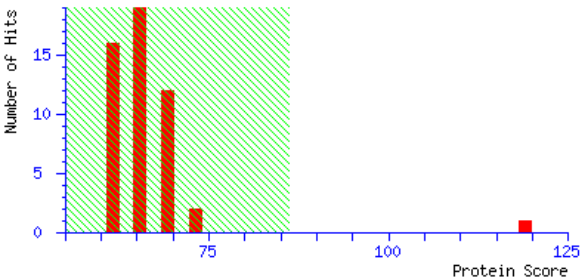


Mascot Search Results

User :  
Email :  
Search title : SampleSetID: 674, AnalysisID: 5211, MaldiWellID: 59827, SpectrumID: 120898, Path=\\161005\\MSMS\\16-85 combined NCBI euk  
Database : NCBI nr 160208 (79581714 sequences; 29080698065 residues)  
Taxonomy : Eukaryota (eucaryotes) (20445761 sequences)  
Timestamp : 24 Oct 2016 at 21:02:10 GMT  
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.  
Top Score : 119 for gi|157167794, AAEL011917-PA [Aedes aegypti]

Mascot Score Histogram

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 86 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Format As Protein Summary (deprecated) Help

Significance threshold p< 0.05 Max. number of hits 20

Re-Search All Search Unmatched

Index

Accession	Mass	Score	Description
1. gi 157167794	27516	119	AAEL011917-PA [Aedes aegypti]
2. gi 922854873	666795	72	e3 ubiquitin-protein ligase rnf213 [Chrysochromulina sp. CCMP291]
3. gi 966976382	852664	72	PREDICTED: nebulin isoform X18 [Macaca mulatta]
4. gi 835979325	266130	71	PREDICTED: putative leucine-rich repeat-containing protein DDB_G0290503 [Setaria italica]
5. gi 556745371	40533	69	PREDICTED: alcohol dehydrogenase class-3-like [Pantholops hodgsonii]
6. gi 119631907	778890	68	nebulin, isoform CRA_d [Homo sapiens]
7. gi 452839594	87020	68	6-phosphofructokinase alpha subunit-like protein [Dothistroma septosporum NZE10]
8. gi 119631905	775357	68	nebulin, isoform CRA_b [Homo sapiens]
9. gi 966976396	881496	68	PREDICTED: nebulin isoform X25 [Macaca mulatta]
10. gi 119631910	775457	68	nebulin, isoform CRA_g [Homo sapiens]
11. gi 954313371	18514	68	hypothetical protein T4E_12042, partial [Trichinella pseudospiralis]
12. gi 966976364	870261	68	PREDICTED: nebulin isoform X9 [Macaca mulatta]
13. gi 966976362	870253	68	PREDICTED: nebulin isoform X8 [Macaca mulatta]
14. gi 966976348	877274	68	PREDICTED: nebulin isoform X1 [Macaca mulatta]
15. gi 966976366	870102	68	PREDICTED: nebulin isoform X10 [Macaca mulatta]
16. gi 966976350	877316	67	PREDICTED: nebulin isoform X2 [Macaca mulatta]
17. gi 944241857	181953	67	hypothetical protein SETIT_000029mg [Setaria italica]
18. gi 954440236	30992	67	hypothetical protein T4D_7133, partial [Trichinella pseudospiralis]
19. gi 212544706	31419	67	conserved hypothetical protein [Talaromyces marneffeii ATCC 18224]
20. gi 966976356	873745	66	PREDICTED: nebulin isoform X5 [Macaca mulatta]

Results List

1. [gi|157167794](#) Mass: 27516 Score: 119 Expect: 2.6e-005 Matches: 12

AAEL011917-PA [Aedes aegypti]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1041.4738	1040.4665	1040.4563	9.81	182	- 189	0	---	R.FESPYDQR.I
1041.4738	1040.4665	1040.4563	9.81	182	- 189	0	21	R.FESPYDQR.I
1296.6404	1295.6331	1295.6258	5.62	180	- 189	1	---	R.VRFESPYDQR.I
1296.6404	1295.6331	1295.6258	5.62	180	- 189	1	28	R.VRFESPYDQR.I
1659.9054	1658.8981	1658.9079	-5.91	241	- 254	0	---	R.VSVHRPWVLVHTMV.-
1675.9045	1674.8972	1674.9028	-3.36	241	- 254	0	---	R.VSVHRPWVLVHTMV.- + Oxidation (M)
1675.9045	1674.8972	1674.9028	-3.36	241	- 254	0	14	R.VSVHRPWVLVHTMV.- + Oxidation (M)
1818.8427	1817.8354	1817.8227	6.99	46	- 62	0	---	R.TASNNAHFCCGGSVLNNR.W
2050.0166	2049.0093	2049.0167	-3.60	27	- 45	0	---	R.IAGGIDAEEGQFPYQVSLR.T
2225.1689	2224.1616	2224.1674	-2.61	100	- 119	0	---	R.IIVHPNFDVTTLANDVAVMR.V
2241.1670	2240.1597	2240.1624	-1.17	100	- 119	0	---	R.IIVHPNFDVTTLANDVAVMR.V + Oxidation (M)
2449.3245	2448.3172	2448.2141	42.1	63	- 86	1	---	R.WIITAASCAQKGEPAGISVMAGSK.S + Oxidation (M)
No match to: 880.4860, 918.4446, 936.4494, 942.5760, 943.5732, 964.4806, 1034.1438, 1069.5068, 1070.4956, 1092.6370, 1274.6362, 1297.6344, 1325.6587, 1328.6764, 1349.6676, 1356.6869, 1365.6539, 1403.7028, 1404.6875, 1414.7764, 1598.8022, 1598.8022,								

1599.8032, 1608.8135, 1637.8694, 1650.8323, 1669.8503, 1678.8468, 1691.8800, 1696.8757, 1718.8705, 1727.8612, 1751.8932, 1790.9150, 1805.9061, 1808.9041, 1817.8647, 1819.8307, 1890.9519, 1913.9663, 1918.9434, 1935.9443, 1986.0540, 1999.0594, 2031.0208, 2047.0057, 2051.0142, 2078.0791, 2079.0591, 2125.0874, 2146.0920, 2174.1213, 2177.1226, 2208.1162, 2242.1606, 2668.3516, 2840.3254

2. [gi|922854873](#) Mass: 666795 Score: 72 Expect: 1.1 Matches: 36

e3 ubiquitin-protein ligase rnf213 [Chrysochromulina sp. CCMP291]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4484	34.5	4595	- 4601	1	---	R.SRETMK.F + Oxidation (M)
918.4446	917.4373	917.4753	-41.35	609	- 616	1	---	R.MPNGKSIR.L + Oxidation (M)
936.4494	935.4421	935.4501	-8.53	2838	- 2844	0	---	R.FPYPEQR.Q
943.5732	942.5659	942.6015	-37.70	5508	- 5515	1	---	R.LPFVLKAR.W
964.4806	963.4733	963.4807	-7.68	5776	- 5783	1	---	R.NLSEARMK.T + Oxidation (M)
1070.4956	1069.4883	1069.5161	-25.95	153	- 160	1	---	R.MCARTLYR.A
1274.6362	1273.6289	1273.6853	-44.24	5422	- 5432	0	---	R.GLDMVATIWR.A
1296.6404	1295.6331	1295.6292	3.03	2827	- 2837	1	---	R.MSALYRGEDVR.F
1296.6404	1295.6331	1295.6292	3.03	2827	- 2837	1	---	R.MSALYRGEDVR.F
1349.6676	1348.6603	1348.6622	-1.43	2816	- 2826	1	---	K.AEQEAEFIEKR.M
1356.6869	1355.6796	1355.7157	-26.59	5153	- 5168	0	---	R.VAEATAAAAAAAAAA.A
1365.6539	1364.6466	1364.6871	-29.63	4323	- 4333	1	---	R.IYDRTGLMQR.I + Oxidation (M)
1403.7028	1402.6955	1402.6986	-2.22	5770	- 5781	1	---	R.MAEINRNLSEAR.M
1414.7764	1413.7691	1413.7827	-9.62	4090	- 4102	1	---	K.IKTSDSPLAEVVR.W
1599.8032	1598.7959	1598.8100	-8.78	1454	- 1466	1	---	R.FQQLRGLQEHMGR.L
1659.9054	1658.8981	1658.8363	37.3	5674	- 5688	0	---	R.EVLDEIISALASEDR.R
1669.8503	1668.8430	1668.9100	-40.12	3458	- 3471	1	---	R.LSELRYAPAPFLHR.F
1675.9045	1674.8972	1674.9305	-19.84	424	- 438	0	---	R.NIVSTIVNYVSNKPK.L
1675.9045	1674.8972	1674.9305	-19.84	424	- 438	0	---	R.NIVSTIVNYVSNKPK.L
1678.8468	1677.8395	1677.8290	6.25	2845	- 2858	1	---	R.QLAALMCRSQDLTR.A + Oxidation (M)
1696.8757	1695.8684	1695.8072	36.1	3202	- 3214	1	---	R.LCLAYQDLMREER.E
1727.8612	1726.8539	1726.7694	48.9	1958	- 1970	1	---	R.TYEMHEWKALMEK.I + 2 Oxidation (M)
1790.9150	1789.9077	1789.8442	35.5	5356	- 5374	0	---	R.TSAGNEAASGDEALATAVR.L
1805.9061	1804.8988	1804.9584	-33.01	5174	- 5188	1	---	R.LTRISPLDDSHPIWR.F
1817.8647	1816.8574	1816.7872	38.6	2337	- 2351	0	---	K.IMMEEAHHALSDDYR.H
1890.9519	1889.9446	1889.8975	24.9	3165	- 3181	0	---	R.ELMQICIGGLGSEAEQR.R
1913.9663	1912.9590	1912.8989	31.4	277	- 293	1	---	K.MPTLTGTATGKWEYSR.G
1986.0540	1985.0467	1985.0007	23.2	784	- 800	0	---	K.SLRPDHLGEWLVS DAYK.H
2047.0057	2045.9984	2045.9986	-0.09	3165	- 3182	1	---	R.ELMQICIGGLGSEAEQRR.L
2078.0791	2077.0718	2076.9680	50.0	2507	- 2524	1	---	K.NLSSMSAQMQDVDPNRLR.V + Oxidation (M)
2079.0591	2078.0518	2078.0718	-9.59	2649	- 2667	0	---	R.SAGDISAEVLADLLLCYIR.A
2177.1226	2176.1153	2176.0834	14.7	5447	- 5465	1	---	R.TQLGEMFPDVKS DAELLQR.V
2208.1162	2207.1089	2207.0503	26.5	4337	- 4354	0	---	K.LWCSTAQFECSPKPEVR.S
2242.1606	2241.1533	2241.2191	-29.35	2946	- 2964	1	---	R.SMLLTIGVVYLR LSTEQR.V
2668.3516	2667.3443	2667.3439	0.17	5422	- 5446	1	---	R.GLDMVATIWR AVSAGAHDEATIR.T
2840.3254	2839.3181	2839.3711	-18.67	5382	- 5406	0	---	R.LQHALSASHTLGDEETNGMHILYFR.M

No match to: 942.5760, 1034.1438, 1041.4738, 1041.4738, 1069.5068, 1092.6370, 1297.6344, 1325.6587, 1328.6764, 1404.6875, 1598.8022, 1598.8022, 1608.8135, 1637.8694, 1650.8323, 1691.8800, 1718.8705, 1751.8932, 1808.9041, 1818.8427, 1819.8307, 1918.9434, 1935.9443, 1999.0594, 2031.0208, 2050.0166, 2051.0142, 2125.0874, 2146.0920, 2174.1213, 2225.1689, 2241.1670, 2449.3245

3. [gi|966976382](#) Mass: 852664 Score: 72 Expect: 1.4 Matches: 44

PREDICTED: nebulin isoform X18 [Macaca mulatta]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4450	38.3	3496	- 3502	1	---	K.KEGYDLR.S
918.4446	917.4373	917.4389	-1.67	3685	- 3692	0	---	K.NNALNMNK.R
936.4494	935.4421	935.4633	-22.69	1951	- 1958	0	---	K.AMEIIEK.K + Oxidation (M)
964.4806	963.4733	963.4848	-11.88	6939	- 6946	0	---	K.HISSVMYK.E
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1070.4956	1069.4883	1069.4862	1.98	2340	- 2347	1	---	K.MQSERYK.K
1296.6404	1295.6331	1295.6768	-33.72	7189	- 7199	0	---	R.SLHMINVQAQR.R
1296.6404	1295.6331	1295.6768	-33.72	7189	- 7199	0	---	R.SLHMINVQAQR.R
1297.6344	1296.6271	1296.5809	35.7	5704	- 5713	1	---	K.DTRYMSSYFK.Y
1328.6764	1327.6691	1327.6442	18.8	7045	- 7056	0	---	K.ATPTPVTPEMER.A
1404.6875	1403.6802	1403.7409	-43.20	6371	- 6382	1	---	K.TVSHLVSENKYK.D
1414.7764	1413.7691	1413.7252	31.0	6181	- 6192	0	---	K.FTSIVDTPEHLR.T
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1608.8135	1607.8062	1607.7977	5.28	7322	- 7336	1	---	R.TGRTGMLPANYVEAI.- + Oxidation (M)
1637.8694	1636.8621	1636.8276	21.1	2331	- 2344	1	---	K.LVLSMNVAKMQSER.E + 2 Oxidation (M)
1678.8468	1677.8395	1677.8032	21.6	1379	- 1394	0	---	K.TSYHTPGDMVSITAAK.M
1691.8800	1690.8727	1690.8600	7.54	6427	- 6441	1	---	K.GKSNYSIMLEPPEVK.H
1696.8757	1695.8684	1695.8553	7.72	5932	- 5946	0	---	K.ERPHHHAGNQTTALK.H
1718.8705	1717.8632	1717.8709	-4.48	1867	- 1882	0	---	K.TSFHTPDMLSVVAAK.K + Oxidation (M)
1727.8612	1726.8539	1726.8634	-5.47	3705	- 3719	0	---	K.TIHVMPDTP EIMLAK.L + 2 Oxidation (M)
1751.8932	1750.8859	1750.8097	43.5	287	- 301	1	---	K.GKWSETPCFEVANAR.M
1805.9061	1804.8988	1804.8600	21.5	4122	- 4137	1	---	R.GIGWMEPGSVEMNRVK.V + Oxidation (M)
1808.9041	1807.8968	1807.9390	-23.32	891	- 906	0	---	K.TIYTAPLMDLQVTQAK.K + Oxidation (M)
1818.8427	1817.8354	1817.8652	-16.36	6885	- 6901	1	---	K.EDVSPGTAIGKTPEMMR.V
1819.8307	1818.8234	1818.8869	-34.89	5271	- 5286	0	---	K.ANVHIPNDMMNHVLAK.K + Oxidation (M)
1890.9519	1889.9446	1889.8869	30.5	716	- 730	0	---	K.CYFPQTITQEYEAIK.K

PREDICTED:	putative	leucine-rich	repeat-containing	protein	DDB_G0290503 [Setaria italica]					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide		
880.4860	879.4787	879.5065	-31.62	12	- 18	1	---	K.YLLESKK.D		
943.5732	942.5659	942.5386	29.0	2011	- 2018	0	---	K.QLEEAALK.V		
1296.6404	1295.6331	1295.5915	32.1	199	- 209	0	---	K.ETEVTTLSCEK.K		
1296.6404	1295.6331	1295.5915	32.1	199	- 209	0	---	K.ETEVTTLSCEK.K		
1403.7028	1402.6955	1402.7303	-24.81	1792	- 1803	1	---	R.NLESVLQSQSEK.I		
1404.6875	1403.6802	1403.7330	-37.58	943	- 954	0	---	K.IEQLEASLMNLK.T + Oxidation (M)		
1598.8022	1597.7949	1597.8423	-29.67	1576	- 1590	0	---	K.NAALAQQQSEANIK.E		
1598.8022	1597.7949	1597.8423	-29.67	1042	- 1056	0	---	K.NAALAQQQSEANIK.E		
1599.8032	1598.7959	1598.8263	-19.02	1309	- 1323	0	---	K.NAALAQQESEANIK.K		
1669.8503	1668.8430	1668.8471	-2.45	1162	- 1175	0	---	K.FIHQAELAAQDEK.N		
1675.9045	1674.8972	1674.8424	32.7	1376	- 1390	1	---	K.EEAINSLQKSNDCLK.T		
1675.9045	1674.8972	1674.8424	32.7	1376	- 1390	1	---	K.EEAINSLQKSNDCLK.T		
1718.8705	1717.8632	1717.8370	15.3	1996	- 2010	0	---	K.DELSVQLNNSTLEK.Q		
1727.8612	1726.8539	1726.9213	-39.01	1309	- 1324	1	---	K.NAALAQQESEANIK.L		
1805.9061	1804.8988	1804.8989	-0.03	1489	- 1503	1	---	K.TELAQQLERISDMQK.T + Oxidation (M)		
1817.8647	1816.8574	1816.8989	-22.81	244	- 259	1	---	K.CNLLSAEVEKAQAEK.E		
1918.9434	1917.9361	1917.9895	-27.81	1867	- 1883	1	---	R.LKEDLSVQLSNSTLDK.Q		
1986.0540	1985.0467	1985.0065	20.3	254	- 270	1	---	K.AQQAQEVQTLLLENQK.L		
2125.0874	2124.0801	2124.1613	-38.20	2227	- 2246	1	---	R.VSLLLETLMQVKGHAVSGVK.V		
2208.1162	2207.1089	2207.0263	37.4	1202	- 1221	0	---	K.DNDSATSEIEQLASLMNLK.T		
2241.1670	2240.1597	2240.1688	-4.06	2114	- 2132	1	---	R.LQYAYDEVSSRVQSLEILK.R		
2242.1606	2241.1533	2241.0960	25.6	1591	- 1608	0	---	K.ELQSDMVQQNQILHFQR.E		
2668.3516	2667.3443	2667.4153	-26.59	324	- 347	1	---	K.LQQGLGLEIGLVKEAELMNLDK.E		
No match to:	918.4446,	936.4494,	942.5760,	964.4806,	1034.1438,	1041.4738,	1041.4738,	1069.5068,	1070.4956,	1092.6370,
1274.6362,	1297.6344,	1325.6587,	1328.6764,	1349.6676,	1356.6869,	1365.6539,	1414.7764,	1608.8135,	1637.8694,	1650.8323,
1659.9054,	1678.8468,	1691.8800,	1696.8757,	1751.8932,	1790.9150,	1808.9041,	1818.8427,	1819.8307,	1890.9519,	1913.9663,
1935.9443,	1999.0594,	2031.0208,	2047.0057,	2050.0166,	2051.0142,	2078.0791,	2079.0591,	2146.0920,	2174.1213,	2177.1226,
2225.1689,	2449.3245,	2840.3254								

PREDICTED:	alcohol dehydrogenase	class-3-like [Pantholops hodgsonii]									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide			
943.5732	942.5659	942.5386	29.0	27	- 35	0	---	R.AGEVLVEVK.A			
964.4806	963.4733	963.4808	-7.72	103	- 110	0	---	K.TNLTCTSR.A			
1092.6370	1091.6297	1091.5757	49.5	102	- 110	1	---	R.KTNLCTSIR.A			
1297.6344	1296.6271	1296.6721	-34.65	275	- 285	1	---	K.VMRQALEASHR.G			
1403.7028	1402.6955	1402.7027	-5.11	359	- 370	1	---	K.GFELMHKGESIR.G			
1404.6875	1403.6802	1403.6463	24.1	111	- 124	0	---	R.ATQGQGVMPDGTSR.F			
1669.8503	1668.8430	1668.8505	-4.48	208	- 223	0	---	R.LAGADMIGVDINPDR.K			
1696.8757	1695.8684	1695.8178	29.8	327	- 340	1	---	R.DVPKIVDWYMEGK.I + Oxidation (M)			
2125.0874	2124.0801	2124.0595	9.71	341	- 358	0	---	K.IQIDPMITHTMPLEDINK.G + Oxidation (M)			
2668.3516	2667.3443	2667.2825	23.2	132	- 154	0	---	K.IHHYMGCSSTFSNYTVLPEIALAK.I + Oxidation (M)			
No match to:	880.4860,	918.4446,	936.4494,	942.5760,	1034.1438,	1041.4738,	1041.4738,	1069.5068,	1070.4956,	1274.6362,	
	1296.6404,	1296.6404,	1325.6587,	1328.6764,	1349.6676,	1356.6869,	1365.6539,	1414.7764,	1598.8022,	1598.8022,	1599.8032,
	1608.8135,	1637.8694,	1650.8323,	1659.9054,	1675.9045,	1675.9045,	1678.8468,	1691.8800,	1718.8705,	1727.8612,	1751.8932,
	1790.9150,	1805.9061,	1808.9041,	1817.8647,	1818.8427,	1819.8307,	1890.9519,	1913.9663,	1918.9434,	1935.9443,	1986.0540,
	1999.0594,	2031.0208,	2047.0057,	2050.0166,	2051.0142,	2078.0791,	2079.0591,	2146.0920,	2174.1213,	2177.1226,	2208.1162,
	2225.1689,	2241.1670,	2242.1606,	2449.3245,	2840.3254						

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4450	38.3	3496	- 3502	1	---	K.KEGYDLR.L
918.4446	917.4373	917.4389	-1.67	3442	- 3449	0	---	K.NNALNMNK.R
936.4494	935.4421	935.4633	-22.69	1951	- 1958	0	---	K.AMEIISEK.K + Oxidation (M)
964.4806	963.4733	963.4848	-11.88	6210	- 6217	0	---	K.HISSVMYK.E
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)

1070.4956	1069.4883	1069.4862	1.95	137	-	145	1	---	K.YRMDGDVAK.T + Oxidation (M)
1274.6362	1273.6289	1273.6203	6.75	5550	-	5559	1	---	K.QYEANKAHWK.W
1296.6404	1295.6331	1295.6768	-33.72	6553	-	6563	0	---	R.SLHMINVQAQR.R
1296.6404	1295.6331	1295.6768	-33.72	6553	-	6563	0	---	R.SLHMINVQAQR.R
1297.6344	1296.6271	1296.5809	35.7	4975	-	4984	1	---	K.DTRYMSSYFK.Y
1325.6587	1324.6514	1324.6875	-27.20	5326	-	5337	1	---	R.AVTDTVSDVKYK.E
1328.6764	1327.6691	1327.6442	18.8	6409	-	6420	0	---	K.ATPTPVTPEMER.A
1356.6869	1355.6796	1355.6755	3.05	6254	-	6265	0	---	K.GIPTPITPEMER.V + Oxidation (M)
1365.6539	1364.6466	1364.6837	-27.14	4391	-	4401	1	---	K.KNALENYPNFR.S
1414.7764	1413.7691	1413.7252	31.0	5452	-	5463	0	---	K.FTSIVDTPEHLR.T
1598.8022	1597.7949	1597.8208	-16.19	4789	-	4802	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1598.8022	1597.7949	1597.8208	-16.19	4789	-	4802	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1608.8135	1607.8062	1607.7977	5.28	6686	-	6700	1	---	R.TGRGTMLPANYVEAI.- + Oxidation (M)
1637.8694	1636.8621	1636.8276	21.1	2331	-	2344	1	---	K.LVLSMNVAKMQSER.E + 2 Oxidation (M)
1678.8468	1677.8395	1677.8032	21.6	1379	-	1394	0	---	K.TSYHTPGDMVSITAAK.M
1691.8800	1690.8727	1690.8600	7.54	5698	-	5712	1	---	K.GKSNIYSIMLEPPEVK.H
1696.8757	1695.8684	1695.8553	7.72	5203	-	5217	0	---	K.ERPHHHAGNQTTALK.H
1718.8705	1717.8632	1717.8709	-4.48	1867	-	1882	0	---	K.TSFHTPVDMLSVVAAK.K + Oxidation (M)
1727.8612	1726.8539	1726.8634	-5.47	3462	-	3476	0	---	K.TIHVMPDTPEIMLAK.L + 2 Oxidation (M)
1751.8932	1750.8859	1750.8196	37.9	2664	-	2679	1	---	K.GIGWMTSGSLEDEKNK.R
1805.9061	1804.8988	1804.9757	-42.60	2598	-	2614	1	---	K.TKFSSPVDMLGVVLANK.C
1808.9041	1807.8968	1807.9390	-23.32	891	-	906	0	---	K.TIYTAPLDMQLVQTQAK.K + Oxidation (M)
1818.8427	1817.8354	1817.8652	-16.36	6156	-	6172	1	---	K.EDVSPGTAIGKTPEMMR.V
1819.8307	1818.8234	1818.8869	-34.89	4542	-	4557	0	---	K.ANVHIPNDMMNHVLAK.R + Oxidation (M)
1890.9519	1889.9446	1889.8869	30.5	716	-	730	0	---	K.CYFPQTITQEYEAIK.K
1918.9434	1917.9361	1918.0101	-38.59	4994	-	5010	1	---	K.AYGYTLGPKDVPFVHVR.R
1935.9443	1934.9370	1934.9118	13.1	1723	-	1738	1	---	K.LKFTYAMDTMEQALNK.S + 2 Oxidation (M)
1986.0540	1985.0467	1985.0193	13.8	4608	-	4624	1	---	K.GIGCYVWDTPQILHAKK.S
1999.0594	1998.0521	1998.0278	12.2	855	-	872	1	---	K.MIGALSINDDPKMLHSLK.T + Oxidation (M)
2031.0208	2030.0135	2029.9271	42.6	1969	-	1986	0	---	K.YSTLMDSMNMVLAQNNAK.I
2047.0057	2045.9984	2045.9220	37.4	1969	-	1986	0	---	K.YSTLMDSMNMVLAQNNAK.I + Oxidation (M)
2051.0142	2050.0069	2050.0517	-21.84	3945	-	3962	1	---	K.DKTSIHIMPDTPEINLAR.A
2079.0591	2078.0518	2078.1016	-23.96	3462	-	3479	1	---	K.TIHVMPDTPEIMLAKLNR.I
2125.0874	2124.0801	2124.0707	4.43	2973	-	2990	1	---	K.DKTIHIMPDTPEIMLAR.Q + Oxidation (M)
2177.1226	2176.1153	2176.1132	0.97	2144	-	2161	1	---	K.YILLPDAMNIELTRNMNR.I
2208.1162	2207.1089	2207.0317	35.0	3685	-	3703	1	---	K.NNALTMKSHLYTEAWDADK.T
2449.3245	2448.3172	2448.2318	34.9	3428	-	3449	1	---	K.FTSITDTPEQVLAKNNALNMNK.R
2668.3516	2667.3443	2667.3690	-9.26	2248	-	2270	1	---	K.IHVMPTDPDILQAKQNQTLYSQK.L
No match to: 942.5760, 943.5732, 1034.1438, 1069.5068, 1092.6370, 1349.6676, 1403.7028, 1404.6875, 1599.8032, 1650.8323, 1659.9054, 1669.8503, 1675.9045, 1675.9045, 1790.9150, 1817.8647, 1913.9663, 2050.0166, 2078.0791, 2146.0920, 2174.1213, 2225.1689, 2241.1670, 2242.1606, 2840.3254									

7. [gi|452839594](#) Mass: 87020 Score: 68 Expect: 2.9 Matches: 14

6-phosphofructokinase alpha subunit-like protein [Dothistroma septosporum NZE10]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1070.4956	1069.4883	1069.5192	-28.89	521	- 529	1	---	K.ARAEYDAFK.I
1274.6362	1273.6289	1273.6415	-9.86	697	- 707	0	---	R.SLQHIETYAGR.T
1598.8022	1597.7949	1597.7525	26.6	460	- 472	0	---	R.EVHWLDAEQWASK.G
1598.8022	1597.7949	1597.7525	26.6	460	- 472	0	---	R.EVHWLDAEQWASK.G
1659.9054	1658.8981	1658.8814	10.1	2	- 16	1	---	M.AQITLTPPAMPYGRK.R + Oxidation (M)
1678.8468	1677.8395	1677.8218	10.5	1	- 15	0	---	-.MAQITLTPPAMPYGRK + 2 Oxidation (M)
1691.8800	1690.8727	1690.8937	-12.41	406	- 423	0	---	R.VGIIHVGAPAGGMNAATR.A
1696.8757	1695.8684	1695.8580	6.14	773	- 789	0	---	R.SPNPGSPALLNGTSAWK.G
1790.9150	1789.9077	1789.9219	-7.91	1	- 16	1	---	-.MAQITLTPPAMPYGRK.R + Oxidation (M)
1818.8427	1817.8354	1817.8829	-26.14	109	- 127	0	---	R.GIDALVICGGDGLTGADK.F
1935.9443	1934.9370	1934.9560	-9.82	128	- 144	1	---	K.FRGEWPSLMDELVATGK.R
2125.0874	2124.0801	2124.0204	28.1	91	- 108	1	---	K.SFMERPGRLTAANNMIER.G + 2 Oxidation (M)
2208.1162	2207.1089	2207.0933	7.10	751	- 769	0	---	K.DEFWMSLIDVVDTLGRPK.A
2840.3254	2839.3181	2839.3790	-21.44	449	- 472	1	---	R.HHDDKPLGVSREVHWLDAEQWASK.G
No match to: 880.4860, 918.4446, 936.4494, 942.5760, 943.5732, 964.4806, 1034.1438, 1041.4738, 1069.5068, 1092.6370, 1296.6404, 1296.6404, 1297.6344, 1325.6587, 1328.6764, 1349.6676, 1356.6869, 1365.6539, 1403.7028, 1404.6875, 1414.7764, 1599.8032, 1608.8135, 1637.8694, 1650.8323, 1669.8503, 1675.9045, 1675.9045, 1718.8705, 1727.8612, 1751.8932, 1805.9061, 1808.9041, 1817.8647, 1819.8307, 1890.9519, 1913.9663, 1918.9434, 1986.0540, 1999.0594, 2031.0208, 2047.0057, 2050.0166, 2051.0142, 2078.0791, 2079.0591, 2146.0920, 2174.1213, 2177.1226, 2225.1689, 2241.1670, 2242.1606, 2449.3245, 2668.3516								

8. [gi|119631905](#) Mass: 775357 Score: 68 Expect: 3 Matches: 44

nebulin, isoform CRA\_b [Homo sapiens]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4450	38.3	3496	- 3502	1	---	K.KEGYDLR.L
918.4446	917.4373	917.4389	-1.67	3442	- 3449	0	---	K.NNALNMNK.R
936.4494	935.4421	935.4633	-22.69	1951	- 1958	0	---	K.AMEIIEK.K + Oxidation (M)
964.4806	963.4733	963.4848	-11.88	6210	- 6217	0	---	K.HISSVMYK.E
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1070.4956	1069.4883	1069.4862	1.95	137	- 145	1	---	K.YRMDGDVAK.T + Oxidation (M)
1274.6362	1273.6289	1273.6203	6.75	5550	- 5559	1	---	K.QYEANKAHWK.W
1296.6404	1295.6331	1295.6768	-33.72	6522	- 6532	0	---	R.SLHMINVQAQR.R
1296.6404	1295.6331	1295.6768	-33.72	6522	- 6532	0	---	R.SLHMINVQAQR.R
1297.6344	1296.6271	1296.5809	35.7	4975	- 4984	1	---	K.DTRYMSSYFK.Y
1325.6587	1324.6514	1324.6875	-27.20	5326	- 5337	1	---	R.AVTDTVSDVKYK.E



1328.6764	1327.6691	1327.6442	18.8	6378	-	6389	0	---	K.ATPTPTPEMER.A
1356.6869	1355.6796	1355.6755	3.05	6254	-	6265	0	---	K.GIPTPTPEMER.V + Oxidation (M)
1365.6539	1364.6466	1364.6837	-27.14	4391	-	4401	1	---	K.KNALENYPNFR.S
1414.7764	1413.7691	1413.7252	31.0	5452	-	5463	0	---	K.FTSIVDTPEHLR.T
1598.8022	1597.7949	1597.8208	-16.19	4789	-	4802	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1598.8022	1597.7949	1597.8208	-16.19	4789	-	4802	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1608.8135	1607.8062	1607.7977	5.28	6655	-	6669	1	---	R.TGRGTMLPANYVEAI.- + Oxidation (M)
1637.8694	1636.8621	1636.8276	21.1	2331	-	2344	1	---	K.LVLSMNVAKMQSER.E + 2 Oxidation (M)
1678.8468	1677.8395	1677.8032	21.6	1379	-	1394	0	---	K.TSYHTPGDMVSITAAK.M
1691.8800	1690.8727	1690.8600	7.54	5698	-	5712	1	---	K.GKSNSYSIMLEPPEVK.H
1696.8757	1695.8684	1695.8553	7.72	5203	-	5217	0	---	K.ERPHHHAGNQTTALK.H
1718.8705	1717.8632	1717.8709	-4.48	1867	-	1882	0	---	K.TSFHTPVDMLSVVAAK.K + Oxidation (M)
1727.8612	1726.8539	1726.8634	-5.47	3462	-	3476	0	---	K.TIHVMPDTPEIMLAK.L + 2 Oxidation (M)
1751.8932	1750.8859	1750.8196	37.9	2664	-	2679	1	---	K.GIGWMTSGSLEDEKNK.R
1805.9061	1804.8988	1804.9757	-42.60	2598	-	2614	1	---	K.TKFSSPVDMLGVVLANK.C
1808.9041	1807.8968	1807.9390	-23.32	891	-	906	0	---	K.TIYTAPLDMLQVTQAK.K + Oxidation (M)
1818.8427	1817.8354	1817.8652	-16.36	6156	-	6172	1	---	K.EDVSPGTAIGKTPEMMR.V
1819.8307	1818.8234	1818.8869	-34.89	4542	-	4557	0	---	K.ANVHIPNDMMNHVLAK.R + Oxidation (M)
1890.9519	1889.9446	1889.8869	30.5	716	-	730	0	---	K.CYFPQTITQEYEAIK.K
1918.9434	1917.9361	1918.0101	-38.59	4994	-	5010	1	---	K.AYGYTLGPKDVPFVHVR.R
1935.9443	1934.9370	1934.9118	13.1	1723	-	1738	1	---	K.LKFTYAMDTMEQALNK.S + 2 Oxidation (M)
1986.0540	1985.0467	1985.0193	13.8	4608	-	4624	1	---	K.GIGCYVWDTPQILHAKK.S
1999.0594	1998.0521	1998.0278	12.2	855	-	872	1	---	K.MIGALSINDDPKMLHSLK.T + Oxidation (M)
2031.0208	2030.0135	2029.9271	42.6	1969	-	1986	0	---	K.YSTLMDSMNMVLAQNNAK.I
2047.0057	2045.9984	2045.9220	37.4	1969	-	1986	0	---	K.YSTLMDSMNMVLAQNNAK.I + Oxidation (M)
2051.0142	2050.0069	2050.0517	-21.84	3945	-	3962	1	---	K.DKTSIHIMPDTPEINLAR.A
2079.0591	2078.0518	2078.1016	-23.96	3462	-	3479	1	---	K.TIHVMPDTPEIMLAKLNR.I
2125.0874	2124.0801	2124.0707	4.43	2973	-	2990	1	---	K.DKTQIHIMPDTPEIMLAR.Q + Oxidation (M)
2177.1226	2176.1153	2176.1132	0.97	2144	-	2161	1	---	K.YILLPDAMNIELTRNMNR.I
2208.1162	2207.1089	2207.0317	35.0	3685	-	3703	1	---	K.NNALTMKSHLYTEAWDADK.T
2449.3245	2448.3172	2448.2318	34.9	3428	-	3449	1	---	K.FTSITDTPEQVLAKNNALNMNK.R
2668.3516	2667.3443	2667.3690	-9.26	2248	-	2270	1	---	K.IHVMPDTPDILQAKQNQTLYSQK.L

No match to: 942.5760, 943.5732, 1034.1438, 1069.5068, 1092.6370, 1349.6676, 1403.7028, 1404.6875, 1599.8032, 1650.8323, 1659.9054, 1669.8503, 1675.9045, 1675.9045, 1790.9150, 1817.8647, 1913.9663, 2050.0166, 2078.0791, 2146.0920, 2174.1213, 2225.1689, 2241.1670, 2242.1606, 2840.3254

9. [gi|966976396](#) Mass: 881496 Score: 68 Expect: 3.1 Matches: 44

PREDICTED: nebulin isoform X25 [Macaca mulatta]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4450	38.3	3496	- 3502	1	---	K.KEGYDLR.S
918.4446	917.4373	917.4389	-1.67	3685	- 3692	0	---	K.NNALNMNK.R
936.4494	935.4421	935.4633	-22.69	1951	- 1958	0	---	K.AMEIIEK.K + Oxidation (M)
964.4806	963.4733	963.4848	-11.88	6974	- 6981	0	---	K.HISSVMYK.E
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1070.4956	1069.4883	1069.4862	1.98	2340	- 2347	1	---	K.MQSEREYK.K
1296.6404	1295.6331	1295.6768	-33.72	7441	- 7451	0	---	R.SLHMINVQAQR.R
1296.6404	1295.6331	1295.6768	-33.72	7441	- 7451	0	---	R.SLHMINVQAQR.R
1297.6344	1296.6271	1296.5809	35.7	5704	- 5713	1	---	K.DTRYMSSYFK.Y
1328.6764	1327.6691	1327.6442	18.8	7297	- 7308	0	---	K.ATPTPTPEMER.A
1404.6875	1403.6802	1403.7409	-43.20	6406	- 6417	1	---	K.TVSHLVSENKYK.D
1414.7764	1413.7691	1413.7252	31.0	6216	- 6227	0	---	K.FTSIVDTPEHLR.T
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1608.8135	1607.8062	1607.7977	5.28	7574	- 7588	1	---	R.TGRGTMLPANYVEAI.- + Oxidation (M)
1637.8694	1636.8621	1636.8276	21.1	2331	- 2344	1	---	K.LVLSMNVAKMQSER.E + 2 Oxidation (M)
1678.8468	1677.8395	1677.8032	21.6	1379	- 1394	0	---	K.TSYHTPGDMVSITAAK.M
1691.8800	1690.8727	1690.8600	7.54	6462	- 6476	1	---	K.GKSNSYSIMLEPPEVK.H
1696.8757	1695.8684	1695.8553	7.72	5932	- 5946	0	---	K.ERPHHHAGNQTTALK.H
1718.8705	1717.8632	1717.8709	-4.48	1867	- 1882	0	---	K.TSFHTPVDMLSVVAAK.K + Oxidation (M)
1727.8612	1726.8539	1726.8634	-5.47	3705	- 3719	0	---	K.TIHVMPDTPPEIMLAK.L + 2 Oxidation (M)
1751.8932	1750.8859	1750.8097	43.5	287	- 301	1	---	K.GKWSETPCFEVANAR.M
1805.9061	1804.8988	1804.8600	21.5	4122	- 4137	1	---	R.GIGWMPEGSVEMNRVK.V + Oxidation (M)
1808.9041	1807.8968	1807.9390	-23.32	891	- 906	0	---	K.TIYTAPLDMLQVTQAK.K + Oxidation (M)
1818.8427	1817.8354	1817.8652	-16.36	6920	- 6936	1	---	K.EDVSPGTAIGKTPEMMR.V
1819.8307	1818.8234	1818.8869	-34.89	5271	- 5286	0	---	K.ANVHIPNDMMNHVLAK.K + Oxidation (M)
1890.9519	1889.9446	1889.8869	30.5	716	- 730	0	---	K.CYFPQTITQEYEAIK.K
1913.9663	1912.9590	1912.9564	1.37	7044	- 7060	1	---	K.ENLSKGTPLPVTPEMER.V + Oxidation (M)
1918.9434	1917.9361	1918.0101	-38.59	5723	- 5739	1	---	K.AYGYTLGPKDVPFVHVR.R
1935.9443	1934.9370	1934.9118	13.1	1723	- 1738	1	---	K.LKFTYAMDTMEQALNK.S + 2 Oxidation (M)
1986.0540	1985.0467	1985.0193	13.8	5337	- 5353	1	---	K.GIGCYVWDTPQILHAKK.S
1999.0594	1998.0521	1998.0278	12.2	855	- 872	1	---	K.MIGALSINDDPKMLHSLK.T + Oxidation (M)
2031.0208	2030.0135	2029.9271	42.6	1969	- 1986	0	---	K.YSTLMSDMNMVLAQNNAK.I
2047.0057	2045.9984	2045.9220	37.4	1969	- 1986	0	---	K.YSTLMSDMNMVLAQNNAK.I + Oxidation (M)
2051.0142	2050.0069	2050.0769	-34.12	2487	- 2504	1	---	K.DKTQIHIMPDTPEIVLAK.A + Oxidation (M)
2079.0591	2078.0518	2078.1016	-23.96	3705	- 3722	1	---	K.TIHVMPDTPPEIMLAKLNR.I
2125.0874	2124.0801	2124.0707	4.43	3216	- 3233	1	---	K.DKTQIHIMPDTPEIMLAR.Q + Oxidation (M)
2177.1226	2176.1153	2176.1132	0.97	2144	- 2161	1	---	K.YILLPDAMNIELTRNMNR.I
2208.1162	2207.1089	2207.0755	15.2	1895	- 1913	0	---	R.NLIHTYNNMLPDAMSFELAK.T

2225.1689 2224.1616 2224.1344 12.2 2975 - 2993 1 --- K.TQIHIMPDTPEIMLARTNK.I + Oxidation (M)  
 2241.1670 2240.1597 2240.1293 13.6 2975 - 2993 1 --- K.TQIHIMPDTPEIMLARTNK.I + 2 Oxidation (M)  
 2449.3245 2448.3172 2448.2318 34.9 3671 - 3692 1 --- K.FTSITDTPEQVLAKNNALNMNK.R  
 2840.3254 2839.3181 2839.4572 -48.98 1758 - 1782 1 --- K.TTIHVPDTPDILLSRVNQITMSNK.L + Oxidation (M)  
**No match to:** 942.5760, 943.5732, 1034.1438, 1069.5068, 1092.6370, 1274.6362, 1325.6587, 1349.6676, 1356.6869, 1365.6539, 1403.7028, 1599.8032, 1650.8323, 1659.9054, 1669.8503, 1675.9045, 1675.9045, 1790.9150, 1817.8647, 2050.0166, 2078.0791, 2146.0920, 2174.1213, 2242.1606, 2668.3516

10. [gi|119631910](#) Mass: 775457 Score: 68 Expect: 3.2 Matches: 44

nebulin, isoform CRA\_g [Homo sapiens]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4450	38.3	3497	3503	1	---	K.KEGYDLR.L
918.4446	917.4373	917.4389	-1.67	3443	3450	0	---	K.NNALNMNK.R
936.4494	935.4421	935.4633	-22.69	1952	1959	0	---	K.AMEIIEK.K + Oxidation (M)
964.4806	963.4733	963.4848	-11.88	6211	6218	0	---	K.HISSVMYK.E
1041.4738	1040.4665	1040.4960	-28.37	2518	2525	1	---	R.MGYEELKR.K + Oxidation (M)
1041.4738	1040.4665	1040.4960	-28.37	2518	2525	1	---	R.MGYEELKR.K + Oxidation (M)
1070.4956	1069.4883	1069.4862	1.95	137	145	1	---	K.YRMDGDVAK.T + Oxidation (M)
1274.6362	1273.6289	1273.6203	6.75	5551	5560	1	---	K.QYEANKAHWK.W
1296.6404	1295.6331	1295.6768	-33.72	6523	6533	0	---	R.SLHMINVQQR.R
1296.6404	1295.6331	1295.6768	-33.72	6523	6533	0	---	R.SLHMINVQQR.R
1297.6344	1296.6271	1296.5809	35.7	4976	4985	1	---	K.DTRYMSSYFK.Y
1325.6587	1324.6514	1324.6875	-27.20	5327	5338	1	---	R.AVTDTVSDVKYK.E
1328.6764	1327.6691	1327.6442	18.8	6379	6390	0	---	K.ATPTVPTEMER.A
1356.6869	1355.6796	1355.6755	3.05	6255	6266	0	---	K.GIPTPITPEMER.V + Oxidation (M)
1365.6539	1364.6466	1364.6837	-27.14	4392	4402	1	---	K.KNALENYPNFR.S
1414.7764	1413.7691	1413.7252	31.0	5453	5464	0	---	K.FTSIVDTPPEHLR.T
1598.8022	1597.7949	1597.8208	-16.19	4790	4803	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1598.8022	1597.7949	1597.8208	-16.19	4790	4803	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1608.8135	1607.8062	1607.7977	5.28	6656	6670	1	---	R.TGRTGMLPANYVEAI.- + Oxidation (M)
1637.8694	1636.8621	1636.8276	21.1	2332	2345	1	---	K.LVLSMNVAKMQSER.E + 2 Oxidation (M)
1678.8468	1677.8395	1677.8032	21.6	1380	1395	0	---	K.TSYHTPGDMVSITAAK.M
1691.8800	1690.8727	1690.8600	7.54	5699	5713	1	---	K.GKSNNYSIMLEPPEVK.H
1696.8757	1695.8684	1695.8553	7.72	5204	5218	0	---	K.ERPHHAGNQTTALK.H
1718.8705	1717.8632	1717.8709	-4.48	1868	1883	0	---	K.TSFHTPVDMLSVVAAK.K + Oxidation (M)
1727.8612	1726.8539	1726.8634	-5.47	3463	3477	0	---	K.TIHVMPDTPEIMLAK.L + 2 Oxidation (M)
1751.8932	1750.8859	1750.8196	37.9	2665	2680	1	---	K.GIGWMTSGSLEDEKNK.R
1805.9061	1804.8988	1804.9757	-42.60	2599	2615	1	---	K.TKFSSPVDMLGVVLANK.C
1808.9041	1807.8968	1807.9390	-23.32	892	907	0	---	K.TIYTAPLDMLQVTQAK.K + Oxidation (M)
1818.8427	1817.8354	1817.8652	-16.36	6157	6173	1	---	K.EDVSPGTAIGKTPEMMR.V
1819.8307	1818.8234	1818.8869	-34.89	4543	4558	0	---	K.ANVHIPNDMMNHVLAK.R + Oxidation (M)
1890.9519	1889.9446	1889.8869	30.5	717	731	0	---	K.CYFPQTITQEYEAIK.K
1918.9434	1917.9361	1918.0101	-38.59	4995	5011	1	---	K.AYGTYLGPDKVPFVHVR.R
1935.9443	1934.9370	1934.9118	13.1	1724	1739	1	---	K.LKFYAMDTMEQALNK.S + 2 Oxidation (M)
1986.0540	1985.0467	1985.0193	13.8	4609	4625	1	---	K.GIGCYVWDTPQILHAKK.S
1999.0594	1998.0521	1998.0278	12.2	856	873	1	---	K.MIGALSINDPKMLHSLK.T + Oxidation (M)
2031.0208	2030.0135	2029.9271	42.6	1970	1987	0	---	K.YSTLMDSMNMVLAQNNAK.I
2047.0057	2045.9984	2045.9220	37.4	1970	1987	0	---	K.YSTLMDSMNMVLAQNNAK.I + Oxidation (M)
2051.0142	2050.0069	2050.0517	-21.84	3946	3963	1	---	K.DKTSIHIMPDTPEINLAR.A
2079.0591	2078.0518	2078.1016	-23.96	3463	3480	1	---	K.TIHVMPDTPEIMLAKLN.R
2125.0874	2124.0801	2124.0707	4.43	2974	2991	1	---	K.DKTQIHIMPDTPEIMLAR.M + Oxidation (M)
2177.1226	2176.1153	2176.1132	0.97	2145	2162	1	---	K.YILLPDAMNIELTRNMNR.I
2208.1162	2207.1089	2207.0317	35.0	3686	3704	1	---	K.NNALTMSKHLYTEAWDADK.T
2449.3245	2448.3172	2448.2318	34.9	3429	3450	1	---	K.FTSITDTPEQVLAKNNALNMNK.R
2668.3516	2667.3443	2667.3690	-9.26	2249	2271	1	---	K.IHVMPDTPDILQAKQNQTLYSQK.L

**No match to:** 942.5760, 943.5732, 1034.1438, 1069.5068, 1092.6370, 1349.6676, 1403.7028, 1404.6875, 1599.8032, 1650.8323, 1659.9054, 1669.8503, 1675.9045, 1675.9045, 1790.9150, 1817.8647, 1913.9663, 2050.0166, 2078.0791, 2146.0920, 2174.1213, 2225.1689, 2241.1670, 2242.1606, 2840.3254

11. [gi|954313371](#) Mass: 18514 Score: 68 Expect: 3.3 Matches: 9

hypothetical protein T4E\_12042, partial [Trichinella pseudospiralis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1296.6404	1295.6331	1295.5897	33.5	135	144	1	---	R.AMLMRCQQR.G + 2 Oxidation (M)
1296.6404	1295.6331	1295.5897	33.5	135	144	1	---	R.AMLMRCQQR.G + 2 Oxidation (M)
1669.8503	1668.8430	1668.7928	30.1	38	52	1	---	R.NGNNSTADSHEVIRR.G
1678.8468	1677.8395	1677.7668	43.3	72	85	0	---	K.LDSQIDHLNDYMAK.V + Oxidation (M)
1790.9150	1789.9077	1789.8669	22.8	71	85	1	---	K.KLDSQIDHLNDYMAK.V
1817.8647	1816.8574	1816.8084	27.0	4	18	1	---	K.HKMPCEETNNIDESVK.I + Oxidation (M)
1890.9519	1889.9446	1889.8867	30.6	119	134	0	---	R.QQEEAAQIEFNNQVR.A
2031.0208	2030.0135	2030.0181	-2.26	19	36	1	---	K.INDGYNGEQTPPTPVRLR.R
2047.0057	2045.9984	2045.9840	7.05	72	88	1	---	K.LDSQIDHLNDYMAKVER.R

**No match to:** 880.4860, 918.4446, 936.4494, 942.5760, 943.5732, 964.4806, 1034.1438, 1041.4738, 1041.4738, 1069.5068, 1070.4956, 1092.6370, 1274.6362, 1297.6344, 1325.6587, 1328.6764, 1349.6676, 1356.6869, 1365.6539, 1403.7028, 1404.6875, 1414.7764, 1598.8022, 1598.8022, 1599.8032, 1608.8135, 1637.8694, 1650.8323, 1659.9054, 1675.9045, 1675.9045, 1691.8800, 1696.8757, 1718.8705, 1727.8612, 1751.8932, 1805.9061, 1808.9041, 1818.8427, 1819.8307, 1913.9663, 1918.9434, 1935.9443, 1986.0540, 1999.0594, 2050.0166, 2051.0142, 2078.0791, 2079.0591, 2125.0874, 2146.0920, 2174.1213, 2177.1226, 2208.1162, 2225.1689, 2241.1670, 2242.1606, 2449.3245, 2668.3516, 2840.3254

12. [gi|966976364](#) Mass: 870261 Score: 68 Expect: 3.3 Matches: 44

PREDICTED: nebulin isoform X9 [Macaca mulatta]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4450	38.3	3496	- 3502	1	---	K.KEGYDLR.S
918.4446	917.4373	917.4389	-1.67	3685	- 3692	0	---	K.NNALNMNK.R
936.4494	935.4421	935.4633	-22.69	1951	- 1958	0	---	K.AMEIIEK.K + Oxidation (M)
964.4806	963.4733	963.4848	-11.88	6939	- 6946	0	---	K.HISSVMYK.E
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1070.4956	1069.4883	1069.4862	1.98	2340	- 2347	1	---	K.MQSEREYK.K
1296.6404	1295.6331	1295.6768	-33.72	7344	- 7354	0	---	R.SLHMINVQAQR.R
1296.6404	1295.6331	1295.6768	-33.72	7344	- 7354	0	---	R.SLHMINVQAQR.R
1297.6344	1296.6271	1296.5809	35.7	5704	- 5713	1	---	K.DTRYMSSYFK.Y
1328.6764	1327.6691	1327.6442	18.8	7200	- 7211	0	---	K.ATPTPTPEMER.A
1404.6875	1403.6802	1403.7409	-43.20	6371	- 6382	1	---	K.TVSHLVSENKYK.D
1414.7764	1413.7691	1413.7252	31.0	6181	- 6192	0	---	K.FTSIVDTPEHLR.T
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1608.8135	1607.8062	1607.7977	5.28	7477	- 7491	1	---	R.TGRTGMLPANYVEAI.- + Oxidation (M)
1637.8694	1636.8621	1636.8276	21.1	2331	- 2344	1	---	K.LVLSMNVAKMQSER.E + 2 Oxidation (M)
1678.8468	1677.8395	1677.8032	21.6	1379	- 1394	0	---	K.TSYHTPGDMVSITAAK.M
1691.8800	1690.8727	1690.8600	7.54	6427	- 6441	1	---	K.GKSNSYIMLEPEVK.H
1696.8757	1695.8684	1695.8553	7.72	5932	- 5946	0	---	K.ERPHHHAGNQTTALK.H
1718.8705	1717.8632	1717.8709	-4.48	1867	- 1882	0	---	K.TSFHTPVDMLSVVAAK.K + Oxidation (M)
1727.8612	1726.8539	1726.8634	-5.47	3705	- 3719	0	---	K.TIHVMPDTPEIMLAK.L + 2 Oxidation (M)
1751.8932	1750.8859	1750.8097	43.5	287	- 301	1	---	K.GKWSETPCFEVANAR.M
1805.9061	1804.8988	1804.8600	21.5	4122	- 4137	1	---	R.GIGWMEGSVEMNRVK.V + Oxidation (M)
1808.9041	1807.8968	1807.9390	-23.32	891	- 906	0	---	K.TIYTAPLDMLQVTQAK.K + Oxidation (M)
1818.8427	1817.8354	1817.8652	-16.36	6885	- 6901	1	---	K.EDVSPGTAIGKTPEMMR.V
1819.8307	1818.8234	1818.8869	-34.89	5271	- 5286	0	---	K.ANVHIPNDMMNHVLAK.K + Oxidation (M)
1890.9519	1889.9446	1889.8869	30.5	716	- 730	0	---	K.CYFPQTITQEYEAIK.K
1913.9663	1912.9590	1912.9564	1.37	7009	- 7025	1	---	K.ENLSKGTPLPVTPEMER.V + Oxidation (M)
1918.9434	1917.9361	1918.0101	-38.59	5723	- 5739	1	---	K.AYGYTLGPKDVPFVHVR.R
1935.9443	1934.9370	1934.9118	13.1	1723	- 1738	1	---	K.LKFTYAMDTMEQALNK.S + 2 Oxidation (M)
1986.0540	1985.0467	1985.0193	13.8	5337	- 5353	1	---	K.GIGCYVWDTPQILHAKK.S
1999.0594	1998.0521	1998.0278	12.2	855	- 872	1	---	K.MIGALSINDDPKMLHSLK.T + Oxidation (M)
2031.0208	2030.0135	2029.9271	42.6	1969	- 1986	0	---	K.YSTLMDSMNMVLAQNNAK.I
2047.0057	2045.9984	2045.9220	37.4	1969	- 1986	0	---	K.YSTLMDSMNMVLAQNNAK.I + Oxidation (M)
2051.0142	2050.0069	2050.0769	-34.12	2487	- 2504	1	---	K.DKTQIHIMPDTPDIVLAK.A + Oxidation (M)
2079.0591	2078.0518	2078.1016	-23.96	3705	- 3722	1	---	K.TIHVMPDTPEIMLAKLNR.I
2125.0874	2124.0801	2124.0707	4.43	3216	- 3233	1	---	K.DKTQIHIMPDTPEIMLAR.Q + Oxidation (M)
2177.1226	2176.1153	2176.1132	0.97	2144	- 2161	1	---	K.YILLPDAMNIELTRNMNR.I
2208.1162	2207.1089	2207.0755	15.2	1895	- 1913	0	---	R.NLIHTYNMLPDAMSFELAK.T
2225.1689	2224.1616	2224.1344	12.2	2975	- 2993	1	---	K.TQIHIMPDTPEIMLARTNK.I + Oxidation (M)
2241.1670	2240.1597	2240.1293	13.6	2975	- 2993	1	---	K.TQIHIMPDTPEIMLARTNK.I + 2 Oxidation (M)
2449.3245	2448.3172	2448.2318	34.9	3671	- 3692	1	---	K.FTSITDTPQVLAKNNALNMNK.R
2840.3254	2839.3181	2839.4572	-48.98	1758	- 1782	1	---	K.TTIHVMPDTPDILLSRVNQITMSNK.L + Oxidation (M)

No match to: 942.5760, 943.5732, 1034.1438, 1069.5068, 1092.6370, 1274.6362, 1325.6587, 1349.6676, 1356.6869, 1365.6539, 1403.7028, 1599.8032, 1650.8323, 1659.9054, 1669.8503, 1675.9045, 1675.9045, 1675.9045, 1790.9150, 1817.8647, 2050.0166, 2078.0791, 2146.0920, 2174.1213, 2242.1606, 2668.3516

13. [gi|966976362](#) Mass: 870253 Score: 68 Expect: 3.5 Matches: 44

PREDICTED: nebulin isoform X8 [Macaca mulatta]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4450	38.3	3496	- 3502	1	---	K.KEGYDLR.S
918.4446	917.4373	917.4389	-1.67	3685	- 3692	0	---	K.NNALNMNK.R
936.4494	935.4421	935.4633	-22.69	1951	- 1958	0	---	K.AMEIIEK.K + Oxidation (M)
964.4806	963.4733	963.4848	-11.88	6939	- 6946	0	---	K.HISSVMYK.E
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1070.4956	1069.4883	1069.4862	1.98	2340	- 2347	1	---	K.MQSEREYK.K
1296.6404	1295.6331	1295.6768	-33.72	7344	- 7354	0	---	R.SLHMINVQAQR.R
1296.6404	1295.6331	1295.6768	-33.72	7344	- 7354	0	---	R.SLHMINVQAQR.R
1297.6344	1296.6271	1296.5809	35.7	5704	- 5713	1	---	K.DTRYMSSYFK.Y
1328.6764	1327.6691	1327.6442	18.8	7200	- 7211	0	---	K.ATPTPTPEMER.A
1404.6875	1403.6802	1403.7409	-43.20	6371	- 6382	1	---	K.TVSHLVSENKYK.D
1414.7764	1413.7691	1413.7252	31.0	6181	- 6192	0	---	K.FTSIVDTPEHLR.T
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1608.8135	1607.8062	1607.7977	5.28	7477	- 7491	1	---	R.TGRTGMLPANYVEAI.- + Oxidation (M)
1637.8694	1636.8621	1636.8276	21.1	2331	- 2344	1	---	K.LVLSMNVAKMQSER.E + 2 Oxidation (M)
1678.8468	1677.8395	1677.8032	21.6	1379	- 1394	0	---	K.TSYHTPGDMVSITAAK.M
1691.8800	1690.8727	1690.8600	7.54	6427	- 6441	1	---	K.GKSNSYIMLEPEVK.H
1696.8757	1695.8684	1695.8553	7.72	5932	- 5946	0	---	K.ERPHHHAGNQTTALK.H
1718.8705	1717.8632	1717.8709	-4.48	1867	- 1882	0	---	K.TSFHTPVDMLSVVAAK.K + Oxidation (M)
1727.8612	1726.8539	1726.8634	-5.47	3705	- 3719	0	---	K.TIHVMPDTPEIMLAK.L + 2 Oxidation (M)
1751.8932	1750.8859	1750.8097	43.5	287	- 301	1	---	K.GKWSETPCFEVANAR.M
1805.9061	1804.8988	1804.8600	21.5	4122	- 4137	1	---	R.GIGWMEGSVEMNRVK.V + Oxidation (M)
1808.9041	1807.8968	1807.9390	-23.32	891	- 906	0	---	K.TIYTAPLDMLQVTQAK.K + Oxidation (M)
1818.8427	1817.8354	1817.8652	-16.36	6885	- 6901	1	---	K.EDVSPGTAIGKTPEMMR.V
1819.8307	1818.8234	1818.8869	-34.89	5271	- 5286	0	---	K.ANVHIPNDMMNHVLAK.K + Oxidation (M)

1890.9519	1889.9446	1889.8869	30.5	716	-	730	0	---	K.CYFPQTITQEYEAIK.K
1913.9663	1912.9590	1912.9564	1.37	7009	-	7025	1	---	K.ENLSKGTPLPVTPEMER.V + Oxidation (M)
1918.9434	1917.9361	1918.0101	-38.59	5723	-	5739	1	---	K.AYGTYLGPQDVPFVHVR.R
1935.9443	1934.9370	1934.9118	13.1	1723	-	1738	1	---	K.LKFTYAMDTMEQALNK.S + 2 Oxidation (M)
1986.0540	1985.0467	1985.0193	13.8	5337	-	5353	1	---	K.GIGCYVWDTPQILHAKK.S
1999.0594	1998.0521	1998.0278	12.2	855	-	872	1	---	K.MIGALSINDDPKMLHSLK.T + Oxidation (M)
2031.0208	2030.0135	2029.9271	42.6	1969	-	1986	0	---	K.YSTLMDSMNMVLAQNNAK.I
2047.0057	2045.9984	2045.9220	37.4	1969	-	1986	0	---	K.YSTLMDSMNMVLAQNNAK.I + Oxidation (M)
2051.0142	2050.0069	2050.0769	-34.12	2487	-	2504	1	---	K.DKTQIHIMPDTPDIVLAK.A + Oxidation (M)
2079.0591	2078.0518	2078.1016	-23.96	3705	-	3722	1	---	K.TIHVMPDTPEIMLAKLNR.I
2125.0874	2124.0801	2124.0707	4.43	3216	-	3233	1	---	K.DKTQIHIMPDTPEIMLAR.Q + Oxidation (M)
2177.1226	2176.1153	2176.1132	0.97	2144	-	2161	1	---	K.YILLPDAMNIELTRNMNR.I
2208.1162	2207.1089	2207.0755	15.2	1895	-	1913	0	---	R.NLIHTYNMLPDAMSFELAK.T
2225.1689	2224.1616	2224.1344	12.2	2975	-	2993	1	---	K.TQIHIMPDTPEIMLARTNK.I + Oxidation (M)
2241.1670	2240.1597	2240.1293	13.6	2975	-	2993	1	---	K.TQIHIMPDTPEIMLARTNK.I + 2 Oxidation (M)
2449.3245	2448.3172	2448.2318	34.9	3671	-	3692	1	---	K.FTSITDTPQVLAKNNALNMNK.R
2840.3254	2839.3181	2839.4572	-48.98	1758	-	1782	1	---	K.TTIHVMPDTPDILLSRVNQITMSNK.L + Oxidation (M)

No match to: 942.5760, 943.5732, 1034.1438, 1069.5068, 1092.6370, 1274.6362, 1325.6587, 1349.6676, 1356.6869, 1365.6539, 1403.7028, 1599.8032, 1650.8323, 1659.9054, 1669.8503, 1675.9045, 1675.9045, 1790.9150, 1817.8647, 2050.0166, 2078.0791, 2146.0920, 2174.1213, 2242.1606, 2668.3516

14. [gi|966976348](#) Mass: 877274 Score: 68 Expect: 3.5 Matches: 44

PREDICTED: nebulin isoform X1 [Macaca mulatta]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4450	38.3	3496	- 3502	1	---	K.KEGYDLR.S
918.4446	917.4373	917.4389	-1.67	3685	- 3692	0	---	K.NNALNMNK.R
936.4494	935.4421	935.4633	-22.69	1951	- 1958	0	---	K.AMEIISEK.K + Oxidation (M)
964.4806	963.4733	963.4848	-11.88	6939	- 6946	0	---	K.HISSVMYK.E
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1070.4956	1069.4883	1069.4862	1.98	2340	- 2347	1	---	K.MQSEREYK.K
1296.6404	1295.6331	1295.6768	-33.72	7406	- 7416	0	---	R.SLHMINVQAQR.R
1296.6404	1295.6331	1295.6768	-33.72	7406	- 7416	0	---	R.SLHMINVQAQR.R
1297.6344	1296.6271	1296.5809	35.7	5704	- 5713	1	---	K.DTRYMSYFYK.Y
1328.6764	1327.6691	1327.6442	18.8	7262	- 7273	0	---	K.ATPTPVTPEMER.A
1404.6875	1403.6802	1403.7409	-43.20	6371	- 6382	1	---	K.TVSHLVSENKYK.D
1414.7764	1413.7691	1413.7252	31.0	6181	- 6192	0	---	K.FTSIVDTPPEHLR.T
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1608.8135	1607.8062	1607.7977	5.28	7539	- 7553	1	---	R.TGRTGMLPANYVEAI.- + Oxidation (M)
1637.8694	1636.8621	1636.8276	21.1	2331	- 2344	1	---	K.LVLSMNVAKMQSER.E + 2 Oxidation (M)
1678.8468	1677.8395	1677.8032	21.6	1379	- 1394	0	---	K.TSYHTPGDMVSITAAM.M
1691.8800	1690.8727	1690.8600	7.54	6427	- 6441	1	---	K.GKSNSYSIMLEPEVK.H
1696.8757	1695.8684	1695.8553	7.72	5932	- 5946	0	---	K.ERPHHHAGNQTTALK.H
1718.8705	1717.8632	1717.8709	-4.48	1867	- 1882	0	---	K.TSFHTPVDMLSVVAAK.K + Oxidation (M)
1727.8612	1726.8539	1726.8634	-5.47	3705	- 3719	0	---	K.TIHVMPDTPEIMLAK.L + 2 Oxidation (M)
1751.8932	1750.8859	1750.8097	43.5	287	- 301	1	---	K.GKWSETPCFEVANAR.M
1805.9061	1804.8988	1804.8600	21.5	4122	- 4137	1	---	R.GIGWMPGSGVEMNRVK.V + Oxidation (M)
1808.9041	1807.8968	1807.9390	-23.32	891	- 906	0	---	K.TIYTAPLDMLQVTQAK.K + Oxidation (M)
1818.8427	1817.8354	1817.8652	-16.36	6885	- 6901	1	---	K.EDVSPGTAIGKTPEMMR.V
1819.8307	1818.8234	1818.8869	-34.89	5271	- 5286	0	---	K.ANVHIPNDMMNHVLAK.K + Oxidation (M)
1890.9519	1889.9446	1889.8869	30.5	716	- 730	0	---	K.CYFPQTTITQEYEAIK.K
1913.9663	1912.9590	1912.9564	1.37	7009	- 7025	1	---	K.ENLSKGTPLPVTPEMER.V + Oxidation (M)
1918.9434	1917.9361	1918.0101	-38.59	5723	- 5739	1	---	K.AYGTYLGPQDVPFVHVR.R
1935.9443	1934.9370	1934.9118	13.1	1723	- 1738	1	---	K.LKFTYAMDTMEQALNK.S + 2 Oxidation (M)
1986.0540	1985.0467	1985.0193	13.8	5337	- 5353	1	---	K.GIGCYVWDTPQILHAKK.S
1999.0594	1998.0521	1998.0278	12.2	855	- 872	1	---	K.MIGALSINDDPKMLHSLK.T + Oxidation (M)
2031.0208	2030.0135	2029.9271	42.6	1969	- 1986	0	---	K.YSTLMDSMNMVLAQNNAK.I
2047.0057	2045.9984	2045.9220	37.4	1969	- 1986	0	---	K.YSTLMDSMNMVLAQNNAK.I + Oxidation (M)
2051.0142	2050.0069	2050.0769	-34.12	2487	- 2504	1	---	K.DKTQIHIMPDTPDIVLAK.A + Oxidation (M)
2079.0591	2078.0518	2078.1016	-23.96	3705	- 3722	1	---	K.TIHVMPDTPEIMLAKLNR.I
2125.0874	2124.0801	2124.0707	4.43	3216	- 3233	1	---	K.DKTQIHIMPDTPEIMLAR.Q + Oxidation (M)
2177.1226	2176.1153	2176.1132	0.97	2144	- 2161	1	---	K.YILLPDAMNIELTRNMNR.I
2208.1162	2207.1089	2207.0755	15.2	1895	- 1913	0	---	R.NLIHTYNMLPDAMSFELAK.T
2225.1689	2224.1616	2224.1344	12.2	2975	- 2993	1	---	K.TQIHIMPDTPEIMLARTNK.I + Oxidation (M)
2241.1670	2240.1597	2240.1293	13.6	2975	- 2993	1	---	K.TQIHIMPDTPEIMLARTNK.I + 2 Oxidation (M)
2449.3245	2448.3172	2448.2318	34.9	3671	- 3692	1	---	K.FTSITDTPQVLAKNNALNMNK.R
2840.3254	2839.3181	2839.4572	-48.98	1758	- 1782	1	---	K.TTIHVMPDTPDILLSRVNQITMSNK.L + Oxidation (M)
No match to: 942.5760, 943.5732, 1034.1438, 1069.5068, 1092.6370, 1274.6362, 1325.6587, 1349.6676, 1356.6869, 1365.6539, 1403.7028, 1599.8032, 1650.8323, 1659.9054, 1669.8503, 1675.9045, 1675.9045, 1790.9150, 1817.8647, 2050.0166, 2078.0791, 2146.0920, 2174.1213, 2242.1606, 2668.3516								

15. [gi|966976366](#) Mass: 870102 Score: 68 Expect: 3.6 Matches: 44

PREDICTED: nebulin isoform X10 [Macaca mulatta]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4450	38.3	3496	- 3502	1	---	K.KEGYDLR.S
918.4446	917.4373	917.4389	-1.67	3685	- 3692	0	---	K.NNALNMNK.R
936.4494	935.4421	935.4633	-22.69	1951	- 1958	0	---	K.AMEIISEK.K + Oxidation (M)
964.4806	963.4733	963.4848	-11.88	6939	- 6946	0	---	K.HISSVMYK.E



1041.4738	1040.4665	1040.4960	-28.37	2517	-	2524	1	---	R.MGYEELKR.K + Oxidation (M)
1041.4738	1040.4665	1040.4960	-28.37	2517	-	2524	1	---	R.MGYEELKR.K + Oxidation (M)
1070.4956	1069.4883	1069.4862	1.98	2340	-	2347	1	---	K.MQSEREYK.K
1296.6404	1295.6331	1295.6768	-33.72	7344	-	7354	0	---	R.SLHMINVQAQR.R
1296.6404	1295.6331	1295.6768	-33.72	7344	-	7354	0	---	R.SLHMINVQAQR.R
1297.6344	1296.6271	1296.5809	35.7	5704	-	5713	1	---	K.DTRYMSSYFK.Y
1328.6764	1327.6691	1327.6408	21.3	6967	-	6977	0	---	R.NQENFSSVLKY.E
1404.6875	1403.6802	1403.7409	-43.20	6371	-	6382	1	---	K.TVSHLVSENKYK.D
1414.7764	1413.7691	1413.7252	31.0	6181	-	6192	0	---	K.FTSIVDTPEHLR.T
1598.8022	1597.7949	1597.8208	-16.19	5518	-	5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1598.8022	1597.7949	1597.8208	-16.19	5518	-	5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1608.8135	1607.8062	1607.7977	5.28	7477	-	7491	1	---	R.TGRTGMLPANYVEAI.- + Oxidation (M)
1637.8694	1636.8621	1636.8276	21.1	2331	-	2344	1	---	K.LVLSMNVAKMQSER.E + 2 Oxidation (M)
1678.8468	1677.8395	1677.8032	21.6	1379	-	1394	0	---	K.TSYHTPGDMVSITAAK.M
1691.8800	1690.8727	1690.8600	7.54	6427	-	6441	1	---	K.GKSNIYSIMLEPPEVK.H
1696.8757	1695.8684	1695.8553	7.72	5932	-	5946	0	---	K.ERPHHHAGNQTTALK.H
1718.8705	1717.8632	1717.8709	-4.48	1867	-	1882	0	---	K.TSFHTPVDMLSVVAAK.K + Oxidation (M)
1727.8612	1726.8539	1726.8634	-5.47	3705	-	3719	0	---	K.TIHVMPDTPEIMLAK.L + 2 Oxidation (M)
1751.8932	1750.8859	1750.8097	43.5	287	-	301	1	---	K.GKWSETPCFEVANAR.M
1805.9061	1804.8988	1804.8600	21.5	4122	-	4137	1	---	R.GIGWMEPGSVEMNRVK.V + Oxidation (M)
1808.9041	1807.8968	1807.9390	-23.32	891	-	906	0	---	K.TIYTAPLDMLQVTQAK.K + Oxidation (M)
1818.8427	1817.8354	1817.8652	-16.36	6885	-	6901	1	---	K.EDVSPGTAIGKTPPEMMR.V
1819.8307	1818.8234	1818.8869	-34.89	5271	-	5286	0	---	K.ANVHIPNDMMNHVLAK.K + Oxidation (M)
1890.9519	1889.9446	1889.8869	30.5	716	-	730	0	---	K.CYFPQTITQEYEAIK.K
1913.9663	1912.9590	1912.9564	1.37	7009	-	7025	1	---	K.ENLSKGTPLPVTPEMER.V + Oxidation (M)
1918.9434	1917.9361	1918.0101	-38.59	5723	-	5739	1	---	K.AYGYTLGPKDVPFVHVR.R
1935.9443	1934.9370	1934.9118	13.1	1723	-	1738	1	---	K.LKFTYAMDTMEQALNK.S + 2 Oxidation (M)
1986.0540	1985.0467	1985.0193	13.8	5337	-	5353	1	---	K.GIGCYVWDTPQILHAKK.S
1999.0594	1998.0521	1998.0278	12.2	855	-	872	1	---	K.MIGALSINDDPKMLHSLK.T + Oxidation (M)
2031.0208	2030.0135	2029.9271	42.6	1969	-	1986	0	---	K.YSTLMDSMNMVLAQNNAK.I
2047.0057	2045.9984	2045.9220	37.4	1969	-	1986	0	---	K.YSTLMDSMNMVLAQNNAK.I + Oxidation (M)
2051.0142	2050.0069	2050.0769	-34.12	2487	-	2504	1	---	K.DKTQIHIMPDTPDIVLAK.A + Oxidation (M)
2079.0591	2078.0518	2078.1016	-23.96	3705	-	3722	1	---	K.TIHVMPDTPEIMLAKLNR.I
2125.0874	2124.0801	2124.0707	4.43	3216	-	3233	1	---	K.DKTQIHIMPDTPEIMLAR.Q + Oxidation (M)
2177.1226	2176.1153	2176.1132	0.97	2144	-	2161	1	---	K.YILLPDAMNIELTRNMNR.I
2208.1162	2207.1089	2207.0755	15.2	1895	-	1913	0	---	R.NLIHTYNMLPDAMSFELAK.T
2225.1689	2224.1616	2224.1344	12.2	2975	-	2993	1	---	K.TQIHIMPDTPEIMLARTNK.I + Oxidation (M)
2241.1670	2240.1597	2240.1293	13.6	2975	-	2993	1	---	K.TQIHIMPDTPEIMLARTNK.I + 2 Oxidation (M)
2449.3245	2448.3172	2448.2318	34.9	3671	-	3692	1	---	K.FTSITDTPQVLAKNNALNMNK.R
2840.3254	2839.3181	2839.4572	-48.98	1758	-	1782	1	---	K.TTIHVMPDTPDILLSRVNQITMSNK.L + Oxidation (M)

No match to: 942.5760, 943.5732, 1034.1438, 1069.5068, 1092.6370, 1274.6362, 1325.6587, 1349.6676, 1356.6869, 1365.6539, 1403.7028, 1599.8032, 1650.8323, 1659.9054, 1669.8503, 1675.9045, 1675.9045, 1675.9045, 1790.9150, 1817.8647, 2050.0166, 2078.0791, 2146.0920, 2174.1213, 2242.1606, 2668.3516

16. [gi|966976350](#) Mass: 877316 Score: 67 Expect: 3.8 Matches: 44

PREDICTED: nebulin isoform X2 [Macaca mulatta]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4450	38.3	3496	- 3502	1	---	K.KEGYDLR.S
918.4446	917.4373	917.4389	-1.67	3685	- 3692	0	---	K.NNALNMNK.R
936.4494	935.4421	935.4633	-22.69	1951	- 1958	0	---	K.AMEIIEK.K + Oxidation (M)
964.4806	963.4733	963.4848	-11.88	6939	- 6946	0	---	K.HISSVMYK.E
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1070.4956	1069.4883	1069.4862	1.98	2340	- 2347	1	---	K.MQSEREYK.K
1296.6404	1295.6331	1295.6768	-33.72	7406	- 7416	0	---	R.SLHMINVQAQR.R
1296.6404	1295.6331	1295.6768	-33.72	7406	- 7416	0	---	R.SLHMINVQAQR.R
1297.6344	1296.6271	1296.5809	35.7	5704	- 5713	1	---	K.DTRYMSSYFK.Y
1328.6764	1327.6691	1327.6442	18.8	7262	- 7273	0	---	K.ATPTPVTPEMER.A
1404.6875	1403.6802	1403.7409	-43.20	6371	- 6382	1	---	K.TVSHLVSENKYK.D
1414.7764	1413.7691	1413.7252	31.0	6181	- 6192	0	---	K.FTSIVDTPEHLR.T
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1608.8135	1607.8062	1607.7977	5.28	7539	- 7553	1	---	R.TGRTGMLPANYVEAI.- + Oxidation (M)
1637.8694	1636.8621	1636.8276	21.1	2331	- 2344	1	---	K.LVLSMNVAKMQSER.E + 2 Oxidation (M)
1678.8468	1677.8395	1677.8032	21.6	1379	- 1394	0	---	K.TSYHTPGDMVSITAAK.M
1691.8800	1690.8727	1690.8600	7.54	6427	- 6441	1	---	K.GKSNIYSIMLEPPEVK.H
1696.8757	1695.8684	1695.8553	7.72	5932	- 5946	0	---	K.ERPHHHAGNQTTALK.H
1718.8705	1717.8632	1717.8709	-4.48	1867	- 1882	0	---	K.TSFHTPVDMLSVVAAK.K + Oxidation (M)
1727.8612	1726.8539	1726.8634	-5.47	3705	- 3719	0	---	K.TIHVMPDTPEIMLAK.L + 2 Oxidation (M)
1751.8932	1750.8859	1750.8097	43.5	287	- 301	1	---	K.GKWSETPCFEVANAR.M
1805.9061	1804.8988	1804.8600	21.5	4122	- 4137	1	---	R.GIGWMEPGSVEMNRVK.V + Oxidation (M)
1808.9041	1807.8968	1807.9390	-23.32	891	- 906	0	---	K.TIYTAPLDMLQVTQAK.K + Oxidation (M)
1818.8427	1817.8354	1817.8652	-16.36	6885	- 6901	1	---	K.EDVSPGTAIGKTPPEMMR.V
1819.8307	1818.8234	1818.8869	-34.89	5271	- 5286	0	---	K.ANVHIPNDMMNHVLAK.K + Oxidation (M)
1890.9519	1889.9446	1889.8869	30.5	716	- 730	0	---	K.CYFPQTITQEYEAIK.K
1913.9663	1912.9590	1912.9564	1.37	7009	- 7025	1	---	K.ENLSKGTPLPVTPEMER.V + Oxidation (M)
1918.9434	1917.9361	1918.0101	-38.59	5723	- 5739	1	---	K.AYGYTLGPKDVPFVHVR.R
1935.9443	1934.9370	1934.9118	13.1	1723	- 1738	1	---	K.LKFTYAMDTMEQALNK.S + 2 Oxidation (M)
1986.0540	1985.0467	1985.0193	13.8	5337	- 5353	1	---	K.GIGCYVWDTPQILHAKK.S

1999.0594	1998.0521	1998.0278	12.2	855	-	872	1	---	K.MIGALSINDDPKMLHSLK.T + Oxidation (M)
2031.0208	2030.0135	2029.9271	42.6	1969	-	1986	0	---	K.YSTLMDSMNMVLAQNNAK.I
2047.0057	2045.9984	2045.9220	37.4	1969	-	1986	0	---	K.YSTLMDSMNMVLAQNNAK.I + Oxidation (M)
2051.0142	2050.0069	2050.0769	-34.12	2487	-	2504	1	---	K.DKTQIHIMPDPDIVLAK.A + Oxidation (M)
2079.0591	2078.0518	2078.1016	-23.96	3705	-	3722	1	---	K.TIHVMPDTPPEIMLAKLN.R
2125.0874	2124.0801	2124.0707	4.43	3216	-	3233	1	---	K.DKTQIHIMPDPPEIMLAR.Q + Oxidation (M)
2177.1226	2176.1153	2176.1132	0.97	2144	-	2161	1	---	K.YILLPDAMNIELTRNMNR.I
2208.1162	2207.1089	2207.0755	15.2	1895	-	1913	0	---	R.NLIHTYNMLPDAMSFELAK.T
2225.1689	2224.1616	2224.1344	12.2	2975	-	2993	1	---	K.TQIHIMPDPPEIMLARTNK.I + Oxidation (M)
2241.1670	2240.1597	2240.1293	13.6	2975	-	2993	1	---	K.TQIHIMPDPPEIMLARTNK.I + 2 Oxidation (M)
2449.3245	2448.3172	2448.2318	34.9	3671	-	3692	1	---	K.FTSITDTPQVLAKNNALNMN.K
2840.3254	2839.3181	2839.4572	-48.98	1758	-	1782	1	---	K.TTIHVMPDTPDILLSRVNQITMSNK.L + Oxidation (M)

No match to: 942.5760, 943.5732, 1034.1438, 1069.5068, 1092.6370, 1274.6362, 1325.6587, 1349.6676, 1356.6869, 1365.6539, 1403.7028, 1599.8032, 1650.8323, 1659.9054, 1669.8503, 1675.9045, 1675.9045, 1790.9150, 1817.8647, 2050.0166, 2078.0791, 2146.0920, 2174.1213, 2242.1606, 2668.3516

17. [gi|944241857](#) Mass: 181953 Score: 67 Expect: 3.8 Matches: 18

hypothetical protein SETIT\_000029mg [Setaria italica]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
943.5732	942.5659	942.5386	29.0	1274	- 1281	0	---	K.QLEEAILK.V
1296.6404	1295.6331	1295.5915	32.1	170	- 180	0	---	K.ETEVTTLSC.EK.K
1296.6404	1295.6331	1295.5915	32.1	170	- 180	0	---	K.ETEVTTLSC.EK.K
1403.7028	1402.6955	1402.7303	-24.81	1182	- 1193	1	---	R.NLESVLEKQSEK.I
1598.8022	1597.7949	1597.8423	-29.67	966	- 980	0	---	K.NAALAQQLQSEANIK.E
1598.8022	1597.7949	1597.8423	-29.67	501	- 515	0	---	K.NAALAQQLQSEANIK.E
1599.8032	1598.7959	1598.8263	-19.02	768	- 782	0	---	K.NAALAQQLQSEANIK.K
1669.8503	1668.8430	1668.8471	-2.45	621	- 634	0	---	K.FIHQAEILAQDEK.N
1718.8705	1717.8632	1717.8370	15.3	1259	- 1273	0	---	K.DELSVQLENNSTLEK.Q
1727.8612	1726.8539	1726.9213	-39.01	768	- 783	1	---	K.NAALAQQLQSEANIKK.L
1805.9061	1804.8988	1804.8989	-0.03	879	- 893	1	---	K.TELAQQLERISDMQK.T + Oxidation (M)
1817.8647	1816.8574	1816.8989	-22.81	215	- 230	1	---	K.CNLLSAEVEKAQQA.EK.E
1986.0540	1985.0467	1985.0065	20.3	225	- 241	1	---	K.AQQAQKEVQTLLEENQK.L
2125.0874	2124.0801	2124.1613	-38.20	1490	- 1509	1	---	R.VSLLEETLMQVKGHAVSGVK.V
2208.1162	2207.1089	2207.0263	37.4	661	- 680	0	---	K.DNDSATSEIEQLASLMNLK.T
2241.1670	2240.1597	2240.1688	-4.06	1377	- 1395	1	---	R.LQYAYDEVSSRVSQLLEIK.R
2242.1606	2241.1533	2241.0960	25.6	981	- 998	0	---	K.ELQSDMVQQNQILHFQ.R.E
2668.3516	2667.3443	2667.4153	-26.59	295	- 318	1	---	K.LQQLGLEIEGLKVEAAELMNNLDK.E

No match to: 880.4860, 918.4446, 936.4494, 942.5760, 964.4806, 1034.1438, 1041.4738, 1041.4738, 1069.5068, 1070.4956, 1092.6370, 1274.6362, 1297.6344, 1325.6587, 1328.6764, 1349.6676, 1356.6869, 1365.6539, 1404.6875, 1414.7764, 1608.8135, 1637.8694, 1650.8323, 1659.9054, 1675.9045, 1675.9045, 1678.8468, 1691.8800, 1696.8757, 1751.8932, 1790.9150, 1808.9041, 1818.8427, 1819.8307, 1890.9519, 1913.9663, 1918.9434, 1935.9443, 1999.0594, 2031.0208, 2047.0057, 2050.0166, 2051.0142, 2078.0791, 2079.0591, 2146.0920, 2174.1213, 2177.1226, 2225.1689, 2449.3245, 2840.3254

18. [gi|954440236](#) Mass: 30992 Score: 67 Expect: 4.1 Matches: 10

hypothetical protein T4D\_7133, partial [Trichinella pseudospiralis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1296.6404	1295.6331	1295.5897	33.5	243	- 252	1	---	R.AMLMRCQQAR.G + 2 Oxidation (M)
1296.6404	1295.6331	1295.5897	33.5	243	- 252	1	---	R.AMLMRCQQAR.G + 2 Oxidation (M)
1669.8503	1668.8430	1668.7928	30.1	146	- 160	1	---	R.NGNNSTADSHVIRRG
1678.8468	1677.8395	1677.7668	43.3	180	- 193	0	---	K.LDSQIDHLNDYMAK.V + Oxidation (M)
1727.8612	1726.8539	1726.8387	8.82	46	- 60	1	---	K.SIFSTVNPDRHDSR.I
1790.9150	1789.9077	1789.8669	22.8	179	- 193	1	---	K.KLDSQIDHLNDYMAK.V
1817.8647	1816.8574	1816.8084	27.0	112	- 126	1	---	K.HKMPCEPCTNIDESVK.I + Oxidation (M)
1890.9519	1889.9446	1889.8867	30.6	227	- 242	0	---	R.QQEEAAQIEFNNQVR.A
2031.0208	2030.0135	2030.0181	-2.26	127	- 144	1	---	K.INDGYNGEQTPPTVRLR.R
2047.0057	2045.9984	2045.9840	7.05	180	- 196	1	---	K.LDSQIDHLNDYMAKVER.R

No match to: 880.4860, 918.4446, 936.4494, 942.5760, 943.5732, 964.4806, 1034.1438, 1041.4738, 1041.4738, 1069.5068, 1070.4956, 1092.6370, 1274.6362, 1297.6344, 1325.6587, 1328.6764, 1349.6676, 1356.6869, 1365.6539, 1403.7028, 1404.6875, 1414.7764, 1598.8022, 1598.8022, 1599.8032, 1608.8135, 1637.8694, 1650.8323, 1659.9054, 1675.9045, 1675.9045, 1691.8800, 1696.8757, 1718.8705, 1751.8932, 1805.9061, 1808.9041, 1818.8427, 1819.8307, 1913.9663, 1918.9434, 1935.9443, 1986.0540, 1999.0594, 2050.0166, 2051.0142, 2078.0791, 2079.0591, 2125.0874, 2146.0920, 2174.1213, 2177.1226, 2208.1162, 2225.1689, 2241.1670, 2242.1606, 2449.3245, 2668.3516, 2840.3254

19. [gi|212544706](#) Mass: 31419 Score: 67 Expect: 4.5 Matches: 11

conserved hypothetical protein [Talaromyces marneffei ATCC 18224]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4662	14.3	196	- 204	1	---	K.GTGSTTKTK.S
1041.4738	1040.4665	1040.5179	-49.33	120	- 127	0	---	R.VQFEVEYK.S
1041.4738	1040.4665	1040.5179	-49.33	120	- 127	0	---	R.VQFEVEYK.S
1297.6344	1296.6271	1296.6384	-8.67	261	- 270	1	---	R.VEDMVYELRK.E + Oxidation (M)
1325.6587	1324.6514	1324.6445	5.21	260	- 269	1	---	R.RVEDMVYELR.K + Oxidation (M)
1365.6539	1364.6466	1364.6168	21.9	190	- 202	1	---	K.NNNEKGTGTTK.T
1598.8022	1597.7949	1597.7948	0.10	174	- 189	0	---	K.SSGITTPPTQPQDAK.N
1598.8022	1597.7949	1597.7948	0.10	174	- 189	0	---	K.SSGITTPPTQPQDAK.N
1669.8503	1668.8430	1668.8723	-17.52	120	- 133	1	---	R.VQFEVEYKSVINSK.N
1999.0594	1998.0521	1998.1149	-31.44	46	- 62	1	---	R.YLLLLDTHQKLQESLQK.Q
2079.0591	2078.0518	2078.0334	8.88	63	- 81	0	---	K.QLSSGFFQLAHANVYSPGR.R

No match to: 918.4446, 936.4494, 942.5760, 943.5732, 964.4806, 1034.1438, 1069.5068, 1070.4956, 1092.6370, 1274.6362, 1296.6404, 1296.6404, 1328.6764, 1349.6676, 1356.6869, 1403.7028, 1404.6875, 1414.7764, 1599.8032, 1608.8135, 1637.8694, 1650.8323, 1659.9054, 1675.9045, 1675.9045, 1678.8468, 1691.8800, 1696.8757, 1718.8705, 1727.8612, 1751.8932, 1790.9150, 1805.9061, 1808.9041, 1817.8647, 1818.8427, 1819.8307, 1890.9519, 1913.9663, 1918.9434, 1935.9443, 1986.0540, 2031.0208,

2047.0057, 2050.0166, 2051.0142, 2078.0791, 2125.0874, 2146.0920, 2174.1213, 2177.1226, 2208.1162, 2225.1689, 2241.1670, 2242.1606, 2449.3245, 2668.3516, 2840.3254

20. [gi|966976356](#) Mass: 873745 Score: 66 Expect: 4.7 Matches: 44

PREDICTED: nebulin isoform X5 [Macaca mulatta]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
880.4860	879.4787	879.4450	38.3	3496	- 3502	1	---	K.KEGYDLR.S
918.4446	917.4373	917.4389	-1.67	3685	- 3692	0	---	K.NNALNMNK.R
936.4494	935.4421	935.4633	-22.69	1951	- 1958	0	---	K.AMEIIEK.K + Oxidation (M)
964.4806	963.4733	963.4848	-11.88	6939	- 6946	0	---	K.HISSVMYK.E
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1041.4738	1040.4665	1040.4960	-28.37	2517	- 2524	1	---	R.MGYEELKR.K + Oxidation (M)
1070.4956	1069.4883	1069.4862	1.98	2340	- 2347	1	---	K.MQSEREYK.K
1296.6404	1295.6331	1295.6768	-33.72	7375	- 7385	0	---	R.SLHMINVQAQR.R
1296.6404	1295.6331	1295.6768	-33.72	7375	- 7385	0	---	R.SLHMINVQAQR.R
1297.6344	1296.6271	1296.5809	35.7	5704	- 5713	1	---	K.DTRYMSSYFK.Y
1328.6764	1327.6691	1327.6442	18.8	7231	- 7242	0	---	K.ATPTPVTPEMER.A
1404.6875	1403.6802	1403.7409	-43.20	6371	- 6382	1	---	K.TVSHLVSENKYK.D
1414.7764	1413.7691	1413.7252	31.0	6181	- 6192	0	---	K.FTSIVDTPPEHLR.T
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1598.8022	1597.7949	1597.8208	-16.19	5518	- 5531	0	---	K.IHIVPDMVEMVTAK.D + Oxidation (M)
1608.8135	1607.8062	1607.7977	5.28	7508	- 7522	1	---	R.TGRGTMLPANYVEAI.- + Oxidation (M)
1637.8694	1636.8621	1636.8276	21.1	2331	- 2344	1	---	K.LVLSMNVAKMQSER.E + 2 Oxidation (M)
1678.8468	1677.8395	1677.8032	21.6	1379	- 1394	0	---	K.TSYHTPGDMVSITAAK.M
1691.8800	1690.8727	1690.8600	7.54	6427	- 6441	1	---	K.GKSNIYSIMLEPPEVK.H
1696.8757	1695.8684	1695.8553	7.72	5932	- 5946	0	---	K.ERPHHHAGNQTTALK.H
1718.8705	1717.8632	1717.8709	-4.48	1867	- 1882	0	---	K.TSFHTPVDMLSVVAK.K + Oxidation (M)
1727.8612	1726.8539	1726.8634	-5.47	3705	- 3719	0	---	K.TIHVMPDTPEIMLAK.L + 2 Oxidation (M)
1751.8932	1750.8859	1750.8097	43.5	287	- 301	1	---	K.GKWSETPCFEVANAR.M
1805.9061	1804.8988	1804.8600	21.5	4122	- 4137	1	---	R.GIGWMEGSVEMNRVK.V + Oxidation (M)
1808.9041	1807.8968	1807.9390	-23.32	891	- 906	0	---	K.TIYTAPLDMLQVTQAK.K + Oxidation (M)
1818.8427	1817.8354	1817.8652	-16.36	6885	- 6901	1	---	K.EDVSPGTAIGKTPEMMR.V
1819.8307	1818.8234	1818.8869	-34.89	5271	- 5286	0	---	K.ANVHIPNDMMNHVLAK.K + Oxidation (M)
1890.9519	1889.9446	1889.8869	30.5	716	- 730	0	---	K.CYFPQTITQEYEAIK.K
1913.9663	1912.9590	1912.9564	1.37	6978	- 6994	1	---	K.ENLSKGTPLPVTPEMER.V + Oxidation (M)
1918.9434	1917.9361	1918.0101	-38.59	5723	- 5739	1	---	K.AYGYTLGPKDVPFVHVR.R
1935.9443	1934.9370	1934.9118	13.1	1723	- 1738	1	---	K.LKFTYAMDTMEQALNK.S + 2 Oxidation (M)
1986.0540	1985.0467	1985.0193	13.8	5337	- 5353	1	---	K.GIGCYVWDTPQILHAKK.S
1999.0594	1998.0521	1998.0278	12.2	855	- 872	1	---	K.MIGALSINDDPKMLHSLK.T + Oxidation (M)
2031.0208	2030.0135	2029.9271	42.6	1969	- 1986	0	---	K.YSTLMDSMNMVLAQNNAK.I
2047.0057	2045.9984	2045.9220	37.4	1969	- 1986	0	---	K.YSTLMDSMNMVLAQNNAK.I + Oxidation (M)
2051.0142	2050.0069	2050.0769	-34.12	2487	- 2504	1	---	K.DKTQIHIMPDTPDIVLAK.A + Oxidation (M)
2079.0591	2078.0518	2078.1016	-23.96	3705	- 3722	1	---	K.TIHVMPDTPEIMLAKLNR.I
2125.0874	2124.0801	2124.0707	4.43	3216	- 3233	1	---	K.DKTQIHIMPDTPEIMLAR.Q + Oxidation (M)
2177.1226	2176.1153	2176.1132	0.97	2144	- 2161	1	---	K.YILLPDAMNIELTRNMNR.I
2208.1162	2207.1089	2207.0755	15.2	1895	- 1913	0	---	R.NLIHTYNMLPDAMSFELAK.T
2225.1689	2224.1616	2224.1344	12.2	2975	- 2993	1	---	K.TQIHIMPDTPEIMLARTNK.I + Oxidation (M)
2241.1670	2240.1597	2240.1293	13.6	2975	- 2993	1	---	K.TQIHIMPDTPEIMLARTNK.I + 2 Oxidation (M)
2449.3245	2448.3172	2448.2318	34.9	3671	- 3692	1	---	K.FTSITDTPQVLAKNNALNMNK.R
2840.3254	2839.3181	2839.4572	-48.98	1758	- 1782	1	---	K.TTIHVMPDTPDILLSRVNQITMSNK.L + Oxidation (M)
No match to: 942.5760, 943.5732, 1034.1438, 1069.5068, 1092.6370, 1274.6362, 1325.6587, 1349.6676, 1356.6869, 1365.6539, 1403.7028, 1599.8032, 1650.8323, 1659.9054, 1669.8503, 1675.9045, 1675.9045, 1790.9150, 1817.8647, 2050.0166, 2078.0791, 2146.0920, 2174.1213, 2242.1606, 2668.3516								

## Search Parameters

Type of search : Sequence Query  
 Enzyme : Trypsin  
 Fixed modifications : [Carbamidomethyl \(C\)](#)  
 Variable modifications : [Oxidation \(M\)](#)  
 Mass values : Monoisotopic  
 Protein Mass : Unrestricted  
 Peptide Mass Tolerance :  $\pm 50$  ppm  
 Fragment Mass Tolerance:  $\pm 0.3$  Da  
 Max Missed Cleavages : 1  
 Instrument type : MALDI-TOF-TOF  
 Query1 (880.4860,1+) : <no title>  
 Query2 (918.4446,1+) : <no title>  
 Query3 (936.4494,1+) : <no title>  
 Query4 (942.5760,1+) : <no title>  
 Query5 (943.5732,1+) : <no title>  
 Query6 (964.4806,1+) : <no title>  
 Query7 (1034.1438,1+) : <no title>  
 Query8 (1041.4738,1+) : <no title>  
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 Query10 (1069.5068,1+) : <no title>  
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Query67 (2449.3245,1+) : <no title>  
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Query69 (2840.3254,1+) : <no title>

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