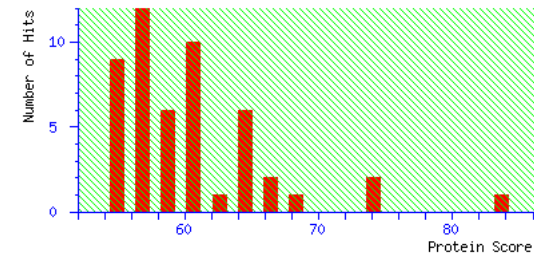


Mascot Search Results

User :
Email :
Search title : SampleSetID: 674, AnalysisID: 5211, MaldiWellID: 59826, SpectrumID: 120894, Path=\\161005\\MSMS\\16-85 combined NCBI euk
Database : NCBIInr 160208 (79581714 sequences; 29080698065 residues)
Taxonomy : Eukaryota (eucaryotes) (20445761 sequences)
Timestamp : 24 Oct 2016 at 20:53:04 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 84 for gi|157113225, AAEL006384-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 157113225	32821	84	AAEL006384-PA [Aedes aegypti]
2. gi 915073449	30892	75	hypothetical protein Z518_04560 [Rhinoclatiella mackenziei CBS 650.93]
3. gi 157140794	30571	75	AAEL015528-PA [Aedes aegypti]
4. gi 255072771	193655	68	predicted protein [Micromonas sp. RCC299]
5. gi 675389835	32207	66	Metalloendopeptidase OMA1, mitochondrial, partial [Stegodyphus mimosarum]
6. gi 71409789	87633	66	hypothetical protein [Trypanosoma cruzi strain CL Brener]
7. gi 299753039	49821	65	miller-Dieker lissencephaly protein [Coprinopsis cinerea okayama7#130]
8. gi 924884380	175589	65	hypothetical protein ACN38_g8607 [Penicillium nordicum]
9. gi 322518684	48330	65	RecName: Full=Nuclear distribution protein PAC1; AltName: Full=Lissencephaly-1 homolog; Short=LIS-1; AltName: Full=n
10. gi 795293311	68745	65	PREDICTED: endonuclease 8-like 3 [Colobus angolensis palliatus]
11. gi 336242517	5712	64	hypothetical protein SMAC_12000 [Sordaria macrospora k-hell]
12. gi 875642868	42136	64	hypothetical protein CIHG_05223 [Coccidioides immitis H538.4]
13. gi 751753175	40103	63	hypothetical protein OIADMADRAFT_41943 [Oidiodendron maius Zn]
14. gi 511006810	74632	62	hypothetical protein HMPREF1544_05059 [Mucor circinelloides f. circinelloides 1006PhL]
15. gi 589985287	632479	62	PREDICTED: dystonin-like [Peromyscus maniculatus bairdii]
16. gi 527303549	144822	62	hypothetical protein FOMPIDRAFT_1157451 [Fomitopsis pinicola FP-58527 SS1]
17. gi 823142681	74396	62	PREDICTED: exocyst complex component EXO70B1-like [Gossypium raimondii]
18. gi 677374751	145337	61	hypothetical protein N329_04449, partial [Haliaeetus albicilla]
19. gi 551503836	76403	61	PREDICTED: caseinolytic peptidase B protein homolog [Xiphophorus maculatus]
20. gi 712911970	57648	60	chaperonin GroEL (chloroplast) [Cerataulina daemon]

Results List

1.	gi 157113225	Mass: 32821	Score: 84	Expect: 0.087	Matches: 7
AAEL006384-PA [Aedes aegypti]					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Ions Peptide
	1521.7461	1520.7388	1520.7776	-25.50	125 - 136 0 --- R.IYVHPEFNVFTR.E
	1521.7461	1520.7388	1520.7776	-25.50	125 - 136 0 20 R.IYVHPEFNVFTR.E
	1844.9191	1843.9118	1843.9428	-16.80	145 - 160 0 --- R.LDRPYDLPSTVDIAR.R
	1844.9191	1843.9118	1843.9428	-16.80	145 - 160 0 31 R.LDRPYDLPSTVDIAR.R
	1877.9161	1876.9088	1876.9948	-45.81	122 - 136 1 --- K.VTRIYVHPEFNVFTR.E
	2328.2629	2327.2556	2327.2525	1.32	95 - 116 0 --- R.LIDPYWLTVVAGDVALSPVGSR.R
	2418.2456	2417.2383	2417.2492	-4.49	125 - 144 1 --- R.IYVHPEFNVFTRENDVAVLR.L
No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1197.5636, 1261.6660, 1301.6093, 1357.7264, 1358.7098, 1376.7114, 1385.7190, 1405.6670, 1414.6940, 1436.7194, 1446.7092, 1465.7672, 1466.7670, 1532.7528, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1611.7694, 1617.8115, 1676.8539, 1707.8973, 1734.8571, 1742.8484, 1763.8722, 1791.8730, 1809.8907, 1819.8888, 1829.8156, 1843.8678, 1873.9242, 1876.8998, 1952.0050, 1987.0083, 1996.9535, 2041.0391, 2094.0942, 2141.0703, 2269.1736, 2309.1104, 2549.2947, 2682.3164, 2683.3115, 2897.4724					
2.	gi 915073449	Mass: 30892	Score: 75	Expect: 0.65	Matches: 11
hypothetical protein Z518_04560 [Rhinoclatiella mackenziei CBS 650.93]					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Ions Peptide
	851.3322	850.3249	850.3239	1.19	17 - 23 0 --- R.SADENCR.A
	1080.4445	1079.4372	1079.4706	-30.92	180 - 188 0 --- K.CDNFNVPSK.K
	1186.6648	1185.6575	1185.6183	33.1	194 - 203 0 --- R.LGFTFEGIFR.Q
	1358.7098	1357.7025	1357.7540	-37.92	120 - 131 1 --- K.TKVPLGWAALMR.I + Oxidation (M)
	1446.7092	1445.7019	1445.6530	33.8	153 - 165 0 --- R.NTSATEAMYIMAK.Y + Oxidation (M)
	1466.7670	1465.7597	1465.8140	-37.06	256 - 269 1 --- R.ASLPDQQGPVTLKI.-

1521.7461 1520.7388 1520.6889 32.8 17 - 30 1 --- R.SADENCRAEAVTAK.W
 1521.7461 1520.7388 1520.6889 32.8 17 - 30 1 --- R.SADENCRAEAVTAK.W
 1987.0083 1986.0010 1986.0186 -8.83 194 - 209 1 --- R.LGFTFEGIFRQHMIYK.N
 2269.1736 2268.1663 2268.0698 42.5 80 - 98 0 --- K.SHLWTLGDESYASLEELR.T
 2328.2629 2327.2556 2327.2195 15.5 54 - 75 1 --- K.GKIVTMEPLTATHAPGLYDSVK.G

No match to: 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1197.5636, 1261.6660, 1301.6093, 1357.7264, 1376.7114, 1385.7190, 1405.6670, 1414.6940, 1436.7194, 1465.7672, 1532.7528, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1611.7694, 1617.8115, 1676.8539, 1707.8973, 1734.8571, 1742.8484, 1763.8722, 1791.8730, 1809.8907, 1819.8888, 1829.8156, 1843.8678, 1844.9191, 1844.9191, 1873.9242, 1876.8998, 1877.9161, 1952.0050, 1996.9535, 2041.0391, 2094.0942, 2141.0703, 2309.1104, 2418.2456, 2549.2947, 2682.3164, 2683.3115, 2897.4724

3. [gil157140794](#) Mass: 30571 Score: 75 Expect: 0.68 Matches: 6

AAEL015528-PA [Aedes aegypti]

Observed	Mr(expt)	Mr(calcd)	ppm	Start	End	Miss	Ions	Peptide
1521.7461	1520.7388	1520.7776	-25.50	105	- 116	0	---	R.IYVHPEFNVFTR.E
1521.7461	1520.7388	1520.7776	-25.50	105	- 116	0	20	R.IYVHPEFNVFTR.E
1844.9191	1843.9118	1843.9428	-16.80	125	- 140	0	---	R.LDRPYDLPSTVDIAR.R
1844.9191	1843.9118	1843.9428	-16.80	125	- 140	0	31	R.LDRPYDLPSTVDIAR.R
1877.9161	1876.9088	1876.9948	-45.81	102	- 116	1	---	K.VTRIYVHPEFNVFTR.E
2418.2456	2417.2383	2417.2492	-4.49	105	- 124	1	---	R.IYVHPEFNVFTRENDVAVLR.L

No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1197.5636, 1261.6660, 1301.6093, 1357.7264, 1376.7114, 1385.7190, 1405.6670, 1414.6940, 1436.7194, 1446.7092, 1465.7672, 1466.7670, 1532.7528, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1611.7694, 1617.8115, 1676.8539, 1707.8973, 1734.8571, 1742.8484, 1763.8722, 1791.8730, 1809.8907, 1819.8888, 1829.8156, 1843.8678, 1873.9242, 1876.8998, 1952.0050, 1987.0083, 1996.9535, 2041.0391, 2094.0942, 2141.0703, 2269.1736, 2309.1104, 2328.2629, 2549.2947, 2682.3164, 2683.3115, 2897.4724

4. [gil255072771](#) Mass: 193655 Score: 68 Expect: 3.2 Matches: 21

predicted protein [Micromonas sp. RCC299]

Observed	Mr(expt)	Mr(calcd)	ppm	Start	End	Miss	Ions	Peptide
965.4107	964.4034	964.4502	-48.46	1566	- 1573	0	---	R.DEFDAQIK.A
1064.4917	1063.4844	1063.5219	-35.26	1162	- 1170	0	---	R.LMAELNETK.A + Oxidation (M)
1064.4917	1063.4844	1063.5298	-42.65	1097	- 1106	0	---	K.ANEYQAQAVAK.A
1197.5636	1196.5563	1196.5496	5.65	949	- 958	1	---	R.NFGKEMDNVK.A + Oxidation (M)
1261.6660	1260.6587	1260.6383	16.2	1187	- 1197	1	---	K.ELKEVMENAK.E
1301.6093	1300.6020	1300.6371	-26.97	1675	- 1687	1	---	R.NDAADRAAAVEK.L
1357.7264	1356.7191	1356.7361	-12.52	771	- 782	1	---	R.DEVVATVRAELR.T
1385.7190	1384.7117	1384.6656	33.3	1596	- 1608	0	---	K.DLLAAHASSEMAEK.Q
1436.7194	1435.7121	1435.6613	35.4	376	- 390	0	---	R.EGMQSSATAGLAGEK.S
1446.7092	1445.7019	1445.6746	18.9	1511	- 1525	1	---	R.SEADAAARAADAQK.A
1465.7672	1464.7599	1464.7936	-22.99	832	- 844	1	---	K.LQAAHDEKIAELK.A
1610.7716	1609.7643	1609.6963	42.2	1198	- 1212	0	---	K.EMADAAATMEALDQK.R + Oxidation (M)
1707.8973	1706.8900	1706.9315	-24.29	658	- 672	1	---	R.ERVELLEAQHAATIK.A
1734.8571	1733.8498	1733.8796	-17.16	172	- 191	0	---	R.AVSTAGSSGGDAASVGTVIK.R
1809.8907	1808.8834	1808.8978	-7.94	1162	- 1177	1	---	R.LMAELNETKAAYAEK.N
1873.9242	1872.9169	1872.9401	-12.40	577	- 595	1	---	K.ALANASASERSSSQAALNR.A
1987.0083	1986.0010	1986.0204	-9.76	917	- 936	1	---	R.MLAAVDDAVADGVARLNAAK.L + Oxidation (M)
2041.0391	2040.0318	2040.0866	-26.87	6	- 22	1	---	R.DHPMVEKIAFIPDLFIR.F
2141.0703	2140.0630	2140.0371	12.1	1708	- 1725	1	---	R.RAVTDDAHWLANELECIC.K
2328.2629	2327.2556	2327.1968	25.3	732	- 754	1	---	K.AAAVELAKNNEASAQLEATVAK.L
2418.2456	2417.2383	2417.1644	30.6	698	- 719	1	---	R.GAYESKIELNANHAELQNAK.D + Oxidation (M)

No match to: 851.3322, 1007.4567, 1034.0704, 1054.4012, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1358.7098, 1376.7114, 1405.6670, 1414.6940, 1466.7670, 1521.7461, 1521.7461, 1532.7528, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1611.7694, 1617.8115, 1676.8539, 1742.8484, 1763.8722, 1791.8730, 1819.8888, 1829.8156, 1843.8678, 1844.9191, 1844.9191, 1876.8998, 1877.9161, 1952.0050, 1996.9535, 2094.0942, 2269.1736, 2309.1104, 2549.2947, 2682.3164, 2683.3115, 2897.4724

5. [gil675389835](#) Mass: 32207 Score: 66 Expect: 4.8 Matches: 10

Metalloendopeptidase OMA1, mitochondrial, partial [Stegodyphus mimosarum]

Observed	Mr(expt)	Mr(calcd)	ppm	Start	End	Miss	Ions	Peptide
1064.4917	1063.4844	1063.4539	28.7	236	- 244	0	---	R.SSCGCPQLR.Y
1064.4917	1063.4844	1063.4539	28.7	236	- 244	0	---	R.SSCGCPQLR.Y
1376.7114	1375.7041	1375.7493	-32.85	19	- 30	1	---	R.IMESVGKQILSR.Y + Oxidation (M)
1385.7190	1384.7117	1384.7211	-6.79	26	- 36	1	---	K.QILSRYPDTR.R
1414.6940	1413.6867	1413.7463	-42.16	45	- 56	1	---	R.ILDANKDLEEV.R
1446.7092	1445.7019	1445.7184	-11.39	251	- 263	0	---	K.EVEAAQMELAR.K + Oxidation (M)
1611.7694	1610.7621	1610.8126	-31.36	187	- 200	1	---	R.ESSAFWSKMAVLQK.S
1791.8730	1790.8657	1790.9349	-38.61	11	- 25	1	---	K.INQFELQRMESVGK.Q
1809.8907	1808.8834	1808.8978	-7.96	221	- 235	1	---	R.SQFLDDLMEAIKLR.S + Oxidation (M)
2269.1736	2268.1663	2268.1267	16.6	201	- 220	1	---	K.SFGKVPNIEFLSTHPSHESR.S

No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1197.5636, 1261.6660, 1301.6093, 1357.7264, 1358.7098, 1405.6670, 1436.7194, 1465.7672, 1466.7670, 1521.7461, 1521.7461, 1532.7528, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1617.8115, 1676.8539, 1707.8973, 1734.8571, 1742.8484, 1763.8722, 1819.8888, 1829.8156, 1843.8678, 1844.9191, 1844.9191, 1873.9242, 1876.8998, 1877.9161, 1952.0050, 1987.0083, 1996.9535, 2041.0391, 2094.0942, 2141.0703, 2309.1104, 2328.2629, 2418.2456, 2549.2947, 2682.3164, 2683.3115, 2897.4724

6. [gil71409789](#) Mass: 87633 Score: 66 Expect: 5.3 Matches: 12

hypothetical protein [Trypanosoma cruzi strain CL Brener]

Observed	Mr(expt)	Mr(calcd)	ppm	Start	End	Miss	Ions	Peptide
1007.4567	1006.4494	1006.4944	-44.70	492	- 499	1	---	K.QYGERQAR.E
1186.6648	1185.6575	1185.6605	-2.48	759	- 769	1	---	R.GELVEALEKAK.N
1414.6940	1413.6867	1413.7463	-42.16	729	- 741	0	---	R.IEAIGALVESQR.A
1676.8539	1675.8466	1675.8166	17.9	596	- 611	1	---	K.FNSIGDGGVPSNKEQK.L
1763.8722	1762.8649	1762.8122	29.9	682	- 696	1	---	R.VTEKYEIEHGASTQR.L
1791.8730	1790.8657	1790.8395	14.7	636	- 653	1	---	K.SDKGSTNGGSQELASTPR.G
1844.9191	1843.9118	1843.9388	-14.63	345	- 362	1	---	R.LATVGNGTEQTRNGELK.D
1844.9191	1843.9118	1843.8483	34.5	268	- 285	1	---	R.HGGIADETSVNDAGMAKR.G + Oxidation (M)
1873.9242	1872.9169	1872.9680	-27.28	2	- 18	0	---	M.DTVQEITVAAIQSELK.A
1877.9161	1876.9088	1876.9200	-5.96	145	- 161	1	---	K.LSDALAEVTAQSDECLR.V
2682.3164	2681.3091	2681.1770	49.3	390	- 417	1	---	R.SAGKTASNSGSGSTCGCAATSNHGLVK.N
2683.3115	2682.3042	2682.3647	-22.53	567	- 591	1	---	R.ELENMKALLGSHQVSTPTASTLSR.Q + Oxidation (M)

No match to: 851.3322, 965.4107, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1197.5636, 1261.6660, 1301.6093, 1357.7264, 1358.7098, 1376.7114, 1385.7190, 1405.6670, 1436.7194, 1446.7092, 1465.7672, 1466.7670, 1521.7461, 1521.7461, 1532.7528, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1611.7694, 1617.8115, 1707.8973, 1734.8571, 1742.8484, 1809.8907, 1819.8888, 1829.8156, 1843.8678, 1876.8998, 1952.0050, 1987.0083, 1996.9535, 2041.0391, 2094.0942, 2141.0703, 2269.1736, 2309.1104, 2328.2629, 2418.2456, 2549.2947, 2897.4724

7. [gi|299753039](#) Mass: 49821 Score: 65 Expect: 6.3 Matches: 10

miller-Dieker lissencephaly protein [Coprinopsis cinerea okayama7#130]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1358.7098	1357.7025	1357.6361	48.9	416	- 428	0	---	K.VNGVDSVDAEPEK.V
1376.7114	1375.7041	1375.7030	0.78	378	- 388	1	---	R.VWELSTGRCLR.I
1436.7194	1435.7121	1435.7130	-0.58	214	- 226	0	---	R.FMPGDQLIVSASR.D + Oxidation (M)
1532.7528	1531.7455	1531.7300	10.1	86	- 99	0	---	R.NAALQEELSMSPAR.R + Oxidation (M)
1676.8539	1675.8466	1675.8716	-14.89	333	- 346	1	---	K.TVKLWDTQTGMIR.N
1707.8973	1706.8900	1706.8410	28.7	214	- 228	1	---	R.FMPGDQLIVSASRDR.T + Oxidation (M)
1763.8722	1762.8649	1762.9267	-35.05	389	- 404	0	---	R.IVEAHSHFVAALAWGR.Q
1809.8907	1808.8834	1808.8733	5.58	147	- 160	1	---	K.IWDWETGEFERTLK.G
2141.0703	2140.0630	2140.0411	10.2	28	- 46	0	---	K.AMLDLYANNHTAAFNALEK.E
2418.2456	2417.2383	2417.1678	29.2	79	- 99	1	---	K.IMELENRNAAALQEELSMSPAR.R + Oxidation (M)
No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1197.5636, 1261.6660, 1301.6093, 1357.7264, 1385.7190, 1405.6670, 1414.6940, 1446.7092, 1465.7672, 1466.7670, 1521.7461, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1611.7694, 1617.8115, 1734.8571, 1742.8484, 1791.8730, 1819.8888, 1829.8156, 1843.8678, 1844.9191, 1844.9191, 1873.9242, 1876.8998, 1877.9161, 1952.0050, 1987.0083, 1996.9535, 2041.0391, 2094.0942, 2269.1736, 2309.1104, 2328.2629, 2549.2947, 2682.3164, 2683.3115, 2897.4724								

8. [gi|924884380](#) Mass: 175589 Score: 65 Expect: 6.5 Matches: 17

hypothetical protein ACN38_g8607 [Penicillium nordicum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1111.5012	1110.4939	1110.4975	-3.26	1355	- 1365	0	---	K.STATSMGDGIR.N + Oxidation (M)
1261.6660	1260.6587	1260.6575	0.99	1439	- 1449	0	---	R.GSLELQHPQPR.Q
1414.6940	1413.6867	1413.7437	-40.27	825	- 836	1	---	R.SQTDLAQRPRSR.S
1436.7194	1435.7121	1435.7168	-3.25	782	- 795	0	---	K.EGHQVTTGVAANPR.F
1446.7092	1445.7019	1445.6899	8.34	282	- 293	1	---	K.DYLEAEPNPSRR.R
1465.7672	1464.7599	1464.7936	-23.02	230	- 243	1	---	R.GSPPEDEVLLKTPR.R
1532.7528	1531.7455	1531.7267	12.3	279	- 292	1	---	R.GGKDYLEAEPNPSR.R
1611.7694	1610.7621	1610.8390	-47.70	1436	- 1449	1	---	R.GHRGSLELQHPQPR.Q
1676.8539	1675.8466	1675.7703	45.6	855	- 868	1	---	R.QDAFHADETSFPRR.M
1707.8973	1706.8900	1706.8336	33.0	718	- 733	1	---	R.STRQGTSSHSQSIGFK.Q
1791.8730	1790.8657	1790.8700	-2.37	448	- 461	1	---	R.WANRPDYEQDKIR.R
1819.8888	1818.8815	1818.9509	-38.16	1108	- 1123	1	---	R.DTEILVTLVRSAAEMR.T + Oxidation (M)
1829.8156	1828.8083	1828.8989	-49.52	224	- 240	1	---	R.SQSMERGSPPEDVLLK.T
1877.9161	1876.9088	1876.9061	1.44	1355	- 1372	1	---	K.STATSMGDGIRNSIQPSR.K
1952.0050	1950.9977	1950.9647	16.9	40	- 57	1	---	K.TSYSIPDDGSPITVSTRR.Q
2309.1104	2308.1031	2308.1958	-40.13	1085	- 1104	1	---	R.IQSQDIVALMDHLTVRDAQR.N
2897.4724	2896.4651	2896.3266	47.8	530	- 554	1	---	K.HNVAPMPHSEMDSELTRNSLLSER.T + Oxidation (M)
No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1136.5402, 1186.6648, 1197.5636, 1301.6093, 1357.7264, 1358.7098, 1376.7114, 1385.7190, 1405.6670, 1466.7670, 1521.7461, 1521.7461, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1617.8115, 1734.8571, 1742.8484, 1763.8722, 1809.8907, 1843.8678, 1844.9191, 1844.9191, 1873.9242, 1876.8998, 1987.0083, 1996.9535, 2041.0391, 2094.0942, 2141.0703, 2269.1736, 2328.2629, 2418.2456, 2549.2947, 2682.3164, 2683.3115								

9. [gi|322518684](#) Mass: 48330 Score: 65 Expect: 6.5 Matches: 10

RecName: Full=Nuclear distribution protein PAC1; AltName: Full=Lissencephaly-1 homolog; Short=LIS-1; AltName: Full=nudF homolog

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1358.7098	1357.7025	1357.6361	48.9	403	- 415	0	---	K.VNGVDSVDAEPEK.V
1376.7114	1375.7041	1375.7030	0.78	365	- 375	1	---	R.VWELSTGRCLR.I
1436.7194	1435.7121	1435.7130	-0.58	201	- 213	0	---	R.FMPGDQLIVSASR.D + Oxidation (M)
1532.7528	1531.7455	1531.7300	10.1	73	- 86	0	---	R.NAALQEELSMSPAR.R + Oxidation (M)
1676.8539	1675.8466	1675.8716	-14.89	320	- 333	1	---	K.TVKLWDTQTGMIR.N
1707.8973	1706.8900	1706.8410	28.7	201	- 215	1	---	R.FMPGDQLIVSASRDR.T + Oxidation (M)
1763.8722	1762.8649	1762.9267	-35.05	376	- 391	0	---	R.IVEAHSHFVAALAWGR.Q
1809.8907	1808.8834	1808.8733	5.58	134	- 147	1	---	K.IWDWETGEFERTLK.G
2141.0703	2140.0630	2140.0411	10.2	15	- 33	0	---	K.AMLDLYANNHTAAFNALEK.E
2418.2456	2417.2383	2417.1678	29.2	66	- 86	1	---	K.IMELENRNAAALQEELSMSPAR.R + Oxidation (M)
No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1197.5636, 1261.6660, 1301.6093, 1357.7264, 1385.7190, 1405.6670, 1414.6940, 1446.7092, 1465.7672, 1466.7670, 1521.7461, 1521.7461, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1611.7694, 1617.8115, 1734.8571, 1742.8484, 1791.8730, 1819.8888, 1829.8156, 1843.8678, 1844.9191, 1844.9191, 1873.9242, 1876.8998, 1877.9161, 1952.0050, 1987.0083, 1996.9535, 2041.0391, 2094.0942, 2269.1736, 2309.1104, 2328.2629, 2549.2947, 2682.3164, 2683.3115, 2897.4724								

10. [gi|795293311](#) Mass: 68745 Score: 65 Expect: 7.1 Matches: 14

PREDICTED: endonuclease 8-like 3 [Colobus angolensis palliatus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
851.3322	850.3249	850.3603	-41.59	136	- 142	0	---	R.NSMESQR.R
1007.4567	1006.4494	1006.4614	-11.89	136	- 143	1	---	R.NSMESQRR.I
1261.6660	1260.6587	1260.6561	2.06	444	- 455	0	---	K.VNISPTISSESK.L
1376.7114	1375.7041	1375.6707	24.3	224	- 233	1	---	R.DFSILFYRCR.K
1446.7092	1445.7019	1445.7489	-32.51	221	- 231	1	---	K.MVRDFSILFYR.C
1521.7461	1520.7388	1520.7486	-6.43	79	- 90	1	---	K.ELFMYFGPKAFR.I + Oxidation (M)
1521.7461	1520.7388	1520.7486	-6.43	79	- 90	1	---	K.ELFMYFGPKAFR.I + Oxidation (M)
1601.8103	1600.8030	1600.8685	-40.92	289	- 302	1	---	R.LPRTNTIISWTSGR.V
1676.8539	1675.8466	1675.8022	26.5	1	- 15	1	---	-MVEGPGCTLNGEKIR.A + Oxidation (M)
1707.8973	1706.8900	1706.8410	28.7	207	- 220	0	---	K.VCQLTDEQTHHLVK.M
1734.8571	1733.8498	1733.8631	-7.67	279	- 292	1	---	K.ENPQHVDCIRLPTR.N
1829.8156	1828.8083	1828.7661	23.1	583	- 597	0	---	K.QCNFFQWAENGPMK.M + Oxidation (M)
2094.0942	2093.0869	2093.0510	17.2	207	- 223	1	---	K.VCQLTDEQTHHLVKMVR.D
2269.1736	2268.1663	2268.0732	41.0	149	- 167	1	---	K.ELDVCSPEFSFLRAENEVK.K
No match to: 965.4107, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1197.5636, 1301.6093, 1357.7264, 1358.7098, 1385.7190, 1405.6670, 1414.6940, 1436.7194, 1465.7672, 1466.7670, 1532.7528, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1610.7716, 1611.7694, 1617.8115, 1742.8484, 1763.8722, 1791.8730, 1809.8907,								

1819.8888, 1843.8678, 1844.9191, 1844.9191, 1873.9242, 1876.8998, 1877.9161, 1952.0050, 1987.0083, 1996.9535, 2041.0391, 2141.0703, 2309.1104, 2328.2629, 2418.2456, 2549.2947, 2682.3164, 2683.3115, 2897.4724

11. [gi|336242517](#) Mass: 5712 Score: 64 Expect: 7.8 Matches: 6

hypothetical protein SMAC_12000 [Sordaria macrospora k-hell]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1357.7264	1356.7191	1356.7150	3.04	7	19	1	---	R.WLVGADAVDAGKR.I
1376.7114	1375.7041	1375.6732	22.5	28	39	0	---	R.LEAWIESNATSR.T
1436.7194	1435.7121	1435.7168	-3.25	40	52	1	---	R.TNVFSTSRTPGPNR.-
1844.9191	1843.9118	1843.9615	-26.92	1	18	1	---	-.MIGLGRWLVGADAVDAGK.R + Oxidation (M)
1844.9191	1843.9118	1843.9615	-26.92	1	18	1	---	-.MIGLGRWLVGADAVDAGK.R + Oxidation (M)
2269.1736	2268.1663	2268.1134	23.3	28	47	1	---	R.LEAWIESNATSRTPNVFSTSR.T
No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1197.5636, 1261.6660, 1301.6093, 1358.7098, 1385.7190, 1405.6670, 1414.6940, 1446.7092, 1465.7672, 1466.7670, 1521.7461, 1521.7461, 1532.7528, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1611.7694, 1617.8115, 1676.8539, 1707.8973, 1734.8571, 1742.8484, 1763.8722, 1791.8730, 1809.8907, 1819.8888, 1829.8156, 1843.8678, 1873.9242, 1876.8998, 1877.9161, 1952.0050, 1987.0083, 1996.9535, 2041.0391, 2094.0942, 2141.0703, 2309.1104, 2328.2629, 2418.2456, 2549.2947, 2682.3164, 2683.3115, 2897.4724								

12. [gi|875642868](#) Mass: 42136 Score: 64 Expect: 8.1 Matches: 12

hypothetical protein CIHG_05223 [Coccidioides immitis H538.4]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1082.5022	1081.4949	1081.4572	34.9	249	257	0	---	R.MEWSEAAAMK.S
1098.4523	1097.4450	1097.4521	-6.48	249	257	0	---	R.MEWSEAAAMK.S + Oxidation (M)
1111.5012	1110.4939	1110.5015	-6.85	307	315	1	---	R.YDESNPKMK.E
1197.5636	1196.5563	1196.5898	-27.95	239	248	1	---	K.NDHLTAKENR.M
1617.8115	1616.8042	1616.8634	-36.62	329	344	1	---	K.GVYGLLGNNRAALGDK.K
1829.8156	1828.8083	1828.8896	-44.47	165	179	0	---	K.QPDAPPRWQEFYAK.D
1844.9191	1843.9118	1843.9792	-36.53	191	206	1	---	K.DIQAATKLPENLQFTR.H
1844.9191	1843.9118	1843.9792	-36.53	191	206	1	---	K.DIQAATKLPENLQFTR.H
1873.9242	1872.9169	1872.9833	-35.43	269	284	1	---	K.SLEWIKDLVDNVDTK.A
1876.8998	1875.8925	1875.8962	-1.98	211	227	1	---	K.SKSELGVYGVNGVNHKEK.G
1952.0050	1950.9977	1951.0765	-40.38	79	96	1	---	K.HVRAPPAFRPPSPGGR.G
2418.2456	2417.2383	2417.2009	15.5	213	234	1	---	K.SSELGVYGVNGVNHKEGVMSIR.T
No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1136.5402, 1186.6648, 1261.6660, 1301.6093, 1357.7264, 1358.7098, 1376.7114, 1385.7190, 1405.6670, 1414.6940, 1436.7194, 1446.7092, 1465.7672, 1466.7670, 1521.7461, 1521.7461, 1532.7528, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1611.7694, 1676.8539, 1707.8973, 1734.8571, 1742.8484, 1763.8722, 1791.8730, 1809.8907, 1819.8888, 1843.8678, 1877.9161, 1987.0083, 1996.9535, 2041.0391, 2094.0942, 2141.0703, 2269.1736, 2309.1104, 2328.2629, 2549.2947, 2682.3164, 2683.3115, 2897.4724								

13. [gi|751753175](#) Mass: 40103 Score: 63 Expect: 11 Matches: 11

hypothetical protein OIIMADRAFT_41943 [Oidiiodendron maius Zn]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
965.4107	964.4034	964.4171	-14.21	286	293	1	---	R.EMDEKGEK.V
1405.6670	1404.6597	1404.6919	-22.88	197	210	0	---	R.ICLSSPSAADAVSK.L
1521.7461	1520.7388	1520.7578	-12.51	139	152	0	---	K.NLVMSIETGGLPK.V + 2 Oxidation (M)
1521.7461	1520.7388	1520.7578	-12.51	139	152	0	---	K.NLVMSIETGGLPK.V + 2 Oxidation (M)
1532.7528	1531.7455	1531.8107	-42.53	266	279	1	---	R.ETGWLSGSSIRLAR.V
1610.7716	1609.7643	1609.8212	-35.36	263	276	1	---	K.YVRETGWLSSGSSIR.L
1617.8115	1616.8042	1616.8630	-36.33	138	152	1	---	K.KNLVMSIETGGLPK.V
1844.9191	1843.9118	1843.8952	9.02	233	249	0	---	K.GLELSPNGAYLPDDR.G
1844.9191	1843.9118	1843.8233	48.0	34	48	0	---	R.SQMQUIYSEMFQHTSK.L
1876.8998	1875.8925	1875.8131	42.3	34	48	0	---	R.SQMQUIYSEMFQHTSK.L + 2 Oxidation (M)
2041.0391	2040.0318	2040.0674	-17.43	78	97	0	---	R.GIAEGAGLVLDVVALNCR.S
No match to: 851.3322, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1197.5636, 1261.6660, 1301.6093, 1357.7264, 1358.7098, 1376.7114, 1385.7190, 1414.6940, 1436.7194, 1446.7092, 1465.7672, 1466.7670, 1521.7461, 1521.7461, 1532.7528, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1611.7694, 1676.8539, 1707.8973, 1734.8571, 1742.8484, 1763.8722, 1791.8730, 1809.8907, 1819.8888, 1829.8156, 1843.8678, 1873.9242, 1877.9161, 1952.0050, 1987.0083, 1996.9535, 2094.0942, 2141.0703, 2269.1736, 2309.1104, 2328.2629, 2418.2456, 2549.2947, 2682.3164, 2683.3115, 2897.4724								

14. [gi|511006810](#) Mass: 74632 Score: 62 Expect: 14 Matches: 12

hypothetical protein HMPREF1544_05059 [Mucor circinelloides f. circinelloides 1006PhL]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1186.6648	1185.6575	1185.6394	15.3	549	558	0	---	K.HLSVDLVEFK.F
1197.5636	1196.5563	1196.6084	-43.53	63	72	0	---	K.HLSMRPDLGR.L + Oxidation (M)
1385.7190	1384.7117	1384.6730	27.9	42	52	1	---	K.VMYKEIDLCK.N
1405.6670	1404.6597	1404.6409	13.4	488	499	1	---	K.KSSVDFSEYSEK.G
1465.7672	1464.7599	1464.7646	-3.23	316	328	0	---	R.FIDMLATQSVNVK.C
1610.7716	1609.7643	1609.8199	-34.52	616	629	1	---	K.YLTTSQIKAIEDTQ.-
1844.9191	1843.9118	1843.9819	-37.98	79	94	0	---	K.LYASSTTTLTYEILK.F
1844.9191	1843.9118	1843.9819	-37.98	79	94	0	---	K.LYASSTTTLTYEILK.F
1952.0050	1950.9977	1950.9720	13.2	46	62	1	---	K.EIDLCKNGFQLAELSK.H
2041.0391	2040.0318	2040.0502	-9.02	287	303	0	---	R.QHIILPEYAHMETFALK.N
2269.1736	2268.1663	2268.1797	-5.89	53	72	1	---	K.NGFQLAELSKHLSMRPDLGR.L
2549.2947	2548.2874	2548.1978	35.2	331	351	1	---	K.VNVEIHYGDSVICLSAIKEK.Q + Oxidation (M)
No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1197.5636, 1261.6660, 1301.6093, 1357.7264, 1358.7098, 1376.7114, 1414.6940, 1436.7194, 1446.7092, 1465.7670, 1466.7672, 1521.7461, 1521.7461, 1532.7528, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1611.7694, 1676.8539, 1707.8973, 1734.8571, 1742.8484, 1763.8722, 1791.8730, 1809.8907, 1819.8888, 1829.8156, 1843.8678, 1873.9242, 1876.8998, 1877.9161, 1987.0083, 1996.9535, 2094.0942, 2141.0703, 2309.1104, 2328.2629, 2418.2456, 2682.3164, 2683.3115, 2897.4724								

15. [gi|589985287](#) Mass: 632479 Score: 62 Expect: 14 Matches: 33

PREDICTED: dystonin-like [Peromyscus maniculatus bairdii]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
965.4107	964.4034	964.4172	-14.24	512	519	0	---	R.DSVICEDK.L
1079.4565	1078.4492	1078.4965	-43.80	3609	3617	1	---	R.EDKDMVQSK.L
1082.5022	1081.4949	1081.4961	-1.12	2631	2639	0	---	K.QLTTEMDTK.W + Oxidation (M)
1111.5012	1110.4939	1110.5240	-27.11	405	413	0	---	R.HHVVTMSER.T + Oxidation (M)
1186.6648	1185.6575	1185.6540	3.01	499	508	0	---	R.LDMLQQIAVR.V
1197.5636	1196.5563	1196.5219	28.8	5124	5131	1	---	K.YMRWMNHK.K + 2 Oxidation (M)
1376.7114	1375.7041	1375.7129	-6.39	2848	2859	1	---	K.AELSRQLGVGMK.S + Oxidation (M)

1385.7190	1384.7117	1384.6987	9.43	1343	-	1354	0	---	R.GVFHALEDELQK.A
1405.6670	1404.6597	1404.7071	-33.74	4893	-	4903	1	---	R.TLIDQHKFEFMK.K + Oxidation (M)
1436.7194	1435.7121	1435.7493	-25.90	1004	-	1015	1	---	K.TSIPIKAICDYR.Q
1466.7670	1465.7597	1465.7467	9.39	3418	-	3430	0	---	R.AAQLEALLHLCGR.F
1521.7461	1520.7388	1520.7697	-20.33	5266	-	5279	0	---	R.VGGGWMALDEFVLK.N
1521.7461	1520.7388	1520.7697	-20.33	5266	-	5279	0	1	R.VGGGWMALDEFVLK.N
1532.7528	1531.7455	1531.7915	-30.05	4184	-	4196	1	---	R.EARLLDVMELAEK.F + Oxidation (M)
1537.8478	1536.8405	1536.7647	49.4	5266	-	5279	0	---	R.VGGGWMALDEFVLK.N + Oxidation (M)
1601.8103	1600.8030	1600.8243	-13.28	2066	-	2079	1	---	K.CNVLGNNKDLVDK.Y
1617.8115	1616.8042	1616.8522	-29.68	2700	-	2712	0	---	R.QQVQILLQEFDR.K
1734.8571	1733.8498	1733.8579	-4.68	3271	-	3286	0	---	K.MMLATEETSPDLVGK.R
1742.8484	1741.8411	1741.8860	-25.74	5408	-	5424	1	---	K.GFHSGEDRALITAAAR.V
1819.8888	1818.8815	1818.9185	-20.36	1806	-	1820	1	---	K.TKIENLMDWLSNVEK.D
1877.9161	1876.9088	1876.8625	24.7	1213	-	1227	1	---	R.DDLHESMFRITEQEK.L
1952.0050	1950.9977	1951.0336	-18.38	776	-	792	1	---	K.LSEIQMTAPLKLTYTDK.L
1987.0083	1986.0010	1985.9602	20.5	215	-	230	1	---	R.TERVHAHETHRPQCTK.R
1996.9535	1995.9462	1995.9394	3.43	5004	-	5019	1	---	K.TLIAEHQTFMEEMTRK.Q + 2 Oxidation (M)
2041.0391	2040.0318	2039.9912	19.9	2569	-	2586	1	---	K.TANKWHQTPPTDTSVK.I
2094.0942	2093.0869	2093.0350	24.8	2519	-	2536	1	---	K.KDMTDISHSYEDLGLLLK.D + Oxidation (M)
2141.0703	2140.0630	2140.0912	-13.19	4564	-	4581	1	---	K.VFANEVNSHREQIIELDK.T
2269.1736	2268.1663	2268.0804	37.9	5329	-	5352	0	---	R.STSMSSHAGQAASPVPAASTPK.I
2309.1104	2308.1031	2308.0470	24.3	4632	-	4649	1	---	K.QFHEAWSKLMWLDESEK.C + Oxidation (M)
2328.2629	2327.2556	2327.1539	43.7	1432	-	1451	1	---	K.MQENQNPENSKALALQNNQK.M + Oxidation (M)
2418.2456	2417.2383	2417.1645	30.5	1016	-	1035	1	---	R.QIEITIIYKDECVLANNSHR.A
2683.3115	2682.3042	2682.2027	37.8	2868	-	2890	0	---	K.TENHVHQLQSACASSHQFQMSK.D
2897.4724	2896.4651	2896.4600	1.77	2818	-	2842	1	---	K.QEIEQQTPLQREALCEDLSALVK.E

No match to: 851.3322, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1080.4445, 1097.4648, 1098.4523, 1136.5402, 1261.6660, 1301.6093, 1357.7264, 1358.7098, 1414.6940, 1446.7092, 1465.7672, 1565.8809, 1567.7930, 1583.7969, 1610.7716, 1611.7694, 1676.8539, 1707.8973, 1763.8722, 1791.8730, 1809.8907, 1829.8156, 1843.8678, 1844.9191, 1844.9191, 1873.9242, 1876.8998, 2549.2947, 2682.3164

16. [gi|527303549](#) Mass: 144822 Score: 62 Expect: 14 Matches: 15

hypothetical protein FOMPIDRAFT_1157451 [Fomitopsis pinicola FP-58527 SS1]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1197.5636	1196.5563	1196.5464	8.29	1161	- 1169	1	---	K.RLMEGCMLR.V + 2 Oxidation (M)
1261.6660	1260.6587	1260.6826	-18.95	368	- 378	1	---	R.EQRAGLPVYTK.S
1301.6093	1300.6020	1300.6623	-46.32	1150	- 1160	1	---	R.QDALDDVERLK.R
1376.7114	1375.7041	1375.6514	38.3	485	- 497	0	---	R.MQNALEGNSAIGR.S + Oxidation (M)
1414.6940	1413.6867	1413.7464	-42.18	279	- 290	0	---	R.VLLQIDDSLQDR.I
1532.7528	1531.7455	1531.7525	-4.55	484	- 497	1	---	K.RMQNALEGNSAIGR.S + Oxidation (M)
1617.8115	1616.8042	1616.7511	32.8	418	- 431	1	---	R.GEGARCINIVCTQPR.R
1844.9191	1843.9118	1843.9369	-13.62	193	- 207	1	---	R.RFGFPRPELNYSSFV.V
1844.9191	1843.9118	1843.9832	-38.70	70	- 85	1	---	K.AIWAENPKSPLTNYLK.A
1876.8998	1875.8925	1875.9187	-13.97	626	- 643	1	---	R.GRHQSDAIPPSIGPDSSR.D
1987.0083	1986.0010	1985.9755	12.9	1	- 17	1	---	-.MTPPNPSFRRPPSHHGR.G + Oxidation (M)
2094.0942	2093.0869	2092.9848	48.8	1099	- 1117	0	---	R.QNLTGGSSHPEMYLVTTSTR.L + Oxidation (M)
2549.2947	2548.2874	2548.2057	32.1	462	- 483	0	---	R.FEHNLPDEHGSVTFCTTGIFLK.R
2683.3115	2682.3042	2682.2391	24.3	1237	- 1260	0	---	R.VAMQSQHNSRPATPMDSPVWSNSR.L
2897.4724	2896.4651	2896.3410	42.9	1266	- 1292	1	---	R.SGYSTPAYMGSAYNSRPSTPSRLSTR.K + Oxidation (M)
No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1357.7264, 1358.7098, 1385.7190, 1405.6670, 1436.7194, 1446.7092, 1465.7672, 1466.7670, 1521.7461, 1521.7461, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1611.7694, 1676.8539, 1707.8973, 1734.8571, 1742.8484, 1763.8722, 1791.8730, 1809.8907, 1819.8888, 1829.8156, 1843.8678, 1873.9242, 1877.9161, 1952.0050, 1996.9535, 2041.0391, 2141.0703, 2269.1736, 2309.1104, 2328.2629, 2418.2456, 2682.3164								

17. [gi|823142681](#) Mass: 74396 Score: 62 Expect: 14 Matches: 11

PREDICTED: exocyst complex component EXO70B1-like [Gossypium raimondii]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1537.8478	1536.8405	1536.8413	-0.48	574	- 586	1	---	R.IQTGWKVPDPQLR.E
1601.8103	1600.8030	1600.8209	-11.17	502	- 515	1	---	K.DSELGKLLGDNWVR.K
1676.8539	1675.8466	1675.8377	5.34	542	- 558	1	---	K.DEGIGGSSNNASKVTLK.E
1734.8571	1733.8498	1733.9062	-32.52	414	- 427	1	---	R.YVMNVKLLVDYSK.T
1742.8484	1741.8411	1741.8523	-6.40	385	- 400	1	---	K.GTFVEFENAVKSEASK.K
1819.8888	1818.8815	1818.8860	-2.48	74	- 89	1	---	K.VILRWDSSSSNPDTSR.H
1876.8998	1875.8925	1875.9360	-23.19	114	- 129	1	---	K.LVVDVSIIRDNEIMDR.A + Oxidation (M)
1952.0050	1950.9977	1950.9469	26.1	130	- 146	1	---	R.AEAAVQLAMSRLEDEFRL + Oxidation (M)
1987.0083	1986.0010	1985.9517	24.9	34	- 49	1	---	K.EVREDMLLIFSSFDNR.L + Oxidation (M)
2418.2456	2417.2383	2417.2348	1.48	401	- 420	1	---	K.KPMQNGEIHPLTRYVMNVVK.L
2683.3115	2682.3042	2682.3549	-18.91	478	- 499	0	---	K.LYEDGALHCIFLMNNLIYVQK.V + Oxidation (M)
No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1197.5636, 1261.6660, 1301.6093, 1357.7264, 1358.7098, 1376.7114, 1385.7190, 1405.6670, 1414.6940, 1436.7194, 1446.7092, 1465.7672, 1466.7670, 1521.7461, 1521.7461, 1532.7528, 1565.8809, 1567.7930, 1583.7969, 1610.7716, 1611.7694, 1617.8115, 1707.8973, 1763.8722, 1791.8730, 1809.8907, 1829.8156, 1843.8678, 1844.9191, 1844.9191, 1873.9242, 1877.9161, 1996.9535, 2041.0391, 2094.0942, 2141.0703, 2269.1736, 2309.1104, 2328.2629, 2549.2947, 2682.3164, 2897.4724								

18. [gi|677374751](#) Mass: 145337 Score: 61 Expect: 15 Matches: 16

hypothetical protein N329_04449, partial [Haliastur albicilla]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1080.4445	1079.4372	1079.4805	-40.05	587	-	595	0 ---	R.SMEELSQEK.R
1186.6648	1185.6575	1185.6255	27.0	417	-	427	1 ---	K.KSSYGPHGVVR.S
1197.5636	1196.5563	1196.6037	-39.59	428	-	439	0 ---	R.SSGYKPSLSK.Q
1405.6670	1404.6597	1404.6741	-10.24	394	-	405	0 ---	R.SESMTTKPMLHK.N + Oxidation (M)
1436.7194	1435.7121	1435.7307	-12.93	689	-	700	0 ---	R.NQSFTELISELR.A
1446.7092	1445.7019	1445.7726	-48.85	735	-	748	1 ---	R.DLAKVQIASTSGEK.S
1466.7670	1465.7597	1465.7017	39.6	1033	-	1044	1 ---	R.MVMSDNNLRNK.T + 2 Oxidation (M)
1610.7716	1609.7643	1609.7808	-10.24	1121	-	1134	1 ---	K.SQATLAYSENNTRR.I
1617.8115	1616.8042	1616.8668	-38.71	11	-	25	1 ---	K.MQLQKSNQVAVSLSR.D
1791.8730	1790.8657	1790.8951	-16.41	769	-	782	1 ---	R.RLQWYAENQDLLDK.D
1829.8156	1828.8083	1828.8625	-29.62	1	-	15	1 ---	-.ETDENTHVEKMLQK.S

1877.9161	1876.9088	1876.9022	3.51	656	-	670	1	---	K.ENQCLMSELIDLREK.I
1987.0083	1986.0010	1986.0381	-18.68	962	-	978	1	---	K.NLQTEIENLKSQNSQLK.L
1996.9535	1995.9462	1995.9398	3.20	1065	-	1081	1	---	K.RNSSNSEPFSLSFNNDR.I
2141.0703	2140.0630	2140.1125	-23.14	917	-	934	1	---	R.LVELEQLLAYKFMESEPK.L + Oxidation (M)
2418.2456	2417.2383	2417.1710	27.9	80	-	100	1	---	K.ELDSNDSVLLAPFVRNEENEK.G
No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1261.6660, 1301.6093, 1357.7264, 1358.7098, 1376.7114, 1385.7190, 1414.6940, 1465.7672, 1521.7461, 1521.7461, 1532.7528, 1537.8478, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1611.7694, 1676.8539, 1707.8973, 1734.8571, 1742.8484, 1763.8722, 1809.8907, 1819.8888, 1843.8678, 1844.9191, 1844.9191, 1873.9242, 1876.8998, 1952.0050, 2041.0391, 2094.0942, 2269.1736, 2309.1104, 2328.2629, 2549.2947, 2682.3164, 2683.3115, 2897.4724									
19. gi 551503836 Mass: 76403 Score: 61 Expect: 17 Matches: 11									
PREDICTED: caseinolytic peptidase B protein homolog [Xiphophorus maculatus]									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1358.7098	1357.7025	1357.7314	-21.23	162	-	173	1	---	R.TNNAQDVSRLIK.E
1446.7092	1445.7019	1445.7474	-31.46	654	-	666	1	---	R.LRLEVVGEDSSSR.T
1465.7672	1464.7599	1464.7217	26.1	184	-	196	0	---	R.LGWLTALMVAAMNR.Q + 2 Oxidation (M)
1466.7670	1465.7597	1465.8253	-44.71	226	-	238	1	---	R.EKGHSLEVLVSR.E
1565.8809	1564.8736	1564.9202	-29.74	530	-	542	1	---	K.DTVIRPILKAHFR.R
1617.8115	1616.8042	1616.7682	22.3	296	-	309	0	---	K.EGEVNTVLQEWEGK.F
1742.8484	1741.8411	1741.8868	-26.24	182	-	196	1	---	R.HRLGWLTALMVAAMNR.Q + Oxidation (M)
1987.0083	1986.0010	1985.9847	8.22	411	-	429	0	---	K.FIGSPPGYIGHEEGQLTK.L
2094.0942	2093.0869	2093.0687	8.69	272	-	291	0	---	R.MLLEAGANPLQTNLSLGHTR.A
2309.1104	2308.1031	2308.1053	-0.92	16	-	37	1	---	R.SLSPCGRVLQTSASGATGPCFR.E
2682.3164	2681.3091	2681.2205	33.1	203	-	227	1	---	K.ALLEAGADPNAGDDFNNVYDTSREK.G
No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1064.4917, 1064.4917, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1197.5636, 1261.6660, 1301.6093, 1357.7264, 1376.7114, 1385.7190, 1405.6670, 1414.6940, 1436.7194, 1521.7461, 1521.7461, 1532.7528, 1537.8478, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1611.7694, 1676.8539, 1707.8973, 1734.8571, 1763.8722, 1791.8730, 1809.8907, 1819.8888, 1829.8156, 1843.8678, 1844.9191, 1844.9191, 1873.9242, 1876.8998, 1877.9161, 1952.0050, 1996.9535, 2041.0391, 2141.0703, 2269.1736, 2328.2629, 2418.2456, 2549.2947, 2682.3164, 2683.3115, 2897.4724									
20. gi 712911970 Mass: 57648 Score: 60 Expect: 20 Matches: 12									
chaperonin GroEL (chloroplast) [Cerataulina daemon]									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1064.4917	1063.4844	1063.5220	-35.29	381	-	390	0	---	R.VGAVTETEMK.D
1064.4917	1063.4844	1063.5220	-35.29	381	-	390	0	---	R.VGAVTETEMK.D
1521.7461	1520.7388	1520.7511	-8.08	487	-	500	0	---	K.FGNLFEEGVVDPK.V
1521.7461	1520.7388	1520.7511	-8.08	487	-	500	0	---	K.FGNLFEEGVVDPK.V
1537.8478	1536.8405	1536.8511	-6.89	456	-	470	0	---	R.IAENAGINGPVIEK.V
1611.7694	1610.7621	1610.7576	2.79	471	-	484	0	---	K.VQQEDFEIGYNAK.N
1676.8539	1675.8466	1675.8525	-3.49	18	-	33	0	---	K.GMEIMVEAVSVTLGPK.G + Oxidation (M)
1763.8722	1762.8649	1762.8890	-13.65	485	-	500	1	---	K.NKFGNLFEEGVVDPK.V
1791.8730	1790.8657	1790.9335	-37.86	181	-	196	1	---	K.GITTELEITEGKIEK.G
1873.9242	1872.9169	1872.9801	-33.75	18	-	35	1	---	K.GMEIMVEAVSVTLGPKGR.N
1877.9161	1876.9088	1876.9683	-31.70	487	-	503	1	---	K.FGNLFEEGVVDPKAVTR.S
1987.0083	1986.0010	1985.9768	12.2	210	-	225	1	---	K.MEVSYPYILLTDKR.I + Oxidation (M)
No match to: 851.3322, 965.4107, 1007.4567, 1034.0704, 1054.4012, 1079.4565, 1080.4445, 1082.5022, 1097.4648, 1098.4523, 1111.5012, 1136.5402, 1186.6648, 1197.5636, 1261.6660, 1301.6093, 1357.7264, 1358.7098, 1376.7114, 1385.7190, 1405.6670, 1414.6940, 1436.7194, 1446.7092, 1465.7672, 1466.7670, 1532.7528, 1565.8809, 1567.7930, 1583.7969, 1601.8103, 1610.7716, 1617.8115, 1707.8973, 1734.8571, 1742.8484, 1809.8907, 1819.8888, 1829.8156, 1843.8678, 1844.9191, 1844.9191, 1876.8998, 1952.0050, 1996.9535, 2041.0391, 2094.0942, 2141.0703, 2269.1736, 2309.1104, 2328.2629, 2418.2456, 2549.2947, 2682.3164, 2683.3115, 2897.4724									

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 : ± 50 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Query1 (851.3322,1+) : <no title>
Query2 (965.4107,1+) : <no title>
Query3 (1007.4567,1+) : <no title>
Query4 (1034.0704,1+) : <no title>
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Query52 (1873.9242,1+) : <no title>
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Query67 (2683.3115,1+) : <no title>
Query68 (2897.4724,1+) : <no title>

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