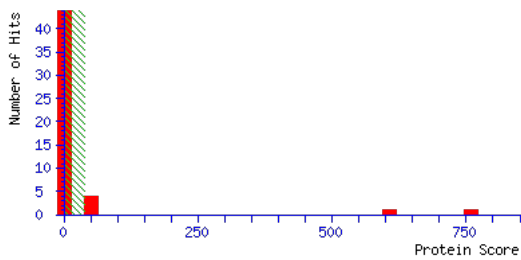


# MASCOT SCIENCE Mascot Search Results

User : Ye-jin Kim  
 Email : yejinil@hotmail.com  
 Search title :  
 MS data file : SN20130111-geno1.mgf  
 Database : NCBI nr 20130106 (22470027 sequences; 7722991751 residues)  
 Taxonomy : Homo sapiens (human) (247607 sequences)  
 : Error tolerant search of all significant protein hits  
 Timestamp : 14 Jan 2013 at 01:23:27 GMT  
 Protein hits : [gi|1160963](#) transmembrane protein [Homo sapiens]  
               [gi|194390140](#) unnamed protein product [Homo sapiens]  
               [gi|14042135](#) unnamed protein product [Homo sapiens]  
               [gi|442920](#) Chain B, X-Ray Structures Of The Antigen-Binding Domains From Three Variants Of Humanized Anti-P185-Her2 Antibody 4d5  
               [gi|39938034](#) immunoglobulin heavy chain variable region [Homo sapiens]  
               [gi|37777958](#) immunoglobulin heavy chain variable region [Homo sapiens]  
               [gi|119602666](#) topoisomerase (DNA) I, mitochondrial, isoform CRA\_b [Homo sapiens]

## 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 > 39 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  [Help](#)

Significance threshold  $p <$   Max. number of hits  Hide error tolerant matches

Standard scoring  MudPIT scoring  Ions score or expect cut-off  Show sub-sets

Show pop-ups  Suppress pop-ups  Sort unassigned  Require bold red

Preferred taxonomy

Error tolerant

1. [gi|1160963](#) Mass: 83616 Score: 759 Matches: 38(18) Sequences: 33(18) emPAI: 1.60  
 transmembrane protein [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> <a href="#">50</a>	402.2269	802.4391	802.4185	25.8	0	26	1.7	1	U	K.SLEDALR.Q
<input checked="" type="checkbox"/> <a href="#">51</a>	424.2040	846.3935	846.3773	19.2	0	30	0.77	1		K.WDSHFR.E
<input checked="" type="checkbox"/> <a href="#">93</a>	490.2666	978.5186	978.5056	13.3	0	31	0.48	1		K.ISSVSEVMK.E
<input checked="" type="checkbox"/> <a href="#">94</a>	501.7945	1001.5745	1001.5505	24.0	1	33	0.36	1		R.TVEGALKER.R
<input checked="" type="checkbox"/> <a href="#">97</a>	508.2966	1014.5787	1014.5611	17.4	1	24	2.4	2		R.RVAQDWLK.E
<input checked="" type="checkbox"/> <a href="#">99</a>	518.3045	1034.5945	1034.5760	17.9	0	47	0.01	1		K.QHITLALAK.Q + Gln->pyro-Glu (N-term Q)
<input checked="" type="checkbox"/> <a href="#">105</a>	558.3130	1114.6114	1114.5870	21.9	0	52	0.0042	1		K.AVDEAADALLK.A
<input checked="" type="checkbox"/> <a href="#">107</a>	575.3061	1148.5976	1148.5826	13.1	0	71	4.8e-05	1		K.LSEQELQFR.R
<input checked="" type="checkbox"/> <a href="#">108</a>	577.3215	1152.6285	1152.5887	34.5	0	23	2.8	1	U	R.ERPPEEVAAR.L
<input checked="" type="checkbox"/> <a href="#">112</a>	589.3375	1176.6604	1176.6251	30.0	1	59	0.00085	1		K.FVNQLKGESR.R
<input checked="" type="checkbox"/> <a href="#">117</a>	623.3138	1244.6130	1244.5885	19.7	0	45	0.022	1		R.YSTSGSSGLTTGK.I
<input checked="" type="checkbox"/> <a href="#">124</a>	636.8723	1271.7300	1271.7085	16.9	1	56	0.0015	1	U	K.QEAVKIESLAK.S
<input checked="" type="checkbox"/> <a href="#">143</a>	653.3605	1304.7064	1304.6837	17.4	1	7	1.1e+02	4		K.LSEQELQFRR.L
<input checked="" type="checkbox"/> <a href="#">145</a>	670.3560	1338.6974	1338.6701	20.4	1	53	0.0024	1		K.ISSVSEVMKESK.Q + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">171</a>	697.9034	1393.7923	1393.7718	14.7	0	39	0.06	1		K.AHQLWLSVEALK.Y
<input checked="" type="checkbox"/> <a href="#">176</a>	714.8347	1427.6549	1427.6239	21.7	0	(43)		1		R.YSTSGSSGLTTGK.I + [+183.0354 at N-term Y]
<input checked="" type="checkbox"/> <a href="#">178</a>	493.6179	1477.8317	1477.7889	29.0	0	36	0.12	1		K.EVAGAKPHITAAEGK.L
<input checked="" type="checkbox"/> <a href="#">179</a>	755.4261	1508.8377	1508.8021	23.6	0	(67)	0.00014	1	U	K.LHNIVDLNVDVVK.K
<input checked="" type="checkbox"/> <a href="#">183</a>	761.9547	1521.8948	1521.8667	18.5	1	75	1.7e-05	1		R.KAHQLWLSVEALK.Y
<input checked="" type="checkbox"/> <a href="#">184</a>	763.4174	1524.8202	1524.8300	-6.45	0	74		1	U	K.LHNIVDLNVDVVK.K + [+16.0279 at M4]
<input checked="" type="checkbox"/> <a href="#">185</a>	764.4322	1526.8499	1526.8205	19.2	0	77	1.1e-05	1	U	K.VVSQYHELVDVQAR.D
<input checked="" type="checkbox"/> <a href="#">186</a>	764.4608	1526.9070	1526.8205	56.6	0	(7)	98	3	U	K.VVSQYHELVDVQAR.D
<input checked="" type="checkbox"/> <a href="#">193</a>	792.4393	1582.8640	1582.8243	25.1	0	64	0.00022	1		R.ELDSITPEVLPGWK.G
<input checked="" type="checkbox"/> <a href="#">194</a>	529.2911	1584.8516	1584.8121	24.9	1	(18)	9	1		R.QAAHTDHLRDVLR.V + Gln->pyro-Glu (N-term Q)
<input checked="" type="checkbox"/> <a href="#">195</a>	534.9666	1601.8781	1601.8386	24.6	1	42	0.032	1		R.QAAHTDHLRDVLR.V
<input checked="" type="checkbox"/> <a href="#">198</a>	551.9828	1652.9265	1652.8920	20.9	1	37	0.11	2	U	K.LHNIVDLNVDVVK.V + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">200</a>	554.9719	1661.8939	1661.8485	27.3	0	16	17	1		K.LSTDLDLSLAHAHR.R
<input checked="" type="checkbox"/> <a href="#">221</a>	579.0173	1734.0300	1733.9788	29.5	2	47	0.0098	1		K.KKEVAGAKPHITAAEGK.L
<input checked="" type="checkbox"/> <a href="#">226</a>	912.4625	1822.9104	1822.8809	16.2	0	108	7.5e-09	1		R.GIEQAVQSHAVAEER.K
<input checked="" type="checkbox"/> <a href="#">257</a>	938.0184	1874.0222	1874.0012	11.2	0	24	2.1	1		K.LFEMVLGPAAYNVPLPK.K + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">260</a>	651.3505	1951.0298	1950.9759	27.6	1	32	0.31	1		R.GIEQAVQSHAVAEER.K
<input checked="" type="checkbox"/> <a href="#">269</a>	1033.0228	2064.0311	2064.0011	14.5	1	76	1.2e-05	1		R.VQEELKSEFEQNLSEK.L

<input checked="" type="checkbox"/>	<a href="#">270</a>	698.3724	2092.0953	2092.0661	14.0	1	49	0.0057	1		R.LRGIEQAVQSHAVAEVEEAR.K	
<input checked="" type="checkbox"/>	<a href="#">284</a>	865.7773	2594.3102	2594.2460	24.8	0	12		31	1	U	K.TDHPEIGEGKPTPALSEEASSSSIR.E
<input checked="" type="checkbox"/>	<a href="#">286</a>	667.3469	2665.3585	2665.3130	17.1	1	(13)		18	1		K.GMSVSDLADKLSTDDLNSLIAHAHR.R
<input checked="" type="checkbox"/>	<a href="#">287</a>	671.4000	2681.5709	2681.3079	98.1	1	52	0.0026	1			K.GMSVSDLADKLSTDDLNSLIAHAHR.R + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">290</a>	944.8817	2831.6233	2831.5253	34.6	0	69	4.1e-05	1			R.QTASVTLQAIQAQNAVQAVNAHSNLIK.A
<input checked="" type="checkbox"/>	<a href="#">294</a>	1065.8890	3194.6453	3194.5731	22.6	2	8		47	1		R.VQEQLKSEFEQNLSEKLEQELQFR.R

Proteins matching the same set of peptides:

<a href="#">gi 31873242</a>	Mass: 82564	Score: 759	Matches: 38(18)	Sequences: 33(18)
hypothetical protein [Homo sapiens]				
<a href="#">gi 48145703</a>	Mass: 83628	Score: 759	Matches: 38(18)	Sequences: 33(18)
IMMT [Homo sapiens]				
<a href="#">gi 154354964</a>	Mass: 83626	Score: 759	Matches: 38(18)	Sequences: 33(18)
mitochondrial inner membrane protein isoform 1 [Homo sapiens]				
<a href="#">gi 154354966</a>	Mass: 82574	Score: 759	Matches: 38(18)	Sequences: 33(18)
mitochondrial inner membrane protein isoform 3 [Homo sapiens]				
<a href="#">gi 189053377</a>	Mass: 83640	Score: 759	Matches: 38(18)	Sequences: 33(18)
unnamed protein product [Homo sapiens]				

2. [gi|194390140](#) Mass: 73111 Score: 586 Matches: 30(15) Sequences: 27(15) emPAI: 1.56  
unnamed protein product [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
<a href="#">51</a>	424.2040	846.3935	846.3773	19.2	0	30	0.77	1	1	K.WDSHFR.E	
<a href="#">93</a>	490.2666	978.5186	978.5056	13.3	0	31	0.48	1	1	K.ISSVSEVMK.E	
<a href="#">94</a>	501.7945	1001.5745	1001.5505	24.0	1	33	0.36	1	1	R.TVEGALKER.R	
<a href="#">97</a>	508.2966	1014.5787	1014.5611	17.4	1	24	2.4	2	1	R.RVAQDWLK.E	
<a href="#">99</a>	518.3045	1034.5945	1034.5760	17.9	0	47	0.01	1	1	K.QHITLALEK.Q + Gln->pyro-Glu (N-term Q)	
<a href="#">105</a>	558.3130	1114.6114	1114.5870	21.9	0	52	0.0042	1	1	K.AVDEAADALLK.A	
<a href="#">107</a>	575.3061	1148.5976	1148.5826	13.1	0	71	4.8e-05	1	1	K.LSEQELQFR.R	
<a href="#">112</a>	589.3375	1176.6604	1176.6251	30.0	1	59	0.00085	1	1	K.FVNQLKGESR.R	
<a href="#">117</a>	623.3138	1244.6130	1244.5885	19.7	0	45	0.022	1	1	R.YSTSGSSGLTTGK.I	
<a href="#">143</a>	653.3605	1304.7064	1304.6837	17.4	1	7	1.1e+02	4	1	K.LSEQELQFR.L	
<a href="#">145</a>	670.3560	1338.6974	1338.6701	20.4	1	53	0.0024	1	1	K.ISSVSEVMKESK.Q + Oxidation (M)	
<a href="#">171</a>	697.9034	1393.7923	1393.7718	14.7	0	39	0.06	1	1	K.AHQLWLSVEALK.Y	
<a href="#">176</a>	714.8347	1427.6549	1427.6239	21.7	0	(43)		1	1	R.YSTSGSSGLTTGK.I + [+183.0354 at N-term Y]	
<a href="#">178</a>	493.6179	1477.8317	1477.7889	29.0	0	36	0.12	1	1	K.EVAGAKPHITAAEGK.L	
<a href="#">183</a>	761.9547	1521.8948	1521.8667	18.5	1	75	1.7e-05	1	1	R.KAHQLWLSVEALK.Y	
<a href="#">193</a>	792.4393	1582.8640	1582.8243	25.1	0	64	0.00022	1	1	R.ELDSITPEVLPQWK.G	
<a href="#">194</a>	529.2911	1584.8516	1584.8121	24.9	1	(18)		9	1	R.QAAAHTDHLRDVLR.V + Gln->pyro-Glu (N-term Q)	
<a href="#">195</a>	534.9666	1601.8781	1601.8386	24.6	1	42	0.032	1	1	R.QAAAHTDHLRDVLR.V	
<input checked="" type="checkbox"/>	<a href="#">198</a>	551.9828	1652.9265	1652.8192	64.9	0	40	1	1	U	K.LHNMIVDLDNVQAR.D + Oxidation (M); [-99.0796 at C-term R]
<a href="#">200</a>	554.9719	1661.8939	1661.8485	27.3	0	16	17	1	1	K.LSTDDLNSLIAHAHR.R	
<a href="#">221</a>	579.0173	1734.0300	1733.9788	29.5	2	47	0.0098	1	1	K.KKEVAGAKPHITAAEGK.L	
<a href="#">226</a>	912.4625	1822.9104	1822.8809	16.2	0	108	7.5e-09	1	1	R.GIEQAVQSHAVAEVEEAR.K	
<a href="#">257</a>	938.0184	1874.0222	1874.0012	11.2	0	24	2.1	1	1	K.LFEMVGLGPAAYNVPLPK.K + Oxidation (M)	
<a href="#">260</a>	651.3505	1951.0298	1950.9759	27.6	1	32	0.31	1	1	R.GIEQAVQSHAVAEVEEAR.K	
<a href="#">269</a>	1033.0228	2064.0311	2064.0011	14.5	1	76	1.2e-05	1	1	R.VQEQLKSEFEQNLSEK.L	
<a href="#">270</a>	698.3724	2092.0953	2092.0661	14.0	1	49	0.0057	1	1	R.LRGIEQAVQSHAVAEVEEAR.K	
<a href="#">286</a>	667.3469	2665.3585	2665.3130	17.1	1	(13)		18	1	K.GMSVSDLADKLSTDDLNSLIAHAHR.R	
<a href="#">287</a>	671.4000	2681.5709	2681.3079	98.1	1	52	0.0026	1	1	K.GMSVSDLADKLSTDDLNSLIAHAHR.R + Oxidation (M)	
<a href="#">290</a>	944.8817	2831.6233	2831.5253	34.6	0	69	4.1e-05	1	1	R.QTASVTLQAIQAQNAVQAVNAHSNLIK.A	
<a href="#">294</a>	1065.8890	3194.6453	3194.5731	22.6	2	8		47	1	R.VQEQLKSEFEQNLSEKLEQELQFR.R	

3. [gi|14042135](#) Mass: 87881 Score: 70 Matches: 4(2) Sequences: 4(2) emPAI: 0.13  
unnamed protein product [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
<input checked="" type="checkbox"/>	<a href="#">146</a>	675.8597	1349.7048	1349.6827	16.4	1	45	0.026	1	U	R.AYEVLKDEDLR.K
<input checked="" type="checkbox"/>	<a href="#">177</a>	739.9044	1477.7943	1477.7776	11.3	2	32	0.3	1	U	R.AYEVLKDEDLRK.K
<input checked="" type="checkbox"/>	<a href="#">186</a>	764.4608	1526.9070	1526.9031	2.52	1	52	0.0032	1	U	K.AIAALISEKLETLR.N
<input checked="" type="checkbox"/>	<a href="#">266</a>	676.6900	2027.0481	2026.9973	25.0	1	9	64	2	U	K.LHPDKNPNNAHGDFLK.I

Proteins matching the same set of peptides:

<a href="#">gi 14042569</a>	Mass: 90981	Score: 70	Matches: 4(2)	Sequences: 4(2)
unnamed protein product [Homo sapiens]				
<a href="#">gi 24308127</a>	Mass: 91021	Score: 70	Matches: 4(2)	Sequences: 4(2)
dnaJ homolog subfamily C member 10 isoform 1 precursor [Homo sapiens]				
<a href="#">gi 25140577</a>	Mass: 91049	Score: 70	Matches: 4(2)	Sequences: 4(2)
ER-resident protein ERdj5 [Homo sapiens]				
<a href="#">gi 37182276</a>	Mass: 86072	Score: 70	Matches: 4(2)	Sequences: 4(2)
disulfide isomerase [Homo sapiens]				
<a href="#">gi 109658554</a>	Mass: 91012	Score: 70	Matches: 4(2)	Sequences: 4(2)
DnaJ (Hsp40) homolog, subfamily C, member 10 [Homo sapiens]				
<a href="#">gi 119631364</a>	Mass: 94501	Score: 70	Matches: 4(2)	Sequences: 4(2)
DnaJ (Hsp40) homolog, subfamily C, member 10, isoform CRA_a [Homo sapiens]				
<a href="#">gi 409971397</a>	Mass: 86081	Score: 70	Matches: 4(2)	Sequences: 4(2)
dnaJ homolog subfamily C member 10 isoform 2 precursor [Homo sapiens]				

4. [gi|442920](#) Mass: 23686 Score: 58 Matches: 2(1) Sequences: 2(1) emPAI: 0.35  
Chain B, X-Ray Structures Of The Antigen-Binding Domains From Three Variants Of Humanized Anti-P185-Her2 Antibody 4d5 And Comparison With Molecular

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
<input checked="" type="checkbox"/>	<a href="#">103</a>	542.7838	1083.5530	1083.5349	16.7	0	33	0.3	1	U	R.IYPTNGYTR.Y
<input checked="" type="checkbox"/>	<a href="#">113</a>	593.8393	1185.6641	1185.6394	20.9	0	51	0.0051	1	1	K.GPSVFLAPSSK.S

Proteins matching the same set of peptides:

[gi|442924](#) Mass: 23708 Score: 58 Matches: 2(1) Sequences: 2(1)  
Chain B, X-Ray Structures Of The Antigen-Binding Domains From Three Variants Of Humanized Anti-P185-Her2 Antibody 4d5 And Comparison With Molecu  
[gi|213424086](#) Mass: 24518 Score: 58 Matches: 2(1) Sequences: 2(1)  
Chain H, Dual Specific Bhl Fab In Complex With Vegf

5. [gi|39938034](#) Mass: 15060 Score: 51 Matches: 2(1) Sequences: 2(1) emPAI: 0.26  
immunoglobulin heavy chain variable region [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">113</a>	593.8393	1185.6641	1185.6394	20.9	0	51	0.0051	1		K.GPSVFLAPSSK.S
<a href="#">282</a>	624.4000	2493.5709	2493.0974	190	0	3	2.3e+02	7	U	R.NQVVLMTNMDPVDSGTYICAR.M + Oxidation (M)

Proteins matching the same set of peptides:

[gi|39938066](#) Mass: 15074 Score: 51 Matches: 2(1) Sequences: 2(1)  
immunoglobulin heavy chain variable region [Homo sapiens]  
[gi|39938122](#) Mass: 15000 Score: 51 Matches: 2(1) Sequences: 2(1)  
immunoglobulin heavy chain variable region [Homo sapiens]

6. [gi|37777958](#) Mass: 16099 Score: 51 Matches: 2(1) Sequences: 2(1) emPAI: 0.24  
immunoglobulin heavy chain variable region [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">113</a>	593.8393	1185.6641	1185.6394	20.9	0	51	0.0051	1		K.GPSVFLAPSSK.S
<a href="#">189</a>	771.8000	1541.5854	1541.7872	-130.83	1	1	4.1e+02	4	U	K.STRTVYMELSSLR.S

7. [gi|119602666](#) Mass: 30466 Score: 16 Matches: 1(0) Sequences: 1(0) emPAI: 0.12  
topoisomerase (DNA) I, mitochondrial, isoform CRA\_b [Homo sapiens]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> <a href="#">199</a>	831.9430	1661.8715	1661.8658	3.47	2	16	14	1	U	-_MAVEEREVIKSLDK.C + Oxidation (M)

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

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> <a href="#">97</a>	508.2966	1014.5787	1014.5458	32.4	1	31	0.51	1		ENRGLDALK
<input checked="" type="checkbox"/> <a href="#">52</a>	430.2000	858.3854	858.4018	-19.02	1	23	4.3	1		MGHQDKK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">101</a>	527.2730	1052.5315	1052.5437	-11.56	1	19	7.7	1		FQNTKMLR + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">110</a>	585.2707	1168.5268	1168.5369	-8.60	1	18	11	1		MDPIRSFGGK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">111</a>	585.2980	1168.5814	1168.5766	4.06	2	18	11	1		LMRDMKTMK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">82</a>	465.3000	928.5854	928.5454	43.2	2	17	12	1		KNIAAERK
<input checked="" type="checkbox"/> <a href="#">240</a>	465.3000	1857.1709	1856.9026	145	1	17	9.6	1		MVAIDQVLDWCHRSGK
<input checked="" type="checkbox"/> <a href="#">136</a>	430.2000	1287.5782	1287.5943	-12.49	0	17	12	1		LGAEGNVDESQK + Acetyl (Protein N-term)
<input checked="" type="checkbox"/> <a href="#">127</a>	430.2000	1287.5782	1287.5943	-12.49	0	17	13	1		LGAEGNVDESQK + Acetyl (Protein N-term)
<input checked="" type="checkbox"/> <a href="#">280</a>	813.1338	2436.3796	2436.1775	82.9	2	17	9.2	1		GGARGTEARALTAAMASGSDSVTR + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">135</a>	430.2000	1287.5782	1287.5943	-12.49	0	17	13	1		LGAEGNVDESQK + Acetyl (Protein N-term)
<input checked="" type="checkbox"/> <a href="#">100</a>	523.3000	1044.5854	1044.5716	13.2	0	16	15	1		LSSAHVYLR
<input checked="" type="checkbox"/> <a href="#">275</a>	762.0973	2283.2700	2283.1490	53.0	1	16	11	1		MPLAGMSLGLSKSEFVPSTSK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">162</a>	465.3000	1392.8782	1392.7435	96.7	1	16	13	1		IPFGSKSNMATLK
<input checked="" type="checkbox"/> <a href="#">154</a>	465.3000	1392.8782	1392.6786	143	1	16	14	1		YEAWLAEAERR
<input checked="" type="checkbox"/> <a href="#">169</a>	465.3000	1392.8782	1392.6521	162	1	16	14	1		LDDEFDNERK
<input checked="" type="checkbox"/> <a href="#">157</a>	465.3000	1392.8782	1392.6350	175	1	16	14	1		MVNASQQACNRR + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">150</a>	465.3000	1392.8782	1392.6350	175	1	16	14	1		MVNASQQACNRR + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">92</a>	467.3000	932.5854	932.4927	99.5	1	16	18	1		NKITSEGGK
<input checked="" type="checkbox"/> <a href="#">95</a>	505.3000	1008.5854	1008.4876	97.0	0	15	15	1		AQTYELER
<input checked="" type="checkbox"/> <a href="#">104</a>	555.3458	1108.6771	1108.6288	43.6	1	15	15	1		CGHGRVLLVR
<input checked="" type="checkbox"/> <a href="#">247</a>	465.3000	1857.1709	1856.9672	110	1	15	15	1		AYEVSWKYQAVTATLK
<input checked="" type="checkbox"/> <a href="#">167</a>	465.3000	1392.8782	1392.6350	175	1	15	16	1		MVNASQQACNRR + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">243</a>	465.3000	1857.1709	1856.9672	110	1	15	15	1		AYEVSWKYQAVTATLK
<input checked="" type="checkbox"/> <a href="#">239</a>	465.3000	1857.1709	1856.9672	110	1	15	15	1		AYEVSWKYQAVTATLK
<input checked="" type="checkbox"/> <a href="#">65</a>	431.2000	860.3854	860.4603	-87.04	0	15	20	1		LQESGTVK
<input checked="" type="checkbox"/> <a href="#">144</a>	668.3662	1334.7178	1334.7055	9.22	0	15	18	1		APGAARPASGLPDR
<input checked="" type="checkbox"/> <a href="#">55</a>	430.2000	858.3854	858.4599	-86.78	0	15	29	1		FPPIETR
<input checked="" type="checkbox"/> <a href="#">129</a>	430.2000	1287.5782	1287.6394	-47.52	2	15	20	1		NARAKGMSFYK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">210</a>	430.2000	1716.7709	1716.8642	-54.37	1	15	18	1		QITQTKSTNATNSNVK + Gln->pyro-Glu (N-term Q)
<input checked="" type="checkbox"/> <a href="#">142</a>	651.3673	1300.7201	1300.6160	80.0	1	14	21	1		HVNERFQDEK
<input checked="" type="checkbox"/> <a href="#">175</a>	467.3000	1398.8782	1398.8347	31.1	0	14	20	1		HIEPTLRPVPLK
<input checked="" type="checkbox"/> <a href="#">214</a>	430.2000	1716.7709	1716.8642	-54.37	1	14	20	1		QITQTKSTNATNSNVK + Gln->pyro-Glu (N-term Q)
<input checked="" type="checkbox"/> <a href="#">106</a>	574.8264	1147.6383	1147.6197	16.2	2	14	22	1		ISVSEKSKDR
<input checked="" type="checkbox"/> <a href="#">255</a>	624.4000	1870.1782	1869.9003	149	1	14	19	1		QPSAGRAPISNPGMSEAGK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">86</a>	465.3000	928.5854	928.5454	43.2	2	14	26	1		KNIAAERK
<input checked="" type="checkbox"/> <a href="#">126</a>	430.2000	1287.5782	1287.5805	-1.82	1	14	24	1		DEYFKNMTPK + Oxidation (M)
<input checked="" type="checkbox"/> <a href="#">78</a>	465.3000	928.5854	928.5454	43.2	2	14	27	1		KNIAAERK
<input checked="" type="checkbox"/> <a href="#">79</a>	465.3000	928.5854	928.5454	43.2	2	14	27	1		KNIAAERK
<input checked="" type="checkbox"/> <a href="#">88</a>	465.3000	928.5854	928.5454	43.2	2	14	27	1		KNIAAERK
<input checked="" type="checkbox"/> <a href="#">71</a>	465.3000	928.5854	928.5454	43.2	2	14	27	1		KNIAAERK
<input checked="" type="checkbox"/> <a href="#">81</a>	465.3000	928.5854	928.5454	43.2	2	14	28	1		KNIAAERK
<input checked="" type="checkbox"/> <a href="#">89</a>	465.3000	928.5854	928.5454	43.2	2	14	28	1		KNIAAERK
<input checked="" type="checkbox"/> <a href="#">285</a>	1300.3000	2598.5854	2598.3289	98.7	2	14	18	1		RPRSEDDLLSQYLSFTKK
<input checked="" type="checkbox"/> <a href="#">83</a>	465.3000	928.5854	928.5454	43.2	2	13	30	1		KNIAAERK
<input checked="" type="checkbox"/> <a href="#">132</a>	430.2000	1287.5782	1287.5943	-12.49	0	13	27	1		LGAEGNVDESQK + Acetyl (Protein N-term)





<input checked="" type="checkbox"/>	<a href="#">291</a>	710.3776	2837.4814	2837.4308	17.8	1	1	2.7e+02	1	VLDSGSQAYDQAPTSPPTSLLSLRHR + Acetyl (Protein N-term)
<input checked="" type="checkbox"/>	<a href="#">38</a>	465.3000	464.2927	464.2053	188	0	1	8.3	1	GGMGK + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">109</a>	577.3644	1152.7142	1152.5312	159	1	1	4.1e+02	1	YFGRDPADGR
<input checked="" type="checkbox"/>	<a href="#">272</a>	1056.0459	2110.0773	2109.9711	50.3	2	1	3.5e+02	1	WEDVKEEMTSALATMRVD
<input checked="" type="checkbox"/>	<a href="#">190</a>	771.8706	1541.7267	1541.6814	29.4	0	1	4e+02	1	MGTSPSSSTALASCSR
<input checked="" type="checkbox"/>	<a href="#">24</a>	465.3000	464.2927	464.2053	188	0	1	8.8	1	GGMGK + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">114</a>	599.3810	1196.7474	1196.6149	111	0	1	4.2e+02	1	AGGPLGNPTTAK
<input checked="" type="checkbox"/>	<a href="#">276</a>	771.8000	2312.3782	2312.0246	153	1	1	3.2e+02	1	QEQNAEDWNLYWRTSSFR + Gln->pyro-Glu (N-term Q)
<input checked="" type="checkbox"/>	<a href="#">191</a>	776.2416	1550.4687	1550.6680	-128.56	0	1	2.8e+02	1	EMFLMAAGPPGGGR + 3 Oxidation (M); Glu->pyro-Glu
<input checked="" type="checkbox"/>	<a href="#">45</a>	624.4000	623.3927	623.3279	104	0	1	2.4e+02	1	YSNIK
<input checked="" type="checkbox"/>	<a href="#">292</a>	771.8000	3083.1709	3083.4030	-75.27	0	1	3.8e+02	1	STLANIFAGVHDSMDSIEVLGEDTYER
<input checked="" type="checkbox"/>	<a href="#">27</a>	465.3000	464.2927	464.2053	188	0	1	10	1	CAGSK
<input checked="" type="checkbox"/>	<a href="#">47</a>	700.4000	699.3927	699.3300	89.7	0	1	5.8e+02	1	SSHGANK
<input checked="" type="checkbox"/>	<a href="#">18</a>	465.3000	464.2927	464.2053	188	0	0	10	1	GGMGK + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">13</a>	431.2000	430.1927	430.2540	-142.31	0	0	14	1	AAAAK
<input checked="" type="checkbox"/>	<a href="#">32</a>	465.3000	464.2927	464.2053	188	0	0	11	1	GGMGK + Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">278</a>	772.2881	2313.8425	2314.0544	-91.56	2	0	4.3e+02	1	GYRMEQPEGCPKVVYELMR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	<a href="#">1</a>	430.2000	429.1927							
<input checked="" type="checkbox"/>	<a href="#">2</a>	430.2000	429.1927							
<input checked="" type="checkbox"/>	<a href="#">3</a>	430.2000	429.1927							
<input checked="" type="checkbox"/>	<a href="#">4</a>	430.2000	429.1927							
<input checked="" type="checkbox"/>	<a href="#">5</a>	430.2000	429.1927							
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<input checked="" type="checkbox"/>	<a href="#">9</a>	430.2000	429.1927							
<input checked="" type="checkbox"/>	<a href="#">10</a>	430.2000	429.1927							
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<input checked="" type="checkbox"/>	<a href="#">15</a>	431.2000	430.1927							
<input checked="" type="checkbox"/>	<a href="#">17</a>	465.3000	464.2927							
<input checked="" type="checkbox"/>	<a href="#">21</a>	465.3000	464.2927							
<input checked="" type="checkbox"/>	<a href="#">23</a>	465.3000	464.2927							
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<input checked="" type="checkbox"/>	<a href="#">28</a>	465.3000	464.2927							
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<input checked="" type="checkbox"/>	<a href="#">35</a>	465.3000	464.2927							
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<input checked="" type="checkbox"/>	<a href="#">40</a>	467.3000	466.2927							
<input checked="" type="checkbox"/>	<a href="#">41</a>	505.3000	504.2927							
<input checked="" type="checkbox"/>	<a href="#">42</a>	505.3000	504.2927							
<input checked="" type="checkbox"/>	<a href="#">43</a>	600.4000	599.3927							
<input checked="" type="checkbox"/>	<a href="#">48</a>	771.8000	770.7927							
<input checked="" type="checkbox"/>	<a href="#">49</a>	776.2442	775.2369							
<input checked="" type="checkbox"/>	<a href="#">137</a>	431.2000	1290.5782							
<input checked="" type="checkbox"/>	<a href="#">141</a>	1300.3000	1299.2927							
<input checked="" type="checkbox"/>	<a href="#">188</a>	771.6567	1541.2989							
<input checked="" type="checkbox"/>	<a href="#">192</a>	518.7857	1553.3352							
<input checked="" type="checkbox"/>	<a href="#">201</a>	834.6810	1667.3474							
<input checked="" type="checkbox"/>	<a href="#">273</a>	1083.6000	2165.1854							

## Search Parameters

Type of search : MS/MS Ion Search  
 Error tolerant search : All significant protein hits  
 Enzyme : Trypsin  
 Variable modifications : [Oxidation \(M\)](#), [Acetyl \(Protein N-term\)](#), [Gln->pyro-Glu \(N-term Q\)](#), [Glu->pyro-Glu \(N-term E\)](#)  
 Mass values : Monoisotopic  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance :  $\pm 200$  ppm  
 Fragment Mass Tolerance :  $\pm 0.2$  Da  
 Max Missed Cleavages : 2  
 Instrument type : Default  
 Number of queries : 298

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