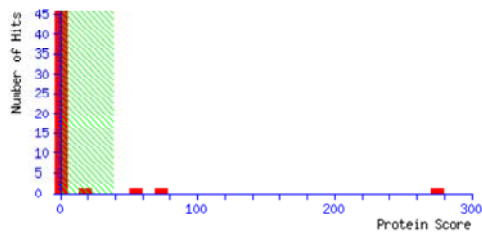



**Mascot Search Results**

User : JPROS  
 Email : pro@jbios.co.jp  
 Search title : D:\JPROS\L046\3\_4micro.wiff (sample number 1)  
 MS data file : mas208.tmp  
 Database : NCBIprot 20180429 (152462470 sequences; 55858910152 residues)  
 Taxonomy : Homo sapiens (human) (327411 sequences)  
 Timestamp : 24 Apr 2019 at 06:01:10 GMT  
 Protein hits : [NP\\_002941.1](#) dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor [Homo sapiens]  
               [EAW80914.1](#) fucosyltransferase 8 (alpha (1,6) fucosyltransferase), isoform CRA\_d [Homo sapiens]  
               [BAG36698.1](#) unnamed protein product [Homo sapiens]  
               [EAW66317.1](#) hCG2039691, partial [Homo sapiens]

### Mascot Score Histogram

Ions score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.  
 Individual ions scores  $> 38$  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	<a href="#">Help</a>
Significance threshold p<	0.05	Max. number of hits
Standard scoring	<input type="radio"/> MudPIT scoring <input checked="" type="radio"/> Display non-significant matches	Show sub-sets
Show pop-ups	<input checked="" type="radio"/> Suppress pop-ups <input type="radio"/> Sort unassigned	Decreasing Score
Preferred taxonomy	All entries	Require bold red

Error tolerant

1. [NP\\_002941.1](#) Mass: 68527 Score: 275 Matches: 13(6) Sequences: 13(6) emPAI: 0.38  
 dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 precursor [Homo sapiens]
- 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="#">232</a>	455.2902	908.5658	908.4967	0.0691	0	31	0.43	1	U	K.IDHILDAL.-
<input checked="" type="checkbox"/> <a href="#">296</a>	530.3097	1058.6049	1058.5356	0.0693	0	38	0.1	1	U	R.QPDSGISSIR.S
<input checked="" type="checkbox"/> <a href="#">306</a>	535.8451	1069.6757	1069.5768	0.0990	0	38	0.089	1	U	R.TVDLSSHAK.V
<input checked="" type="checkbox"/> <a href="#">357</a>	635.8557	1269.6968	1269.5877	0.1091	0	45	0.019	1	U	R.DVPAYSQDTFK.V
<input checked="" type="checkbox"/> <a href="#">373</a>	651.4337	1300.8528	1300.7350	0.1178	0	73	1.6e-05	1	U	K.ALTSEIALLQSR.L
<input checked="" type="checkbox"/> <a href="#">380</a>	656.3724	1310.7301	1310.6143	0.1159	0	65	0.00021	1	U	R.SEDLLDYGPF.R
<input checked="" type="checkbox"/> <a href="#">400</a>	716.8960	1431.7774	1431.6113	0.1661	0	66	0.00013	1	U	K.GEDEENNLEVR.E
<input checked="" type="checkbox"/> <a href="#">401</a>	718.4239	1434.8333	1434.6990	0.1343	0	38	0.09	1	U	K.NIEIDSPYEISR.A
<input checked="" type="checkbox"/> <a href="#">407</a>	740.9539	1479.8932	1479.7722	0.1210	0	16	8.9	1	U	K.TILPAAQDVVYR.D
<input checked="" type="checkbox"/> <a href="#">435</a>	552.0197	1653.0374	1652.8846	0.1528	0	54	0.00083	1	U	K.VTAEVVLALHGGGSTR.A
<input checked="" type="checkbox"/> <a href="#">436</a>	830.5263	1659.0380	1658.8879	0.1501	0	24	0.87	1	U	R.ATSFLLALEPEAR.L
<input checked="" type="checkbox"/> <a href="#">445</a>	582.0535	1743.1387	1742.9713	0.1674	1	64	3.5e-05	1	U	K.VACITEQVLTLVNKR.I + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">469</a>	670.7238	2009.1497	2008.9677	0.1820	0	23	1.6	1	U	K.VHYENNSPFLTITSMTR.V

Proteins matching the same set of peptides:

[CAG33023.1](#) Mass: 68564 Score: 275 Matches: 13(6) Sequences: 13(6)  
 RPN1 [Homo sapiens]  
[BAD97315.1](#) Mass: 68537 Score: 275 Matches: 13(6) Sequences: 13(6)  
 ribophorin I variant, partial [Homo sapiens]

2. [EAW80914.1](#) Mass: 51782 Score: 78 Matches: 3(2) Sequences: 3(2) emPAI: 0.15  
 fucosyltransferase 8 (alpha (1,6) fucosyltransferase), isoform CRA\_d [Homo sapiens]
- 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="#">261</a>	479.3286	956.6426	956.5542	0.0884	0	18	8.3	1	U	R.VLEBQLVK.A
<input checked="" type="checkbox"/> <a href="#">392</a>	667.9322	1333.8498	1333.7129	0.1369	0	58	0.0006	1	U	R.VYLATDDPSLLK.E
<input checked="" type="checkbox"/> <a href="#">398</a>	710.4178	1418.8210	1418.7518	0.0693	0	43	0.025	1	U	R.IPEGPIDQGPVIGR.V

Proteins matching the same set of peptides:

[BAF85102.1](#) Mass: 66474 Score: 78 Matches: 3(2) Sequences: 3(2)  
 unnamed protein product [Homo sapiens]  
[NP\\_835368.1](#) Mass: 66474 Score: 78 Matches: 3(2) Sequences: 3(2)  
 alpha-(1,6)-fucosyltransferase isoform a [Homo sapiens]  
[XP\\_016876625.1](#) Mass: 70347 Score: 78 Matches: 3(2) Sequences: 3(2)

alpha-(1,6)-fucosyltransferase isoform X1 [Homo sapiens]  
[XP\\_016876629.1](#) Mass: 62866 Score: 78 Matches: 3(2) Sequences: 3(2)  
 alpha-(1,6)-fucosyltransferase isoform X2 [Homo sapiens]

3. [BAG36698.1](#) Mass: 65980 Score: 63 Matches: 3(1) Sequences: 3(1) emPAI: 0.06  
 unnamed protein product [Homo sapiens]  
 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="#">305</a>	533.3160	1064.6174	1064.5138	0.1036	0	19	8.9	1	U	K.AQYEDIAQK.S
<input checked="" type="checkbox"/> <a href="#">374</a>	651.9040	1301.7934	1301.7078	0.0856	0	37	0.094	1	U	R.SLDLDSIIAEVK.A
<input checked="" type="checkbox"/> <a href="#">406</a>	738.4803	1474.9461	1474.7780	0.1681	0	55	0.001	1	U	R.FLEQQNQVLQTK.W

Proteins matching the same set of peptides:  
[NP\\_006112.3](#) Mass: 65999 Score: 63 Matches: 3(1) Sequences: 3(1)  
 keratin, type II cytoskeletal 1 [Homo sapiens]  
[AAG41947.1](#) Mass: 66027 Score: 63 Matches: 3(1) Sequences: 3(1)  
 keratin 1 [Homo sapiens]  
[AFA52002.1](#) Mass: 66013 Score: 63 Matches: 3(1) Sequences: 3(1)  
 keratin 1 [Homo sapiens]  
[AFA52003.1](#) Mass: 66029 Score: 63 Matches: 3(1) Sequences: 3(1)  
 keratin 1 [Homo sapiens]  
[AFA52004.1](#) Mass: 65930 Score: 63 Matches: 3(1) Sequences: 3(1)  
 keratin 1 [Homo sapiens]  
[AFA52005.1](#) Mass: 66086 Score: 63 Matches: 3(1) Sequences: 3(1)  
 keratin 1 [Homo sapiens]  
[AFA52007.1](#) Mass: 66071 Score: 63 Matches: 3(1) Sequences: 3(1)  
 keratin 1 [Homo sapiens]

4. [EAW66317.1](#) Mass: 1934 Score: 13 Matches: 1(0) Sequences: 1(0)  
 hCG2039691, partial [Homo sapiens]  
 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="#">156</a>	422.2909	842.5672	842.3995	0.1677	1	13	30	1	U	K.GNTHTRGT.-

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="#">231</a>	455.2703	908.5261	908.4030	0.1230	0	19	7.9	1		LVCMAQGR + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">154</a>	421.7883	841.5620	841.5022	0.0599	0	19	6.6	1		GITLSVRP
<input checked="" type="checkbox"/> <a href="#">454</a>	897.9941	1793.9736	1793.9321	0.0416	0	18	6.8	1		CLGHLFLSLGMVYLR + Carbamidomethyl (C); Oxidation
<input checked="" type="checkbox"/> <a href="#">155</a>	421.7939	841.5733	841.5022	0.0711	0	18	8.2	1		GITLSVRP
<input checked="" type="checkbox"/> <a href="#">309</a>	538.3752	1074.7359	1074.5855	0.1503	1	17	8.2	1		MLALSEQKR
<input checked="" type="checkbox"/> <a href="#">286</a>	523.3197	1044.6248	1044.5564	0.0684	0	17	12	1		LSSDGLQVAR
<input checked="" type="checkbox"/> <a href="#">291</a>	523.3411	1044.6676	1044.6179	0.0497	0	17	13	1		ILAINSSSLK
<input checked="" type="checkbox"/> <a href="#">274</a>	513.3264	1024.6382	1024.6030	0.0353	0	16	16	1		IGGIGTVPVGR
<input checked="" type="checkbox"/> <a href="#">288</a>	523.3288	1044.6430	1044.5564	0.0867	0	15	19	1		LSSDGLQVAR
<input checked="" type="checkbox"/> <a href="#">283</a>	523.3145	1044.6144	1044.6583	-0.0439	0	15	21	1		LLTTFLEPIK
<input checked="" type="checkbox"/> <a href="#">289</a>	523.3294	1044.6442	1044.6583	-0.0141	0	15	21	1		LLTTFLEPIK
<input checked="" type="checkbox"/> <a href="#">115</a>	412.7827	823.5508	823.4487	0.1021	1	15	13	1		VPRCPFR
<input checked="" type="checkbox"/> <a href="#">176</a>	428.7934	855.5722	855.5429	0.0292	0	14	21	1		LVLSSLPK
<input checked="" type="checkbox"/> <a href="#">290</a>	523.3371	1044.6597	1044.5273	0.1324	1	14	27	1		EMAKASAPQL
<input checked="" type="checkbox"/> <a href="#">284</a>	523.3147	1044.6148	1044.5199	0.0949	1	13	32	1		AEKDNAEIR
<input checked="" type="checkbox"/> <a href="#">210</a>	445.1384	888.2623	888.4553	-0.1930	0	13	21	1		GDDVAVSVK
<input checked="" type="checkbox"/> <a href="#">119</a>	413.2965	824.5784	824.4253	0.1531	0	13	16	1		HVQASQR
<input checked="" type="checkbox"/> <a href="#">287</a>	523.3262	1044.6379	1044.6179	0.0200	0	12	40	1		ILAINSSSLK
<input checked="" type="checkbox"/> <a href="#">285</a>	523.3170	1044.6195	1044.6583	-0.0388	0	12	42	1		LLTTFLEPIK
<input checked="" type="checkbox"/> <a href="#">211</a>	445.1539	888.2933	888.3825	-0.0892	0	12	44	1		QETGDDPK
<input checked="" type="checkbox"/> <a href="#">152</a>	420.2000	838.3854	838.3677	0.0177	0	12	29	1		MDAVMTR + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">383</a>	657.8621	1313.7097	1313.6146	0.0951	1	11	45	1		ERASDVDMVR
<input checked="" type="checkbox"/> <a href="#">455</a>	599.3000	1794.8782	1794.9740	-0.0959	0	11	41	1		VPEHIPPLNAPSVQAR
<input checked="" type="checkbox"/> <a href="#">218</a>	446.1181	890.2216	890.4028	-0.1812	0	11	13	1		AQAACANSR
<input checked="" type="checkbox"/> <a href="#">221</a>	446.2888	890.5630	890.4134	0.1496	1	10	72	1		WEDKDAK
<input checked="" type="checkbox"/> <a href="#">332</a>	411.2099	1230.6078	1230.6179	-0.0101	0	10	71	1		TPQPAKPYACR
<input checked="" type="checkbox"/> <a href="#">269</a>	493.3316	984.6486	984.5063	0.1423	0	10	55	1		SVCPVDLPR
<input checked="" type="checkbox"/> <a href="#">175</a>	428.7908	855.5670	855.5178	0.0493	0	10	52	1		LSIIPASR
<input checked="" type="checkbox"/> <a href="#">228</a>	451.2916	900.5687	900.5029	0.0658	1	10	79	1		LQEIDKR
<input checked="" type="checkbox"/> <a href="#">402</a>	481.3108	1440.9107	1440.7361	0.1746	1	10	35	1		EYTSNVFLQGKR
<input checked="" type="checkbox"/> <a href="#">292</a>	523.3521	1044.6897	1044.5273	0.1624	1	9	63	1		EMAKASAPQL
<input checked="" type="checkbox"/> <a href="#">103</a>	409.2673	816.5201	816.3986	0.1215	0	9	74	1		MAVMPPR + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">220</a>	446.2743	890.5340	890.4168	0.1172	0	9	94	1		TADLGSPEK
<input checked="" type="checkbox"/> <a href="#">181</a>	430.3057	858.5968	858.4382	0.1587	0	9	95	1		CGKPGNVK + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">174</a>	428.2897	854.5649	854.5086	0.0563	1	9	58	1		LRVGAPSR
<input checked="" type="checkbox"/> <a href="#">241</a>	462.2415	922.4685	922.4113	0.0572	0	9	86	1		TCTCRPSR
<input checked="" type="checkbox"/> <a href="#">315</a>	599.3000	1196.5854	1196.5898	-0.0043	0	9	84	1		TNVEHLSGGQR
<input checked="" type="checkbox"/> <a href="#">244</a>	465.2809	928.5473	928.4290	0.1183	0	9	98	1		EYQAAYGK
<input checked="" type="checkbox"/> <a href="#">180</a>	429.2339	856.4532	856.4767	-0.0234	0	8	1.1e+02	1		TPATQAIR
<input checked="" type="checkbox"/> <a href="#">253</a>	476.2839	950.5532	950.5185	0.0347	1	8	97	1		ASGNKTVFK
<input checked="" type="checkbox"/> <a href="#">170</a>	427.2744	852.5342	852.5657	-0.0315	1	8	67	1		LARPRLK
<input checked="" type="checkbox"/> <a href="#">128</a>	416.2563	830.4981	830.3923	0.1058	0	8	1e+02	1		FEGPFR
<input checked="" type="checkbox"/> <a href="#">157</a>	423.2514	844.4882	844.3749	0.1134	0	8	1.3e+02	1		ESICHEK
<input checked="" type="checkbox"/> <a href="#">109</a>	411.2159	820.4173	820.3749	0.0424	0	8	76	1		CTANDLK + Carbamidomethyl (C)
<input checked="" type="checkbox"/> <a href="#">467</a>	664.4136	1990.2191	1990.0272	0.1919	1	8	27	1		VFLTGGDLPALDGARADFR
<input checked="" type="checkbox"/> <a href="#">97</a>	409.1689	816.3232	816.3661	-0.0429	1	8	1e+02	1		CPRGNDR

<input checked="" type="checkbox"/>	<a href="#">123</a>	415.1883	828.3620	828.4705	-0.1085	0	8	92	1	DQVVGLAK
<input checked="" type="checkbox"/>	<a href="#">158</a>	423.2660	844.5175	844.3902	0.1273	0	8	1.4e+02	1	MGFTFAR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">239</a>	458.8282	915.6419	915.4848	0.1571	0	8	98	1	LVCLAIGN + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">432</a>	401.1953	1600.7523	1600.7708	-0.0185	0	8	94	1	EYHIPCPYQAVPK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">244</a>	445.2000	888.3854	888.4739	-0.0884	0	7	1.6e+02	1	MTVLGQPK + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">85</a>	405.2617	808.5089	808.3571	0.1518	1	7	69	1	KGACDMK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">219</a>	446.1309	890.2472	890.4466	-0.1994	1	7	63	1	MPLSCRK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">101</a>	409.2644	816.5143	816.3912	0.1231	0	7	1.2e+02	1	AAGPVSCR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">255</a>	476.2985	950.5825	950.4314	0.1511	0	7	1.3e+02	1	MGACDLIR + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">92</a>	408.3413	814.6681	814.4912	0.1769	1	7	33	1	ATVTKAPK
<input checked="" type="checkbox"/>	<a href="#">390</a>	445.2000	1332.5782	1332.7006	-0.1224	1	7	1.3e+02	1	MAALKALVSGCGR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">168</a>	426.2929	850.5712	850.3716	0.1997	1	7	1e+02	1	RDCSGSTR
<input checked="" type="checkbox"/>	<a href="#">411</a>	519.0002	1553.9788	1553.8565	0.1222	0	7	50	1	ASSEQALWLLPAR
<input checked="" type="checkbox"/>	<a href="#">248</a>	474.2740	946.5334	946.5447	-0.0114	1	7	1.6e+02	1	TLGKSNSIK
<input checked="" type="checkbox"/>	<a href="#">278</a>	517.3210	1032.6274	1032.5209	0.1066	1	7	1.5e+02	1	CTCPVLKGR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">443</a>	431.7090	1722.8071	1722.8002	0.0069	1	7	1.1e+02	1	YTGWTYYADSVKGR
<input checked="" type="checkbox"/>	<a href="#">166</a>	425.7991	849.5836	849.4127	0.1710	1	7	1.3e+02	1	EAMTRAR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">273</a>	506.3201	1010.6256	1010.5145	0.1112	1	7	1.2e+02	1	EGHAKAAK
<input checked="" type="checkbox"/>	<a href="#">108</a>	411.2099	820.4052	820.4807	-0.0754	0	7	1.1e+02	1	ILIGYSR
<input checked="" type="checkbox"/>	<a href="#">171</a>	427.2775	852.5404	852.4705	0.0699	1	6	1e+02	1	KSASFVK
<input checked="" type="checkbox"/>	<a href="#">126</a>	415.2620	828.5095	828.4818	0.0277	0	6	1.3e+02	1	QSVVQIR
<input checked="" type="checkbox"/>	<a href="#">246</a>	469.3466	936.6786	936.5393	0.1394	0	6	65	1	EAVPVPVR
<input checked="" type="checkbox"/>	<a href="#">351</a>	420.2000	1257.5782	1257.6863	-0.1082	1	6	1.7e+02	1	APRGLVETMLR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">429</a>	401.1878	1600.7222	1600.7708	-0.0486	0	6	1.3e+02	1	EYHIPCPYQAVPK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">256</a>	476.3164	950.6182	950.4491	0.1690	1	6	1.5e+02	1	CTKVGGS DK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">453</a>	447.1516	1784.5772	1784.7610	-0.1839	0	6	13	1	SRPYEGFDPMSPAR + Carbamidomethyl (C); Oxidation
<input checked="" type="checkbox"/>	<a href="#">195</a>	435.8093	869.6040	869.4971	0.1069	0	6	1.2e+02	1	VDLATVPR
<input checked="" type="checkbox"/>	<a href="#">252</a>	476.2000	950.3854	950.4426	-0.0571	1	6	1.8e+02	1	CGIRSCQK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">202</a>	441.2632	880.5118	880.4225	0.0893	0	6	1.6e+02	1	GSFLAACR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">412</a>	519.3000	1554.8782	1554.8294	0.0488	0	6	1.4e+02	1	DGLELEPDFNVVPK
<input checked="" type="checkbox"/>	<a href="#">122</a>	414.8002	827.5859	827.4865	0.0994	1	6	1.4e+02	1	VPDTRK
<input checked="" type="checkbox"/>	<a href="#">265</a>	488.3050	974.5954	974.5297	0.0656	1	5	2.1e+02	1	NWTLASKR
<input checked="" type="checkbox"/>	<a href="#">259</a>	479.2845	956.5545	956.5113	0.0432	1	5	1.9e+02	1	LMKVHSDK
<input checked="" type="checkbox"/>	<a href="#">98</a>	409.2132	816.4118	816.4164	-0.0046	0	5	1.9e+02	1	CAALTGPK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">270</a>	494.3322	986.6499	986.4716	0.1783	1	5	1.9e+02	1	MNSAAGHRK + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">375</a>	435.2720	1302.7943	1302.6667	0.1276	0	5	1.7e+02	1	VVETELQEGATK
<input checked="" type="checkbox"/>	<a href="#">178</a>	429.1174	856.2202	856.3762	-0.1561	0	5	36	1	HACAGWR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	<a href="#">179</a>	429.2000	856.3854	856.4766	-0.0912	0	5	2.4e+02	1	NELAALAR
<input checked="" type="checkbox"/>	<a href="#">213</a>	445.1754	888.3363	888.4552	-0.1190	0	5	2.5e+02	1	DGSEAGLIK
<input checked="" type="checkbox"/>	<a href="#">240</a>	462.2329	922.4513	922.4430	0.0083	0	5	2e+02	1	IESSACVSK
<input checked="" type="checkbox"/>	<a href="#">198</a>	437.2579	872.5012	872.3884	0.1127	1	5	2.7e+02	1	CFMKGSK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">280</a>	519.3000	1036.5854	1036.5124	0.0730	0	5	2e+02	1	GHMVQPAGPK + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">234</a>	455.3272	908.6398	908.5080	0.1318	0	5	1.2e+02	1	QPGAVGGPVK
<input checked="" type="checkbox"/>	<a href="#">162</a>	424.3315	846.6485	846.4559	0.1926	1	5	93	1	ELSRASAGK
<input checked="" type="checkbox"/>	<a href="#">100</a>	409.2622	816.5099	816.4164	0.0935	0	5	2.1e+02	1	EGIPVMR + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">316</a>	599.4229	1196.8312	1196.7128	0.1184	1	5	68	1	LSKDPNIVIAK
<input checked="" type="checkbox"/>	<a href="#">169</a>	426.2951	850.5756	850.4153	0.1603	1	5	1.6e+02	1	ALKMCCR + Carbamidomethyl (C); Oxidation (M)
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<input checked="" type="checkbox"/>	<a href="#">451</a>	445.1626	1776.6211	1776.8022	-0.1811	0	3	86	1	TSEHINEGETAMLVCK + 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 : 486

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