	Q9HRL1|Q9HRL1	1	1557.7675	-1.6	350	362	5	33.1	28	A	LWIEDPRDDLSLS	G	-0.5	3.5	
16	Q9HRL1|Q9HRL1	1	1940.948	-0.6	350	366	6	58.2	27	A	LWIEDPRDDLSLSGQPT	G	-0.8	3.5	
16	Q9HRL1|Q9HRL1	1	2070.984	-2.2	131	149	2	52.4	27	A	SVPFHFWAPEAYEGAPAPV	S	0.1	4.24	
16	Q9HRL1|Q9HRL1	1	2142.0211	-0.8	130	149	3	134.1	26	T	ASVPFHFWAPEAYEGAPAPV	S	0.2	4.24	
17	Q9HM69|CSG	1	1186.6081	-20.2	716	726	5	28.4	28	V	ELLQGDASIEI	N	0.3	2.94	
17	Q9HM69|CSG	1	1308.7877	4.2	840	852	9	54.4	19	V	AVLGAALLALRQN	-	1.1	11.04	
17	Q9HM69|CSG	1	1909.8541	9.4	598	614	6	43.8	26	T	FDEEDIDISELRQGSAS	A	-0.8	3.38	
17	Q9HM69|CSG	1	2542.0831	12.0	591	613	9	73.9	22	I	SVDSDDTFDEEDIDISELRQGSA	S	-1.0	3.12	
17	Q9HM69|CSG	1	2762.2267	6.9	746	770	7	24.5	23	S	NVEPGNYTVEADDGDNTDRQNVEIV	E	-1.1	3.28	
18	Q9HMF1|Q9HMF1	1	1198.5982	-7.7	160	169	1	71.4	27	V	RLEGELPEWA	T	-0.9	3.96	
18	Q9HMF1|Q9HMF1	1	1411.7095	-0.6	158	169	2	70.8	27	V	NVRLEGELPEWA	T	-0.7	3.96	
18	Q9HMF1|Q9HMF1	1	1664.7682	-3.6	222	235	5	27.2	26	S	SIFPTDDRTEDWLA	R	-0.7	3.5	
18	Q9HMF1|Q9HMF1	1	1832.9156	1.6	192	208	6	30.5	28	V	LEYTGPGVESLSVPERT	T	-0.4	3.96	
18	Q9HMF1|Q9HMF1	1	2193.0073	1.6	581	599	6	52.7	26	L	NIDEETYARIEQGDDVEVV	D	-0.8	3.32	
19	Q9HSA8|Q9HSA8	1	953.4971	9.1	61	68	1	37.6	25	V	FGEYRGLL	E	0.0	6.88	
19	Q9HSA8|Q9HSA8	1	1274.5965	0.0	83	92	3	41.6	27	T	YTFDMRTQTI	D	-0.6	6.7	
19	Q9HSA8|Q9HSA8	1	1349.6979	-2.0	61	72	2	27.3	27	V	FGEYRGLLEPGI	N	-0.1	4.26	
19	Q9HSA8|Q9HSA8	1	2203.1677	2.0	61	80	5	119.1	24	V	FGEYRGLLEPGINVIPPFVS	R	0.4	4.26	
20	Q9HSS1|Q9HSS1	1	940.4866	-2.6	249	258	4	35.7	25	A	LAGALEDGPV	S	0.6	3	
20	Q9HSS1|Q9HSS1	1	1207.635	-3.4	153	164	3	75.4	27	V	GFVGFGEIARGV	A	0.9	6.98	
20	Q9HSS1|Q9HSS1	1	1232.6401	-6.0	210	220	3	42.6	28	V	FAPLTEETRGL	V	-0.2	4.26	
20	Q9HSS1|Q9HSS1	1	1593.8151	-0.8	149	164	6	57.8	27	A	DATVGFVGFGEIARGV	A	0.8	4.08	
20	Q9HSS1|Q9HSS1	1	1646.8152	-2.7	210	224	5	37.1	28	V	FAPLTEETRGLVDEA	A	-0.2	3.68	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
21	Q9HMT7|Q9HMT7	1	1702.7322	-0.9	44	59	5	127.6	23	V	DVDTEAYEESHAPGAI	G	-0.7	3.5	
21	Q9HMT7|Q9HMT7	1	2369.1751	4.1	178	199	6	64.7	26	L	VDVRSPEEFSGEILAPPGLQET	A	-0.4	3.58	
21	Q9HMT7|Q9HMT7	1	2564.0074	4.8	126	147	3	66.1	15	L	DGGRDYWMDNDYPTSEEPPSFS	A	-1.7	3.32	
22	Q9HMX1|Q9HMX1	1	1760.8329	-1.8	111	126	4	53.3	27	L	SRDVIPNQGYNDPSTV	R	-1.0	3.88	
22	Q9HMX1|Q9HMX1	1	1987.0011	1.2	109	126	6	61.7	28	T	LLSRDVIPNQGYNDPSTV	R	-0.5	3.88	
22	Q9HMX1|Q9HMX1	1	2330.0146	0.6	497	519	7	43.6	22	A	NALGDGIRDAIDPESEGGSEEEA	A	-1.0	3.28	
23	Q9HMW4|Q9HMW4	1	1578.7467	-1.8	402	415	2	47.1	27	T	LHPTWGPYAPENPT	T	-1.1	5.12	
23	Q9HMW4|Q9HMW4	1	2202.097	-6.2	252	270	5	37.0	27	A	AFNGNLGPWDLKRWSQQSV	M	-0.8	10.08	
23	Q9HMW4|Q9HMW4	1	2393.0692	-0.8	231	251	5	72.2	24	A	KPYVEAEDADGLEQDEEVMRA	A	-1.1	3.62	
23	Q9HMW4|Q9HMW4	1	2577.1904	-5.4	229	251	7	35.5	24	A	LAKPYVEAEDADGLEQDEEVMRA	A	-0.8	3.62	
24	Q9HHP3|Q9HHP3	1	1600.7594	-3.8	228	241	4	50.5	28	A	AVDPESGDQVWRRS	L	-1.2	4.3	
24	Q9HHP3|Q9HHP3	1	1671.7965	-2.1	227	241	5	38.2	27	V	AAVDPESGDQVWRRS	L	-1.0	4.3	
24	Q9HHP3|Q9HHP3	1	1911.8599	3.6	111	126	6	85.4	26	T	SFDINENTRSWNVETT	G	-1.2	3.82	
25	Q9HR04|Q9HR04	1	789.4232	-22.5	16	24	6	30.0	28	A	TGAATLSGL	A	0.9	6.02	
25	Q9HR04|Q9HR04	1	1239.6248	-3.4	76	87	2	29.9	27	S	IYLGGGEGGRYV	A	0.0	6.82	
25	Q9HR04|Q9HR04	1	1950.8344	-1.3	94	109	4	60.9	23	I	NQYYDDFSATQQTQRS	S	-1.9	3.88	
25	Q9HR04|Q9HR04	1	2037.8664	-1.0	94	110	5	22.4	22	I	NQYYDDFSATQQTQRSS	Q	-1.8	3.88	
25	Q9HR04|Q9HR04	1	2491.2442	6.1	52	75	7	52.7	25	A	IVQERPAPGGESIADLPDLEGELS	I	-0.4	3.44	
26	Q9HM89|EF1A	1	1440.7937	-6.2	235	249	6	34.7	26	I	SGIGTVPVGRIETGV	M	0.5	6.98	
26	Q9HM89|EF1A	1	1521.71	-5.7	165	178	2	50.6	27	V	KDLFGQVGFNPDDA	K	-0.6	3.6	
26	Q9HM89|EF1A	1	1764.8319	2.8	162	178	4	87.0	28	V	SGVKDLFGQVGFNPDDA	K	-0.3	3.6	
27	Q9HQF4|Q9HQF4	1	1538.7577	-1.6	102	116	4	93.5	27	A	TEDGDPSVPGPIVRT	E	-0.7	3.7	
27	Q9HQF4|Q9HQF4	1	2168.9797	0.8	226	244	4	33.1	26	S	MAGEDVDYSPRTRNPDVFT	V	-1.0	3.96	
27	Q9HQF4|Q9HQF4	1	2539.1926	0.4	102	125	7	57.1	25	A	TEDGDPSVPGPIVRTEEGQDIEVT	L	-0.8	3.32	
28	Q9HQP2|Q9HQP2	1	799.4804	20.8	227	235	7	26.5	25	S	VLAGVATAV	Y	2.3	6.02	
28	Q9HQP2|Q9HQP2	1	1263.6976	-0.5	162	172	2	38.8	25	L	GLLPGYFLQRT	L	0.2	9.84	
28	Q9HQP2|Q9HQP2	1	1269.5778	-19.5	208	217	2	32.1	24	V	FEQFRAWDAT	G	-0.7	4.08	
28	Q9HQP2|Q9HQP2	1	2104.9491	0.6	746	763	3	27.0	25	V	VFYDGPRDLSQGDFYQQA	Y	-0.9	3.6	
29	Q9HNL7|Q9HNL7	1	1920.9444	0.0	28	44	3	84.2	28	S	AYWQPGEGMLVEKPFGI	G	-0.1	4.26	
29	Q9HNL7|Q9HNL7	1	2451.2798	2.9	2	23	6	101.7	24	M	VEKPTSGSLFGVPYNFERPKLS	A	-0.5	9.62	
30	Q9HS12|Q9HS12	1	731.4694	-15.4	23	28	3	32.0	21	V	FRALLL	A	1.9	11.04	
30	Q9HS12|Q9HS12	1	876.4263	24.2	511	518	4	48.2	27	S	ETVTAMPL	Q	0.7	3.3	Oxidation (M)
30	Q9HS12|Q9HS12	1	974.5913	5.0	23	31	6	35.6	20	V	FRALLLAAT	L	1.6	11.04	
31	Q9HRR0|Q9HRR0	1	1333.6051	3.3	7	17	1	55.2	27	S	NYGDIHRYEPA	S	-1.5	5.22	
31	Q9HRR0|Q9HRR0	1	1459.6653	1.0	109	120	3	64.1	27	T	SMFENTVEQFKT	A	-0.7	4.26	
31	Q9HRR0|Q9HRR0	1	1530.7024	3.9	109	121	4	78.9	27	T	SMFENTVEQFKTA	L	-0.5	4.26	
32	Q9HMX0|Q9HMX0	1	1880.9785	2.3	188	205	6	36.1	27	S	NALQHLFSGIDPFAGVPV	L	0.6	4.94	
32	Q9HMX0|Q9HMX0	1	1968.0105	2.3	187	205	7	78.8	27	T	SNALQHLFSGIDPFAGVPV	L	0.5	4.94	
33	Q9HRR1|Q9HRR1	1	1544.7583	-5.9	177	189	4	30.5	28	A	TWRSQNTDNTIPI	L	-1.1	6.78	
33	Q9HRR1|Q9HRR1	1	2719.1198	13.6	151	174	4	124.0	20	V	NIDEFDDYDTWENDYGDAGIGKPA	K	-1.3	3.16	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
34	Q9HM85|EF2	1	1379.8024	-3.0	614	625	6	38.8	23	A	LIDADIRLLEPI	Q	0.8	3.7	
34	Q9HM85|EF2	1	1786.8407	18.2	155	169	3	67.9	28	I	SELQEGPEEMQERLL	S	-1.2	3.68	
35	Q9HP48|Q9HP48	1	1821.7694	6.5	204	220	5	74.7	23	V	FESGVDHFEVDDDGALA	A	-0.3	3.32	
35	Q9HP48|Q9HP48	1	1892.8065	2.0	204	221	6	53.6	23	V	FESGVDHFEVDDDGALAA	A	-0.1	3.32	
36	Q9HHR4|Q9HHR4	1	1340.818	-0.9	235	247	6	24.3	20	A	LIGVGYIIGPRIA	A	1.5	9.84	
37	Q9HNS6|Q9HNS6	1	1063.5815	10.7	71	81	3	30.2	24	I	GFGPIVGPHIA	F	0.9	7.84	
37	Q9HNS6|Q9HNS6	1	1361.7456	-5.9	68	81	5	98.4	26	T	NAIGFGPIVGPHIA	F	0.9	7.84	
38	Q9HPG8|Q9HPG8	1	1317.6241	0.8	661	670	2	67.9	28	V	EFDDYFLRTL	E	-0.4	3.7	
39	Q9HP88|Q9HP88	1	1498.7126	0.7	171	183	4	77.5	27	T	AFRDYASTDMLPL	A	0.0	3.88	
39	Q9HP88|Q9HP88	1	1689.9301	-2.5	397	412	4	55.1	25	I	LLPIAPGLDDTPEIRA	Q	0.2	3.7	
41	Q9HRU7|Q9HRU7	1	2158.1827	-1.2	186	204	8	25.4	24	T	VWLGYLDVIRPVFDALSPV	L	1.0	3.88	
42	Q9HRJ5|Q9HRJ5	1	1243.6561	-15.1	96	106	5	36.8	29	A	TTPLSRAEWLA	A	-0.1	6.98	
43	Q9HMS7|Q9HMS7	1	1167.5924	-8.2	363	372	3	29.3	26	S	AFTPERFSLT	V	-0.1	6.98	
44	Q9HP84|HTR4	1	731.4582	-4.6	324	330	3	29.2	21	T	GILGFIL	V	2.7	6.02	
45	Q9HRL8|Q9HRL8	1	1015.5603	2.3	170	178	2	32.2	27	A	GVRIPAWFA	F	0.9	11.04	
45	Q9HRL8|Q9HRL8	1	1826.8799	-5.1	192	208	3	64.0	27	A	NLAEVGRNPFDTPEAPT	E	-0.8	3.82	
46	Q9HNY2|Q9HNY2	1	1026.5458	18.7	233	243	5	29.1	26	T	VPGADASALRA	G	0.4	6.78	
46	Q9HNY2|Q9HNY2	1	1126.6234	-16.4	230	241	7	29.2	26	A	LITVPGADASAL	R	1.2	3.1	
49	Q9HRL2|Q9HRL2	1	1401.7041	-7.1	244	256	2	78.2	28	T	WLPDAHVQAPTPA	S	-0.2	4.94	
50	Q9HPB1|SECY	1	1135.5696	-0.9	421	429	1	47.3	27	V	MERYIPQVT	V	-0.5	6.88	
53	Q9HS26|Q9HS26	1	1711.7577	2.6	16	31	3	55.7	25	A	GDDSEPEIDFYGGKLA	S	-0.8	3.42	
54	Q9HRL9|Q9HRL9	1	1556.841	-0.2	548	562	9	68.5	27	V	ATLGSLDVILGEVDR	-	0.6	3.7	
55	Q9HPA9|Q9HPA9	1	930.4771	-2.6	509	518	4	31.6	29	A	QGNVGLSSGI	T	0.3	6.02	
56	Q9HQQ9|Q9HQQ9	1	2003.9622	-1.7	350	367	6	32.8	27	V	AYDPVAAEKMAEQRPEVT	Y	-0.8	4.16	
57	Q9HR32|TOP6A	1	1459.7154	9.7	7	19	6	34.2	28	T	SDETEARDQLLAI	A	-0.6	3.58	
57	Q9HR32|TOP6A	1	2300.0419	2.5	20	39	3	44.0	25	I	AEQFYDQFADGDIPRMSLPT	R	-0.6	3.5	
58	Q9HSM2|MUTS1	1	1156.6088	1.1	328	338	4	29.4	28	A	RDALGDVLGEI	Y	0.2	3.7	
60	Q9HQ54|Q9HQ54	1	1227.6612	-15.1	794	807	8	32.9	27	S	AGGVALAGWGVVTA	A	1.5	6.02	
61	Q9HMU8|Q9HMU8	1	1186.671	-7.0	47	56	4	79.6	26	I	NILLDFVRPT	T	0.5	6.78	
63	Q9HN92|Q9HN92	1	955.5273	-2.9	1	8	2	42.7	26	-	MNVRPQVI	A	0.2	11.04	
63	Q9HN92|Q9HN92	1	971.5222	-5.1	1	8	2	30.3	28	-	MNVRPQVI	A	0.2	11.04	Oxidation (M)
63	Q9HN92|Q9HN92	1	1026.5644	0.6	1	9	3	55.2	26	-	MNVRPQVIA	T	0.4	11.04	
66	Q9HSM4|DHE42	1	1255.6925	-3.7	241	251	5	57.3	27	A	LLLDDWGARVV	A	0.8	3.88	
68	Q9HPQ2|Q9HPQ2	1	1402.6517	-0.1	332	343	3	71.1	27	A	YVVDNYGYSRPA	T	-0.7	6.58	
69	Q9HNK1|Q9HNK1	1	762.4276	-28.7	116	123	5	32.9	27	A	AIALFGTA	I	1.9	6.02	
69	Q9HNK1|Q9HNK1	1	1311.6558	-25.3	579	591	4	26.1	26	T	IADLDDDLPGGVI	I	0.5	2.74	
73	Q9HRS4|Q9HRS4	1	2054.809	6.7	16	35	5	81.0	17	A	AADQGIDPWTADDHEGGDGE	-	-1.3	3.22	
74	P25964|BACS1	1	1426.6187	-1.9	219	231	1	29.5	24	V	FMHSESPPAPEQA	T	-0.9	4.24	
76	Q9HS86|Q9HS86	1	1261.5939	-0.5	95	106	3	42.6	27	I	AAGEFERADIPS	S	-0.4	3.82	
78	P16102|BACH	1	962.5338	4.1	156	163	4	29.4	25	T	SALLFRWA	F	1.0	11.04	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
78	P16102|BACH	1	1220.6401	-1.6	191	201	5	33.8	27	A	GTAEIFDTLRV	L	0.3	4.08	
80	Q9HS72|SECE	1	1605.8436	-1.7	1	14	6	33.3	27	-	MDVPLELSAYTRVL	R	0.5	4.08	
82	Q9HR22|Q9HR22	1	1658.8304	2.2	72	86	5	36.5	28	V	YSELFLGAIGHPEQV	L	0.2	4.24	
83	Q9HHI2|Q9HHI2	1	731.4582	-6.0	40	46	4	24.0	21	L	IVFGAIL	L	3.0	6.02	
83	Q9HHI2|Q9HHI2	1	731.4582	-4.6	41	47	4	24.1	21	I	VFGAILL	M	2.9	6.02	
84	Q9HQ64|Q9HQ64	1	1716.8907	-1.9	79	94	5	71.3	28	V	YNALVNQGIEGNAKRA	A	-0.6	9.72	
89	Q9HSA0|Q9HSA0	1	1260.6251	-2.2	39	50	2	52.5	28	A	FEHGLPSGPHLA	D	-0.2	6.02	
90	Q9HN43|CAPPA	1	930.4771	-1.8	326	334	5	31.5	29	L	AVIDRTADA	Y	0.2	3.88	
90	Q9HN43|CAPPA	1	1267.6561	11.5	308	319	2	45.9	26	L	RDADLGAPPFPI	D	-0.2	3.88	
91	Q9HN02|Q9HN02	1	1096.5917	-0.8	163	171	4	52.0	25	V	LFDYLTRAV	N	0.7	6.7	
94	Q9HNQ9|Q9HNQ9	1	1122.5094	7.9	209	218	2	44.0	26	S	GGFWESVDRA	M	-0.5	4.08	
95	Q9HMZ3|Q9HMZ3	1	2517.1237	3.8	413	432	4	53.9	24	V	EYLWYVGDYPSYDERNQHIA	R	-1.2	4.06	
98	Q9HHI3|Q9HHI3	1	1145.5088	-12.1	69	79	4	32.6	23	V	SLPDSVETDPS	I	-0.8	2.88	
99	Q9HPM1|Q9HPM1	1	1026.5458	18.7	164	174	6	30.5	26	I	ADGTRPAVAVA	T	0.4	6.78	
102	Q9HR62|Q9HR62	1	958.5964	20.2	21	29	5	14.1	14	A	FRVGLAVVV	L	2.3	11.04	
104	Q9HPG5|TRPE1	1	940.4866	8.2	11	20	5	27.3	24	T	ALADDGPAIV	R	0.9	2.92	
105	Q9HN22|Q9HN22	1	1719.8104	2.4	149	165	8	48.7	27	A	AAFLADIDHSAYGTTPA	Q	0.3	3.88	
115	Q9HNY9|Q9HNY9	1	745.4446	-18.0	121	127	3	27.1	24	A	IAGTRKT	T	-0.6	11.48	
118	Q9HSL1|Q9HSL1	1	1629.8111	4.1	123	140	2	32.4	28	T	EYTGGGGGGGGRLPSLPV	S	-0.3	6.88	
119	Q9HP01|Q9HP01	1	1123.6825	-12.5	13	23	5	22.2	22	V	GSPRARLAALL	A	0.5	12.4	
122	Q9HRS9|Q9HRS9	1	1311.6533	-25.4	184	195	2	51.5	26	S	WLPDAMVAPTPV	S	0.7	3.1	Oxidation (M)
128	Q9HMB7|Q9HMB7	1	1423.662	3.4	123	134	2	74.1	27	A	REEDDFSIFAPV	L	-0.4	3.58	
131	Q9HQE2|Q9HQE2	1	1498.8104	-11.5	114	127	7	36.3	28	L	DRLRDAGLDVAVVT	N	0.2	4.18	
135	Q9HMY7|Q9HMY7	1	731.4582	-6.0	104	110	4	24.0	21	L	LAFVGII	V	3.0	6.02	
136	Q9HRL4|Q9HRL4	1	1369.6514	2.0	83	93	3	56.1	27	T	LYRNFDDIDVT	N	-0.5	3.6	
137	Q9HSW2|Q9HSW2	1	713.4799	27.2	22	27	4	25.1	13	S	IRSLLI	I	1.9	11.04	
138	Q9HP66|Q9HP66	1	830.5266	9.9	117	124	5	25.1	18	V	FLGLLAVV	L	3.0	6.02	
138	Q9HP66|Q9HP66	1	986.6165	7.9	115	124	6	19.3	19	T	GVFLGLLAVV	L	2.8	6.02	
139	Q9HPT9|Q9HPT9	1	2263.0128	2.7	61	82	6	56.9	25	A	ALDLPGHGDSDDIETDPGPETL	D	-0.8	3.22	
143	Q9HMQ8|Q9HMQ8	1	731.4218	6.7	196	202	3	26.9	25	A	IAAFLPT	F	1.8	6.02	
145	Q9HRA8|Q9HRA8	1	799.4803	8.0	319	326	4	31.5	26	T	ALKAVGEI	G	1.0	6.94	
148	Q9HMH4|Q9HMH4	1	1344.5358	5.1	56	67	4	53.9	20	A	SFSYDDPDADTL	G	-0.9	2.74	
150	Q9HN79|Q9HN79	1	1037.6485	-14.6	51	61	7	21.6	19	A	VSAVGLVAPLI	G	2.3	6.02	
155	P33518|COX1	1	1447.6765	8.2	143	155	4	29.3	28	I	DADDMAFPRINAI	A	-0.1	3.6	
157	Q9HN37|Q9HN37	1	1314.8275	-13.2	539	550	8	25.2	17	A	LVFQVKLSVVIA	A	2.1	10.1	
160	Q07971|Q07971	1	1216.5611	-20.9	258	267	3	25.7	24	A	EQLEEAWEAI	Q	-0.7	2.96	
162	Q9HS00|Q9HS00	1	799.4804	13.9	492	500	8	32.1	25	T	AAVVAATVV	R	2.6	6.02	
162	Q9HS00|Q9HS00	1	1449.8919	-24.6	192	205	7	25.0	21	S	NVLTQLKPVLGVGI	G	1.0	10.1	
169	Q9HN36|Q9HN36	1	731.4581	-4.6	259	264	3	39.6	21	T	FNLLLL	V	2.4	6.02	
173	Q9HMB4|Q9HMB4	1	1621.8141	1.0	448	461	1	57.5	28	A	EFIRDYVPFVPGPS	A	0.0	4.08	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
174	Q9HS30|Q9HS30	1	1222.7173	-1.5	59	70	6	24.5	21	A	LLADLPVEAGIL	V	1.5	3	
178	Q9HMU6|Q9HMU6	1	1231.6098	-6.7	114	124	0	46.9	28	V	GDSPPRWHAPL	L	-1.1	7.84	
179	O54610|O54610	1	745.4222	1.7	427	433	5	26.3	25	T	EATLTLV	G	1.2	3.3	
187	Q9HRJ8|Q9HRJ8	1	731.4582	-6.0	396	402	4	22.6	21	V	LLGAVFL	Y	2.8	6.02	
190	Q9HMV1|Q9HMV1	1	763.3752	-13.6	48	54	2	28.2	27	A	TFLEPGT	T	0.0	3.3	
192	Q9HHV2|Q9HHV2	1	930.5022	-28.9	355	364	6	29.3	29	A	AITLTLGDGA	E	1.0	3.1	
193	Q9HMC9|Q9HMC9	1	1137.6758	0.7	533	543	6	27.1	22	S	NNASVVLLIPV	A	1.6	6.02	
204	Q9HP76|Q9HP76	1	968.5807	-8.2	119	126	3	25.9	23	I	RWSIPIVV	R	1.2	11.04	
206	Q9HPQ6|Q9HPQ6	1	997.4393	14.3	25	32	3	26.5	24	A	LVDWYTDS	H	-0.3	2.92	
211	Q9HPY6|Q9HPY6	1	731.4694	-20.0	390	395	3	34.3	21	A	FARLLL	A	1.9	11.04	
213	Q9HQB8|Q9HQB8	1	955.5273	10.8	61	70	4	25.5	25	A	VPMRAAGAAI	D	1.1	11.04	
220	Q9HMJ2|Q9HMJ2	1	876.4263	24.2	149	156	4	36.3	27	A	EVSMLADI	D	1.1	3	
228	Q9HNJ2|Q9HNJ2	1	745.4222	0.3	116	122	5	31.9	26	S	LVTETAL	F	1.2	3.3	
229	Q9HMU9|Q9HMU9	1	1069.4393	-3.3	37	45	1	35.1	20	A	GYGYFFDTT	T	-0.3	3.1	
232	Q9HPQ1|Q9HPQ1	1	731.4582	-4.6	376	382	3	29.2	21	A	GLIGFLL	F	2.6	6.02	
233	Q9HPQ5|Q9HPQ5	1	1041.4516	-1.0	205	212	2	23.7	23	A	NWYSTERS	R	-2.0	6.88	
237	Q9HM88|Q9HM88	1	1187.567	-5.2	56	68	6	37.0	27	A	SEIGTGAPSDALA	A	0.2	3	
239	Q9HQU3|Q9HQU3	1	731.4582	-6.0	143	149	3	36.3	21	V	IIGLGFL	A	2.7	6.02	
255	Q9HRJ0|Q9HRJ0	1	1122.5227	-3.9	141	152	9	28.4	26	A	MAAADTSVSALA	L	1.1	3.1	Oxidation (M)
258	O51975|O51975	1	713.4799	27.2	190	195	4	21.2	13	L	RSLLII	F	1.9	11.04	
258	O51975|O51975	1	1314.8169	-5.2	184	194	6	21.6	17	S	LCKTRLRSLLI	I	0.7	11.32	
260	Q9HME2|Q9HME2	1	1988.0078	0.6	2	18	9	42.4	27	M	VWIIDNLVTMVEHFTTA	A	0.9	4.06	
264	Q9HQU8|Q9HQU8	1	2107.9698	-0.5	13	30	4	41.1	26	A	RLTDQDEFTPPESFVEQA	N	-1.1	3.5	
265	Q9HQE1|Q9HQE1	1	930.477	-1.8	226	234	4	33.0	29	T	ADLLSERGA	N	-0.2	4.08	
273	Q9HQ63|DHSD	1	1038.5386	-1.6	121	130	5	27.0	25	A	SVPTFLTGAF	-	1.1	6.02	
277	Q9HNE6|Q9HNE6	1	1203.607	-4.0	275	284	3	29.4	29	V	TWMDRVQGVL	-	0.1	6.78	
278	Q9HQ90|Q9HQ90	1	1066.5771	27.4	239	249	6	28.8	23	A	QAALRAGADLV	R	0.6	6.78	Gln->pyro-Glu (N-term Q)
279	Q9HMQ2|ASSY	1	1365.6564	-2.7	146	156	3	44.5	27	L	GLTREWEIEYA	A	-0.7	3.96	
304	Q9HMB0|Q9HMB0	1	896.4127	-0.6	10	17	3	35.0	24	L	LYTTPTDS	D	-0.7	3.1	
307	Q48325|TBPB	1	1409.7514	13.3	87	99	5	28.0	25	I	RELGIDVTSNPPI	E	-0.2	4.08	
310	Q9HRW7|Q9HRW7	1	1618.7012	8.1	2	15	5	47.8	25	M	SDALDAFDHDAWRT	A	-0.9	3.86	
319	Q9HRR2|Q9HRR2	1	1688.8661	-1.7	42	54	5	47.2	28	V	DYLELLETLYYRV	N	0.0	3.82	
323	Q9HSW6|CDC61	1	1098.6172	-23.7	145	154	6	36.6	27	I	LIVLDEVDAI	G	1.6	2.88	
324	Q9HML8|PSTB2	1	1516.6682	-26.0	88	100	4	22.5	21	S	VSDLDTYYGEERA	L	-1.0	3.58	
328	Q9HQH2|Q9HQH2	1	1441.6838	-2.0	152	163	3	30.7	26	V	NTRLQTFDGEYV	M	-0.9	4.08	
331	Q9HRJ7|Q9HRJ7	1	1901.0557	-15.9	90	109	8	26.0	25	L	LLGGVGGLYMLQGAGLGARV	A	1.0	9.84	
344	Q9HQV2|Q9HQV2	1	2003.9371	-3.2	216	236	8	29.0	27	T	GAVLLFRAGAMGNEPASGDGD	-	0.0	3.7	
354	Q9HNB8|Q9HNB8	1	1293.6717	-8.5	12	24	4	34.3	27	A	SGHLAPLFDAAPV	R	0.7	4.94	
387	Q9HSQ7|Q9HSQ7	1	944.512	-11.1	208	214	2	32.3	29	A	LFTYRFV	N	1.0	9.84	
401	Q9HQ23|Q9HQ23	1	1222.7074	22.2	104	115	7	20.4	20	V	NLAVWGPALALV	G	1.6	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
432	Q9HRH6|Q9HRH6	1	1480.731	2.6	143	156	6	38.8	27	A	SYTGLRWLAGGAET	-	-0.2	6.88	
433	Q9HSE5|Q9HSE5	1	799.4804	20.8	81	89	8	27.2	25	S	AAAAVVTVV	L	2.6	6.02	
441	Q9HS52|SYP	1	1698.861	27.7	449	465	8	29.3	27	I	AAEIVMVPLGEDSAARA	A	0.6	3.82	
458	Q9HRK3|Q9HRK3	1	731.4582	-6.0	47	52	3	24.0	21	I	IQFVLI	G	2.7	6.02	
471	Q9HMW6|Q9HMW6	1	799.4804	20.8	2	10	7	26.1	25	M	LAGAATVVV	F	2.3	6.02	
472	Q9HQV6|Q9HQV6	1	731.4582	-4.6	26	32	3	36.8	21	V	LFGGLLL	I	2.5	6.02	
482	Q9HMK6|Q9HMK6	1	1727.9166	-19.4	184	199	7	36.0	28	T	EKDVSEARRDAVLAGI	T	-0.4	4.56	
490	Q9HR54|Q9HR54	1	958.5964	20.2	335	343	4	24.0	14	V	LFRAGGLLL	V	1.6	11.04	
534	Q9HPI6|Q9HPI6	1	882.5175	26.2	15	24	5	33.2	23	T	LPAAIGGITA	Y	1.5	6.02	
576	Q9HRR3|Q9HRR3	1	1093.4716	7.5	42	49	1	31.5	26	L	TYEYFERS	R	-1.6	4.26	
595	Q9HRR7|Q9HRR7	1	1289.6364	-27.7	41	55	6	32.6	27	A	ADAGGPHLAPGVSAA	A	0.3	4.94	
596	Q9HQB1|Q9HQB1	1	958.6328	-17.7	70	77	4	19.6	14	V	KAVFRLLI	E	1.6	11.48	
609	Q9HRR6|Q9HRR6	1	1286.6295	-1.0	95	104	1	30.2	28	A	DFFEFEARKV	E	-0.5	4.44	
632	Q9HRE8|RTCA	1	1227.6711	-16.9	95	107	7	29.2	28	T	SVEVGTAGSIPLV	F	1.1	3.3	
650	Q9HRP9|Q9HRP9	1	1255.6633	-1.4	86	98	6	28.4	27	V	GPDAVTGAVRRAS	E	-0.2	10.88	
652	Q48295|ARCC	1	1170.6132	-4.8	66	76	5	28.2	27	A	ESAAEKPLDVL	G	-0.1	3.82	
654	Q9HSE7|Q9HSE7	1	930.4771	6.3	36	44	4	29.8	29	S	LDAVRETGA	T	-0.1	4.08	
689	Q9HRP5|Q9HRP5	1	745.4222	0.3	84	90	5	28.3	26	V	TIETAVL	Y	1.3	3.3	
694	Q9HPV1|Q9HPV1	1	958.5964	20.2	33	41	5	14.3	14	A	IAAFGLVRI	S	2.1	11.04	
719	O54633|O54633	1	1186.671	-5.3	54	64	5	26.9	26	A	ARIVEIAFAPT	A	1.0	6.98	
748	Q9HR26|Q9HR26	1	1449.8344	15.2	18	31	8	24.5	21	T	VLSFGAYIGALRAL	D	1.5	9.84	
768	Q9HPH6|Q9HPH6	1	731.4429	14.9	112	118	6	24.0	21	S	LSSVTIL	S	2.0	6.02	
901	Q9HHQ7|Q9HHQ7	1	731.4581	-6.0	125	130	3	24.0	21	I	LLNFIL	H	2.5	6.02	
1001	Q9HRF3|Q9HRF3	1	713.4799	27.2	85	90	4	15.6	13	T	RLSLLL	D	1.7	11.04	

END OF LIST VI

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
VII. Purple membrane; elastase digest; nLC-MALDI MS/MS; AVLI search specificity															
1	P02945|BACR	1	731.4582	-4.6	231	237	3	57.7	20	V	GFGLILL	R	2.6	6.02	
1	P02945|BACR	1	799.4916	6.8	187	193	3	38.5	23	V	LRNVTVV	L	1.1	11.04	
1	P02945|BACR	1	822.4024	-10.6	95	100	1	26.9	24	A	RYADWL	F	-0.8	6.7	
1	P02945|BACR	1	828.3918	23.3	92	97	1	30.7	23	I	YWARYA	D	-0.7	9.58	
1	P02945|BACR	1	834.4276	-5.5	194	200	2	30.7	24	V	LWSAYPV	V	0.7	5.92	
1	P02945|BACR	1	835.4514	-12.2	220	226	3	28.5	23	L	LFMVLDV	S	2.5	3.1	
1	P02945|BACR	1	857.4395	-4.1	18	24	0	32.2	26	I	TGRPEWI	W	-1.0	6.98	
1	P02945|BACR	1	887.4786	-25.8	124	132	4	60.2	27	A	LVGADGIMI	G	1.8	3.1	
1	P02945|BACR	1	917.4276	0.1	174	181	1	37.9	25	A	ESMRPEVA	S	-0.8	4.26	
1	P02945|BACR	1	930.4811	-6.2	201	209	3	68.7	27	V	VWLIGSEGA	G	0.9	3.3	
1	P02945|BACR	1	958.6215	-6.1	229	237	4	44.1	13	A	KVGFGLILL	R	2.0	10.1	
1	P02945|BACR	1	991.5015	-7.5	98	105	1	29.0	25	A	DWLFTTPL	L	0.4	3.1	
1	P02945|BACR	1	1005.5356	-1.8	238	246	2	37.5	24	L	RSRAIFGEA	E	-0.3	10.88	
1	P02945|BACR	1	1016.5331	20.5	165	173	1	27.3	25	V	LFFGFTSKA	E	0.9	10.1	
1	P02945|BACR	1	1043.5499	-2.0	112	121	4	72.5	27	A	LLVDADQGTI	L	0.7	2.92	
1	P02945|BACR	1	1062.6186	-2.5	182	190	2	56.9	20	A	STFKVLRNV	T	0.2	11.48	
1	P02945|BACR	1	1081.5556	1.9	16	24	1	61.4	24	A	QITGRPEWI	W	-0.7	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1098.5822	2.5	16	24	1	50.6	25	A	QITGRPEWI	W	-0.7	6.98	
1	P02945|BACR	1	1116.6907	4.9	227	237	5	53.5	15	V	SAKVGFGLILL	R	1.7	10.1	
1	P02945|BACR	1	1140.5451	-2.4	48	57	1	23.9	23	V	SDPDAKKFYA	I	-1.2	6.8	
1	P02945|BACR	1	1156.6029	6.2	18	26	1	56.0	25	I	TGRPEWIWL	A	-0.5	6.98	
1	P02945|BACR	1	1156.634	0.3	112	122	5	106.5	25	A	LLVDADQGTIL	A	0.9	2.92	
1	P02945|BACR	1	1215.7115	-8.0	101	111	5	62.7	23	L	FTTPLLLLDLA	L	1.6	3.1	
1	P02945|BACR	1	1216.5612	-20.1	242	253	2	22.5	22	A	IFGEAEAPEPSA	G	-0.2	3.02	
1	P02945|BACR	1	1227.64	22.3	18	27	2	56.7	25	I	TGRPEWIWLA	L	-0.2	6.98	
1	P02945|BACR	1	1227.6711	-24.1	112	123	6	113.1	25	A	LLVDADQGTILA	L	1.0	2.92	
1	P02945|BACR	1	1242.5822	-3.0	92	100	2	36.3	23	I	YWARYADWL	F	-0.6	6.64	
1	P02945|BACR	1	1253.6292	-0.8	48	58	2	66.4	25	V	SDPDAKKFYAI	T	-0.7	6.8	
1	P02945|BACR	1	1314.8136	-2.6	231	242	5	70.3	16	V	GFGLILLRSRAI	F	1.2	12.4	
1	P02945|BACR	1	1340.7241	-0.5	18	28	3	28.5	25	I	TGRPEWIWLAL	G	0.1	6.98	
1	P02945|BACR	1	1361.8031	1.8	182	193	4	76.5	20	A	STFKVLRNVTVV	L	0.8	11.48	
1	P02945|BACR	1	1380.719	-3.1	16	26	2	71.8	25	A	QITGRPEWIWL	A	-0.3	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1381.703	16.1	95	105	2	74.5	24	A	RYADWLFTTPL	L	-0.1	6.7	
1	P02945|BACR	1	1409.7919	-15.3	201	214	5	111.2	24	V	VWLIGSEGAGIVPL	N	1.3	3.3	
1	P02945|BACR	1	1451.7561	1.0	16	27	3	88.0	24	A	QITGRPEWIWLA	L	-0.1	6.98	Gln->pyro-Glu (N-term Q)
1	P02945|BACR	1	1468.7827	11.0	16	27	3	61.8	25	A	QITGRPEWIWLA	L	-0.1	6.98	
1	P02945|BACR	1	1607.8712	4.1	95	107	4	77.8	24	A	RYADWLFTTPLLL	L	0.5	6.7	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
1	P02945|BACR	1	1629.9018	4.5	98	111	6	64.6	23	A	DWLFTTPLLLLDLA	L	1.2	2.92	
1	P02945|BACR	1	1671.923	-12.1	126	143	7	91.6	25	V	GADGIMIGTGLVGALTKV	Y	1.1	6.76	
1	P02945|BACR	1	1678.8025	-3.5	76	91	1	123.4	25	L	GYGLTMVPFGGEQNPI	Y	0.0	3.3	
1	P02945|BACR	1	1686.8325	-4.8	238	253	3	82.3	26	L	RSRAIFGEAEAPEPSA	G	-0.6	4.56	
1	P02945|BACR	1	1694.7974	-7.2	76	91	1	115.0	24	L	GYGLTMVPFGGEQNPI	Y	0.0	3.3	Oxidation (M)
1	P02945|BACR	1	1718.9832	0.8	231	246	6	57.5	21	V	GFGLILLRSRAIFGEA	E	0.9	10.88	
1	P02945|BACR	1	1720.9552	-1.7	95	108	5	101.0	22	A	RYADWLFTTPLLLL	D	0.7	6.7	
1	P02945|BACR	1	1754.9104	-2.2	13	27	4	33.0	25	V	SQAQITGRPEWIWLA	L	-0.3	6.98	
1	P02945|BACR	1	1801.8828	1.1	92	105	3	76.1	25	I	YWARYADWLFTTPL	L	-0.1	6.64	
1	P02945|BACR	1	1835.9669	-4.5	48	64	4	95.0	25	V	SDPDAKKFYAITTLVPA	I	0.0	6.8	
1	P02945|BACR	1	1884.0754	0.5	124	143	9	110.6	21	A	LVGADGIMIGTGLVGALTKV	Y	1.4	6.76	
1	P02945|BACR	1	2020.1033	-2.5	95	111	7	127.6	24	A	RYADWLFTTPLLLLDLA	L	0.7	3.88	
1	P02945|BACR	1	2440.2831	-0.2	92	111	8	75.3	25	I	YWARYADWLFTTPLLLLDLA	L	0.6	3.88	
2	P00772|ELA1	1	701.3609	-4.8	62	66	0	27.2	27	I	RQNWV	M	-1.6	11.04	
2	P00772|ELA1	1	800.3851	9.2	54	61	1	46.1	23	A	HTCGGTLI	R	0.7	7.16	
2	P00772|ELA1	1	882.5287	0.6	138	146	2	30.3	21	L	GVLPRAGTI	L	0.7	11.04	
2	P00772|ELA1	1	943.4512	-7.2	223	231	2	49.9	23	V	NGQYAVHGV	T	-0.2	7.76	
2	P00772|ELA1	1	1004.4862	-2.5	62	69	1	45.1	25	I	RQNWVMTA	A	-0.7	11.04	
2	P00772|ELA1	1	1040.4675	2.4	45	53	0	25.3	22	L	QYRSGSSWA	H	-1.2	9.84	
2	P00772|ELA1	1	1066.6499	0.0	138	148	4	54.4	19	L	GVLPRAGTILA	N	1.1	11.04	
2	P00772|ELA1	1	1097.5254	3.6	34	42	0	71.2	24	A	QRNSWPSQI	S	-1.6	11.04	Gln->pyro-Glu (N-term Q)
2	P00772|ELA1	1	1114.5519	10.2	34	42	0	55.5	25	A	QRNSWPSQI	S	-1.6	11.04	
2	P00772|ELA1	1	1123.6713	-5.1	136	146	3	39.4	20	V	QLGVLPRAGTI	L	0.6	11.04	
2	P00772|ELA1	1	1240.5836	-0.2	43	53	1	63.8	23	I	SLQYRSGSSWA	H	-0.7	9.84	
2	P00772|ELA1	1	1244.5462	6.2	105	114	1	72.6	22	V	VHPYWNTDDV	A	-1.0	3.88	
2	P00772|ELA1	1	1307.7925	-5.4	136	148	5	22.4	19	V	QLGVLPRAGTILA	N	1.0	11.04	
2	P00772|ELA1	1	1315.5833	10.9	105	115	2	62.6	23	V	VHPYWNTDDVA	A	-0.7	3.88	
2	P00772|ELA1	1	1343.6146	-2.2	104	114	2	75.6	23	I	VVHPYWNTDDV	A	-0.5	3.88	
2	P00772|ELA1	1	1386.6204	4.4	105	116	3	96.9	22	V	VHPYWNTDDVAA	G	-0.5	3.88	
2	P00772|ELA1	1	1414.6517	1.6	104	115	3	81.2	24	I	VVHPYWNTDDVA	A	-0.3	3.88	
2	P00772|ELA1	1	1485.6889	-1.8	104	116	4	89.6	23	I	VVHPYWNTDDVAA	G	-0.2	3.88	
2	P00772|ELA1	1	1529.7223	-0.3	29	42	1	71.0	25	V	GGTEAQRNSWPSQI	S	-1.3	6.98	
2	P00772|ELA1	1	1590.8729	-1.2	124	137	5	31.5	24	L	RLAQSVTLNSYVQL	G	0.2	9.84	
2	P00772|ELA1	1	1712.8522	-17.2	101	114	3	92.1	25	V	QKIVVHPYWNTDDV	A	-0.6	5.1	
2	P00772|ELA1	1	1715.8955	0.2	156	171	3	67.9	26	I	TGWGLTRTNGQLAQTL	Q	-0.4	11.04	
2	P00772|ELA1	1	1770.9992	0.3	132	148	6	37.3	22	L	NSYVQLGVLPRAGTILA	N	0.7	9.84	
2	P00772|ELA1	1	1801.0098	-0.6	130	146	5	127.3	22	V	TLNSYVQLGVLPRAGTI	L	0.5	9.84	
2	P00772|ELA1	1	1815.8024	-2.5	83	98	2	130.9	22	V	VGEHNLNQNDGTEQYV	G	-1.4	3.82	
2	P00772|ELA1	1	1905.8533	-0.6	105	121	5	119.4	23	V	VHPYWNTDDVAAGYDIA	L	-0.3	3.6	
2	P00772|ELA1	1	1914.8708	1.0	82	98	3	132.9	23	V	VVGEHNLNQNDGTEQYV	G	-1.0	3.82	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
2	P00772|ELA1	1	1933.8847	9.8	104	120	5	65.5	25	I	VVHPYWNTDDVAAGYDI	A	-0.2	3.6	
2	P00772|ELA1	1	1971.8923	2.7	83	100	3	147.5	23	V	VGEHNLNQNDGTEQYVGV	Q	-1.0	3.82	
2	P00772|ELA1	1	1985.131	-3.7	130	148	7	109.7	21	V	TLNSYVQLGVLPRAGTILA	N	0.8	9.84	
2	P00772|ELA1	1	2004.9218	-0.4	104	121	6	144.5	24	I	VVHPYWNTDDVAAGYDIA	L	-0.1	3.6	
2	P00772|ELA1	1	2043.0498	3.2	156	174	4	103.5	26	I	TGWGLTRTNGQLAQTLQQA	Y	-0.6	11.04	
2	P00772|ELA1	1	2070.9607	-2.5	82	100	4	154.5	24	V	VVGEHNLNQNDGTEQYVGV	Q	-0.7	3.82	
2	P00772|ELA1	1	2118.0058	2.6	104	122	7	34.4	26	I	VVHPYWNTDDVAAGYDIAL	L	0.2	3.6	
2	P00772|ELA1	1	2231.0899	-4.3	104	123	8	137.8	26	I	VVHPYWNTDDVAAGYDIALL	R	0.3	3.6	
2	P00772|ELA1	1	2341.1299	-5.7	83	103	4	96.7	25	V	VGEHNLNQNDGTEQYVGVQKI	V	-1.0	4.42	
2	P00772|ELA1	1	2374.1594	-0.3	101	121	7	130.5	26	V	QKIVVHPYWNTDDVAAGYDIA	L	-0.2	4.16	
2	P00772|ELA1	1	2440.1983	4.2	82	103	5	110.4	26	V	VVGEHNLNQNDGTEQYVGVQKI	V	-0.8	4.42	
3	Q9HR99|Q9HR99	1	1419.6154	-3.6	122	134	2	65.3	21	V	DAGETLEHTFETA	G	-0.7	3.68	
3	Q9HR99|Q9HR99	1	1473.6195	-5.4	106	119	0	75.8	18	A	SGFGTMDKDGNQFA	V	-0.8	3.88	
3	Q9HR99|Q9HR99	1	1491.7246	-7.0	57	70	1	84.6	26	A	VAPDGGFKFEPSEL	T	-0.3	3.82	
3	Q9HR99|Q9HR99	1	1562.7617	-5.1	56	70	2	78.5	25	I	AVAPDGGFKFEPSEL	T	-0.1	3.82	
3	Q9HR99|Q9HR99	1	1671.7563	-1.6	106	121	2	133.1	23	A	SGFGTMDKDGNQFAVV	D	-0.2	3.88	
3	Q9HR99|Q9HR99	1	1687.7512	-4.7	106	121	2	54.8	21	A	SGFGTMDKDGNQFAVV	D	-0.2	3.88	Oxidation (M)
3	Q9HR99|Q9HR99	1	1691.8407	0.9	57	72	2	105.2	26	A	VAPDGGFKFEPSELTV	S	0.0	3.82	
3	Q9HR99|Q9HR99	1	1762.8778	-3.5	56	72	3	119.1	26	I	AVAPDGGFKFEPSELTV	S	0.1	3.82	
3	Q9HR99|Q9HR99	1	2131.9222	7.6	122	140	3	152.5	22	V	DAGETLEHTFETAGEYTYV	C	-0.7	3.58	
3	Q9HR99|Q9HR99	1	2212.0107	4.0	100	121	3	56.4	25	I	SIPDGASGFGTMDKDGNQFAVV	D	-0.1	3.6	
3	Q9HR99|Q9HR99	1	2307.1019	5.5	48	70	3	104.2	25	A	SQSGGNTIAVAPDGGFKFEPSEL	T	-0.3	3.82	
3	Q9HR99|Q9HR99	1	2507.218	5.4	48	72	4	128.2	26	A	SQSGGNTIAVAPDGGFKFEPSELTV	S	-0.2	3.82	
3	Q9HR99|Q9HR99	1	3073.3611	0.4	106	134	5	91.2	21	A	SGFGTMDKDGNQFAVVDAGETLEHTFETA	G	-0.4	3.74	
4	Q9HMW9|Q9HMW9	1	978.5287	8.2	636	643	1	55.1	23	A	FHLQPPQL	F	-0.4	7.84	
4	Q9HMW9|Q9HMW9	1	1166.6084	-23.3	616	624	2	48.3	24	A	YVINREQFV	S	-0.1	6.88	
4	Q9HMW9|Q9HMW9	1	1367.618	-8.8	133	143	0	37.8	21	L	QYQSPTWKEMA	N	-1.5	6.86	
4	Q9HMW9|Q9HMW9	1	1368.686	-1.2	614	624	3	41.0	25	A	MAYVINREQFV	S	0.3	6.88	
4	Q9HMW9|Q9HMW9	1	1467.7358	-1.0	616	627	3	38.3	25	A	YVINREQFVSDV	F	-0.1	4.08	
4	Q9HMW9|Q9HMW9	1	1567.7307	-7.4	120	132	1	33.7	23	A	GYGPDNKYELNWL	Q	-1.2	4.08	
4	Q9HMW9|Q9HMW9	1	1695.7926	-3.9	133	146	1	89.6	23	L	QYQSPTWKEMANTI	R	-1.1	6.86	
4	Q9HMW9|Q9HMW9	1	1736.8958	0.9	619	633	2	89.0	25	I	NREQFVSDVFKGRGV	G	-0.7	10.08	
4	Q9HMW9|Q9HMW9	1	1857.9335	-0.5	595	610	1	105.2	26	I	DTYYVGFNMTKVPKPV	R	-0.3	9.46	
4	Q9HMW9|Q9HMW9	1	1864.9544	0.1	619	635	3	92.1	26	I	NREQFVSDVFKGRGVGA	F	-0.5	10.08	
4	Q9HMW9|Q9HMW9	1	2112.1116	2.3	616	633	4	95.5	25	A	YVINREQFVSDVFKGRGV	G	-0.2	9.72	
4	Q9HMW9|Q9HMW9	1	2159.0973	0.5	592	610	2	39.7	26	V	STIDTYYVGFNMTKVPKPV	R	-0.1	9.46	
4	Q9HMW9|Q9HMW9	1	2240.1702	-3.3	616	635	5	56.5	26	A	YVINREQFVSDVFKGRGVGA	F	-0.1	9.72	
4	Q9HMW9|Q9HMW9	1	2314.1892	-0.5	614	633	5	97.4	25	A	MAYVINREQFVSDVFKGRGV	G	0.0	9.72	
4	Q9HMW9|Q9HMW9	1	2442.2478	1.7	614	635	6	52.0	26	A	MAYVINREQFVSDVFKGRGVGA	F	0.1	9.72	
5	Q48302|Q48302	1	904.5059	-11.4	82	89	2	33.8	24	V	VFVVPTPF	-	1.8	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
5	Q48302|Q48302	1	979.4723	-5.6	40	49	2	47.4	24	A	GYAERGIGSA	A	-0.3	6.88	
5	Q48302|Q48302	1	1050.5094	1.8	39	49	3	50.1	24	A	AGYAERGIGSA	A	-0.1	6.88	
5	Q48302|Q48302	1	1149.5778	-2.2	40	51	4	63.8	25	A	GYAERGIGSAAV	G	0.2	6.88	
5	Q48302|Q48302	1	1220.6149	-4.8	39	51	5	54.4	25	A	AGYAERGIGSAAV	G	0.4	6.88	
5	Q48302|Q48302	1	1234.6306	-2.8	37	49	5	68.2	25	A	LAAGYAERGIGSA	A	0.3	6.88	
5	Q48302|Q48302	1	1277.6364	-0.9	40	53	5	103.4	26	A	GYAERGIGSAAVGA	I	0.3	6.88	
5	Q48302|Q48302	1	1305.6677	2.4	36	49	6	72.1	25	A	ALAAGYAERGIGSA	A	0.4	6.88	
5	Q48302|Q48302	1	1348.6735	-0.3	39	53	6	95.6	26	A	AGYAERGIGSAAVGA	I	0.4	6.88	
5	Q48302|Q48302	1	1359.6922	-0.2	54	66	4	29.3	26	A	IAEDPDLFGTGLI	L	0.6	2.88	
5	Q48302|Q48302	1	1386.6813	-1.9	14	27	3	47.5	25	A	ETGSNMPAITPKAA	A	-0.4	6.94	
5	Q48302|Q48302	1	1457.7184	-10.2	13	27	4	101.0	25	L	AETGSNMPAITPKAA	A	-0.2	6.94	
5	Q48302|Q48302	1	1473.7133	-1.8	13	27	4	38.4	26	L	AETGSNMPAITPKAA	A	-0.2	6.94	Oxidation (M)
5	Q48302|Q48302	1	1475.7732	-4.6	36	51	8	49.2	26	A	ALAAGYAERGIGSAAV	G	0.8	6.88	
5	Q48302|Q48302	1	1603.8318	0.6	36	53	9	83.8	25	A	ALAAGYAERGIGSAAVGA	I	0.7	6.88	
6	Q9HMI3|Q9HMI3	1	1172.619	-5.7	556	566	3	53.9	26	V	GGPFLDRVELA	-	0.2	4.08	
6	Q9HMI3|Q9HMI3	1	1475.7157	-0.9	390	402	0	61.1	26	A	TFSNPRGYNPNPI	Q	-1.2	9.84	
6	Q9HMI3|Q9HMI3	1	1577.8202	-2.9	178	190	2	59.0	25	I	DLTQQYAPFLRNL	A	-0.5	6.7	
6	Q9HMI3|Q9HMI3	1	1648.8573	-5.1	178	191	3	50.7	25	I	DLTQQYAPFLRNLA	I	-0.3	6.7	
6	Q9HMI3|Q9HMI3	1	1696.8056	-0.3	331	345	4	30.1	25	I	NRDEIVDSIYQGFAA	S	-0.3	3.7	
6	Q9HMI3|Q9HMI3	1	1951.8912	1.1	220	236	1	140.2	24	V	GTGPFEFDQLDNETQRV	R	-1.1	3.58	
6	Q9HMI3|Q9HMI3	1	1994.9585	-4.4	460	477	4	89.1	25	V	LLHPGTDIDDVPADQNYI	A	-0.4	3.42	
6	Q9HMI3|Q9HMI3	1	2310.1339	1.6	198	219	6	64.2	26	I	LSRDQIESLGADAQPELGTDPV	G	-0.5	3.42	
6	Q9HMI3|Q9HMI3	1	2494.2551	2.2	196	219	8	98.1	25	A	AILSRDQIESLGADAQPELGTDPV	G	-0.2	3.42	
6	Q9HMI3|Q9HMI3	1	2565.2922	2.0	195	219	9	44.2	25	A	AAILSRDQIESLGADAQPELGTDPV	G	-0.1	3.42	
6	Q9HMI3|Q9HMI3	1	3202.4691	5.2	207	236	5	72.6	23	L	GADAQPELGTDPVGTGPFEFDQLDNETQRV	R	-0.9	3.28	
7	Q9HN93|Q9HN93	1	1332.6099	-2.1	98	108	1	38.4	24	V	SFEWVSNTHNI	L	-0.5	5.12	
7	Q9HN93|Q9HN93	1	1564.7481	-6.4	103	117	4	51.3	25	V	SNTHNILIDAQPDGA	D	-0.5	3.88	
7	Q9HN93|Q9HN93	1	1610.7002	1.7	38	53	3	96.9	21	A	QAYDGWFSGDAKGGAV	G	-0.4	3.88	Gln->pyro-Glu (N-term Q)
7	Q9HN93|Q9HN93	1	1761.737	6.6	240	254	1	54.0	20	A	FEPDTELGHDEYDPV	G	-1.3	3.38	
7	Q9HN93|Q9HN93	1	2213.0389	4.4	98	117	5	147.7	25	V	SFEWVSNTHNILIDAQPDGA	D	-0.3	3.7	
7	Q9HN93|Q9HN93	1	2418.0401	5.8	38	61	4	176.6	21	A	QAYDGWFSGDAKGGAVGNYDGTTV	D	-0.5	3.6	Gln->pyro-Glu (N-term Q)
7	Q9HN93|Q9HN93	1	2583.1726	4.9	62	87	5	52.4	24	V	DRTGTDEVTIDVGVDANGGTYGFGPA	A	-0.4	3.36	
7	Q9HN93|Q9HN93	1	3291.4229	0.9	38	69	5	83.0	20	A	QAYDGWFSGDAKGGAVGNYDGTTVDRTGTDEV	T	-0.8	3.64	Gln->pyro-Glu (N-term Q)
7	Q9HN93|Q9HN93	1	3444.5018	-2.8	206	237	2	41.2	19	V	SYYRRTPAPDSSGAFDYEPGGDTDDQPAIPEA	D	-1.2	3.58	
7	Q9HN93|Q9HN93	1	3505.5547	15.3	38	71	6	63.8	22	A	QAYDGWFSGDAKGGAVGNYDGTTVDRTGTDEVTI	D	-0.6	3.64	Gln->pyro-Glu (N-term Q)
9	Q9HMG3|Q9HMG3	1	1037.5254	8.9	35	43	3	48.2	23	I	AQDVLEHRA	S	-0.7	5.22	
9	Q9HMG3|Q9HMG3	1	2207.0131	1.1	44	65	1	85.0	24	A	STVPETDFPEPYNRSIGGGGGA	G	-0.7	3.82	
9	Q9HMG3|Q9HMG3	1	2335.0717	-1.4	44	67	2	107.0	24	A	STVPETDFPEPYNRSIGGGGGAGA	V	-0.6	3.82	
9	Q9HMG3|Q9HMG3	1	2434.1401	4.2	44	68	3	63.2	25	A	STVPETDFPEPYNRSIGGGGGAGAV	A	-0.4	3.82	
9	Q9HMG3|Q9HMG3	1	2505.1772	3.0	44	69	4	107.0	25	A	STVPETDFPEPYNRSIGGGGGAGAVA	G	-0.3	3.82	

Supplementary Table 1

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
9	Q9HMG3|Q9HMG3	1	2690.2573	1.8	44	72	5	60.5	25	A	STVPETDFPEPYNRSIGGGGGAGAVAGGA	E	-0.3	3.82	
10	Q9HN95|Q9HN95	1	940.5018	5.1	454	463	1	65.8	23	V	LAPGSPGFPV	-	0.6	6.02	
10	Q9HN95|Q9HN95	1	1403.6874	-2.0	29	40	2	42.0	26	L	YTFYPPLQAHPA	F	-0.4	7.7	
10	Q9HN95|Q9HN95	1	1450.8224	-0.3	140	151	4	44.5	22	A	YLAWYTILPKLA	G	0.8	9.52	
10	Q9HN95|Q9HN95	1	1516.7714	-4.5	28	40	3	87.6	26	V	LYTFYPPLQAHPA	F	-0.1	7.7	
10	Q9HN95|Q9HN95	1	1729.8828	-3.6	26	40	4	58.0	26	A	NVLYTFYPPLQAHPA	F	0.0	7.7	
10	Q9HN95|Q9HN95	1	2062.9901	1.4	176	193	2	62.7	25	V	GFHHQYTDPGIAEGFKFI	A	-0.4	6.02	
11	Q9HRQ9|Q9HRQ9	1	1398.6681	-6.8	102	113	1	57.9	23	V	KWVWEGSTGHNV	H	-0.8	7.82	
11	Q9HRQ9|Q9HRQ9	1	1626.8002	-1.5	79	93	3	90.2	25	V	KVGPNNQNVFDPAEV	Y	-0.8	4.08	
11	Q9HRQ9|Q9HRQ9	1	2306.0716	-13.4	102	122	3	96.1	23	V	KWVWEGSTGHNVHATSVPDEA	G	-0.7	5.18	
11	Q9HRQ9|Q9HRQ9	1	2445.1812	8.3	79	101	5	87.2	26	V	KVGPNNQNVFDPAEVYVSPGDTV	K	-0.5	3.7	
12	Q9HSS1|Q9HSS1	1	940.4866	-2.6	249	258	4	35.7	23	A	LAGALEDGPV	S	0.6	3	
12	Q9HSS1|Q9HSS1	1	1207.635	-3.4	153	164	3	75.4	24	V	GFVGFGEIARGV	A	0.9	6.98	
12	Q9HSS1|Q9HSS1	1	1232.6401	-6.0	210	220	1	42.6	25	V	FAPLTEETRGL	V	-0.2	4.26	
12	Q9HSS1|Q9HSS1	1	1593.8151	-0.8	149	164	5	57.8	25	A	DATVGFVGFGEIARGV	A	0.8	4.08	
12	Q9HSS1|Q9HSS1	1	1646.8152	-2.7	210	224	3	37.1	26	V	FAPLTEETRGLVDEA	A	-0.2	3.68	
13	Q9HMF1|Q9HMF1	1	1198.5982	-7.7	160	169	1	71.4	24	V	RLEGELPEWA	T	-0.9	3.96	
13	Q9HMF1|Q9HMF1	1	1411.7095	-0.6	158	169	2	70.8	24	V	NVRLEGELPEWA	T	-0.7	3.96	
13	Q9HMF1|Q9HMF1	1	2193.0073	1.6	581	599	5	52.7	24	L	NIDEETYARIEQGDDVEVV	D	-0.8	3.32	
14	Q9HRS0|Q9HRS0	1	1286.6156	-0.9	119	129	1	52.0	25	V	RFVWESGGHNV	H	-0.5	7.84	
14	Q9HRS0|Q9HRS0	1	1475.6067	-1.2	219	230	0	64.6	17	A	YFFMKYGGDYGE	-	-0.7	4.08	
14	Q9HRS0|Q9HRS0	1	1917.8956	-1.5	183	200	1	84.7	24	V	TDSPPENKGYQTIVPDSA	K	-1.1	3.7	
15	Q9HM89|EF1A	1	1440.7937	-6.2	235	249	3	34.7	24	I	SGIGTVPVGRIETGV	M	0.5	6.98	
15	Q9HM89|EF1A	1	1521.71	-5.7	165	178	2	50.6	24	V	KDLFGQVGFNPDDA	K	-0.6	3.6	
15	Q9HM89|EF1A	1	1764.8319	2.8	162	178	3	87.0	25	V	SGVKDLFGQVGFNPDDA	K	-0.3	3.6	
16	Q9HS26|Q9HS26	1	731.4251	2.1	61	67	4	22.9	22	A	GMLVALI	F	2.8	6.02	Oxidation (M)
16	Q9HS26|Q9HS26	1	1711.7577	2.6	16	31	2	55.7	23	A	GDDSEPEIDFYGGKLA	S	-0.8	3.42	
16	Q9HS26|Q9HS26	1	2144.1517	0.0	310	328	7	33.6	24	A	SDSLWIARELSVLPFVEAI	N	0.8	3.82	
17	Q9HMW4|Q9HMW4	1	1745.8161	0.0	273	285	2	26.7	25	A	FERAEDYYLRQWA	K	-1.3	4.44	
17	Q9HMW4|Q9HMW4	1	2202.097	-6.2	252	270	3	37.0	26	A	AFNGNLGPWDLKRWSQQSV	M	-0.8	10.08	
17	Q9HMW4|Q9HMW4	1	2393.0692	-0.8	231	251	5	72.2	23	A	KPYVEAEDADGLEQDEEVMRA	A	-1.1	3.62	
17	Q9HMW4|Q9HMW4	1	2577.1904	-5.4	229	251	7	35.5	24	A	LAKPYVEAEDADGLEQDEEVMRA	A	-0.8	3.62	
18	Q9HRR1|Q9HRR1	1	1544.7583	-5.9	177	189	0	30.5	26	A	TWRSQNTDNTIPI	L	-1.1	6.78	
18	Q9HRR1|Q9HRR1	1	2719.1198	13.6	151	174	3	124.0	19	V	NIDEFDDYDTWENDYGDAGIGKPA	K	-1.3	3.16	
19	Q9HHR4|Q9HHR4	1	1340.818	-0.9	235	247	6	24.3	18	A	LIGVGYIIGPRIA	A	1.5	9.84	
20	Q9HRL3|Q9HRL3	1	1845.9221	-3.5	631	648	6	28.9	26	A	RGADTFDQGVIDGIVNAV	S	0.2	3.6	
20	Q9HRL3|Q9HRL3	1	1916.9592	-2.6	630	648	7	58.8	26	L	ARGADTFDQGVIDGIVNAV	S	0.3	3.6	
20	Q9HRL3|Q9HRL3	1	2133.0702	3.5	631	651	7	28.6	26	A	RGADTFDQGVIDGIVNAVSSI	S	0.3	3.6	
21	Q9HM69|CSG	1	1186.6081	-20.2	716	726	4	28.4	26	V	ELLQGDASIEI	N	0.3	2.94	
21	Q9HM69|CSG	1	1308.7877	4.2	840	852	9	54.4	18	V	AVLGAALLALRQN	-	1.1	11.04	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
21	Q9HM69|CSG	1	2542.0831	12.0	591	613	4	73.9	21	I	SVDSDDTFDEEDIDISELRQGSA	S	-1.0	3.12	
22	Q9HM85|EF2	1	1379.8024	-3.0	614	625	6	38.8	21	A	LIDADIRLLEPI	Q	0.8	3.7	
22	Q9HM85|EF2	1	1786.8407	18.2	155	169	2	67.9	26	I	SELQEGPEEMQERLL	S	-1.2	3.68	
23	Q9HP48|Q9HP48	1	1821.7694	6.5	204	220	4	74.7	21	V	FESGVDHFEVDDDGALA	A	-0.3	3.32	
23	Q9HP48|Q9HP48	1	1892.8065	2.0	204	221	5	53.6	20	V	FESGVDHFEVDDDGALAA	A	-0.1	3.32	
24	Q9HMX1|Q9HMX1	1	887.548	8.0	315	323	6	19.1	19	A	GFIAALLAL	V	2.6	6.02	
24	Q9HMX1|Q9HMX1	1	1760.8329	-1.8	111	126	1	53.3	25	L	SRDVIPNQGYNDPSTV	R	-1.0	3.88	
24	Q9HMX1|Q9HMX1	1	2330.0146	0.6	497	519	5	43.6	20	A	NALGDGIRDAIDPESEGGSEEEA	A	-1.0	3.28	
26	Q9HMT7|Q9HMT7	1	1702.7322	-0.9	44	59	3	127.6	21	V	DVDTEAYEESHAPGAI	G	-0.7	3.5	
27	Q9HS12|Q9HS12	1	731.4694	-15.4	23	28	3	32.0	20	V	FRALLL	A	1.9	11.04	
27	Q9HS12|Q9HS12	1	1293.6717	-8.0	137	147	2	24.5	24	V	TAYDQRLPFLA	R	-0.1	6.7	
28	Q9HRL1|Q9HRL1	1	1517.7878	-0.8	335	347	4	52.8	25	I	NSALSLFYYSRVV	K	0.6	9.58	
28	Q9HRL1|Q9HRL1	1	2070.984	-2.2	131	149	1	52.4	25	A	SVPFHFWAPEAYEGAPAPV	S	0.1	4.24	
29	Q9HSM4|DHE42	1	1255.6925	-3.7	241	251	5	57.3	25	A	LLLDDWGARVV	A	0.8	3.88	
33	Q9HPA9|Q9HPA9	1	930.4771	-2.6	509	518	2	31.6	27	A	QGNVGLSSGI	T	0.3	6.02	
34	Q9HSA8|Q9HSA8	1	953.4971	9.1	61	68	1	37.6	23	V	FGEYRGLL	E	0.0	6.88	
34	Q9HSA8|Q9HSA8	1	1349.6979	-2.0	61	72	2	27.3	25	V	FGEYRGLLEPGI	N	-0.1	4.26	
36	Q9HRJ5|Q9HRJ5	1	1243.6561	-15.1	96	106	3	36.8	26	A	TTPLSRAEWLA	A	-0.1	6.98	
37	Q9HNY2|Q9HNY2	1	1126.6234	-16.4	230	241	5	29.2	24	A	LITVPGADASAL	R	1.2	3.1	
38	Q9HP84|HTR4	1	830.5266	9.9	327	334	5	17.1	17	L	GFILVALV	G	3.1	6.02	
39	Q9HP76|Q9HP76	1	968.5807	-8.2	119	126	2	25.9	22	I	RWSIPIVV	R	1.2	11.04	
39	Q9HP76|Q9HP76	1	1277.6616	-20.6	467	481	8	32.3	26	V	TAAAISGAFTAAVGA	A	1.4	6.02	
40	Q9HR98|Q9HR98	1	2059.9698	5.3	134	153	7	70.0	26	V	SFVDATDPDAVADAIRPETA	F	-0.1	3.36	
43	Q9HRS4|Q9HRS4	1	2054.809	6.7	16	35	4	81.0	15	A	AADQGIDPWTADDHEGGDGE	-	-1.3	3.22	
44	Q9HS72|SECE	1	1605.8436	-1.7	1	14	4	33.3	25	-	MDVPLELSAYTRVL	R	0.5	4.08	
45	Q9HPG8|Q9HPG8	1	1317.6241	0.8	661	670	1	67.9	25	V	EFDDYFLRTL	E	-0.4	3.7	
46	Q9HHN1|Q9HHN1	1	2336.1934	1.3	166	188	7	49.8	26	A	GAILSGVYMGDKQSPLSDTTLLA	S	0.3	3.88	
47	Q9HN92|Q9HN92	1	955.5273	-2.9	1	8	2	42.7	24	-	MNVRPQVI	A	0.2	11.04	
47	Q9HN92|Q9HN92	1	971.5222	-5.1	1	8	2	30.3	27	-	MNVRPQVI	A	0.2	11.04	Oxidation (M)
47	Q9HN92|Q9HN92	1	1026.5644	0.6	1	9	3	55.2	24	-	MNVRPQVIA	T	0.4	11.04	
48	Q9HSM2|MUTS1	1	1156.6088	1.1	328	338	4	29.4	25	A	RDALGDVLGEI	Y	0.2	3.7	
50	Q9HQ64|Q9HQ64	1	1716.8907	-1.9	79	94	5	71.3	25	V	YNALVNQGIEGNAKRA	A	-0.6	9.72	
51	Q9HR22|Q9HR22	1	1658.8304	2.2	72	86	4	36.5	26	V	YSELFLGAIGHPEQV	L	0.2	4.24	
52	Q9HPQ2|Q9HPQ2	1	1402.6517	-0.1	332	343	2	71.1	24	A	YVVDNYGYSRPA	T	-0.7	6.58	
53	Q9HN43|CAPPA	1	930.4771	-1.8	326	334	4	31.5	27	L	AVIDRTADA	Y	0.2	3.88	
53	Q9HN43|CAPPA	1	1267.6561	11.5	308	319	2	45.9	24	L	RDADLGAPPFPI	D	-0.2	3.88	
54	P25964|BACS1	1	1426.6187	-1.9	219	231	0	29.5	20	V	FMHSESPPAPEQA	T	-0.9	4.24	
55	Q9HNK1|Q9HNK1	1	762.4276	-28.7	116	123	4	32.9	25	A	AIALFGTA	I	1.9	6.02	
57	Q9HSB5|Q9HSB5	1	1955.051	-18.3	22	41	9	33.7	26	V	QGAIDAGATIGPRVMVSLLA	V	0.9	6.78	Oxidation (M)
59	Q9HHI2|Q9HHI2	1	731.4582	-6.0	40	46	4	24.0	20	L	IVFGAIL	L	3.0	6.02	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
59	Q9HHI2|Q9HHI2	1	731.4582	-4.6	41	47	4	24.1	20	I	VFGAILL	M	2.9	6.02	
61	Q9HMZ3|Q9HMZ3	1	2517.1237	3.8	413	432	3	53.9	23	V	EYLWYVGDYPSYDERNQHIA	R	-1.2	4.06	
66	P16102|BACH	1	1220.6401	-1.6	191	201	3	33.8	25	A	GTAEIFDTLRV	L	0.3	4.08	
67	Q9HRL9|Q9HRL9	1	1556.841	-0.2	548	562	7	68.5	25	V	ATLGSLDVILGEVDR	-	0.6	3.7	
69	Q9HQP2|Q9HQP2	1	2104.9491	0.6	746	763	2	27.0	23	V	VFYDGPRDLSQGDFYQQA	Y	-0.9	3.6	
71	Q9HNR0|Q9HNR0	1	745.4044	25.6	464	470	3	24.9	23	A	MSPLAVL	S	1.9	6.02	Oxidation (M)
76	Q9HN02|Q9HN02	1	1096.5917	-0.8	163	171	3	52.0	23	V	LFDYLTRAV	N	0.7	6.7	
80	Q9HPM1|Q9HPM1	1	1026.5458	18.7	164	174	5	30.5	24	I	ADGTRPAVAVA	T	0.4	6.78	
83	Q9HMB7|Q9HMB7	1	1423.662	3.4	123	134	1	74.1	24	A	REEDDFSIFAPV	L	-0.4	3.58	
84	Q9HMY7|Q9HMY7	1	731.4582	-6.0	104	110	4	24.0	20	L	LAFVGII	V	3.0	6.02	
86	Q9HN37|Q9HN37	1	1314.8275	-13.2	539	550	7	25.2	16	A	LVFQVKLSVVIA	A	2.1	10.1	
87	Q9HND8|VATI	1	1530.7678	-4.5	364	376	2	44.1	26	I	NRPQYTEIDPTVV	L	-0.9	4.08	
88	Q9HPT9|Q9HPT9	1	2263.0128	2.7	61	82	3	56.9	23	A	ALDLPGHGDSDDIETDPGPETL	D	-0.8	3.22	
89	Q9HRN3|Q9HRN3	1	1649.8009	-0.5	84	100	4	26.4	25	V	SSPGGAVSGSEVQYRAV	K	-0.2	6.88	
90	Q9HQB8|Q9HQB8	1	955.5273	10.8	61	70	4	25.5	24	A	VPMRAAGAAI	D	1.1	11.04	
91	Q9HHV1|Q9HHV1	1	1972.0425	14.0	132	149	8	26.0	24	L	RAMTALAFRHAATDRVVA	E	0.3	12.1	Oxidation (M)
92	Q9HN47|PRIL	1	1397.5228	4.0	315	327	2	14.7	13	A	YGNCVNPDDLCDA	I	-0.5	2.82	
95	Q9HN22|Q9HN22	1	1719.8104	2.4	149	165	6	48.7	25	A	AAFLADIDHSAYGTTPA	Q	0.3	3.88	
96	Q9HRL8|Q9HRL8	1	1015.5603	2.3	170	178	2	32.2	25	A	GVRIPAWFA	F	0.9	11.04	
98	Q9HP01|Q9HP01	1	1009.6172	3.3	21	31	5	19.5	19	A	ALLAPSGGLLV	A	1.8	6.02	
98	Q9HP01|Q9HP01	1	1123.6825	-12.5	13	23	5	22.2	20	V	GSPRARLAALL	A	0.5	12.4	
103	Q9HME2|Q9HME2	1	1988.0078	0.6	2	18	6	42.4	26	M	VWIIDNLVTMVEHFTTA	A	0.9	4.06	
106	Q9HQ90|Q9HQ90	1	1066.5771	27.4	239	249	6	28.8	21	A	QAALRAGADLV	R	0.6	6.78	Gln->pyro-Glu (N-term Q)
108	Q9HSA0|Q9HSA0	1	1260.6251	-2.2	39	50	1	52.5	26	A	FEHGLPSGPHLA	D	-0.2	6.02	
110	Q9HQ63|DHSD	1	1038.5386	-1.6	121	130	2	27.0	22	A	SVPTFLTGAF	-	1.1	6.02	
113	Q9HSW2|Q9HSW2	1	713.4799	27.2	23	28	3	21.2	13	I	RSLLII	S	1.9	11.04	
114	Q9HRJ8|Q9HRJ8	1	731.4582	-6.0	396	402	4	22.6	20	V	LLGAVFL	Y	2.8	6.02	
115	Q9HRT4|Q9HRT4	1	1449.8555	0.6	208	224	9	19.1	19	V	GVPTAIGGAGVALAVVV	L	1.9	6.02	
119	Q9HNP7|Q9HNP7	1	1784.9632	19.9	270	288	8	43.2	23	V	RLGTVSGEEVGLVGASALA	D	0.7	4.26	
125	Q9HP66|Q9HP66	1	830.5266	9.9	117	124	5	25.1	17	V	FLGLLAVV	L	3.0	6.02	
127	Q9HPQ1|Q9HPQ1	1	731.4582	-4.6	376	382	3	29.2	20	A	GLIGFLL	F	2.6	6.02	
130	Q9HQH2|Q9HQH2	1	1441.6838	-2.0	152	163	1	30.7	24	V	NTRLQTFDGEYV	M	-0.9	4.08	
132	Q9HQU3|Q9HQU3	1	731.4582	-6.0	143	149	3	36.3	20	V	IIGLGFL	A	2.7	6.02	
135	Q9HM88|Q9HM88	1	1187.567	-5.2	56	68	3	37.0	25	A	SEIGTGAPSDALA	A	0.2	3	
137	Q9HQ19|Q9HQ19	1	1208.7016	5.7	23	34	5	20.3	19	V	LLVSATIGPEPI	T	1.2	3.3	
142	Q9HP88|Q9HP88	1	1689.9301	-2.5	397	412	4	55.1	24	I	LLPIAPGLDDTPEIRA	Q	0.2	3.7	
149	Q9HMH4|Q9HMH4	1	1344.5358	5.1	56	67	1	53.9	16	A	SFSYDDPDADTL	G	-0.9	2.74	
151	Q9HRJ0|Q9HRJ0	1	1122.5227	-3.9	141	152	6	28.4	23	A	MAAADTSVSALA	L	1.1	3.1	Oxidation (M)
156	Q9HMQ2|ASSY	1	1365.6564	-2.7	146	156	2	44.5	25	L	GLTREWEIEYA	A	-0.7	3.96	
161	Q9HNE6|Q9HNE6	1	1203.607	-4.0	275	284	2	29.4	26	V	TWMDRVQGVL	-	0.1	6.78	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
166	Q9HHV2|Q9HHV2	1	930.5022	-28.9	355	364	4	29.3	27	A	AITLTLGDGA	E	1.0	3.1	
170	Q9HPN9|Q9HPN9	1	1468.7998	-9.8	273	286	6	26.4	25	A	TPELSRAVAADRLA	A	0.0	7.04	
174	Q9HPQ3|Q9HPQ3	1	731.4429	14.9	247	253	3	23.0	20	A	VTSSILL	V	2.0	6.02	
178	Q9HSW6|CDC61	1	1098.6172	-23.7	145	154	6	36.6	24	I	LIVLDEVDAI	G	1.6	2.88	
182	Q48325|TBPB	1	1409.7514	13.3	87	99	3	28.0	24	I	RELGIDVTSNPPI	E	-0.2	4.08	
187	Q07971|Q07971	1	1216.5611	-20.9	258	267	3	25.7	21	A	EQLEEAWEAI	Q	-0.7	2.96	
188	P33518|COX1	1	1447.6765	8.2	143	155	4	29.3	25	I	DADDMAFPRINAI	A	-0.1	3.6	
189	Q9HS30|Q9HS30	1	1222.7173	-1.5	59	70	6	24.5	19	A	LLADLPVEAGIL	V	1.5	3	
190	Q9HR04|Q9HR04	1	789.4232	-22.5	16	24	3	30.0	25	A	TGAATLSGL	A	0.9	6.02	
192	Q9HRR2|Q9HRR2	1	1688.8661	-1.7	42	54	4	47.2	26	V	DYLELLETLYYRV	N	0.0	3.82	
193	Q9HMJ2|Q9HMJ2	1	876.4263	24.2	149	156	3	36.3	25	A	EVSMLADI	D	1.1	3	
195	Q9HMU6|Q9HMU6	1	1231.6098	-6.7	114	124	0	46.9	26	V	GDSPPRWHAPL	L	-1.1	7.84	
198	O54559|O54559	1	1159.6714	-15.3	107	118	4	25.2	23	L	VGGVFVGIGTRV	G	1.4	11.04	
208	Q9HNB8|Q9HNB8	1	1293.6717	-8.5	12	24	3	34.3	24	A	SGHLAPLFDAAPV	R	0.7	4.94	
212	Q9HRJ7|Q9HRJ7	1	1901.0557	-15.9	90	109	8	26.0	25	L	LLGGVGGLYMLQGAGLGARV	A	1.0	9.84	
232	Q9HSQ7|Q9HSQ7	1	944.512	-11.1	208	214	1	32.3	26	A	LFTYRFV	N	1.0	9.84	
236	Q9HR54|Q9HR54	1	958.5964	20.2	335	343	4	24.0	13	V	LFRAGGLLL	V	1.6	11.04	
241	Q9HN79|Q9HN79	1	1037.6485	-14.6	51	61	6	21.6	18	A	VSAVGLVAPLI	G	2.3	6.02	
246	Q9HQU8|Q9HQU8	1	2107.9698	-0.5	13	30	2	41.1	24	A	RLTDQDEFTPPESFVEQA	N	-1.1	3.5	
254	Q9HSE1|Q9HSE1	1	1227.6459	4.5	11	24	6	25.2	25	L	GGGIAGLTAAQELA	E	0.7	3.3	
260	Q9HRP5|Q9HRP5	1	745.4222	0.3	84	90	3	28.3	23	V	TIETAVL	Y	1.3	3.3	
271	Q9HRH6|Q9HRH6	1	1480.731	2.6	143	156	4	38.8	25	A	SYTGLRWLAGGAET	-	-0.2	6.88	
273	Q9HR62|Q9HR62	1	958.5964	20.2	21	29	5	14.1	13	A	FRVGLAVVV	L	2.3	11.04	
282	Q9HRK3|Q9HRK3	1	731.4582	-6.0	47	52	3	24.0	20	I	IQFVLI	G	2.7	6.02	
286	O54662|O54662	1	1167.5515	28.6	78	88	4	24.0	23	I	MTVAMTIGIEA	G	1.4	3.3	2 Oxidation (M)
289	O54610|O54610	1	1439.7094	-0.3	193	203	1	27.0	25	A	FLTPRMPWMYV	H	0.4	9.84	
294	Q9HMW6|Q9HMW6	1	799.4804	20.8	2	10	6	26.1	23	M	LAGAATVVV	F	2.3	6.02	
296	Q9HQV6|Q9HQV6	1	731.4582	-4.6	26	32	3	36.8	20	V	LFGGLLL	I	2.5	6.02	
303	Q9HNW7|Q9HNW7	1	917.5334	-4.3	345	352	5	22.8	21	A	LLADLRAF	-	1.2	6.78	
309	Q9HPF1|Q9HPF1	1	1453.7525	27.7	7	22	7	25.3	24	V	GDTGPLDAALAARAGV	T	0.4	3.88	
332	Q9HPY6|Q9HPY6	1	731.4694	-20.0	390	395	3	34.3	20	A	FARLLL	A	1.9	11.04	
375	Q9HQY5|Q9HQY5	1	745.4222	-3.6	142	148	3	23.1	23	L	LVTTAEL	N	1.2	3.3	
382	Q9HRS8|Q9HRS8	1	731.4582	-6.0	94	100	5	21.2	20	A	AFALIVV	G	3.3	6.02	
385	Q9HQZ0|Q9HQZ0	1	1137.6645	9.1	513	522	5	20.8	20	A	ILELDVNPLL	A	1.2	3	
388	Q9HRR7|Q9HRR7	1	1289.6364	-27.7	41	55	5	32.6	25	A	ADAGGPHLAPGVSAA	A	0.3	4.94	
397	Q9HHW5|Q9HHW5	1	731.4582	-6.0	88	94	3	22.4	20	L	FIGLGIL	I	2.7	6.02	
405	Q9HRR6|Q9HRR6	1	1286.6295	-1.0	95	104	1	30.2	26	A	DFFEFEARKV	E	-0.5	4.44	
420	Q9HRC9|Q9HRC9	1	1805.0564	9.8	74	91	7	16.3	16	L	ILRVGTKTGVAFGFGVLA	A	1.3	11.48	
421	Q9HQ23|Q9HQ23	1	1222.7074	22.2	104	115	7	20.4	18	V	NLAVWGPALALV	G	1.6	6.02	
433	Q48295|ARCC	1	1170.6132	-4.8	66	76	4	28.2	25	A	ESAAEKPLDVL	G	-0.1	3.82	

hit	**accession**	**z**	**mass**	**ppm**	**start**	**end**	**mc**	**score**	**id**	**-**	**sequence**	**+**	**gravy**	**pI**	**modification**
447	Q9HS52|SYP	1	1698.861	27.7	449	465	7	29.3	26	I	AAEIVMVPLGEDSAARA	A	0.6	3.82	
458	Q9HMQ8|Q9HMQ8	1	1005.5131	10.5	77	87	3	26.9	24	I	VGTGAGLYPTA	A	0.6	5.92	
462	Q9HNS6|Q9HNS6	1	1063.5815	10.7	71	81	3	30.2	22	I	GFGPIVGPHIA	F	0.9	7.84	
463	Q9HMT5|Q9HMT5	1	1289.5888	9.2	257	268	3	26.8	25	L	NDQGYINPEAVA	R	-0.7	3	
469	Q9HPV1|Q9HPV1	1	958.5964	20.2	33	41	5	14.3	13	A	IAAFGLVRI	S	2.1	11.04	
508	Q9HRK2|Q9HRK2	1	1139.5975	-1.7	120	128	2	24.9	23	V	AFLYETQRL	-	-0.1	6.88	
548	Q9HQM2|Q9HQM2	1	1687.8054	-27.5	27	43	4	23.6	23	V	FVLTDDHTGAPSSTAVA	A	0.3	3.88	
553	Q9HP32|PYRG	1	940.4978	-14.5	535	543	3	23.5	23	V	LERADVAPA	G	0.0	4.08	
647	Q9HS38|Q9HS38	1	1717.7287	-7.9	135	150	4	20.7	18	L	DAASMRDFETGMAVSV	R	0.2	3.7	2 Oxidation (M)
661	Q9HHQ7|Q9HHQ7	1	731.4581	-6.0	125	130	3	24.0	20	I	LLNFIL	H	2.5	6.02	
670	Q9HQB1|Q9HQB1	1	958.6328	-17.7	70	77	4	19.6	13	V	KAVFRLLI	E	1.6	11.48	

END OF LIST VII

hit	**accession**	**z**	**mass**	**ppm**	**start**	**end**	**mc**	**score**	**id**	**-**	**sequence**	**+**	**gravy**	**pI**	**modification**
VIII. Purple membrane; trypsin digest; nLC-MALDI MS/MS; KR search specificity															
1	Q9HMW9|Q9HMW9	1	936.4851	7.2	613	620	0	57.7	13	K	AMAYVINR	E	0.6	9.84	
1	Q9HMW9|Q9HMW9	1	1097.5393	-4.6	621	629	0	51.2	13	R	EQFVSDVFK	G	-0.1	4.08	
1	Q9HMW9|Q9HMW9	1	1394.6678	3.3	431	443	0	53.1	13	R	ATGVEAVDDYTVR	L	-0.1	3.7	
1	Q9HMW9|Q9HMW9	1	1613.8009	3.1	238	252	0	39.6	13	R	LVSNPGQSEDAIQTR	K	-0.8	4.08	
1	Q9HMW9|Q9HMW9	1	1740.7777	20.9	337	351	0	29.6	13	K	VMDLFDAPTNYENGR	T	-0.8	3.7	
1	Q9HMW9|Q9HMW9	1	2016.0139	-2.7	613	629	1	100.8	15	K	AMAYVINREQFVSDVFK	G	0.2	6.94	
1	Q9HMW9|Q9HMW9	1	2211.0498	-1.4	173	191	0	26.7	13	K	QGEHEAFTLGWVADYPRPR	N	-1.0	5.34	Gln->pyro-Glu (N-term Q)
1	Q9HMW9|Q9HMW9	1	2466.1598	6.9	192	214	0	183.2	13	R	NFMQLVQPDNTIYGGETAANGAR	L	-0.5	4.08	
2	Q9HRQ9|Q9HRQ9	1	1835.9126	2.0	164	182	0	154.6	14	K	VIVNENGQAPSGGGGPVER	S	-0.5	4.26	
2	Q9HRQ9|Q9HRQ9	1	2021.029	-1.0	162	182	1	143.6	15	K	GKVIVNENGQAPSGGGGPVER	S	-0.6	7.1	
2	Q9HRQ9|Q9HRQ9	1	2445.1812	9.0	80	102	0	153.1	15	K	VGPNNQNVFDPAEVYVSPGDTVK	W	-0.5	3.7	
3	Q9HHP3|Q9HHP3	1	1761.905	-0.3	161	178	0	118.3	16	R	ANTGSPFLGNAPVFVSGK	I	0.2	10.1	
3	Q9HHP3|Q9HHP3	1	1811.8479	0.9	199	214	0	150.5	13	R	WTFSFEDTGPNSVGLR	D	-0.5	4.08	
3	Q9HHP3|Q9HHP3	1	2026.9848	3.4	179	197	0	127.8	14	K	ILSWDSSSVVAYDATTGQK	R	-0.1	3.88	
4	Q9HMW4|Q9HMW4	1	944.4828	7.5	363	370	0	66.0	15	R	ANGWTQLR	N	-1.0	11.04	
4	Q9HMW4|Q9HMW4	1	1345.6878	0.9	327	338	0	108.2	15	R	VSIPSTDVPEFR	D	-0.1	4.08	
4	Q9HMW4|Q9HMW4	1	1367.6292	-2.5	265	275	0	78.3	13	R	WSQQSVMAFER	A	-0.6	6.98	
4	Q9HMW4|Q9HMW4	1	1972.9854	-3.3	321	338	1	31.0	15	K	GGEIDRVSIPSTDVPEFR	D	-0.5	4.06	
4	Q9HMW4|Q9HMW4	1	2071.9673	-2.6	481	497	0	39.3	13	K	LNQETTSWPNLMSNYFK	T	-0.9	6.86	
4	Q9HMW4|Q9HMW4	1	3212.5163	-2.0	396	425	0	64.3	13	R	AGVQNTLHPTWGPYAPENPTTFSGSLDEAR	R	-0.8	4.42	
5	Q9HHN1|Q9HHN1	1	775.3864	24.6	2	7	0	36.4	15	M	VEFEPR	S	-1.0	4.26	
5	Q9HHN1|Q9HHN1	1	1128.4611	-2.3	8	16	0	54.4	13	R	SYEDFDPEK	R	-2.1	3.58	
5	Q9HHN1|Q9HHN1	1	1711.7537	1.6	397	411	0	132.0	13	R	DLNDEYDLDGTSLSR	T	-1.2	3.36	
5	Q9HHN1|Q9HHN1	1	1723.857	-2.8	293	308	0	65.9	14	R	GFAEAWQIIYSGTGPK	T	-0.1	6.86	
5	Q9HHN1|Q9HHN1	1	2593.2661	-8.3	178	201	0	69.4	13	K	QSPLSDTTLLASGVSDVDLWDHVR	G	-0.1	3.86	Gln->pyro-Glu (N-term Q)
6	Q9HSA8|Q9HSA8	1	932.4062	6.9	82	88	0	30.3	13	R	TYTFDMR	T	-0.9	6.7	
6	Q9HSA8|Q9HSA8	1	1165.5768	-0.3	56	65	0	45.2	13	K	QALTVFGEYR	G	-0.1	6.88	Gln->pyro-Glu (N-term Q)
6	Q9HSA8|Q9HSA8	1	1182.6033	-3.0	56	65	0	84.7	13	K	QALTVFGEYR	G	-0.1	6.88	
6	Q9HSA8|Q9HSA8	1	1518.7678	-5.7	103	116	0	94.5	14	R	DNSPVTADAVVYIR	V	0.1	3.88	
6	Q9HSA8|Q9HSA8	1	1706.9719	1.5	66	81	0	124.7	13	R	GLLEPGINVIPPFVSR	T	0.6	6.98	
7	Q9HMZ3|Q9HMZ3	1	727.3653	-0.4	14	19	0	18.8	13	R	FATYAR	G	0.0	9.84	
7	Q9HMZ3|Q9HMZ3	1	1081.4828	-0.1	552	560	0	59.6	13	R	YNGEFEAPR	E	-1.5	4.26	
7	Q9HMZ3|Q9HMZ3	1	1188.5809	1.6	565	575	0	35.8	15	R	ATGVTLDEMPR	N	-0.3	4.08	
7	Q9HMZ3|Q9HMZ3	1	1364.6394	-5.4	371	382	0	78.1	13	K	NVEDAVMNAFQK	G	-0.4	4.08	
7	Q9HMZ3|Q9HMZ3	1	2302.0641	13.5	245	265	0	112.7	15	R	VPADASPEEIGPSEIEDFSWK	Q	-0.7	3.44	
7	Q9HMZ3|Q9HMZ3	1	3103.4258	-8.0	434	461	0	28.1	13	R	SLATVFETAGVDYGILYEDEQNDGNDIR	R	-0.5	3.28	
8	Q9HN95|Q9HN95	1	739.4341	15.8	336	343	0	51.9	13	R	GGLAGLPR	R	0.3	11.04	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
8	Q9HN95|Q9HN95	1	917.4971	3.3	155	162	0	43.8	13	K	LFSDPLAR	V	0.2	6.78	
8	Q9HN95|Q9HN95	1	1064.5403	-0.4	224	233	0	75.2	13	R	GGSGYIGWLR	A	-0.1	9.84	
8	Q9HN95|Q9HN95	1	1331.6735	4.6	222	233	1	31.3	15	R	QRGGSGYIGWLR	A	-0.7	11.14	Gln->pyro-Glu (N-term Q)
8	Q9HN95|Q9HN95	1	1823.9377	2.1	403	421	0	119.3	13	R	LSVNGSIPSALSGPADSPR	I	-0.1	6.78	
9	Q9HMI3|Q9HMI3	1	1258.7397	-0.3	189	200	0	70.0	13	R	NLAIFAAAILSR	D	1.5	11.04	
9	Q9HMI3|Q9HMI3	1	1769.7421	-2.5	139	152	0	119.1	13	R	FIDDEYDYYLGSDR	S	-1.1	3.36	
9	Q9HMI3|Q9HMI3	1	1925.8432	5.6	138	152	1	34.1	13	R	RFIDDEYDYYLGSDR	S	-1.4	3.76	
9	Q9HMI3|Q9HMI3	1	2143.0626	3.8	238	257	0	80.6	16	R	LTAFDDYWGGAPSVSAVIFK	T	0.5	3.88	
10	Q9HP76|Q9HP76	1	968.5807	0.2	120	127	0	49.2	13	R	WSIPIVVR	F	1.2	11.04	
10	Q9HP76|Q9HP76	1	1104.7019	-9.3	342	351	0	26.9	13	R	LPPNLALVLR	V	1.0	11.04	
10	Q9HP76|Q9HP76	1	1966.9748	3.8	389	407	0	83.0	14	R	QFAAGTAEEFQAAATSVLR	V	0.2	4.26	
10	Q9HP76|Q9HP76	1	2048.9691	-3.3	60	77	0	63.6	15	R	VIEDELGPVDDVFDAFNR	E	-0.2	3.32	
10	Q9HP76|Q9HP76	1	2070.0058	-0.9	128	146	0	77.2	15	R	FVGQGQAFSLENLADEFAK	T	0.0	3.82	
11	Q9HMX1|Q9HMX1	1	934.4509	3.2	18	25	0	34.6	13	R	STDGLWTR	I	-1.0	6.78	
11	Q9HMX1|Q9HMX1	1	1250.6078	-2.8	408	418	0	13.8	13	K	SFGQQPTVTMR	K	-0.6	11.04	
11	Q9HMX1|Q9HMX1	1	1272.7038	-1.3	101	112	0	62.1	14	R	STAQSLPTLLSR	D	0.0	11.04	
11	Q9HMX1|Q9HMX1	1	1673.8009	-1.7	113	127	0	84.0	14	R	DVIPNQGYNDPSTVR	S	-1.0	3.88	
11	Q9HMX1|Q9HMX1	1	1711.8417	5.2	392	407	0	83.7	15	R	GPALQVAEEEWVDAAK	S	-0.3	3.68	
11	Q9HMX1|Q9HMX1	1	1744.9724	-3.0	85	100	0	13.4	13	R	VVDVQLALSTFIEGVR	S	1.0	4.08	
12	Q9HRR3|Q9HRR3	1	1119.5237	0.2	41	48	0	61.3	13	R	LTYEYFER	S	-1.0	4.26	
12	Q9HRR3|Q9HRR3	1	1287.5917	1.4	237	246	1	48.2	13	R	EGYMYDLNKR	Y	-1.6	6.88	
12	Q9HRR3|Q9HRR3	1	1522.8719	1.3	130	144	0	118.7	13	K	LSALNPELAILGGQK	L	0.4	6.94	
12	Q9HRR3|Q9HRR3	1	1845.8381	4.7	13	29	0	54.5	13	R	TDGTGIVSPDDETPTWR	E	-1.1	3.5	
13	Q9HN93|Q9HN93	1	1380.627	1.2	50	63	0	119.1	13	K	GGAVGNYDGTTVDR	T	-0.7	3.88	
13	Q9HN93|Q9HN93	1	2638.2511	13.4	64	90	0	152.5	13	R	TGTDEVTIDVGVDANGGTYGFGPAAVR	V	0.0	3.5	
14	Q9HNQ9|Q9HNQ9	1	1138.5043	-3.9	208	217	0	83.5	13	R	SGGFWESVDR	A	-0.8	4.08	
14	Q9HNQ9|Q9HNQ9	1	1210.5618	4.5	70	80	0	56.3	13	K	AAFDAEPTSFR	S	-0.3	4.08	
14	Q9HNQ9|Q9HNQ9	1	1957.888	0.7	2	17	0	131.4	13	M	SWFEVPDVDLSQYSMR	Q	-0.5	3.7	
14	Q9HNQ9|Q9HNQ9	1	1973.8829	0.5	2	17	0	31.0	13	M	SWFEVPDVDLSQYSMR	Q	-0.5	3.7	Oxidation (M)
15	Q9HPB1|SECY	1	813.4861	10.3	361	366	0	24.9	14	R	WQVLIR	I	0.6	11.04	
15	Q9HPB1|SECY	1	1457.7085	1.1	399	411	0	14.7	13	R	QIQNSGMQIPGFR	K	-0.6	11.04	Gln->pyro-Glu (N-term Q)
15	Q9HPB1|SECY	1	1474.7351	2.6	399	411	0	121.4	14	R	QIQNSGMQIPGFR	K	-0.6	11.04	
15	Q9HPB1|SECY	1	1486.8945	2.8	287	299	0	58.0	13	K	LIYASVLPMILVR	A	1.9	9.84	
15	Q9HPB1|SECY	1	1585.8035	0.7	399	412	1	54.9	14	R	QIQNSGMQIPGFRK	N	-0.9	11.48	Gln->pyro-Glu (N-term Q)
16	Q9HS26|Q9HS26	1	912.4453	1.9	427	433	0	28.5	13	R	FNINSYR	R	-0.9	9.84	
16	Q9HS26|Q9HS26	1	1017.5243	-3.9	309	317	0	56.8	16	R	ASDSLWIAR	E	0.2	6.78	
16	Q9HS26|Q9HS26	1	1661.8988	2.2	375	389	0	124.2	13	R	AIQDFLLESVATTVR	R	0.6	4.08	
17	Q9HRL4|Q9HRL4	1	1611.7199	-0.5	86	99	0	99.7	13	R	NFDDIDVTNATTMR	W	-0.6	3.6	
17	Q9HRL4|Q9HRL4	1	1797.7992	-0.1	86	100	1	116.9	13	R	NFDDIDVTNATTMRW	-	-0.7	3.6	
18	Q9HRF2|Q9HRF2	1	1164.5411	7.9	13	23	0	24.7	13	R	GPESFDLTSGR	I	-0.9	4.08	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
18	Q9HRF2|Q9HRF2	1	1169.6404	-2.6	267	278	0	59.8	13	R	IGLPASIEGTGR	A	0.2	6.98	
18	Q9HRF2|Q9HRF2	1	1875.94	1.4	246	262	0	131.8	14	R	GVEINAADMLPDLSYLR	R	0.2	3.7	
19	P33518|COX1	1	1506.7314	5.0	33	47	0	57.8	14	R	SYTPLSDVGGGLGER	T	-0.4	4.08	
19	P33518|COX1	1	2872.2253	6.8	535	557	0	153.7	13	R	VDSTDPWDLEETDQFTNDWAWFR	A	-1.2	3.22	
20	P02945|BACR	1	986.6277	28.3	230	238	0	72.2	13	K	VGFGLILLR	S	2.0	11.04	
20	P02945|BACR	1	1451.7078	4.0	173	185	0	80.3	14	K	AESMRPEVASTFK	V	-0.5	7.1	
20	P02945|BACR	1	1467.7028	-0.9	173	185	0	31.3	13	K	AESMRPEVASTFK	V	-0.5	7.1	Oxidation (M)
20	P02945|BACR	1	2276.0193	3.3	239	262	1	57.5	13	R	SRAIFGEAEAPEPSAGDGAAATSD	-	-0.4	3.5	
21	Q9HS72|SECE	1	1393.6911	-2.2	1	12	0	106.8	13	-	MDVPLELSAYTR	V	0.0	4.08	
21	Q9HS72|SECE	1	1409.6861	-3.6	1	12	0	75.9	13	-	MDVPLELSAYTR	V	0.0	4.08	Oxidation (M)
21	Q9HS72|SECE	1	1692.8359	0.9	16	30	0	101.4	15	R	LASTPSWEEFSQIAK	I	-0.4	4.26	
22	Q9HN94|Q9HN94	1	1435.7096	-2.0	41	53	0	38.1	14	R	QFAFSPGTSEPIR	V	-0.4	6.98	
22	Q9HN94|Q9HN94	1	2175.9233	5.0	22	40	0	159.3	13	R	DPGVYQADDDSYDVYVEAR	Q	-1.0	3.26	
23	Q9HSQ7|Q9HSQ7	1	1085.5216	-2.6	139	147	0	36.7	13	R	LNMDFFATK	Q	0.2	6.76	
23	Q9HSQ7|Q9HSQ7	1	2074.9776	3.1	148	165	1	28.7	13	K	QTGEMMSILSNDVNRLER	F	-0.7	4.44	Gln->pyro-Glu (N-term Q)
23	Q9HSQ7|Q9HSQ7	1	2244.3093	3.7	52	73	0	113.7	13	R	VLDLAPPVLLGLAIDSVIQGNK	A	1.0	3.88	
24	Q9HND9|Q9HND9	1	1728.9522	2.7	8	26	0	175.6	13	K	AAAALAVGLAALAAGYAER	G	1.2	6.88	
25	Q9HRJ0|Q9HRJ0	1	1391.6681	1.3	26	38	0	45.0	13	R	ADEQPPDPLPGTR	T	-1.6	3.7	
25	Q9HRJ0|Q9HRJ0	1	1529.8566	-1.4	173	187	0	127.8	13	R	TPVVGTAVFNALVSR	R	1.0	11.04	
26	Q9HSQ2|HTPX	1	1401.7187	-0.1	89	102	0	72.6	14	K	VANMGVPNAFAVGR	K	0.6	11.04	
26	Q9HSQ2|HTPX	1	1608.6726	-5.7	55	68	0	100.0	13	R	SVGAEDMDEQEFPR	I	-1.3	3.5	
27	Q9HRS0|Q9HRS0	1	773.4395	-18.0	21	28	0	19.2	16	R	ALSVAASR	G	0.9	11.04	
27	Q9HRS0|Q9HRS0	1	1177.5979	-6.5	191	201	0	32.6	14	K	GYQTIVPDSAK	T	-0.5	6.68	
27	Q9HRS0|Q9HRS0	1	2529.2962	3.1	178	201	1	117.6	15	K	GTIIVTDSPPENKGYQTIVPDSAK	T	-0.5	4.3	
28	Q9HRL3|Q9HRL3	1	825.5072	9.3	624	631	0	35.1	13	K	GVTLPLAR	G	0.8	11.04	
28	Q9HRL3|Q9HRL3	1	2323.1161	5.7	606	623	0	131.9	13	R	TLLYNNYYQDEYQVWLAK	G	-0.8	4.08	
29	Q9HRR1|Q9HRR1	1	1136.5614	-6.2	267	276	0	43.1	13	K	SFVAFARPEN	-	0.0	6.98	
29	Q9HRR1|Q9HRR1	1	1596.8835	1.9	180	193	0	105.2	13	R	SQNTDNTIPILIIR	S	0.0	6.78	
30	Q9HHR4|Q9HHR4	1	1001.5142	4.5	331	339	0	36.8	16	K	SETATQIPR	T	-1.0	6.98	
30	Q9HHR4|Q9HHR4	1	1047.5713	2.6	450	459	0	68.1	13	K	TGYLLGATPR	K	0.0	9.84	
30	Q9HHR4|Q9HHR4	1	1381.6838	3.9	211	223	0	40.9	13	K	TTLETAFSAGQTR	G	-0.4	6.98	
31	Q9HR99|Q9HR99	1	1494.7025	-0.7	99	113	0	145.5	13	K	ISIPDGASGFGTMDK	D	0.0	3.88	
31	Q9HR99|Q9HR99	1	1510.6974	-5.7	99	113	0	34.1	13	K	ISIPDGASGFGTMDK	D	0.0	3.88	Oxidation (M)
32	Q9HQP2|Q9HQP2	1	888.4454	3.3	213	220	0	19.1	15	R	AWDATGLR	D	-0.3	6.78	
32	Q9HQP2|Q9HQP2	1	1277.6768	1.4	379	389	0	60.0	13	R	TIGEAQPFLFR	T	0.1	6.98	
32	Q9HQP2|Q9HQP2	1	1353.6718	0.8	741	752	0	65.3	13	K	FSAPVVFYDGPR	D	0.2	6.7	
33	Q9HP89|Q9HP89	1	1329.7405	-3.2	225	237	0	71.3	13	R	LSPYLAAGNIGVR	E	0.6	9.84	
33	Q9HP89|Q9HP89	1	1364.6394	-15.5	308	320	0	34.9	13	R	GETGYPLVDAGMR	Q	-0.4	4.08	
33	Q9HP89|Q9HP89	1	1964.8864	-4.0	238	256	0	36.0	13	R	EVWAAVADAYDDATGNAAR	N	-0.2	3.5	
34	Q9HNE6|Q9HNE6	1	981.5607	0.8	213	222	0	62.2	13	R	AGDILGPLAR	F	0.5	6.78	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
34	Q9HNE6|Q9HNE6	1	1594.8905	4.8	92	106	0	79.4	13	R	GGLPMLVPLLGFPER	Y	0.7	6.98	
35	Q9HQ04|Q9HQ04	1	1459.7419	-2.8	207	220	0	84.0	16	R	QPYGIGDQVAIGSR	E	-0.4	6.7	
35	Q9HQ04|Q9HQ04	1	1475.762	1.2	221	233	0	55.3	14	R	EGVVQEVDVFVTR	I	0.3	3.82	
36	Q9HRM1|Q9HRM1	1	874.4483	9.9	119	125	0	33.2	15	K	GVVQWMR	T	0.1	11.04	
36	Q9HRM1|Q9HRM1	1	1464.6845	0.6	39	52	0	98.9	13	R	ATYESAEVPTGNAR	L	-0.8	4.26	
37	Q9HSC3|LONH	1	728.4181	11.5	430	436	0	39.6	15	R	DLGGLVR	V	0.4	6.78	
37	Q9HSC3|LONH	1	1638.8002	2.1	464	476	0	71.9	13	R	SIEQQFVDNYIQR	R	-0.9	4.08	
38	Q9HRT0|Q9HRT0	1	1146.5669	1.8	505	514	0	44.7	14	R	VPDVDAVYNR	V	-0.4	3.88	
38	Q9HRT0|Q9HRT0	1	1271.6721	-5.0	559	570	0	76.5	15	R	LLGDTDSPVSLR	A	0.0	3.88	
39	Q9HSC9|Q9HSC9	1	1300.6201	-1.6	80	89	0	47.1	13	K	QQVFFDTFNR	F	-0.7	6.78	
39	Q9HSC9|Q9HSC9	1	1435.7282	1.3	94	105	0	68.5	15	R	SLYNWLLPMGSR	L	0.0	9.84	
40	Q9HS12|Q9HS12	1	1504.8613	4.2	471	485	0	28.0	13	R	SFSGILTGTILALGR	A	1.1	11.04	
40	Q9HS12|Q9HS12	1	1694.9641	-5.5	486	502	0	76.0	13	R	AIGETAPLIMIGAPTIK	F	1.0	6.94	
41	Q9HRL8|Q9HRL8	1	877.5021	7.5	118	125	0	32.8	13	K	YSLLGGLR	A	0.5	9.84	
41	Q9HRL8|Q9HRL8	1	1553.8566	-2.5	29	43	0	81.1	13	R	VGPWGLGTIVVDSVR	L	0.8	6.78	
42	Q9HMG3|Q9HMG3	1	1721.7897	-0.6	43	57	0	111.8	13	R	ASTVPETDFPEPYNR	S	-1.2	3.82	
43	Q9HR22|Q9HR22	1	1270.6823	2.3	234	244	0	108.6	15	R	IPNVPFGFQPR	D	-0.2	11.04	
44	Q9HPD4|RL3	1	1209.6254	-1.2	234	244	0	104.0	13	R	IGNLGPWNPSR	V	-0.8	11.04	
45	Q9HMU9|Q9HMU9	1	764.3817	-3.5	260	265	1	22.5	15	R	FNTRDL	-	-0.9	6.78	
45	Q9HMU9|Q9HMU9	1	773.4184	13.6	2	8	0	57.1	15	M	SWAAIAR	K	0.5	11.04	
45	Q9HMU9|Q9HMU9	1	1784.9421	-1.3	206	221	0	23.9	15	R	QFLNQIPPTDAITTAR	A	-0.3	6.78	
46	P25964|BACS1	1	1323.6652	-0.1	206	215	0	53.4	13	K	VPYVYFFYAR	R	0.6	9.44	
46	P25964|BACS1	1	1780.0135	-6.3	149	164	0	48.3	13	R	VVPDVPEQIGLFNLLK	N	0.6	4.08	
47	Q9HMX0|Q9HMX0	1	1013.5869	4.0	52	60	0	37.8	14	R	NLEISLGIR	Y	0.4	6.98	
47	Q9HMX0|Q9HMX0	1	1448.814	0.7	305	317	0	58.6	13	K	VFSINGIGNLFIR	A	1.1	11.04	
48	Q9HRN3|Q9HRN3	1	1578.7638	2.4	83	98	0	90.9	13	R	VSSPGGAVSGSEVQYR	A	-0.3	6.88	
49	Q9HRR2|Q9HRR2	1	1801.9502	0.7	40	53	0	90.6	13	R	IVDYLELLETLYYR	V	0.3	3.82	
50	Q9HN07|Q9HN07	1	1281.6353	4.1	599	609	0	90.4	13	R	TPANTAELFYR	L	-0.5	6.88	
51	Q9HN25|Q9HN25	1	1841.9312	7.6	129	144	0	89.8	15	K	LNANFIEPGSLSYVYR	N	0.0	6.82	
52	Q9HHS5|Q9HHS5	1	1571.674	1.1	75	88	0	89.3	13	R	YAAGDIDDEEFTAR	R	-0.8	3.42	
53	Q9HQU7|Q9HQU7	1	1514.7518	0.1	184	196	0	88.3	15	R	AEGWEPFSVLQPR	Y	-0.6	4.26	
54	Q9HRL1|Q9HRL1	1	950.5338	-0.8	159	167	0	69.5	13	K	AAGFAVLFR	V	1.6	11.04	
54	Q9HRL1|Q9HRL1	1	998.5185	8.9	349	356	0	13.4	13	K	ALWIEDPR	D	-0.5	4.08	
55	Q9HMK7|Q9HMK7	1	1190.6196	0.6	197	208	0	59.3	15	R	YGIAWGAVGAAR	N	0.7	9.84	
55	Q9HMK7|Q9HMK7	1	1898.005	3.5	110	126	0	23.6	14	K	TWITNSPIADVAVVWAR	D	0.6	6.78	
56	Q9HR16|Q9HR16	1	1222.671	-5.2	78	88	0	56.9	13	R	AVTLPTFFATR	L	0.8	11.04	
56	Q9HR16|Q9HR16	1	1261.6303	1.6	13	24	0	22.8	15	R	DVGPVVTGFSER	A	0.0	4.08	
57	Q9HSF7|TF2B7	1	1304.6724	0.6	136	146	0	78.7	15	R	NLQFALSEIDR	M	-0.2	4.08	
58	Q9HMD1|SECG	1	1768.7904	1.7	19	33	0	74.4	13	R	YFDSEDSNALQIDPR	S	-1.1	3.5	
59	Q9HRZ2|Q9HRZ2	1	1436.7663	2.9	184	195	0	62.2	13	K	LANLLFAYELDR	R	0.4	4.08	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
60	Q9HQ64|Q9HQ64	1	1147.5986	1.2	10	19	0	69.0	14	R	SGSTTWLLQR	L	-0.5	11.04	
61	Q9HPU7|Q9HPU7	1	813.4861	2.1	153	159	0	31.4	13	R	WLAAVVR	G	1.5	11.04	
61	Q9HPU7|Q9HPU7	1	2368.2427	-3.8	14	35	0	34.7	13	R	SQFVPSWLVPEAAGDLPLTVSR	L	0.3	4.08	
62	Q9HR80|Q9HR80	1	1071.5746	3.1	14	23	0	28.7	14	R	SGMPLAEVLR	I	0.5	6.98	
62	Q9HR80|Q9HR80	1	1157.5903	1.6	4	13	0	34.9	15	R	TVAFMYALSR	S	0.9	9.84	
63	Q9HNN6|Q9HNN6	1	1107.5423	-6.8	48	56	0	47.7	13	R	FLDWMATPK	R	0.0	6.76	
63	Q9HNN6|Q9HNN6	1	1315.6884	0.9	565	575	0	15.5	14	R	LPFERPETATR	A	-1.1	7.12	
64	P33741|HTR1	1	716.3969	8.4	2	7	0	29.5	17	M	TIAWAR	R	0.3	11.04	
64	P33741|HTR1	1	1697.7567	0.6	85	99	0	32.4	13	R	TDEFGSLADSIEQMR	Q	-0.7	3.58	
65	Q9HPA6|Q9HPA6	1	1378.6364	-0.2	165	175	0	61.1	13	K	YQEQAQELQDK	M	-2.2	3.82	
66	Q9HRR0|Q9HRR0	1	1189.6417	-3.9	80	89	0	54.1	13	K	EFLPDVMIVK	K	0.9	4.08	
67	O51960|O51960	1	1084.5513	1.7	2	10	0	52.8	13	M	SELPENIQR	Q	-1.4	4.26	
68	Q9HND8|VATI	1	1016.4716	-2.5	709	716	0	51.8	13	K	YNPFGYTR	N	-1.3	9.58	
69	Q9HQ63|DHSD	1	833.4396	8.5	8	15	0	50.4	14	R	GLVADFGR	W	0.5	6.78	
70	Q9HRC9|Q9HRC9	1	1080.4699	0.7	104	111	0	48.9	13	R	FDPEWMTR	T	-1.3	4.08	
71	Q9HT02|Q9HT02	1	965.4389	9.9	230	237	0	48.0	13	R	EGVNNFMR	T	-0.8	6.98	
72	Q9HQ52|THYX	1	2101.999	1.9	158	176	0	47.5	15	R	AVEDYQELLGLGMPPEDAR	F	-0.5	3.5	
73	Q9HT01|Q9HT01	1	1299.5996	0.4	612	622	0	45.6	13	R	LYNWFGSGNSR	S	-0.9	9.84	
74	Q9HR62|Q9HR62	1	1118.6448	1.3	305	315	0	43.4	13	R	APSVPVPSLPR	S	0.1	11.04	
75	Q9HRL2|Q9HRL2	1	923.4899	5.5	267	274	0	43.3	13	K	MGTYALLR	F	0.6	9.84	
76	Q9HRC5|Q9HRC5	1	915.445	7.6	192	198	0	17.4	14	R	ISYYSQR	N	-1.1	9.58	
76	Q9HRC5|Q9HRC5	1	1128.5564	3.3	180	189	0	25.8	13	R	LAWDSVPADR	I	-0.3	3.88	
77	Q9HPQ5|Q9HPQ5	1	2024.9843	4.7	23	40	0	42.3	15	K	TYLEYTPTGESIPAAAWR	R	-0.4	4.26	
78	Q9HRL9|Q9HRL9	1	1336.7139	14.1	344	355	0	41.9	13	R	LGGVVWDIPEPR	A	0.0	4.08	
79	Q9HSL5|Q9HSL5	1	1148.5251	5.1	49	58	0	41.7	13	K	AGGSYYYVNR	A	-0.8	9.44	
80	Q9HQU6|Q9HQU6	1	871.4916	4.6	16	22	0	39.5	16	K	LVEWIGR	V	0.5	6.98	
81	Q9HN76|Q9HN76	1	975.5576	4.4	83	90	0	38.6	13	R	FTLPMVLR	A	1.2	11.04	
82	P16102|BACH	1	887.4249	4.4	252	258	0	23.2	13	R	WVANNER	T	-1.4	6.98	
82	P16102|BACH	1	1140.6695	15.2	243	251	0	14.6	13	K	YVFAFILLR	W	2.0	9.84	
83	Q48290|FTSZ	1	1550.8014	-3.3	181	194	0	37.0	13	K	AFSVMDQIIAETVK	G	0.7	4.08	
84	P57699|ATKB	1	934.472	-19.4	320	328	0	23.2	13	K	TGTITTGER	V	-0.8	6.98	
85	Q9HN02|Q9HN02	1	948.4777	8.2	170	178	0	35.9	14	R	AVNQFTGGR	A	-0.5	11.04	
86	Q9HR92|HTR6	1	758.4439	3.7	14	20	0	35.6	15	R	ALPGFVR	R	0.9	11.04	
87	Q9HRM0|Q9HRM0	1	1309.6918	-6.3	39	50	0	35.2	13	R	EAFGSTPFILTK	F	0.3	6.94	
88	Q9HNK1|Q9HNK1	1	962.5008	1.7	352	360	0	34.1	14	R	VFMSAVGPR	G	0.8	11.04	
89	Q9HRQ7|Q9HRQ7	1	1329.6758	-5.4	153	162	1	33.7	14	R	YVIRYPEFPF	-	0.1	6.82	
90	Q9HQ81|Q9HQ81	1	1109.5506	1.6	414	423	0	33.0	13	R	GVFYPSDAVR	T	0.1	6.7	
91	Q9HN58|Q9HN58	1	1186.5328	4.4	1	9	0	32.7	13	-	MELAEYFER	A	-0.7	3.96	
92	Q9HQQ6|Q9HQQ6	1	1133.706	-7.9	216	225	0	31.5	13	R	IILTLYSLAK	T	1.6	9.72	
93	Q9HS60|Q9HS60	1	773.4296	-1.0	170	175	1	30.6	15	K	SWLGRR	L	-1.2	12.4	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
94	Q9HQP7|Q9HQP7	1	1949.0945	-2.5	38	56	0	30.5	13	R	LGIATAALPNQADLLAELR	R	0.6	4.08	
95	Q9HSE0|Q9HSE0	1	773.4144	6.1	116	122	1	19.6	16	R	SPATRSR	T	-1.6	12.4	
96	Q9HSA3|MFNA	1	1386.7078	29.6	211	224	0	29.1	15	K	MGQAPVPAGGFLAR	D	0.4	11.04	Oxidation (M)
97	Q9HPJ9|GCSPA	1	773.4031	20.7	48	54	0	28.5	16	K	SEQAALR	G	-0.7	6.98	
98	Q9HNI9|Q9HNI9	1	1349.7496	3.6	143	153	0	28.2	13	R	VTPFPLNFLFR	G	0.8	11.04	
99	Q9HRC1|Q9HRC1	1	1728.9128	23.8	1	17	1	15.9	13	-	MRTVGVVVNPIAGMGGR	V	0.6	12.4	Oxidation (M)
100	Q9HSE1|Q9HSE1	1	1835.953	-18.7	117	133	0	28.0	14	R	EWVSAIQPQIAGGEVPR	R	-0.2	4.26	
101	O52005|O52005	1	772.4265	13.6	254	260	0	28.0	15	K	IGPVTMR	M	0.5	11.04	
102	Q9HNG0|Q9HNG0	1	960.5392	4.5	267	274	0	27.9	13	K	ENLVFALR	A	0.6	6.98	
103	Q9HPX5|Q9HPX5	1	1593.8475	-3.5	116	130	0	27.5	13	R	AVQDPQSLLGQPSVR	A	-0.4	6.78	
104	Q9HR54|Q9HR54	1	992.508	2.8	246	253	0	27.0	14	R	DAISVFWR	T	0.5	6.78	
105	Q9HMH6|Q9HMH6	1	1437.7616	-6.0	100	112	0	26.7	14	R	VIVFKPGDFSSSR	A	0.2	10.08	
106	Q9HPT0|Q9HPT0	1	852.4494	2.8	414	420	0	26.4	13	R	LFAFAER	H	0.7	6.98	
107	Q9HHH4|Q9HHH4	1	1673.8009	-0.7	142	154	1	14.9	14	R	DVITRWEENLEDR	R	-1.5	3.92	
108	Q9HRS2|Q9HRS2	1	787.4017	6.9	318	323	0	24.9	17	R	FVFYGR	A	0.6	9.84	
109	Q9HR04|Q9HR04	1	2764.3344	3.0	86	108	0	24.2	14	R	YVALIDLINQYYDDFSATQQTQR	S	-0.5	3.6	
110	Q9HNM8|Q9HNM8	1	773.4031	20.7	2	9	0	23.9	16	M	ALDASAAR	E	0.3	6.78	
111	Q9HQV1|Q9HQV1	1	846.4422	7.3	1	6	0	23.8	14	-	MLEWLR	E	0.1	6.98	
112	Q9HNS2|Q9HNS2	1	1231.6131	2.4	160	171	0	23.6	15	R	LANAAMNFGPAR	W	0.2	11.04	
113	Q9HP84|HTR4	1	865.5749	7.9	26	33	0	22.7	13	K	AIALLPLR	S	1.7	11.04	
114	Q9HMW2|Q9HMW2	1	741.3598	1.6	91	95	0	22.3	13	R	AFYWR	R	-0.4	9.84	
115	Q9HPR5|Q9HPR5	1	968.5767	9.8	344	353	0	22.2	13	R	NLGGIGAVLR	Y	0.9	11.04	
116	Q9HRK2|Q9HRK2	1	1265.5888	-2.0	13	23	0	22.1	13	R	TEPGLSDQYTR	A	-1.5	4.08	
117	Q9HRY6|Q9HRY6	1	1409.7011	-12.8	16	27	1	21.8	13	R	TVERDDAAHLQR	S	-1.3	5.28	
118	Q9HNB2|Q9HNB2	1	927.5753	-28.4	581	588	0	21.1	16	R	IIATLELR	E	1.2	6.98	
119	Q9HHI4|Q9HHI4	1	927.5389	-0.8	516	523	0	20.9	16	R	VLEALDIR	V	0.8	4.08	
120	Q9HSJ6|Q9HSJ6	1	1547.7831	-8.3	212	225	0	20.8	15	R	IEAGIEEFVASVER	L	0.3	3.8	
121	Q9HHS8|GVPO2	1	927.5389	10.9	63	70	0	20.5	16	R	ILAEVVER	S	0.9	4.26	
123	Q9HMY6|Q9HMY6	1	1047.5536	19.6	154	163	0	20.2	13	R	GVVVMPSGFR	E	1.0	11.04	
124	Q9HP19|Q9HP19	1	1194.5373	28.5	1	11	0	19.8	13	-	MDGMSGELTVR	Q	-0.2	4.08	
125	Q9HNT0|Q9HNT0	1	1673.7645	21.1	11	24	1	19.6	14	R	GDVTEWPTDDDRLR	Y	-1.6	3.76	
126	Q9HQS2|Q9HQS2	1	897.5072	0.3	13	19	0	19.5	13	R	LLDPWVR	A	0.2	6.78	
127	Q9HQS6|Q9HQS6	1	1141.6608	-5.8	74	84	0	18.8	14	R	VVAFANAVVPR	V	1.4	11.04	
128	Q9HQ42|Q9HQ42	1	728.4293	-4.0	274	279	1	18.2	15	R	VRDLAR	R	-0.5	10.88	
129	Q9HHW0|Q9HHW0	1	1017.4736	1.0	2	9	0	18.0	13	M	ELCTMLHR	E	0.0	7.16	Oxidation (M)
130	Q9HQS5|Q9HQS5	1	773.4085	22.1	121	125	1	17.4	16	R	WWRAR	Y	-1.8	12.4	
131	Q9HQZ6|Q9HQZ6	1	813.4708	16.3	326	333	0	17.4	13	R	ADLAIVGR	E	1.0	6.78	
132	Q9HRH2|Q9HRH2	1	846.4195	28.2	292	299	0	17.3	14	K	SQASDALR	E	-0.7	6.78	
133	Q9HRF4|Q9HRF4	1	728.4181	11.5	207	212	0	17.2	15	R	LDLNVR	V	0.1	6.78	
134	Q9HN17|Q9HN17	1	716.3817	29.6	203	209	0	17.2	17	R	VGESAVR	F	0.1	6.98	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
135	Q9HQ56|Q9HQ56	1	1105.555	16.7	395	405	0	17.1	13	R	AIVASNMASAR	G	0.7	11.04	Oxidation (M)
136	O51999|O51999	1	813.4708	20.8	924	931	0	17.0	13	K	LDVGALAR	G	0.9	6.78	
137	Q9HN83|SYW1	1	773.433	-18.9	67	73	1	16.8	16	R	RVAAAMR	N	0.4	12.4	
138	Q9HQM4|Q9HQM4	1	2143.0393	-14.7	302	320	1	16.8	14	K	EQIEDIIGAVADDRTDDIR	E	-0.6	3.58	
139	Q9HMS7|Q9HMS7	1	1500.8816	-3.8	7	20	0	16.7	13	R	AQALLALFPAFLAR	L	1.4	11.04	
140	Q9HQB1|Q9HQB1	1	927.5389	-0.8	16	23	0	16.7	16	R	EIVDLIAR	R	0.9	4.08	
141	Q9HRS1|Q9HRS1	1	773.4283	0.8	153	159	1	16.2	15	R	IEEGKAK	L	-1.3	7.06	
142	Q9HPN3|Q9HPN3	1	1889.0119	-25.4	22	38	2	16.2	15	K	RTLEAADVVYSPGRLSR	T	-0.4	9.84	
143	Q9HM88|Q9HM88	1	1346.7307	-6.9	157	169	0	16.2	13	R	GVLNGTANFVLSR	M	0.5	11.04	
144	Q9HR33|Q9HR33	1	773.4144	14.5	224	230	1	16.0	16	R	LTGDGRR	F	-1.5	10.88	
145	Q9HSS1|Q9HSS1	1	1409.684	-0.6	134	146	0	16.0	13	R	GGWAWNDAPAPLR	L	-0.6	6.78	
146	Q9HSS0|Q9HSS0	1	1017.5356	-26.9	18	26	1	15.9	15	R	RDVFAPSAR	H	-0.5	10.88	
147	Q9HS67|Q9HS67	1	1272.741	-29.6	1	11	1	15.9	14	-	MRPMGLLSKLK	S	0.0	11.64	
148	Q9HRH6|Q9HRH6	1	1336.7602	-20.5	19	31	0	15.8	13	R	VAPLSLPEIVDGK	A	0.5	4.08	
149	Q9HI31|Q9HI31	1	1027.6138	-29.5	53	60	1	15.7	15	K	QTRELIIR	N	-0.5	10.88	
150	Q9HRA1|Q9HRA1	1	887.548	8.7	100	107	0	15.6	13	R	AAPYILLK	D	1.1	9.72	
151	Q9HQ54|Q9HQ54	1	1158.6357	17.1	505	515	0	15.5	14	R	LTGNTIAVNTR	S	0.0	11.04	
152	Q9HP79|Q9HP79	1	813.4821	7.0	225	231	1	15.3	13	R	ELRAAVR	A	-0.1	10.88	
153	Q9HSL0|Q9HSL0	1	1119.556	-19.1	44	52	0	15.1	13	R	LTPQEVDYR	L	-1.2	4.08	
155	Q9HQD7|HUTG	1	1629.8071	-25.6	197	212	1	14.9	13	R	DQGGRIVTSDAVAADR	D	-0.4	4.18	
160	Q9HNA3|Q9HNA3	1	1140.6727	-9.5	62	73	1	14.4	13	R	VGVALAAAARSR	G	0.9	12.4	
161	Q9HS87|Q9HS87	1	842.4974	11.9	161	168	0	14.3	13	R	GIIQGSLR	E	0.4	11.04	
163	Q9HPK0|GCSPB	1	1552.7158	-27.8	303	316	0	14.2	13	R	QSAGGDYELYTPPR	S	-1.3	4.08	
167	Q9HRU7|Q9HRU7	1	1829.0638	-7.9	759	775	0	13.9	13	K	AIVPFAFVVTPGVMLLR	R	1.8	11.04	
168	Q9HN78|LIPA	1	1024.589	-6.6	172	179	2	15.6	13	R	RQVPVRDR	R	-1.7	12.1	
176	Q9HRT5|Q9HRT5	1	739.4453	-10.8	421	427	1	14.8	13	R	RVAAPAR	R	-0.1	12.4	
178	Q9HMG7|Q9HMG7	1	1598.7551	-15.3	40	52	0	13.1	13	R	YGGYQMPLETVWR	A	-0.6	6.82	

END OF LIST VIII

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
IX. Purple membrane; trypsin digest; nLC-MALDI MS/MS; no search specificity															
1	P02945|BACR	1	799.3348	29.8	249	257	0	38.9	32	A	PEPSAGDGA	A	-0.9	3	
1	P02945|BACR	1	830.5378	0.4	232	238	0	27.5	22	G	FGLILLR	S	2.0	11.04	
1	P02945|BACR	1	870.3719	2.3	249	258	0	88.0	30	A	PEPSAGDGAA	A	-0.6	3	
1	P02945|BACR	1	887.5593	-4.1	231	238	0	44.5	25	V	GFGLILLR	S	1.7	11.04	
1	P02945|BACR	1	903.3934	0.7	251	261	0	107.0	33	E	PSAGDGAAATS	D	-0.1	3.1	
1	P02945|BACR	1	986.6277	28.3	230	238	0	72.2	14	K	VGFGLILLR	S	2.0	11.04	
1	P02945|BACR	1	988.4648	6.1	173	181	0	53.3	35	K	AESMRPEVA	S	-0.5	4.26	
1	P02945|BACR	1	1069.508	-0.7	48	56	0	55.4	33	V	SDPDAKKFY	A	-1.5	6.8	
1	P02945|BACR	1	1129.4887	5.5	249	261	0	121.7	32	A	PEPSAGDGAAATS	D	-0.5	3	
1	P02945|BACR	1	1175.5723	1.3	87	95	0	57.4	35	G	EQNPIYWAR	Y	-1.4	6.88	
1	P02945|BACR	1	1200.5258	2.1	248	261	0	138.7	32	E	APEPSAGDGAAATS	D	-0.3	3	
1	P02945|BACR	1	1216.5612	-9.3	241	252	0	106.0	33	R	AIFGEAEAPEPS	A	-0.2	3.02	
1	P02945|BACR	1	1227.64	-0.6	18	27	0	34.6	34	I	TGRPEWIWLA	L	-0.2	6.98	
1	P02945|BACR	1	1232.5938	-1.3	86	95	0	64.9	35	G	GEQNPIYWAR	Y	-1.3	6.88	
1	P02945|BACR	1	1240.689	-8.9	33	43	0	60.5	33	L	MGLGTLYFLVK	G	1.2	9.72	
1	P02945|BACR	1	1242.5822	-4.3	92	100	0	36.6	33	I	YWARYADWL	F	-0.6	6.64	
1	P02945|BACR	1	1287.5983	-7.6	241	253	0	99.9	34	R	AIFGEAEAPEPSA	G	0.0	3.02	
1	P02945|BACR	1	1289.6153	-1.9	85	95	0	78.3	35	F	GGEQNPIYWAR	Y	-1.2	6.88	
1	P02945|BACR	1	1323.6129	0.8	173	184	0	44.3	34	K	AESMRPEVASTF	K	-0.2	4.26	
1	P02945|BACR	1	1380.6707	3.6	174	185	0	52.5	35	A	ESMRPEVASTFK	V	-0.7	7.1	
1	P02945|BACR	1	1381.703	0.6	95	105	0	63.3	34	A	RYADWLFTTPL	L	-0.1	6.7	
1	P02945|BACR	1	1451.7078	4.0	173	185	0	80.3	35	K	AESMRPEVASTFK	V	-0.5	7.1	
1	P02945|BACR	1	1459.6943	2.9	239	252	0	113.3	35	R	SRAIFGEAEAPEPS	A	-0.5	3.96	
1	P02945|BACR	1	1530.7314	-0.6	239	253	0	98.6	35	R	SRAIFGEAEAPEPSA	G	-0.4	3.96	
1	P02945|BACR	1	1533.7365	3.7	83	95	0	46.3	35	V	PFGGEQNPIYWAR	Y	-0.9	6.88	
1	P02945|BACR	1	1587.7053	-1.2	241	257	0	139.4	33	R	AIFGEAEAPEPSAGDGA	A	-0.2	2.88	
1	P02945|BACR	1	1587.7529	-2.3	239	254	0	76.2	35	R	SRAIFGEAEAPEPSAG	D	-0.4	3.96	
1	P02945|BACR	1	1658.7424	-3.7	241	258	0	131.6	33	R	AIFGEAEAPEPSAGDGAA	A	-0.1	2.88	
1	P02945|BACR	1	1702.7798	-0.5	239	255	0	36.8	34	R	SRAIFGEAEAPEPSAGD	G	-0.6	3.68	
1	P02945|BACR	1	1759.8013	0.4	239	256	0	109.7	34	R	SRAIFGEAEAPEPSAGDG	A	-0.6	3.68	
1	P02945|BACR	1	1763.8454	1.9	81	95	0	92.1	35	T	MVPFGGEQNPIYWAR	Y	-0.4	6.88	
1	P02945|BACR	1	1801.8828	2.9	92	105	0	74.3	36	I	YWARYADWLFTTPL	L	-0.1	6.64	
1	P02945|BACR	1	1830.8384	2.1	239	257	0	122.9	34	R	SRAIFGEAEAPEPSAGDGA	A	-0.4	3.68	
1	P02945|BACR	1	1901.8755	-2.6	239	258	0	172.1	34	R	SRAIFGEAEAPEPSAGDGAA	A	-0.3	3.68	
1	P02945|BACR	1	1917.8592	3.5	241	261	0	180.4	34	R	AIFGEAEAPEPSAGDGAAATS	D	0.0	2.88	
1	P02945|BACR	1	1972.9126	5.8	239	259	0	67.9	35	R	SRAIFGEAEAPEPSAGDGAAA	T	-0.2	3.68	
1	P02945|BACR	1	2073.9603	-3.5	239	260	0	94.0	35	R	SRAIFGEAEAPEPSAGDGAAAT	S	-0.2	3.68	

hit	**accession**	**z**	**mass**	**ppm**	**start**	**end**	**mc**	**score**	**id**	**-**	**sequence**	**+**	**gravy**	**pI**	**modification**
1	P02945|BACR	1	2160.9923	0.6	239	261	0	194.1	35	R	SRAIFGEAEAPEPSAGDGAAATS	D	-0.3	3.68	
1	P02945|BACR	1	2276.0193	3.3	239	262	0	57.5	34	R	SRAIFGEAEAPEPSAGDGAAATSD	-	-0.4	3.5	
2	Q9HMW9|Q9HMW9	1	936.4851	7.2	613	620	0	57.7	32	K	AMAYVINR	E	0.6	9.84	
2	Q9HMW9|Q9HMW9	1	958.4582	5.1	598	605	0	51.9	35	Y	YVGFNMTK	V	-0.1	9.72	
2	Q9HMW9|Q9HMW9	1	1097.5393	-4.6	621	629	0	51.2	33	R	EQFVSDVFK	G	-0.1	4.08	
2	Q9HMW9|Q9HMW9	1	1149.5931	-2.5	632	642	0	61.1	34	R	GVGAFHLQPPQ	L	-0.1	7.84	
2	Q9HMW9|Q9HMW9	1	1164.5928	4.2	622	631	0	60.0	34	E	QFVSDVFKGR	G	-0.3	10.08	Gln->pyro-Glu (N-term Q)
2	Q9HMW9|Q9HMW9	1	1222.5692	-1.5	596	605	0	45.5	34	D	TYYVGFNMTK	V	-0.3	9.52	
2	Q9HMW9|Q9HMW9	1	1262.6772	-2.0	632	643	0	87.5	33	R	GVGAFHLQPPQL	F	0.2	7.84	
2	Q9HMW9|Q9HMW9	1	1340.6547	-1.3	613	623	0	61.9	34	K	AMAYVINREQF	V	0.1	6.88	
2	Q9HMW9|Q9HMW9	1	1394.6678	3.3	431	443	0	53.1	35	R	ATGVEAVDDYTVR	L	-0.1	3.7	
2	Q9HMW9|Q9HMW9	1	1409.7456	-4.0	632	644	0	91.6	33	R	GVGAFHLQPPQLF	S	0.4	7.84	
2	Q9HMW9|Q9HMW9	1	1450.6803	-1.7	594	605	0	89.4	35	T	IDTYYVGFNMTK	V	-0.2	6.62	
2	Q9HMW9|Q9HMW9	1	1496.7776	-1.9	632	645	0	101.4	34	R	GVGAFHLQPPQLFS	D	0.3	7.84	
2	Q9HMW9|Q9HMW9	1	1551.7279	-8.2	593	605	0	68.9	34	S	TIDTYYVGFNMTK	V	-0.2	6.62	
2	Q9HMW9|Q9HMW9	1	1562.7881	-5.1	129	140	0	37.9	35	E	LNWLQYQSPTWK	E	-1.1	9.72	
2	Q9HMW9|Q9HMW9	1	1613.8009	3.1	238	252	0	39.6	35	R	LVSNPGQSEDAIQTR	K	-0.8	4.08	
2	Q9HMW9|Q9HMW9	1	1691.8307	1.2	128	140	0	44.7	35	Y	ELNWLQYQSPTWK	E	-1.3	6.86	
2	Q9HMW9|Q9HMW9	1	1737.8284	1.2	591	605	0	141.8	35	S	VSTIDTYYVGFNMTK	V	0.1	6.62	
2	Q9HMW9|Q9HMW9	1	1753.8233	-3.3	591	605	0	63.5	34	S	VSTIDTYYVGFNMTK	V	0.1	6.62	Oxidation (M)
2	Q9HMW9|Q9HMW9	1	1911.8924	-1.9	589	605	0	101.2	35	S	SSVSTIDTYYVGFNMTK	V	0.0	6.62	
2	Q9HMW9|Q9HMW9	1	1998.9245	-1.9	588	605	0	72.5	35	N	SSSVSTIDTYYVGFNMTK	V	-0.1	6.62	
2	Q9HMW9|Q9HMW9	1	2016.0139	-2.7	613	629	0	100.8	36	K	AMAYVINREQFVSDVFK	G	0.2	6.94	
2	Q9HMW9|Q9HMW9	1	2466.1598	6.9	192	214	0	183.2	36	R	NFMQLVQPDNTIYGGETAANGAR	L	-0.5	4.08	
3	Q9HN93|Q9HN93	1	1326.5517	-2.5	38	49	0	109.9	30	A	QAYDGWFSGDAK	G	-1.0	3.88	Gln->pyro-Glu (N-term Q)
3	Q9HN93|Q9HN93	1	1380.627	1.2	50	63	0	119.1	34	K	GGAVGNYDGTTVDR	T	-0.7	3.88	
3	Q9HN93|Q9HN93	1	1414.6153	-2.9	37	49	0	85.5	31	A	AQAYDGWFSGDAK	G	-0.8	3.88	
3	Q9HN93|Q9HN93	1	2638.2511	13.4	64	90	0	152.5	36	R	TGTDEVTIDVGVDANGGTYGFGPAAVR	V	0.0	3.5	
3	Q9HN93|Q9HN93	1	2689.1681	8.6	38	63	0	199.5	33	A	QAYDGWFSGDAKGGAVGNYDGTTVDR	T	-0.8	3.88	Gln->pyro-Glu (N-term Q)
3	Q9HN93|Q9HN93	1	2719.1409	12.1	211	237	0	72.8	31	R	TPAPDSSGAFDYEPGGDTDDQPAIPEA	D	-1.0	2.64	
3	Q9HN93|Q9HN93	1	2875.242	13.1	210	237	0	89.1	33	R	RTPAPDSSGAFDYEPGGDTDDQPAIPEA	D	-1.1	3.22	
4	Q9HHN1|Q9HHN1	1	775.3864	24.6	2	7	0	36.4	34	M	VEFEPR	S	-1.0	4.26	
4	Q9HHN1|Q9HHN1	1	968.5906	23.8	36	45	0	27.7	27	A	VGIVLLGLDA	Q	2.2	3.1	
4	Q9HHN1|Q9HHN1	1	1128.4611	-2.3	8	16	0	54.4	28	R	SYEDFDPEK	R	-2.1	3.58	
4	Q9HHN1|Q9HHN1	1	1483.7056	1.4	189	201	0	86.8	34	A	SGVSDVDLWDHVR	G	-0.4	4.16	
4	Q9HHN1|Q9HHN1	1	1596.7267	0.6	398	411	0	95.5	34	D	LNDEYDLDGTSLSR	T	-1.0	3.5	
4	Q9HHN1|Q9HHN1	1	1667.8268	0.8	187	201	0	111.2	35	L	LASGVSDVDLWDHVR	G	0.1	4.16	
4	Q9HHN1|Q9HHN1	1	1711.7537	1.6	397	411	0	132.0	33	R	DLNDEYDLDGTSLSR	T	-1.2	3.36	
4	Q9HHN1|Q9HHN1	1	1723.857	-2.8	293	308	0	65.9	35	R	GFAEAWQIIYSGTGPK	T	-0.1	6.86	
4	Q9HHN1|Q9HHN1	1	1780.9108	-0.5	186	201	0	134.0	35	T	LLASGVSDVDLWDHVR	G	0.3	4.16	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
4	Q9HHN1|Q9HHN1	1	2593.2661	-8.3	178	201	0	69.4	36	K	QSPLSDTTLLASGVSDVDLWDHVR	G	-0.1	3.86	Gln->pyro-Glu (N-term Q)
5	Q9HN95|Q9HN95	1	739.4341	15.8	336	343	0	51.9	26	R	GGLAGLPR	R	0.3	11.04	
5	Q9HN95|Q9HN95	1	898.4508	8.3	413	421	0	35.3	32	A	LSGPADSPR	I	-0.8	6.78	
5	Q9HN95|Q9HN95	1	917.4971	3.3	155	162	0	43.8	33	K	LFSDPLAR	V	0.2	6.78	
5	Q9HN95|Q9HN95	1	1064.5403	-0.4	224	233	0	75.2	33	R	GGSGYIGWLR	A	-0.1	9.84	
5	Q9HN95|Q9HN95	1	1353.6888	0.3	408	421	0	92.4	34	G	SIPSALSGPADSPR	I	-0.3	6.78	
5	Q9HN95|Q9HN95	1	1410.7103	0.2	407	421	0	115.7	34	N	GSIPSALSGPADSPR	I	-0.3	6.78	
5	Q9HN95|Q9HN95	1	1623.8216	-0.6	405	421	0	151.7	35	S	VNGSIPSALSGPADSPR	I	-0.2	6.78	
5	Q9HN95|Q9HN95	1	1823.9377	2.1	403	421	0	119.3	35	R	LSVNGSIPSALSGPADSPR	I	-0.1	6.78	
6	Q9HMW4|Q9HMW4	1	944.4828	7.5	363	370	0	66.0	35	R	ANGWTQLR	N	-1.0	11.04	
6	Q9HMW4|Q9HMW4	1	1159.5873	0.9	329	338	0	58.4	35	S	IPSTDVPEFR	D	-0.5	4.08	
6	Q9HMW4|Q9HMW4	1	1317.5585	5.5	507	518	0	39.5	32	S	GEPGYGDENRQP	S	-2.3	3.82	
6	Q9HMW4|Q9HMW4	1	1345.6878	0.9	327	338	0	108.2	35	R	VSIPSTDVPEFR	D	-0.1	4.08	
6	Q9HMW4|Q9HMW4	1	1367.6292	-2.5	265	275	0	78.3	34	R	WSQQSVMAFER	A	-0.6	6.98	
6	Q9HMW4|Q9HMW4	1	1539.747	1.2	396	409	0	47.5	35	R	AGVQNTLHPTWGPY	A	-0.6	7.76	
6	Q9HMW4|Q9HMW4	1	2071.9673	-2.6	481	497	0	39.3	35	K	LNQETTSWPNLMSNYFK	T	-0.9	6.86	
6	Q9HMW4|Q9HMW4	1	2250.0706	1.5	396	416	0	84.5	36	R	AGVQNTLHPTWGPYAPENPTT	F	-0.8	5.12	
6	Q9HMW4|Q9HMW4	1	2484.171	-5.4	396	418	0	58.7	35	R	AGVQNTLHPTWGPYAPENPTTFS	G	-0.7	5.12	
6	Q9HMW4|Q9HMW4	1	3212.5163	-2.0	396	425	0	64.3	36	R	AGVQNTLHPTWGPYAPENPTTFSGSLDEAR	R	-0.8	4.42	
7	Q9HRR3|Q9HRR3	1	1119.5237	0.2	41	48	0	61.3	35	R	LTYEYFER	S	-1.0	4.26	
7	Q9HRR3|Q9HRR3	1	1287.5917	1.4	237	246	0	48.2	34	R	EGYMYDLNKR	Y	-1.6	6.88	
7	Q9HRR3|Q9HRR3	1	1414.6729	-1.5	18	29	0	88.5	35	G	IVSPDDETPTWR	E	-1.1	3.7	
7	Q9HRR3|Q9HRR3	1	1522.8719	1.3	130	144	0	118.7	30	K	LSALNPELAILGGQK	L	0.4	6.94	
7	Q9HRR3|Q9HRR3	1	1629.7635	1.1	15	29	0	102.4	35	D	GTGIVSPDDETPTWR	E	-0.9	3.7	
7	Q9HRR3|Q9HRR3	1	1744.7904	-3.6	14	29	0	120.5	33	T	DGTGIVSPDDETPTWR	E	-1.1	3.5	
7	Q9HRR3|Q9HRR3	1	1845.8381	4.7	13	29	0	54.5	34	R	TDGTGIVSPDDETPTWR	E	-1.1	3.5	
7	Q9HRR3|Q9HRR3	1	1914.9072	-0.1	15	31	0	67.4	35	D	GTGIVSPDDETPTWRER	K	-1.3	4.06	
8	Q9HSA8|Q9HSA8	1	1140.6655	-3.2	72	81	0	31.6	31	G	INVIPPFVSR	T	0.8	11.04	
8	Q9HSA8|Q9HSA8	1	1165.5768	-0.3	56	65	0	45.2	34	K	QALTVFGEYR	G	-0.1	6.88	Gln->pyro-Glu (N-term Q)
8	Q9HSA8|Q9HSA8	1	1182.6033	-3.0	56	65	0	84.7	34	K	QALTVFGEYR	G	-0.1	6.88	
8	Q9HSA8|Q9HSA8	1	1222.5983	3.1	56	66	0	59.0	34	K	QALTVFGEYRG	L	-0.2	6.88	Gln->pyro-Glu (N-term Q)
8	Q9HSA8|Q9HSA8	1	1239.6248	0.0	56	66	0	70.3	34	K	QALTVFGEYRG	L	-0.2	6.88	
8	Q9HSA8|Q9HSA8	1	1423.7823	0.2	69	81	0	54.2	32	L	EPGINVIPPFVSR	T	0.2	6.98	
8	Q9HSA8|Q9HSA8	1	1518.7678	-5.7	103	116	0	94.5	35	R	DNSPVTADAVVYIR	V	0.1	3.88	
8	Q9HSA8|Q9HSA8	1	1649.9505	1.9	67	81	0	71.8	29	G	LLEPGINVIPPFVSR	T	0.7	6.98	
8	Q9HSA8|Q9HSA8	1	1706.9719	1.5	66	81	0	124.7	30	R	GLLEPGINVIPPFVSR	T	0.6	6.98	
9	Q48302|Q48302	1	1104.5927	4.0	34	44	0	51.0	33	G	LAALAAGYAER	G	0.6	6.88	
9	Q48302|Q48302	1	1315.6442	-3.0	13	25	0	72.7	35	L	AETGSNMPAITPK	A	-0.5	6.94	
9	Q48302|Q48302	1	1331.7197	2.0	31	44	0	95.2	33	L	AVGLAALAAGYAER	G	0.9	6.88	
9	Q48302|Q48302	1	1541.8123	-2.9	11	25	0	90.7	35	T	ILAETGSNMPAITPK	A	0.1	6.94	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
9	Q48302|Q48302	1	1728.9522	2.7	26	44	0	175.6	32	K	AAAALAVGLAALAAGYAER	G	1.2	6.88	
9	Q48302|Q48302	1	1729.892	0.9	9	25	0	97.7	35	L	STILAETGSNMPAITPK	A	0.0	6.94	
10	Q9HNQ9|Q9HNQ9	1	1138.5043	-3.9	208	217	0	83.5	32	R	SGGFWESVDR	A	-0.8	4.08	
10	Q9HNQ9|Q9HNQ9	1	1210.5618	4.5	70	80	0	56.3	34	K	AAFDAEPTSFR	S	-0.3	4.08	
10	Q9HNQ9|Q9HNQ9	1	1537.7083	-1.4	5	17	0	128.5	34	F	EVPDVDLSQYSMR	Q	-0.7	3.7	
10	Q9HNQ9|Q9HNQ9	1	1684.7767	0.8	4	17	0	108.9	34	W	FEVPDVDLSQYSMR	Q	-0.4	3.7	
10	Q9HNQ9|Q9HNQ9	1	1870.856	8.1	3	17	0	91.1	34	S	WFEVPDVDLSQYSMR	Q	-0.5	3.7	
10	Q9HNQ9|Q9HNQ9	1	1957.888	0.7	2	17	0	131.4	34	M	SWFEVPDVDLSQYSMR	Q	-0.5	3.7	
11	Q9HHP3|Q9HHP3	1	1761.905	-0.3	161	178	0	118.3	35	R	ANTGSPFLGNAPVFVSGK	I	0.2	10.1	
11	Q9HHP3|Q9HHP3	1	1811.8479	0.9	199	214	0	150.5	35	R	WTFSFEDTGPNSVGLR	D	-0.5	4.08	
11	Q9HHP3|Q9HHP3	1	2026.9848	3.4	179	197	0	127.8	36	K	ILSWDSSSVVAYDATTGQK	R	-0.1	3.88	
11	Q9HHP3|Q9HHP3	1	2262.0077	0.5	100	119	0	166.7	33	A	LTPDEFGGSYTSFDINENTR	S	-1.0	3.58	
12	Q9HMX1|Q9HMX1	1	934.4509	3.2	18	25	0	34.6	34	R	STDGLWTR	I	-1.0	6.78	
12	Q9HMX1|Q9HMX1	1	1163.5757	-0.7	409	418	0	76.7	35	S	FGQQPTVTMR	K	-0.6	11.04	
12	Q9HMX1|Q9HMX1	1	1272.7038	-1.3	101	112	0	62.1	33	R	STAQSLPTLLSR	D	0.0	11.04	
12	Q9HMX1|Q9HMX1	1	1274.5602	1.9	269	279	0	92.2	33	N	VGVMTYDDYGR	F	-0.5	3.88	
12	Q9HMX1|Q9HMX1	1	1583.7943	-1.0	389	402	0	51.6	35	R	SLRGPALQVAEEEW	V	-0.5	3.96	
12	Q9HMX1|Q9HMX1	1	1673.8009	-1.7	113	127	0	84.0	35	R	DVIPNQGYNDPSTVR	S	-1.0	3.88	
12	Q9HMX1|Q9HMX1	1	1711.8417	5.2	392	407	0	83.7	35	R	GPALQVAEEEWVDAAK	S	-0.3	3.68	
13	Q9HMI3|Q9HMI3	1	1258.7397	-0.3	189	200	0	70.0	28	R	NLAIFAAAILSR	D	1.5	11.04	
13	Q9HMI3|Q9HMI3	1	1613.7573	-1.6	210	225	0	109.2	34	D	AQPELGTDPVGTGPFE	F	-0.6	2.94	
13	Q9HMI3|Q9HMI3	1	1769.7421	-2.5	139	152	0	119.1	29	R	FIDDEYDYYLGSDR	S	-1.1	3.36	
13	Q9HMI3|Q9HMI3	1	1925.8432	5.6	138	152	0	34.1	33	R	RFIDDEYDYYLGSDR	S	-1.4	3.76	
13	Q9HMI3|Q9HMI3	1	2143.0626	3.8	238	257	0	80.6	36	R	LTAFDDYWGGAPSVSAVIFK	T	0.5	3.88	
14	Q9HRQ9|Q9HRQ9	1	1835.9126	2.0	164	182	0	154.6	35	K	VIVNENGQAPSGGGGPVER	S	-0.5	4.26	
14	Q9HRQ9|Q9HRQ9	1	2021.029	-1.0	162	182	0	143.6	35	K	GKVIVNENGQAPSGGGGPVER	S	-0.6	7.1	
14	Q9HRQ9|Q9HRQ9	1	2445.1812	9.0	80	102	0	153.1	36	K	VGPNNQNVFDPAEVYVSPGDTVK	W	-0.5	3.7	
15	Q9HMK0|Q9HMK0	1	1676.7318	2.6	177	190	0	132.9	33	D	YASDVEAQEYFAER	M	-0.9	3.68	
15	Q9HMK0|Q9HMK0	1	1791.7587	3.1	176	190	0	33.1	31	E	DYASDVEAQEYFAER	M	-1.1	3.5	
15	Q9HMK0|Q9HMK0	1	2374.9826	9.3	171	190	0	50.2	30	L	TTDHEDYASDVEAQEYFAER	M	-1.4	3.68	
15	Q9HMK0|Q9HMK0	1	2488.0666	8.2	170	190	0	161.8	32	E	LTTDHEDYASDVEAQEYFAER	M	-1.2	3.68	
16	Q9HM69|CSG	1	1029.5455	2.5	603	611	0	46.9	35	D	IDISELRQG	S	-0.4	4.08	
16	Q9HM69|CSG	1	1144.5724	5.7	602	611	0	47.3	35	E	DIDISELRQG	S	-0.7	3.7	
16	Q9HM69|CSG	1	1607.7315	-2.8	598	610	0	70.6	34	T	FDEEDIDISELRQ	G	-1.1	3.38	
16	Q9HM69|CSG	1	1664.7529	1.4	598	611	0	107.5	34	T	FDEEDIDISELRQG	S	-1.0	3.38	
16	Q9HM69|CSG	1	1898.8568	7.4	101	118	0	44.2	34	G	GSDEGVPLQMPIPEDQST	G	-0.8	2.84	
17	Q9HRS0|Q9HRS0	1	1608.7606	0.8	97	111	0	60.2	35	K	VGPNGSNVFKPAEMY	V	-0.4	6.86	
17	Q9HRS0|Q9HRS0	1	1818.9	-0.2	178	194	0	104.8	36	K	GTIIVTDSPPENKGYQT	I	-0.8	4.08	
17	Q9HRS0|Q9HRS0	1	2529.2962	3.1	178	201	0	117.6	36	K	GTIIVTDSPPENKGYQTIVPDSAK	T	-0.5	4.3	
18	Q9HMZ3|Q9HMZ3	1	1081.4828	-0.1	552	560	0	59.6	32	R	YNGEFEAPR	E	-1.5	4.26	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
18	Q9HMZ3|Q9HMZ3	1	1188.5809	1.6	565	575	0	35.8	35	R	ATGVTLDEMPR	N	-0.3	4.08	
18	Q9HMZ3|Q9HMZ3	1	1364.6394	-5.4	371	382	0	78.1	35	K	NVEDAVMNAFQK	G	-0.4	4.08	
18	Q9HMZ3|Q9HMZ3	1	2302.0641	13.5	245	265	0	112.7	36	R	VPADASPEEIGPSEIEDFSWK	Q	-0.7	3.44	
19	Q9HSQ7|Q9HSQ7	1	1085.5216	-2.6	139	147	0	36.7	34	R	LNMDFFATK	Q	0.2	6.76	
19	Q9HSQ7|Q9HSQ7	1	1522.8833	-9.8	177	190	0	37.4	30	R	LSVMVLAIGVYLFV	V	2.6	5.92	
19	Q9HSQ7|Q9HSQ7	1	2154.9553	4.5	358	376	0	91.7	34	M	NEPSRIEENPDADELVVDD	G	-1.3	3.24	
19	Q9HSQ7|Q9HSQ7	1	2244.3093	3.7	52	73	0	113.7	27	R	VLDLAPPVLLGLAIDSVIQGNK	A	1.0	3.88	
20	Q9HMG3|Q9HMG3	1	1563.7205	-1.7	45	57	0	42.1	34	S	TVPETDFPEPYNR	S	-1.5	3.82	
20	Q9HMG3|Q9HMG3	1	1650.7526	2.5	45	58	0	61.0	34	S	TVPETDFPEPYNRS	I	-1.4	3.82	
20	Q9HMG3|Q9HMG3	1	1721.7897	-0.6	43	57	0	111.8	34	R	ASTVPETDFPEPYNR	S	-1.2	3.82	
20	Q9HMG3|Q9HMG3	1	1808.8217	2.2	43	58	0	100.7	34	R	ASTVPETDFPEPYNRS	I	-1.2	3.82	
21	Q9HP76|Q9HP76	1	968.5807	0.2	120	127	0	49.2	29	R	WSIPIVVR	F	1.2	11.04	
21	Q9HP76|Q9HP76	1	1104.7019	-9.3	342	351	0	26.9	20	R	LPPNLALVLR	V	1.0	11.04	
21	Q9HP76|Q9HP76	1	1966.9748	3.8	389	407	0	83.0	35	R	QFAAGTAEEFQAAATSVLR	V	0.2	4.26	
21	Q9HP76|Q9HP76	1	2048.9691	-3.3	60	77	0	63.6	35	R	VIEDELGPVDDVFDAFNR	E	-0.2	3.32	
21	Q9HP76|Q9HP76	1	2070.0058	-0.9	128	146	0	77.2	36	R	FVGQGQAFSLENLADEFAK	T	0.0	3.82	
22	P33518|COX1	1	1506.7314	5.0	33	47	0	57.8	35	R	SYTPLSDVGGGLGER	T	-0.4	4.08	
22	P33518|COX1	1	2872.2253	6.8	535	557	0	153.7	32	R	VDSTDPWDLEETDQFTNDWAWFR	A	-1.2	3.22	
23	Q9HRM1|Q9HRM1	1	1292.5997	6.0	41	52	0	74.5	34	T	YESAEVPTGNAR	L	-1.0	4.26	
23	Q9HRM1|Q9HRM1	1	1464.6845	0.6	39	52	0	98.9	35	R	ATYESAEVPTGNAR	L	-0.8	4.26	
24	Q9HQP2|Q9HQP2	1	1006.5236	9.6	382	389	0	39.6	33	G	EAQPFLFR	T	-0.2	6.98	
24	Q9HQP2|Q9HQP2	1	1176.6291	3.8	380	389	0	68.4	33	T	IGEAQPFLFR	T	0.2	6.98	
24	Q9HQP2|Q9HQP2	1	1277.6768	1.4	379	389	0	60.0	33	R	TIGEAQPFLFR	T	0.1	6.98	
24	Q9HQP2|Q9HQP2	1	1353.6718	0.8	741	752	0	65.3	34	K	FSAPVVFYDGPR	D	0.2	6.7	
25	Q9HPB1|SECY	1	1474.7351	2.6	399	411	0	121.4	35	R	QIQNSGMQIPGFR	K	-0.6	11.04	
25	Q9HPB1|SECY	1	1486.8945	2.8	287	299	0	58.0	25	K	LIYASVLPMILVR	A	1.9	9.84	
25	Q9HPB1|SECY	1	1585.8035	0.7	399	412	0	54.9	35	R	QIQNSGMQIPGFRK	N	-0.9	11.48	Gln->pyro-Glu (N-term Q)
26	Q9HRL4|Q9HRL4	1	1611.7199	-0.5	86	99	0	99.7	33	R	NFDDIDVTNATTMR	W	-0.6	3.6	
26	Q9HRL4|Q9HRL4	1	1797.7992	-0.1	86	100	0	116.9	33	R	NFDDIDVTNATTMRW	-	-0.7	3.6	
27	Q9HN94|Q9HN94	1	1435.7096	-2.0	41	53	0	38.1	35	R	QFAFSPGTSEPIR	V	-0.4	6.98	
27	Q9HN94|Q9HN94	1	2175.9233	5.0	22	40	0	159.3	31	R	DPGVYQADDDSYDVYVEAR	Q	-1.0	3.26	
28	Q9HRU5|Q9HRU5	1	941.4355	-0.2	38	46	0	39.9	32	R	LSWHAGGQS	G	-0.5	7.84	
28	Q9HRU5|Q9HRU5	1	1522.6841	-2.2	38	51	0	95.8	33	R	LSWHAGGQSGTYYP	L	-0.7	7.7	
28	Q9HRU5|Q9HRU5	1	1722.8002	-2.6	38	53	0	101.2	34	R	LSWHAGGQSGTYYPLS	N	-0.4	7.7	
29	Q9HRL3|Q9HRL3	1	825.5072	9.3	624	631	0	35.1	28	K	GVTLPLAR	G	0.8	11.04	
29	Q9HRL3|Q9HRL3	1	1832.8369	7.9	610	623	0	45.9	35	Y	NNYYQDEYQVWLAK	G	-1.4	4.08	
29	Q9HRL3|Q9HRL3	1	2323.1161	5.7	606	623	0	131.9	36	R	TLLYNNYYQDEYQVWLAK	G	-0.8	4.08	
30	Q9HSQ2|HTPX	1	1401.7187	-0.1	89	102	0	72.6	35	K	VANMGVPNAFAVGR	K	0.6	11.04	
30	Q9HSQ2|HTPX	1	1422.5721	1.3	57	68	0	55.0	29	V	GAEDMDEQEFPR	I	-1.8	3.5	
30	Q9HSQ2|HTPX	1	1608.6726	-5.7	55	68	0	100.0	30	R	SVGAEDMDEQEFPR	I	-1.3	3.5	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
31	Q9HRR1|Q9HRR1	1	1136.5614	-6.2	267	276	0	43.1	34	K	SFVAFARPEN	-	0.0	6.98	
31	Q9HRR1|Q9HRR1	1	1596.8835	1.9	180	193	0	105.2	32	R	SQNTDNTIPILIIR	S	0.0	6.78	
31	Q9HRR1|Q9HRR1	1	3091.5058	26.2	17	51	0	88.7	36	K	GVVGSAALAGAGTAGTAVLESVTNPTGSGGGQTNY	F	0.3	3.3	
32	Q9HRF2|Q9HRF2	1	1169.6404	-2.6	267	278	0	59.8	33	R	IGLPASIEGTGR	A	0.2	6.98	
32	Q9HRF2|Q9HRF2	1	1875.94	1.4	246	262	0	131.8	36	R	GVEINAADMLPDLSYLR	R	0.2	3.7	
33	Q9HRJ0|Q9HRJ0	1	1391.6681	1.3	26	38	0	45.0	35	R	ADEQPPDPLPGTR	T	-1.6	3.7	
33	Q9HRJ0|Q9HRJ0	1	1529.8566	-1.4	173	187	0	127.8	32	R	TPVVGTAVFNALVSR	R	1.0	11.04	
34	Q9HS12|Q9HS12	1	1694.9641	-5.5	486	502	0	76.0	31	R	AIGETAPLIMIGAPTIK	F	1.0	6.94	
35	Q9HHR4|Q9HHR4	1	1001.5142	4.5	331	339	0	36.8	35	K	SETATQIPR	T	-1.0	6.98	
35	Q9HHR4|Q9HHR4	1	1047.5713	2.6	450	459	0	68.1	32	K	TGYLLGATPR	K	0.0	9.84	
35	Q9HHR4|Q9HHR4	1	1381.6838	3.9	211	223	0	40.9	34	K	TTLETAFSAGQTR	G	-0.4	6.98	
35	Q9HHR4|Q9HHR4	1	1728.9258	17.9	433	450	0	32.1	32	S	VVAIAAAVAGDTSQDLKT	G	0.7	3.88	
36	Q9HS72|SECE	1	1393.6911	-2.2	1	12	0	106.8	35	-	MDVPLELSAYTR	V	0.0	4.08	
36	Q9HS72|SECE	1	1409.6861	-3.6	1	12	0	75.9	34	-	MDVPLELSAYTR	V	0.0	4.08	Oxidation (M)
36	Q9HS72|SECE	1	1692.8359	0.9	16	30	0	101.4	35	R	LASTPSWEEFSQIAK	I	-0.4	4.26	
37	Q9HS26|Q9HS26	1	1017.5243	-3.9	309	317	0	56.8	35	R	ASDSLWIAR	E	0.2	6.78	
37	Q9HS26|Q9HS26	1	1661.8988	2.2	375	389	0	124.2	33	R	AIQDFLLESVATTVR	R	0.6	4.08	
38	Q9HNN6|Q9HNN6	1	1107.5423	-6.8	48	56	0	47.7	35	R	FLDWMATPK	R	0.0	6.76	
38	Q9HNN6|Q9HNN6	1	1525.8141	-3.9	25	39	0	107.1	34	R	GLLPSFVHTSGPITT	L	0.5	7.84	
39	Q9HQV3|Q9HQV3	1	1134.6033	-1.6	19	28	0	46.9	33	H	ALDVFSQLSR	S	0.3	6.78	
39	Q9HQV3|Q9HQV3	1	1453.7314	3.9	16	28	0	112.9	34	S	QAHALDVFSQLSR	S	-0.1	7.84	Gln->pyro-Glu (N-term Q)
40	Q9HQF4|Q9HQF4	1	1437.71	3.6	102	115	0	49.9	35	A	TEDGDPSVPGPIVR	T	-0.7	3.7	
40	Q9HQF4|Q9HQF4	1	1538.7577	-2.6	102	116	0	79.0	35	A	TEDGDPSVPGPIVRT	E	-0.7	3.7	
41	Q9HQ04|Q9HQ04	1	1346.7195	1.4	222	233	0	53.7	34	E	GVVQEVDVFVTR	I	0.6	4.08	
41	Q9HQ04|Q9HQ04	1	1459.7419	-6.2	207	220	0	50.6	35	R	QPYGIGDQVAIGSR	E	-0.4	6.7	
41	Q9HQ04|Q9HQ04	1	1475.762	1.2	221	233	0	55.3	35	R	EGVVQEVDVFVTR	I	0.3	3.82	
42	P25964|BACS1	1	1780.0135	-6.3	149	164	0	48.3	31	R	VVPDVPEQIGLFNLLK	N	0.6	4.08	
43	Q9HQA6|Q9HQA6	1	1176.5411	1.8	96	105	0	77.9	35	D	FEDATDINPR	K	-1.2	3.7	
43	Q9HQA6|Q9HQA6	1	1291.5681	5.1	95	105	0	63.1	33	D	DFEDATDINPR	K	-1.4	3.5	
44	Q9HP89|Q9HP89	1	1329.7405	-3.2	225	237	0	71.3	32	R	LSPYLAAGNIGVR	E	0.6	9.84	
44	Q9HP89|Q9HP89	1	1964.8864	-4.0	238	256	0	36.0	33	R	EVWAAVADAYDDATGNAAR	N	-0.2	3.5	
45	O59634|O59634	1	1647.7893	0.3	26	40	0	39.3	35	L	EYTPTGESIPAAAWR	R	-0.6	4.26	
45	O59634|O59634	1	2024.9843	4.7	23	40	0	42.3	36	K	TYLEYTPTGESIPAAAWR	R	-0.4	4.26	
46	Q9HS51|Q9HS51	1	1767.7336	-0.2	78	93	0	36.8	29	L	GNDDADEIGLNPHDWT	V	-1.4	3.36	
46	Q9HS51|Q9HS51	1	1880.8177	-1.9	77	93	0	114.6	32	T	LGNDDADEIGLNPHDWT	V	-1.0	3.36	
47	Q9HRT0|Q9HRT0	1	1146.5669	1.8	505	514	0	44.7	35	R	VPDVDAVYNR	V	-0.4	3.88	
47	Q9HRT0|Q9HRT0	1	1271.6721	-5.0	559	570	0	76.5	35	R	LLGDTDSPVSLR	A	0.0	3.88	
48	Q9HR22|Q9HR22	1	1270.6823	-3.5	234	244	0	84.6	35	R	IPNVPFGFQPR	D	-0.2	11.04	
49	Q9HR99|Q9HR99	1	1494.7025	-1.1	99	113	0	104.3	35	K	ISIPDGASGFGTMDK	D	0.0	3.88	
49	Q9HR99|Q9HR99	1	1510.6974	-5.7	99	113	0	34.1	34	K	ISIPDGASGFGTMDK	D	0.0	3.88	Oxidation (M)

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
50	Q9HNR0|Q9HNR0	1	1259.6186	-3.8	340	350	0	61.6	35	N	SYYVAPSFAQK	Y	-0.2	9.52	
51	Q9HSC3|LONH	1	728.4181	11.5	430	436	0	39.6	35	R	DLGGLVR	V	0.4	6.78	
51	Q9HSC3|LONH	1	1638.8002	-1.5	464	476	0	53.9	35	R	SIEQQFVDNYIQR	R	-0.9	4.08	
52	Q9HNE6|Q9HNE6	1	981.5607	-0.4	213	222	0	47.6	29	R	AGDILGPLAR	F	0.5	6.78	
52	Q9HNE6|Q9HNE6	1	1594.8905	0.6	92	106	0	71.4	31	R	GGLPMLVPLLGFPER	Y	0.7	6.98	
54	Q9HPU7|Q9HPU7	1	2006.0837	-1.2	17	35	0	42.3	33	F	VPSWLVPEAAGDLPLTVSR	L	0.4	4.08	
55	Q9HRN3|Q9HRN3	1	1578.7638	2.4	83	98	0	90.9	35	R	VSSPGGAVSGSEVQYR	A	-0.3	6.88	
56	Q9HMU9|Q9HMU9	1	773.4184	0.0	2	8	0	53.1	35	M	SWAAIAR	K	0.5	11.04	
57	Q9HN07|Q9HN07	1	1281.6353	-3.2	599	609	0	76.0	34	R	TPANTAELFYR	L	-0.5	6.88	
58	Q9HN92|Q9HN92	1	1428.834	-4.4	15	28	0	124.1	30	L	LSLVPVALYAAGQK	A	1.0	9.72	
59	Q9HRL8|Q9HRL8	1	877.5021	0.6	118	125	0	32.5	29	K	YSLLGGLR	A	0.5	9.84	
60	Q9HRJ9|Q9HRJ9	1	1439.6892	-1.7	27	39	0	63.7	34	A	SSGYQSATEELIR	N	-0.7	4.26	
61	Q9HHJ8|Q9HHJ8	1	927.5138	26.3	601	609	0	39.6	33	Q	AGNVAVERL	V	0.4	6.98	
62	Q9HR16|Q9HR16	1	1222.671	-5.2	78	88	0	56.9	32	R	AVTLPTFFATR	L	0.8	11.04	
63	Q9HT01|Q9HT01	1	1299.5996	0.4	612	622	0	45.6	33	R	LYNWFGSGNSR	S	-0.9	9.84	
64	Q9HMX0|Q9HMX0	1	1013.5869	3.2	52	60	0	34.9	32	R	NLEISLGIR	Y	0.4	6.98	
64	Q9HMX0|Q9HMX0	1	1448.814	-2.2	305	317	0	42.3	31	K	VFSINGIGNLFIR	A	1.1	11.04	
68	Q9HND8|VATI	1	1016.4716	-2.5	709	716	0	51.8	34	K	YNPFGYTR	N	-1.3	9.58	
69	Q9HQU7|Q9HQU7	1	1514.7518	-0.3	184	196	0	47.6	35	R	AEGWEPFSVLQPR	Y	-0.6	4.26	
71	Q9HPD4|RL3	1	1209.6254	-1.2	234	244	0	104.0	33	R	IGNLGPWNPSR	V	-0.8	11.04	
72	Q9HRL1|Q9HRL1	1	950.5338	-0.8	159	167	0	69.5	30	K	AAGFAVLFR	V	1.6	11.04	
74	Q9HSF7|TF2B7	1	1304.6724	0.6	136	146	0	78.7	35	R	NLQFALSEIDR	M	-0.2	4.08	
75	Q9HT00|GLMS	1	773.4032	19.7	423	430	0	41.4	35	S	TGDAAALR	D	0.0	6.78	
78	Q9HQ63|DHSD	1	776.4181	8.4	9	15	0	38.3	33	G	LVADFGR	W	0.6	6.78	
81	Q9HN25|Q9HN25	1	1841.9312	-2.3	129	144	0	64.6	36	K	LNANFIEPGSLSYVYR	N	0.0	6.82	
87	Q9HSL5|Q9HSL5	1	1148.5251	5.1	49	58	0	41.7	34	K	AGGSYYYVNR	A	-0.8	9.44	
88	Q9HNB2|Q9HNB2	1	773.4283	-12.8	409	417	0	36.1	35	V	VTTAALAAG	V	1.5	6.02	
93	Q9HHS5|Q9HHS5	1	1571.674	0.0	75	88	0	80.9	31	R	YAAGDIDDEEFTAR	R	-0.8	3.42	
94	Q9HT02|Q9HT02	1	965.4389	9.9	230	237	0	48.0	34	R	EGVNNFMR	T	-0.8	6.98	
105	Q9HP72|HEM1	1	773.4395	-27.4	160	167	0	39.4	35	T	SLGTAAVR	L	0.7	11.04	
107	Q9HRL9|Q9HRL9	1	1336.7139	-6.4	344	355	0	36.2	33	R	LGGVVWDIPEPR	A	0.0	4.08	
110	P00772|ELA1	1	1695.8257	-0.1	101	114	0	67.3	35	V	QKIVVHPYWNTDDV	A	-0.6	5.1	Gln->pyro-Glu (N-term Q)
111	P71416|P71416	1	865.5749	5.9	26	33	0	22.6	20	K	AIALLPLR	S	1.7	11.04	
112	Q9HQW0|Q9HQW0	1	1017.5455	-24.7	127	136	0	37.6	35	P	SSVISDAALR	A	0.6	6.78	
113	Q9HQ64|Q9HQ64	1	1147.5986	-2.1	10	19	0	43.5	34	R	SGSTTWLLQR	L	-0.5	11.04	
114	Q9HMK7|Q9HMK7	1	1190.6196	-1.3	197	208	0	36.7	34	R	YGIAWGAVGAAR	N	0.7	9.84	
117	Q9HSJ6|Q9HSJ6	1	950.5226	10.9	13	22	0	34.6	30	G	FGAAAVVFAV	L	2.5	6.02	
118	Q9HP32|PYRG	1	1190.6329	-10.6	18	30	0	35.9	34	F	VTGGVMSGLGKGI	T	0.9	10.1	Oxidation (M)
125	Q9HPA6|Q9HPA6	1	1378.6364	-0.2	165	175	0	61.1	34	K	YQEQAQELQDK	M	-2.2	3.82	
126	Q9HNK1|Q9HNK1	1	962.5008	1.7	352	360	0	34.1	34	R	VFMSAVGPR	G	0.8	11.04	

hit	accession	z	mass	ppm	start	end	mc	score	id	-	sequence	+	gravy	pI	modification
128	Q9HRD0|Q9HRD0	1	2143.007	0.4	345	364	0	51.8	35	E	EQPEDIPSAGDLFDPGTTVR	V	-0.8	3.42	
129	Q9HP01|Q9HP01	1	887.5328	25.8	79	87	0	40.7	25	F	VTSLLLSVG	I	1.9	6.02	
130	Q9HRC9|Q9HRC9	1	1080.4699	-4.0	104	111	0	44.8	32	R	FDPEWMTR	T	-1.3	4.08	
132	Q9HMD1|SECG	1	1768.7904	-2.8	19	33	0	55.1	33	R	YFDSEDSNALQIDPR	S	-1.1	3.5	
134	Q9HRU7|Q9HRU7	1	986.6277	23.3	884	892	0	19.7	14	L	VVFAALLVR	N	2.5	11.04	
136	Q9HQQ5|Q9HQQ5	1	841.5273	-22.0	174	182	0	34.1	31	G	ATVAVLVGL	Y	2.5	6.02	
139	Q9HQ03|Q9HQ03	1	927.5277	11.3	7	15	0	36.6	33	D	LLADVLDGI	D	1.6	2.92	
150	P16102|BACH	1	971.6089	10.0	118	126	0	26.5	22	P	MILLALGLL	A	3.0	6.02	Oxidation (M)
158	Q9HNT9|Q9HNT9	1	773.4031	19.7	3	10	0	41.6	35	I	SDLAAAAR	S	0.3	6.78	
159	Q9HPX0|Q9HPX0	1	1835.8618	28.4	293	310	0	38.5	35	D	RMRGDGMAIAAGGIQTTD	T	-0.2	6.92	Oxidation (M)
160	Q9HRZ2|Q9HRZ2	1	1436.7663	-3.6	184	195	0	44.4	33	K	LANLLFAYELDR	R	0.4	4.08	
163	Q9HR62|Q9HR62	1	1118.6448	1.3	305	315	0	43.4	29	R	APSVPVPSLPR	S	0.1	11.04	
164	Q9HRY9|Q9HRY9	1	1728.9444	7.2	18	36	0	46.5	32	A	VAVLAGGAVIGMTVLGGTQ	S	1.5	6.02	Oxidation (M)
169	Q9HMS1|Q9HMS1	1	1367.6609	-7.7	45	57	0	48.9	34	K	LLEGGLTFDPSGY	L	0.1	3	
170	Q9HR07|Q9HR07	1	1321.8194	-24.1	8	20	0	27.3	26	A	VRSRPLVVAALAA	A	1.2	12.4	
197	O51960|O51960	1	1084.5513	1.7	2	10	0	52.8	34	M	SELPENIQR	Q	-1.4	4.26	
199	Q9HS48|Q9HS48	1	773.4283	-3.5	68	76	0	35.6	35	A	SATVAVAGV	A	1.8	6.02	
202	Q9HQW3|Q9HQW3	1	986.6277	23.3	124	132	0	19.1	14	L	LAFRIVIVG	C	2.3	11.04	
213	Q9HS33|Q9HS33	1	971.6419	-27.3	298	306	0	26.6	24	F	IIAGFIILI	P	3.4	6.02	
220	Q9HSA0|Q9HSA0	1	1260.6251	5.0	39	50	0	36.0	35	A	FEHGLPSGPHLA	D	-0.2	6.02	
230	Q9HN82|ENDA	1	950.5338	-0.8	68	76	0	31.0	30	E	AGFAARFLV	Y	1.6	11.04	
234	Q9HN85|Q9HN85	1	1182.6033	-3.0	179	189	0	43.2	34	G	AGALTSPTFYR	E	0.0	9.84	
285	Q9HNZ0|NADB	1	773.4105	10.1	216	224	0	38.6	35	G	VAMAALAGA	D	2.1	6.02	
301	Q9HSJ5|Q9HSJ5	1	1728.9774	-13.6	10	28	0	33.4	33	L	AGAAVAALALASVAVAYLQ	F	1.8	5.92	
339	Q9HQ52|THYX	1	2101.999	1.9	158	176	0	47.5	36	R	AVEDYQELLGLGMPPEDAR	F	-0.5	3.5	
344	Q9HN76|Q9HN76	1	975.5576	4.4	83	90	0	38.6	29	R	FTLPMVLR	A	1.2	11.04	
375	Q48290|FTSZ	1	1550.8014	-3.3	181	194	0	37.0	34	K	AFSVMDQIIAETVK	G	0.7	4.08	
394	Q9HQQ6|Q9HQQ6	1	1133.706	-7.9	216	225	0	31.5	23	R	IILTLYSLAK	T	1.6	9.72	
395	Q9HNU0|Q9HNU0	1	813.4708	16.3	268	275	0	41.8	32	A	DALVAAVR	A	1.2	6.78	
454	P17103|Y1111	1	1024.6029	-26.4	308	315	0	30.0	30	D	REEPLIIR	R	-0.6	7.12	
508	Q9HRM0|Q9HRM0	1	1309.6918	-6.3	39	50	0	35.2	33	R	EAFGSTPFILTK	F	0.3	6.94	
536	O51958|O51958	1	981.5719	-11.8	371	378	0	29.2	29	N	AERLRLQP	V	-1.0	10.88	
635	Q9HSM8|Q9HSM8	1	981.5859	-26.1	268	278	0	29.1	29	A	AATLLPLAGGV	G	1.6	6.02	

END OF LIST IX