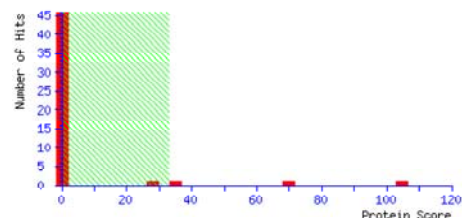


MATRIX SCIENCE Mascot Search Results

User : JPROS  
Email : pro@jbios.co.jp  
Search title : D:\JPROS\Q007\WT3\_8micro.wiff (sample number 1)  
MS data file : masA7A.tmp  
Database : UP589\_M\_musculus M\_musculus\_20240121 (63447 sequences; 28585060 residues)  
Timestamp : 22 Jan 2024 at 08:40:49 GMT  
Protein hits : [P18872](#) Guanine nucleotide-binding protein G(o) subunit alpha OS=Mus musculus OX=10090 GN=Gnao1 PE=1 SV=3  
[A0A0G2JG40](#) Guanine nucleotide binding protein, alpha 12 (Fragment) OS=Mus musculus OX=10090 GN=Gna12 PE=1 SV=1  
[A0A0U1RPN8](#) fructose-bisphosphate aldolase (Fragment) OS=Mus musculus OX=10090 GN=Aldoa PE=1 SV=1  
[Q9Z1G3](#) V-type proton ATPase subunit C 1 OS=Mus musculus OX=10090 GN=Atp6v1c1 PE=1 SV=4

Mascot Score Histogram

Ions score is  $-10 \times \log(P)$ , where P is the probability that the observed match is a random event.  
Individual ions scores > 33 indicate identity or extensive homology ( $p < 0.05$ ).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As Peptide Summary [Help](#)

Significance threshold  $p < 0.05$  Max. number of hits AUTO

Standard scoring ☐ MudPIT scoring ☒ Display non-significant matches ☒ Show sub-sets 0

Show pop-ups ☒ Suppress pop-ups ☐ Sort unassigned Decreasing Score Require bold red ☐

Select All Select None Search Selected ☐ Error tolerant

1. [P18872](#) Mass: 40059 Score: 105 Matches: 9(4) Sequences: 7(3) emPAI: 0.31  
Guanine nucleotide-binding protein G(o) subunit alpha OS=Mus musculus OX=10090 GN=Gnao1 PE=1 SV=3  
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/>	<a href="#">215</a>	446.2216	890.4286	890.4610	-0.0324	0	30	0.17	1	U	R.LFDVGGQR.S
<input checked="" type="checkbox"/>	<a href="#">261</a>	483.2123	964.4100	964.4470	-0.0371	0	34	0.059	1	U	K.MVCDVVSR.M + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">316</a>	529.2820	1056.5494	1056.6179	-0.0685	0	56	0.00047	1	U	K.LLLLGA GESGK.S
<input checked="" type="checkbox"/>	<a href="#">317</a>	529.2919	1056.5692	1056.6179	-0.0487	0	(48)	0.003	1	U	K.LLLLGA GESGK.S
<input checked="" type="checkbox"/>	<a href="#">318</a>	529.3511	1056.6876	1056.6179	0.0697	0	(14)	5.8	1	U	K.LLLLGA GESGK.S
<input checked="" type="checkbox"/>	<a href="#">421</a>	482.5388	1444.5945	1444.6834	-0.0889	0	38	0.018	1	U	K.IIHEDGFSGEDVK.Q
<input checked="" type="checkbox"/>	<a href="#">438</a>	528.5538	1582.6396	1582.7297	-0.0901	1	35	0.035	1	U	R.AMDTLGV EYGDKER.K
<input checked="" type="checkbox"/>	<a href="#">441</a>	838.3725	1674.7304	1674.8213	-0.0909	0	20	1.1	1	U	R.IGAGDYQPT EQDILR.T
<input checked="" type="checkbox"/>	<a href="#">461</a>	717.3583	2149.0531	2149.1895	-0.1364	0	20	1.1	1	U	K.QYKPVVYSNTIQSLAAIVR.A

Proteins matching the same set of peptides:

[P18872-2](#) Mass: 40011 Score: 105 Matches: 9(4) Sequences: 7(3)  
Isoform Alpha-2 of Guanine nucleotide-binding protein G(o) subunit alpha OS=Mus musculus OX=10090 GN=Gnao1

2. [A0A0G2JG40](#) Mass: 37045 Score: 73 Matches: 3(2) Sequences: 1(1) emPAI: 0.10  
Guanine nucleotide binding protein, alpha 12 (Fragment) OS=Mus musculus OX=10090 GN=Gna12 PE=1 SV=1  
☐ Check to include this hit in error tolerant search

	Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
	<a href="#">316</a>	529.2820	1056.5494	1056.6179	-0.0685	0	56	0.00047	1	U	K.ILLLGA GESGK.S
	<a href="#">317</a>	529.2919	1056.5692	1056.6179	-0.0487	0	(48)	0.003	1	U	K.ILLLGA GESGK.S
	<a href="#">318</a>	529.3511	1056.6876	1056.6179	0.0697	0	(14)	5.8	1	U	K.ILLLGA GESGK.S

Proteins matching the same set of peptides:

[Q9D034](#) Mass: 19924 Score: 73 Matches: 3(2) Sequences: 1(1)  
Guanine nucleotide binding protein, alpha 13 OS=Mus musculus OX=10090 GN=Gna13 PE=1 SV=1  
[P27601](#) Mass: 44027 Score: 73 Matches: 3(2) Sequences: 1(1)

Guanine nucleotide-binding protein subunit alpha-13 OS=Mus musculus OX=10090 GN=Gnal3 PE=1 SV=1  
[P27600](#) Mass: 44067 Score: 73 Matches: 3(2) Sequences: 1(1)  
 Guanine nucleotide-binding protein subunit alpha-12 OS=Mus musculus OX=10090 GN=Gnal2 PE=1 SV=3

3. [A0A0U1RPN8](#) Mass: 20609 Score: 36 Matches: 2(1) Sequences: 2(1) emPAI: 0.19  
 fructose-bisphosphate aldolase (Fragment) OS=Mus musculus OX=10090 GN=Aldoa PE=1 SV=1  
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> <a href="#">410</a>	666.8202	1331.6258	1331.6932	-0.0675	0	36	0.044	1	U	K.GILAADESTGSIK.R
<input checked="" type="checkbox"/> <a href="#">416</a>	448.2208	1341.6405	1341.7041	-0.0636	0	10	15	1	U	K.ADDGRPFPPQVIK.S

Proteins matching the same set of peptides:

[A0A0U1RPT5](#) Mass: 22611 Score: 36 Matches: 2(1) Sequences: 2(1)  
 fructose-bisphosphate aldolase (Fragment) OS=Mus musculus OX=10090 GN=Aldoa PE=1 SV=1  
[D3YV98](#) Mass: 20823 Score: 36 Matches: 2(1) Sequences: 2(1)  
 fructose-bisphosphate aldolase (Fragment) OS=Mus musculus OX=10090 GN=Aldoa PE=1 SV=1  
[D3YWI1](#) Mass: 25780 Score: 36 Matches: 2(1) Sequences: 2(1)  
 Fructose-bisphosphate aldolase (Fragment) OS=Mus musculus OX=10090 GN=Aldoa PE=1 SV=8  
[D3Z510](#) Mass: 19561 Score: 36 Matches: 2(1) Sequences: 2(1)  
 fructose-bisphosphate aldolase (Fragment) OS=Mus musculus OX=10090 GN=Aldoa PE=1 SV=2  
[A6Z144](#) Mass: 45092 Score: 36 Matches: 2(1) Sequences: 2(1)  
 Fructose-bisphosphate aldolase OS=Mus musculus OX=10090 GN=Aldoa PE=1 SV=1  
[P05064](#) Mass: 39331 Score: 36 Matches: 2(1) Sequences: 2(1)  
 Fructose-bisphosphate aldolase A OS=Mus musculus OX=10090 GN=Aldoa PE=1 SV=2

4. [Q9Z1G3](#) Mass: 43860 Score: 26 Matches: 1(0) Sequences: 1(0)  
 V-type proton ATPase subunit C 1 OS=Mus musculus OX=10090 GN=Atp6v1c1 PE=1 SV=4  
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> <a href="#">348</a>	551.7624	1101.5103	1101.5666	-0.0563	0	26	0.41	1	U	K.GVTQIDNDLK.S

Peptide matches not assigned to protein hits: (no details means no match)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> <a href="#">245</a>	466.2062	930.3979	930.5175	-0.1195	0	23	0.92	1		AAAVPVEFK
<input checked="" type="checkbox"/> <a href="#">246</a>	466.3000	930.5854	930.4771	0.1084	0	18	2.9	1		LEGPGTTTR
<input checked="" type="checkbox"/> <a href="#">194</a>	439.2194	876.4243	876.4818	-0.0574	0	18	3.1	1		VGASFLQR
<input checked="" type="checkbox"/> <a href="#">266</a>	485.2959	968.5772	968.5403	0.0369	1	18	2.6	1		TQLNKTHK
<input checked="" type="checkbox"/> <a href="#">140</a>	422.7422	843.4699	843.5066	-0.0367	0	16	4.7	1		VTTPTVVK
<input checked="" type="checkbox"/> <a href="#">193</a>	439.2138	876.4131	876.4818	-0.0686	0	16	5.2	1		VGASFLQR
<input checked="" type="checkbox"/> <a href="#">169</a>	428.7501	855.4857	855.5429	-0.0573	0	15	4.6	1		LVLSSLPK
<input checked="" type="checkbox"/> <a href="#">451</a>	897.8667	1793.7188	1793.9094	-0.1907	1	15	3.5	1		MLSDGRTIITFPNGTR + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">241</a>	463.2541	924.4936	924.4413	0.0522	0	13	6.7	1		SPGSPTSHR
<input checked="" type="checkbox"/> <a href="#">135</a>	421.7320	841.4494	841.4334	0.0160	0	13	7.2	1		VTWDPPK
<input checked="" type="checkbox"/> <a href="#">167</a>	428.7420	855.4694	855.5429	-0.0735	0	13	7.6	1		LVLSSLPK
<input checked="" type="checkbox"/> <a href="#">142</a>	423.2239	844.4333	844.4654	-0.0321	0	13	10	1		TAEVLANK
<input checked="" type="checkbox"/> <a href="#">138</a>	421.7428	841.4711	841.5062	-0.0351	0	13	7.4	1		VAPAIFPK
<input checked="" type="checkbox"/> <a href="#">304</a>	523.2776	1044.5406	1044.6179	-0.0772	0	12	10	1		ILAINSSSLK
<input checked="" type="checkbox"/> <a href="#">190</a>	437.2004	872.3863	872.5079	-0.1216	1	12	12	1		ISKETQR
<input checked="" type="checkbox"/> <a href="#">66</a>	403.2033	804.3921	804.4025	-0.0104	1	12	7	1		RTVGGQR + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">143</a>	423.2245	844.4345	844.4654	-0.0309	0	12	11	1		TAEVLANK
<input checked="" type="checkbox"/> <a href="#">275</a>	491.7749	981.5353	981.5243	0.0109	1	12	8.8	1		AEPKTHHK
<input checked="" type="checkbox"/> <a href="#">80</a>	408.2091	814.4037	814.5276	-0.1239	0	12	8.8	1		LSTLILR
<input checked="" type="checkbox"/> <a href="#">197</a>	441.3072	880.5999	880.4477	0.1522	1	11	7.7	1		KCIQDFK
<input checked="" type="checkbox"/> <a href="#">229</a>	451.2098	900.4051	900.5579	-0.1528	1	11	14	1		LMKLLQR
<input checked="" type="checkbox"/> <a href="#">336</a>	538.3031	1074.5917	1074.4917	0.1000	0	11	15	1		NECFLEHK + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">94</a>	412.2844	822.5542	822.3654	0.1888	0	11	8.3	1		NASASMAR + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">82</a>	409.1656	816.3167	816.3977	-0.0810	0	11	13	1		LEAAEER
<input checked="" type="checkbox"/> <a href="#">195</a>	439.2226	876.4306	876.4818	-0.0512	0	11	17	1		VGASFLQR
<input checked="" type="checkbox"/> <a href="#">144</a>	423.2252	844.4359	844.4654	-0.0295	0	10	17	1		TAEVLANK
<input checked="" type="checkbox"/> <a href="#">61</a>	400.2000	798.3854	798.4487	-0.0633	0	10	8.4	1		ELGTGLLP
<input checked="" type="checkbox"/> <a href="#">427</a>	485.5000	1453.4782	1453.6694	-0.1912	0	10	4.3	1		FGCSTVLQPTGGK + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">137</a>	421.7424	841.4703	841.5062	-0.0358	0	10	14	1		VAPAIFPK
<input checked="" type="checkbox"/> <a href="#">242</a>	463.2712	924.5279	924.4626	0.0653	0	10	15	1		MEFLELK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">306</a>	525.1933	1048.3720	1048.5409	-0.1690	1	10	17	1		IPSMKGICK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">168</a>	428.7488	855.4830	855.4273	0.0558	0	10	15	1		ICLQDHK
<input checked="" type="checkbox"/> <a href="#">211</a>	444.2000	886.3854	886.4661	-0.0806	0	10	22	1		AQTPAFPR
<input checked="" type="checkbox"/> <a href="#">244</a>	466.2018	930.3890	930.5134	-0.1244	1	10	22	1		DTKNVNLK
<input checked="" type="checkbox"/> <a href="#">95</a>	412.7347	823.4548	823.3317	0.1232	0	9	13	1		VMCEGGR + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">240</a>	461.2152	920.4159	920.4967	-0.0808	1	9	23	1		KSLDFPSK
<input checked="" type="checkbox"/> <a href="#">302</a>	523.2604	1044.5063	1044.6233	-0.1170	1	9	23	1		RIFPPPIR
<input checked="" type="checkbox"/> <a href="#">76</a>	406.2695	810.5245	810.4599	0.0645	0	9	10	1		QPTPIQK
<input checked="" type="checkbox"/> <a href="#">71</a>	405.2384	808.4623	808.4304	0.0320	1	8	13	1		AHRGPGSK
<input checked="" type="checkbox"/> <a href="#">90</a>	411.2411	820.4677	820.3385	0.1292	0	8	19	1		TSHSDMK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">439</a>	401.1315	1600.4969	1600.6398	-0.1429	1	8	2.4	1		EMNCFRENNDWK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">73</a>	405.2501	808.4856	808.4304	0.0552	1	8	15	1		AHRGPGSK
<input checked="" type="checkbox"/> <a href="#">220</a>	447.3087	892.6029	892.4767	0.1263	1	8	22	1		KAPSSFTTR
<input checked="" type="checkbox"/> <a href="#">363</a>	583.3490	1164.6834	1164.5696	0.1138	0	8	26	1		KPATSTMVSEV + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">373</a>	403.3000	1206.8782	1206.7336	0.1446	1	8	2.7	1		HVKDELELLK
<input checked="" type="checkbox"/> <a href="#">315</a>	529.2465	1056.4785	1056.4811	-0.0026	0	8	31	1		GMPPPSNWR + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">257</a>	477.2669	952.5193	952.5454	-0.0261	1	7	28	1		ELSHLRK
<input checked="" type="checkbox"/> <a href="#">230</a>	451.2527	900.4909	900.3470	0.1440	0	7	34	1		GFMEMDR + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">382</a>	421.2000	1260.5782	1260.6965	-0.1184	0	7	30	1		AEVVTLPYLYK

265	485.2731	968.5316	968.6131	-0.0815	1	7	29	1	LVKLINNR
228	451.2083	900.4020	900.4487	-0.0467	0	7	35	1	MLGVPDNR
323	536.1572	1070.2998	1070.4889	-0.1891	0	7	7	1	CACSSIVFK + 2 Carbamidomethyl (C)
292	507.1616	1012.3086	1012.5052	-0.1966	0	7	13	1	EICFAFVK + Carbamidomethyl (C)
151	425.7454	849.4762	849.4014	0.0748	0	7	36	1	TQMAEVR + Oxidation (M)
404	444.2000	1329.5782	1329.7041	-0.1259	1	7	28	1	HSVFTAGKGVAEK
466	737.6635	2209.9685	2210.0967	-0.1282	0	7	20	1	LGEHNINVLEGNQFIDAAK
346	545.1714	1088.3282	1088.4999	-0.1717	1	7	9.5	1	GDFGSHGERK
232	451.3176	900.6206	900.5392	0.0814	1	7	34	1	SIKNKPSK
153	425.7518	849.4891	849.4014	0.0876	0	7	38	1	TQMAEVR + Oxidation (M)
172	432.2036	862.3926	862.4661	-0.0735	0	7	36	1	VLGSGAFGR
277	494.1528	986.2910	986.4677	-0.1767	1	7	13	1	KCYVMTGR + Oxidation (M)
79	407.2157	812.4168	812.4028	0.0140	0	7	20	1	ELHSAEK
250	472.2603	942.5060	942.5974	-0.0914	1	7	36	1	IVSVTIRR
253	476.2498	950.4849	950.4379	0.0471	1	7	38	1	KDGEIMDK + Oxidation (M)
303	523.2621	1044.5096	1044.6233	-0.1136	1	7	39	1	RIFFFPIR
370	400.2000	1197.5782	1197.6288	-0.0506	1	6	34	1	ELAPSPACVR
149	425.2539	848.4932	848.4578	0.0354	0	6	38	1	FAVPMLR + Oxidation (M)
175	433.2258	864.4370	864.4341	0.0029	1	6	40	1	REETIFA
375	411.1507	1230.4301	1230.5993	-0.1691	0	6	23	1	GAAPPAATAYDR
219	447.3049	892.5952	892.4589	0.1363	1	6	37	1	MGRLSWK + Oxidation (M)
405	444.2000	1329.5782	1329.6062	-0.0280	0	6	35	1	TAEPSEAHSHHK
272	488.2521	974.4897	974.5470	-0.0573	1	6	46	1	IIKLCEEK
136	421.7391	841.4636	841.3674	0.0962	0	6	34	1	VTCSMSSK
332	536.1739	1070.3333	1070.5331	-0.1998	0	6	16	1	ICASHIGWK + Carbamidomethyl (C)
337	540.3966	1078.7787	1078.6499	0.1288	0	6	9	1	LESVHIILR
239	459.2438	916.4730	916.4800	-0.0071	0	6	52	1	INVCVGQK + Carbamidomethyl (C)
132	421.2371	840.4597	840.5069	-0.0472	1	6	27	1	KAAPALLSA
366	585.3335	1168.6524	1168.5109	0.1415	0	6	40	1	LPDSSDHQDR
342	545.1342	1088.2539	1088.4267	-0.1728	0	6	1.8	1	TAFSDCTCK + 2 Carbamidomethyl (C)
92	411.2484	820.4823	820.3473	0.1351	0	6	33	1	CGHVFCR
403	444.2000	1329.5782	1329.6062	-0.0280	0	6	39	1	TAEPSEAHSHHK
218	447.2573	892.5000	892.4436	0.0564	1	6	46	1	MAAANGSK + Oxidation (M)
125	419.6770	837.3395	837.3651	-0.0256	0	6	34	1	MSTEAQR + Oxidation (M)
408	444.2000	1329.5782	1329.6057	-0.0275	1	6	40	1	DGMGMVEYLK + 2 Oxidation (M)
249	472.2602	942.5059	942.5862	-0.0803	1	5	46	1	IALKETIR
293	508.2376	1014.4607	1014.5709	-0.1102	0	5	51	1	IEVVAELSR
351	565.2890	1128.5634	1128.5788	-0.0154	1	5	48	1	SPYHSRNIR
216	446.2560	890.4975	890.5226	-0.0250	0	5	56	1	IGGISGIFK
335	536.1865	1070.3585	1070.5430	-0.1845	0	5	25	1	TLP CSPVAGGL + Carbamidomethyl (C)
199	441.7568	881.4990	881.4164	0.0826	0	5	42	1	TIITSGEMK + Oxid

☑	<a href="#">305</a>	523.3266	1044.6386	1044.4989	0.1397	0	3	80	1	GDGYPGVAGPR
☑	<a href="#">264</a>	485.2000	968.3854	968.4750	-0.0895	0	3	67	1	CHTPDIVK + Carbamidomethyl (C)
☑	<a href="#">385</a>	422.2491	1263.7256	1263.5877	0.1379	1	3	73	1	AVKNSAESDGMR
☑	<a href="#">105</a>	413.2549	824.4952	824.4365	0.0587	1	3	49	1	NSVGHRR
☑	<a href="#">103</a>	413.2464	824.4782	824.3586	0.1196	0	3	49	1	MTDDSLK + Oxidation (M)
☑	<a href="#">273</a>	491.7699	981.5252	981.5607	-0.0355	1	3	72	1	KSEQLLHK
☑	<a href="#">330</a>	536.1693	1070.3241	1070.4525	-0.1284	1	3	26	1	AFKCEECGK + Carbamidomethyl (C)
☑	<a href="#">223</a>	448.7602	895.5059	895.3957	0.1102	0	3	73	1	VDSMDSVK + Oxidation (M)
☑	<a href="#">386</a>	422.5715	1264.6928	1264.7027	-0.0099	1	3	77	1	TNKELLVFSSK
☑	<a href="#">285</a>	503.2822	1004.5499	1004.6019	-0.0520	1	3	91	1	EIIRTVMK
☑	<a href="#">412</a>	445.2000	1332.5782	1332.7150	-0.1368	1	3	79	1	TLSPAQQRAFSK
☑	<a href="#">187</a>	435.7532	869.4918	869.5157	-0.0239	0	3	68	1	LILQMPR
☑	<a href="#">86</a>	411.2113	820.4081	820.3563	0.0518	0	3	62	1	TGGENTDK
☑	<a href="#">426</a>	485.2491	1452.7254	1452.6411	0.0843	0	3	70	1	DVIEDCLMALCR + Carbamidomethyl (C)
☑	<a href="#">81</a>	408.2681	814.5216	814.3353	0.1863	0	3	70	1	SGMAFLAC + Oxidation (M)
☑	<a href="#">84</a>	411.1438	820.2730	820.4265	-0.1536	0	3	58	1	LTPGMFR
☑	<a href="#">96</a>	413.0746	824.1347	824.2979	-0.1632	1	3	3.4	1	KCPACGSC + Carbamidomethyl (C)
☑	<a href="#">394</a>	427.2000	1278.5782	1278.6905	-0.1123	1	3	75	1	GARTSPGPAGPR
☑	<a href="#">119</a>	419.1680	836.3215	836.3698	-0.0483	0	3	59	1	QAAGMESK + Oxidation (M)
☑	<a href="#">274</a>	491.7714	981.5283	981.5243	0.0040	1	3	76	1	AEPKTTTHK
☑	<a href="#">235</a>	455.3016	908.5887	908.5304	0.0583	1	3	73	1	QAPKGRPR
☑	<a href="#">110</a>	414.2896	826.5646	826.4522	0.1124	1	3	49	1	RPDARGR
☑	<a href="#">146</a>	424.2821	846.5496	846.3970	0.1525	1	3	94	1	EAEKEEL
☑	<a href="#">234</a>	455.2765	908.5384	908.4715	0.0669	1	3	85	1	EYISNKR
☑	<a href="#">347</a>	547.2986	1092.5827	1092.4870	0.0958	0	3	1e+02	1	CSAEAEATVR + Carbamidomethyl (C)
☑	<a href="#">154</a>	425.7521	849.4897	849.4742	0.0155	1	2	1.1e+02	1	TSLVMRK + Oxidation (M)
☑	<a href="#">209</a>	444.2000	886.3854	886.2918	0.0937	0	2	1.2e+02	1	GSVCCCCR + Carbamidomethyl (C)
☑	<a href="#">171</a>	430.1969	858.3792	858.5035	-0.1243	1	2	1.1e+02	1	SRTILNR
☑	<a href="#">152</a>	425.7464	849.4782	849.3552	0.1230	0	2	1.1e+02	1	GYGMHNR + Oxidation (M)
☑	<a href="#">89</a>	411.2411	820.4676	820.4629	0.0047	0	2	72	1	AIVLCFR
☑	<a href="#">339</a>	543.6411	1085.2676	1085.4634	-0.1958	0	2	8.8	1	DFLMTCNSR
☑	<a href="#">329</a>	536.1674	1070.3203	1070.4525	-0.1322	0	2	31	1	AYICAECNK + Carbamidomethyl (C)
☑	<a href="#">321</a>	536.1475	1070.2805	1070.4339	-0.1534	0	2	15	1	DMENYEVK + Oxidation (M)
☑	<a href="#">74</a>	405.2728	808.5310	808.3636	0.1673	0	2	53	1	EMNSIIS + Oxidation (M)
☑	<a href="#">148</a>	424.2918	846.5691	846.3970	0.1720	1	2	1e+02	1	EAEKEEL
☑	<a href="#">145</a>	424.0713	846.1281	846.2922	-0.1641	0	2	0.62	1	TMMVSSC + Carbamidomethyl (C); 2 O:
☑	<a href="#">325</a>	536.1614	1070.3082	1070.4815	-0.1733	0	2	27	1	QLNGSVNR + Oxidation (M)
☑	<a href="#">85</a>	411.1788	820.3431	820.4807	-0.1376	0	2	77	1	ILIGYSR
☑	<a href="#">69</a>	405.2229	808.4313	808.4304	0.0009	0	2	59	1	ARNHNSK
☑	<a href="#">374</a>	615.3781	1228.7417	1228.6346	0.1071	1	2	90	1	CTLRNPPTAPR
☑	<a href="#">227</a>	450.2470	898.4795	898.4218	0.0577	0	2	1e+02	1	FATMTANK + Oxidation (M)
☑	<a href="#">440</a>	555.3415	1663.0028	1662.8511	0.1516	1	2	56	1	APKVHPLNNSCEIK
☑	<a href="#">202</a>	443.6451	885.2756	885.4014	-0.1258	0	2	54	1	HASMAEPK + Oxidation (M)
☑	<a href="#">164</a>	427.2464	852.4783	852.4718	0.0065	0	2	84	1	AAWRPPR
☑	<a href="#">282</a>	498.7780	995.5415	995.5301	0.0114	1	2	1.1e+02	1	WLEHRQK
☑	<a href="#">422</a>	483.3141	1446.9205	1446.7388	0.1817	0	1	55	1	VIPOGADSTMLATK + Oxidation (M)
☑	<a href="#">296</a>	514.2525	1026.4905	1026.5029	-0.0124	1	1	1.2e+02	1	EAARCAPGR
☑	<a href="#">413</a>	445.2000	1332.5782	1332.7150	-0.1368	1	1	1.1e+02	1	TLSPAQQRAFSK
☑	<a href="#">188</a>	435.7567	869.4989	869.3589	0.1400	0	1	98	1	EFGENMK + Oxidation (M)
☑	<a href="#">224</a>	448.7620	895.5094	895.3957	0.1137	0	1	1.1e+02	1	DMDVSVSK + Oxidation (M)
☑	<a href="#">401</a>	439.2496	1314.7269	1314.7143	0.0126	0	1	1.1e+02	1	EGLLQLTNATQK
☑	<a href="#">276</a>	491.7754	981.5362	981.4992	0.0370	1	1	1.1e+02	1	QRAEDVHK
☑	<a href="#">457</a>	494.0054	1971.9924	1971.8522	0.1401	1	1	85	1	LECMLESECTALCENRK + 2 Carbamidomethyl (C)
☑	<a href="#">200</a>	441.7684	881.5223	881.3549	0.1675	1	1	1e+02	1	SRSMDSPS + Oxidation (M)
☑	<a href="#">210</a>	444.2000	886.3854	886.4984	-0.1130	1	1	1.5e+02	1	QRIDISR
☑	<a href="#">258</a>	477.2741	952.5337	952.4865	0.0472	0	1	1.1e+02	1	EYNLLSK
☑	<a href="#">289</a>	504.2541	1006.4936	1006.6175	-0.1239	0	1	1.3e+02	1	LVPVNIQPK
☑	<a href="#">156</a>	425.7540	849.4934	849.3287	0.1647	0	1	1.4e+02	1	SNDPDMR + Oxidation (M)
☑	<a href="#">122</a>	419.2925	836.5704	836.4062	0.1642	0	1	74	1	LMQNSTK + Oxidation (M)
☑	<a href="#">464</a>	737.6628	2209.9666	2210.1167	-0.1501	1	1	76	1	ALFASQEMWLSHRQTHLR
☑	<a href="#">203</a>	444.1527	886.2909	886.4483	-0.1574	0	1	1e+02	1	AGPAWMVR
☑	<a href="#">205</a>	444.2000	886.3854	886.4589	-0.0734	0	1	1.6e+02	1	YSFFVPK
☑	<a href="#">198</a>	441.3124	880.6102	880.4654	0.1447	0	1	78	1	VNSLSSFK
☑	<a href="#">124</a>	419.3126	836.6107	836.5232	0.0876	1	1	52	1	PINLPKR
☑	<a href="#">383</a>	422.2415	1263.7026	1263.5877	0.1149	1	1	1.2e+02	1	AVKNSAESDGMR
☑	<a href="#">445</a>	441.7709	1763.0546	1762.9400	0.1147	1	1	58	1	DSRLLMASGPALYVVR + Oxidation (M)
☑	<a href="#">158</a>	425.7580	849.5015	849.3902	0.1113	0	1	1.5e+02	1	TEGPAMTK + Oxidation (M)
☑	<a href="#">186</a>	435.2566	868.4986	868.3419	0.1567	0	1	1.1e+02	1	SPSSTCK + Carbamidomethyl (C)
☑	<a href="#">331</a>	536.1732	1070.3318	1070.4129	-0.0812	0	1	50	1	CVNMMNMR + Carbamidomethyl (C); Ox:
☑	<a href="#">106</a>	413.2606	824.5066	824.3712	0.1355	0	1	83	1	QHCPGQR
☑	<a href="#">377</a>	413.1000	1236.2782	1236.4726	-0.1944	0	1	2.5	1	TFQCEMCFR + Carbamidomethyl (C); O:
☑	<a href="#">458</a>	660.6000	1978.7782	1978.9678	-0.1897	1	1	51	1	CGMILQEAMKWAPTVTK + Carbamidomethyl (C)
☑	<a href="#">183</a>	434.7516	867.4886	867.4008	0.0879	0	1	1.1e+02	1	LSTMSDSK
☑	<a href="#">191</a>	437.2405	872.4665	872.4716	-0.0051	0	1	1.7e+02	1	VGNALNSK
☑	<a href="#">341</a>	545.1211	1088.2277	1088.4267	-0.1990	0	1	2.2	1	TAFSDCTCK + 2 Carbamidomethyl (C)
☑	<a href="#">256</a>	477.2618	952.5090	952.5454	-0.0364	1	1	1.3e+02	1	ELSHLRK
☑	<a href="#">221</a>	447.3154	892.6163	892.4589	0.1575	1	1	1.1e+02	1	MGRLSWK + Oxidation (M)
☑	<a href="#">311</a>	526.3392	1050.6639	1050.4869	0.1770	0	1	1.1e+02	1	TEAYLPDDK
☑	<a href="#">139</a>	422.2616	842.5087	842.4974	0.0113	1	1	1.4e+02	1	GAKAINAAK
☑	<a href="#">126</a>	419.7563	837.4980	837.4708	0.0272	0	0	1.1e+02	1	APGGPSKPK
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☑	<a href="#">64</a>	400.2190	798.4235	798.4964	-0.0728	0	0	82	1	LGGGVGVIK
☑	<a href="#">396</a>	427.2404	1278.6992	1278.6979	0.0014	0	0	1.3e+02	1	MPPGLEPARPR
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☑	<a href="#">248</a>	468.2688	934.5230	934.4793	0.0436	0	0	1.7e+02	1	ISMEVAASK
☑	<a href="#">68</a>	405.2216	808.4287	808.4919	-0.0632	1	0	85	1	APRVAPAK
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☑	<a href="#">123</a>	419.3047	836.5949	836.4062	0.1887	0	0	78	1	LMQNSTK + Oxidation (M)
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## Search Parameters

Type of search : MS/MS Ion Search  
Enzyme : Trypsin  
Variable modifications : [Carbamidomethyl \(C\)](#), [Oxidation \(M\)](#)  
Mass values : Monoisotopic  
Protein Mass : Unrestricted  
Peptide Mass Tolerance :  $\pm 0.2$  Da  
Fragment Mass Tolerance:  $\pm 0.2$  Da  
Max Missed Cleavages : 1  
Instrument type : Default  
Number of queries : 469

Mascot: <http://www.matrixscience.com/>