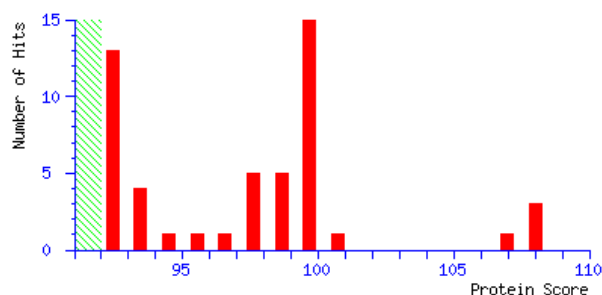


Mascot Search Results

User :
 Email :
 Search title : SampleSetID: 692, AnalysisID: 5361, MaldiWellID: 60697, SpectrumID: 127319, Path=\\161031\\MSMS\\run 65 NCBI all ok 1
 Database : NCBI nr 160208 (79581714 sequences; 29080698065 residues)
 Timestamp : 28 Nov 2016 at 13:23:59 GMT
 Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
 Top Score : 108 for gi|585185897, PREDICTED: beta-actin-like protein 2-like isoform X1 [Leptonychotes weddellii]

Mascot Score Histogram

Protein score is $-10 \times \log(P)$, where P is the probability that the observed match is a random event.
 Protein scores greater than 92 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 [Help](#)

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

Index

Accession	Mass	Score	Description
1. gi 585185897	42238	108	PREDICTED: beta-actin-like protein 2-like isoform X1 [Leptonychotes weddellii]
2. gi 562839756	42188	108	PREDICTED: beta-actin-like protein 2 isoform X1 [Tupaia chinensis]
3. gi 301781394	42256	108	PREDICTED: beta-actin-like protein 2 [Ailuropoda melanoleuca]
4. gi 57043600	42232	107	PREDICTED: beta-actin-like protein 2 [Canis lupus familiaris]
5. gi 585185899	37460	101	PREDICTED: beta-actin-like protein 2-like isoform X2 [Leptonychotes weddellii]
6. gi 826324799	37384	100	PREDICTED: beta-actin-like protein 2 isoform X2 [Propithecus coquereli]
7. gi 562839758	37410	100	PREDICTED: beta-actin-like protein 2 isoform X2 [Tupaia chinensis]
8. gi 667261017	42181	100	PREDICTED: beta-actin-like protein 2 isoform X1 [Galeopterus variegatus]
9. gi 472378785	37478	100	PREDICTED: beta-actin-like protein 2 isoform X2 [Odobenus rosmarus divergens]
10. gi 478497113	41870	100	PREDICTED: beta-actin-like protein 2 [Ceratotherium simum simum]
11. gi 617572918	42206	100	PREDICTED: beta-actin-like protein 2 isoform X1 [Erinaceus europaeus]
12. gi 686718468	37541	100	PREDICTED: beta-actin-like protein 2 isoform X2 [Pongo abelii]
13. gi 826324796	42162	99	PREDICTED: beta-actin-like protein 2 isoform X1 [Propithecus coquereli]
14. gi 410948613	42246	99	PREDICTED: beta-actin-like protein 2 isoform X1 [Felis catus]
15. gi 505801923	42149	99	PREDICTED: beta-actin-like protein 2 isoform X1 [Sorex araneus]
16. gi 507934246	42253	99	PREDICTED: beta-actin-like protein 2 isoform X1 [Condylura cristata]
17. gi 591306586	42246	99	PREDICTED: beta-actin-like protein 2 isoform X1 [Panthera tigris altaica]
18. gi 585679916	42240	99	PREDICTED: beta-actin-like protein 2-like [Elephantulus edwardii]
19. gi 586489862	42182	99	PREDICTED: beta-actin-like protein 2-like isoform X1 [Chrysochloris asiatica]
20. gi 829821249	37402	99	PREDICTED: beta-actin-like protein 2 isoform X2 [Microcebus murinus]

Results List

1. [gi|585185897](#) Mass: 42238 Score: 108 Expect: 0.0013 Matches: 9

PREDICTED: beta-actin-like protein 2-like isoform X1 [Leptonychotes weddellii]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7330	1514.7257	1514.7419	-10.66	86	- 96	0	---	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.8385	-20.31	185	- 197	1	---	R.DLTDYLMKILTER.G
1622.8273	1621.8200	1621.8419	-13.48	314	- 327	1	---	R.MQKEIITLAPSTMK.I + 2 Oxidation (M)
1638.8357	1637.8284	1637.8161	7.50	361	- 374	1	---	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	- 211	1	---	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	- 255	0	---	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	- 255	0	60	R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	- 19	0	---	M.TDELSALVVDNGSGMCK.A
2229.1194	2228.1121	2228.0783	15.2	293	- 313	0	---	K.DLYANIVLSGGSTMYPGIADR.M + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042,								

2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2345.1975, 2633.3140, 2762.4597, 3154.6409, 3268.7122

2. [gi|562839756](#) Mass: 42188 Score: 108 Expect: 0.0013 Matches: 9

PREDICTED: beta-actin-like protein 2 isoform X1 [Tupaia chinensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7330	1514.7257	1514.7419	-10.66	86	-	96	0	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.8385	-20.31	185	-	197	1	R.DLTDYLMKILTER.G
1622.8273	1621.8200	1621.8419	-13.48	314	-	327	1	R.MQKEIITLAPSTMK.I + 2 Oxidation (M)
1638.8357	1637.8284	1637.8161	7.50	361	-	374	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	-	211	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
2012.0171	2011.0098	2010.8697	69.7	1	-	19	0	-.MADELALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	292	-	313	1	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)

No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1910.9115, 1922.9425, 1938.9855, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2345.1975, 2633.3140, 2762.4597, 3154.6409, 3268.7122

3. [gi|301781394](#) Mass: 42256 Score: 108 Expect: 0.0013 Matches: 9

PREDICTED: beta-actin-like protein 2 [Ailuropoda melanoleuca]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7330	1514.7257	1514.7419	-10.66	86	-	96	0	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.8385	-20.31	185	-	197	1	R.DLTDYLMKILTER.G
1622.8273	1621.8200	1621.8419	-13.48	314	-	327	1	R.MQKEIITLAPSTMK.I + 2 Oxidation (M)
1638.8357	1637.8284	1637.8161	7.50	361	-	374	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	-	211	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0	M.TDELSALVVDNGSGMCK.A
2229.1194	2228.1121	2228.0783	15.2	293	-	313	0	K.DLYANIVLSGGSTMYPGIADR.M + Oxidation (M)

No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2345.1975, 2633.3140, 2762.4597, 3154.6409, 3268.7122

4. [gi|57043600](#) Mass: 42232 Score: 107 Expect: 0.0016 Matches: 9

PREDICTED: beta-actin-like protein 2 [Canis lupus familiaris]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1237.6570	1236.6497	1236.6094	32.6	317	-	327	0	K.EIMTLAPSTMK.I + Oxidation (M)
1515.7330	1514.7257	1514.7419	-10.66	86	-	96	0	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.8385	-20.31	185	-	197	1	R.DLTDYLMKILTER.G
1638.8357	1637.8284	1637.8161	7.50	361	-	374	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	-	211	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0	M.TDELSALVVDNGSGMCK.A
2229.1194	2228.1121	2228.0783	15.2	293	-	313	0	K.DLYANIVLSGGSTMYPGIADR.M + Oxidation (M)

No match to: 983.5242, 1128.5931, 1128.5931, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1622.8273, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2345.1975, 2633.3140, 2762.4597, 3154.6409, 3268.7122

5. [gi|585185899](#) Mass: 37460 Score: 101 Expect: 0.0063 Matches: 8

PREDICTED: beta-actin-like protein 2-like isoform X2 [Leptonchotes weddellii]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1610.8131	1609.8058	1609.8385	-20.31	143	-	155	1	R.DLTDYLMKILTER.G
1622.8273	1621.8200	1621.8419	-13.48	272	-	285	1	R.MQKEIITLAPSTMK.I + 2 Oxidation (M)
1638.8357	1637.8284	1637.8161	7.50	319	-	332	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	156	-	169	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	198	-	213	0	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	198	-	213	0	R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0	M.TDELSALVVDNGSGMCK.A
2229.1194	2228.1121	2228.0783	15.2	251	-	271	0	K.DLYANIVLSGGSTMYPGIADR.M + Oxidation (M)

No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2345.1975, 2633.3140, 2762.4597, 3154.6409, 3268.7122

6. [gi|826324799](#) Mass: 37384 Score: 100 Expect: 0.008 Matches: 8

PREDICTED: beta-actin-like protein 2 isoform X2 [Propithecus coquereli]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
----------	----------	----------	-----	-------	-----	------	------	---------

1610.8131 1609.8058 1609.8385 -20.31 143 - 155 1 --- R.DLTDYLMKILTER.G
 1622.8273 1621.8200 1621.8419 -13.48 272 - 285 1 --- R.MQKEIITLAPSTMK.V + 2 Oxidation (M)
 1638.8357 1637.8284 1637.8161 7.50 319 - 332 1 --- K.QEYDEAGPPIVHRK.C
 1656.8834 1655.8761 1655.8267 29.8 156 - 169 1 --- R.GYNFTTTAEREIVR.D
 1790.8844 1789.8771 1789.8846 -4.19 198 - 213 0 --- R.SYELPDGQVITIGNER.F
 1790.8844 1789.8771 1789.8846 -4.19 198 - 213 0 60 R.SYELPDGQVITIGNER.F
 1910.9115 1909.9042 1909.8398 33.8 2 - 19 0 --- M.TDELSALVVDNGSGMCK.A
 2345.1975 2344.1902 2344.1369 22.7 250 - 271 1 --- R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)
 No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1515.7330, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122

7. [gi|562839758](#) Mass: 37410 Score: 100 Expect: 0.008 Matches: 8

PREDICTED: beta-actin-like protein 2 isoform X2 [Tupaia chinensis]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1610.8131	1609.8058	1609.8385	-20.31	143	-	155	1 ---	R.DLTDYLMKILTER.G
1622.8273	1621.8200	1621.8419	-13.48	272	-	285	1 ---	R.MQKEIITLAPSTMK.I + 2 Oxidation (M)
1638.8357	1637.8284	1637.8161	7.50	319	-	332	1 ---	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	156	-	169	1 ---	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	198	-	213	0 ---	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	198	-	213	0 60	R.SYELPDGQVITIGNER.F
2012.0171	2011.0098	2010.8697	69.7	1	-	19	0 ---	- .MADDELSALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	250	-	271	1 ---	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1515.7330, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1910.9115, 1922.9425, 1938.9855, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122								

8. [gi|667261017](#) Mass: 42181 Score: 100 Expect: 0.008 Matches: 8

PREDICTED: beta-actin-like protein 2 isoform X1 [Galeopterus variegatus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7330	1514.7257	1514.7419	-10.66	86	-	96	0 ---	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.8385	-20.31	185	-	197	1 ---	R.DLTDYLMKILTER.G
1638.8357	1637.8284	1637.8161	7.50	361	-	374	1 ---	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	-	211	1 ---	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0 ---	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0 60	R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0 ---	M.TDELSALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	292	-	313	1 ---	R.KDLYANTVLSGGSTMYPGIADR.I + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1622.8273, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122								

9. [gi|472378785](#) Mass: 37478 Score: 100 Expect: 0.0083 Matches: 8

PREDICTED: beta-actin-like protein 2 isoform X2 [Odobenus rosmarus divergens]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1610.8131	1609.8058	1609.8385	-20.31	143	-	155	1 ---	R.DLTDYLMKILTER.G
1622.8273	1621.8200	1621.8419	-13.48	272	-	285	1 ---	R.MQKEIITLAPSTMK.I + 2 Oxidation (M)
1638.8357	1637.8284	1637.8161	7.50	319	-	332	1 ---	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	156	-	169	1 ---	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	198	-	213	0 ---	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	198	-	213	0 60	R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0 ---	M.TDELSALVVDNGSGMCK.A
2229.1194	2228.1121	2228.0783	15.2	251	-	271	0 ---	K.DLYANIVLSGGSTMYPGIADR.M + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1515.7330, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2345.1975, 2633.3140, 2762.4597, 3154.6409, 3268.7122								

10. [gi|478497113](#) Mass: 41870 Score: 100 Expect: 0.0083 Matches: 8

PREDICTED: beta-actin-like protein 2 [Ceratotherium simum simum]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7330	1514.7257	1514.7419	-10.66	86	-	96	0 ---	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.7848	13.0	358	-	371	1 ---	K.QEYDEAGPPIAHRK.C
1656.8834	1655.8761	1655.8267	29.8	195	-	208	1 ---	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	237	-	252	0 ---	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	237	-	252	0 60	R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0 ---	M.TDELSALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	289	-	310	1 ---	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)
3154.6409	3153.6336	3153.5337	31.7	118	-	145	1 ---	R.EKMMFEAFNTPAMYVAIQAVLSLYASGR.T + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1515.7330, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2345.1975, 2633.3140, 2762.4597, 3154.6409, 3268.7122								

1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1622.8273, 1638.8357, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3268.7122

11. [gi|617572918](#) Mass: 42206 Score: 100 Expect: 0.0085 Matches: 9

PREDICTED: beta-actin-like protein 2 isoform X1 [Erinaceus europaeus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7330	1514.7257	1514.7419	-10.66	86	-	96	0	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.8385	-20.31	185	-	197	1	R.DLTDYLMKILTER.G
1638.8357	1637.8284	1637.8161	7.50	361	-	374	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	-	211	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1894.9287	1893.9214	1893.8448	40.4	2	-	19	0	M.AEDEL SALVVDNGSGMCK.A
1910.9115	1909.9042	1909.8397	33.8	2	-	19	0	M.AEDEL SALVVDNGSGMCK.A + Oxidation (M)
2345.1975	2344.1902	2344.1369	22.7	292	-	313	1	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1622.8273, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122								

12. [gi|686718468](#) Mass: 37541 Score: 100 Expect: 0.0085 Matches: 8

PREDICTED: beta-actin-like protein 2 isoform X2 [Pongo abelii]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1610.8131	1609.8058	1609.8385	-20.31	143	-	155	1	R.DLTDYLMKILTER.G
1622.8273	1621.8200	1621.8419	-13.48	272	-	285	1	R.MQKEITLAPSTMK.I + 2 Oxidation (M)
1638.8357	1637.8284	1637.8161	7.50	319	-	332	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	156	-	169	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	198	-	213	0	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	198	-	213	0	R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0	M.TDELSALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	250	-	271	1	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1515.7330, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122								

13. [gi|826324796](#) Mass: 42162 Score: 99 Expect: 0.0091 Matches: 8

PREDICTED: beta-actin-like protein 2 isoform X1 [Propithecus coquereli]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1610.8131	1609.8058	1609.8385	-20.31	185	-	197	1	R.DLTDYLMKILTER.G
1622.8273	1621.8200	1621.8419	-13.48	314	-	327	1	R.MQKEITLAPSTMK.V + 2 Oxidation (M)
1638.8357	1637.8284	1637.8161	7.50	361	-	374	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	-	211	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0	M.TDELSALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	292	-	313	1	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1515.7330, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122								

14. [gi|410948613](#) Mass: 42246 Score: 99 Expect: 0.0094 Matches: 8

PREDICTED: beta-actin-like protein 2 isoform X1 [Felis catus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7330	1514.7257	1514.7419	-10.66	86	-	96	0	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.8385	-20.31	185	-	197	1	R.DLTDYLMKILTER.G
1638.8357	1637.8284	1637.8161	7.50	361	-	374	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	-	211	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0	M.TDELSALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	292	-	313	1	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1622.8273, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122								

15. [gi|505801923](#) Mass: 42149 Score: 99 Expect: 0.0094 Matches: 8

PREDICTED: beta-actin-like protein 2 isoform X1 [Sorex araneus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7330	1514.7257	1514.7419	-10.66	86	-	96	0	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.8385	-20.31	185	-	197	1	R.DLTDYLMKILTER.G
1638.8357	1637.8284	1637.8161	7.50	361	-	374	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	-	211	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	K.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	60 K.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0	M.TDELSALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	292	-	313	1	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1622.8273, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122								

16. [gi|507934246](#) Mass: 42253 Score: 99 Expect: 0.0094 Matches: 8

PREDICTED: beta-actin-like protein 2 isoform X1 [Condylura cristata]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7330	1514.7257	1514.7419	-10.66	86	-	96	0	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.8385	-20.31	185	-	197	1	R.DLTDYLMKILTER.G
1638.8357	1637.8284	1637.8161	7.50	361	-	374	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	-	211	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	60 R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0	M.TDELSALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	292	-	313	1	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1622.8273, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122								

17. [gi|591306586](#) Mass: 42246 Score: 99 Expect: 0.0094 Matches: 8

PREDICTED: beta-actin-like protein 2 isoform X1 [Panthera tigris altaica]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7330	1514.7257	1514.7419	-10.66	86	-	96	0	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.8385	-20.31	185	-	197	1	R.DLTDYLMKILTER.G
1638.8357	1637.8284	1637.8161	7.50	361	-	374	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	-	211	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	60 R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0	M.TDELSALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	292	-	313	1	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1622.8273, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122								

18. [gi|585679916](#) Mass: 42240 Score: 99 Expect: 0.0094 Matches: 8

PREDICTED: beta-actin-like protein 2-like [Elephantulus edwardii]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7330	1514.7257	1514.7419	-10.66	86	-	96	0	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.8385	-20.31	185	-	197	1	R.DLTDYLMKILTER.G
1638.8357	1637.8284	1637.8161	7.50	361	-	374	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	-	211	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	60 R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0	M.TDELSALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	292	-	313	1	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)
No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1622.8273, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122								

19. [gi|586489862](#) Mass: 42182 Score: 99 Expect: 0.0094 Matches: 8

PREDICTED: beta-actin-like protein 2-like isoform X1 [Chrysochloris asiatica]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1515.7330	1514.7257	1514.7419	-10.66	86	-	96	0	K.IWHHTFYNELR.V
1610.8131	1609.8058	1609.8385	-20.31	185	-	197	1	R.DLTDYLMKILTER.G
1638.8357	1637.8284	1637.8161	7.50	361	-	374	1	K.QEYDEAGPPIVHRK.C
1656.8834	1655.8761	1655.8267	29.8	198	-	211	1	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	240	-	255	0	60 R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0	M.TDELSALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	292	-	313	1	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)

No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1622.8273, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122

20. [gi|829821249](#) Mass: 37402 Score: 99 Expect: 0.0094 Matches: 8

PREDICTED: beta-actin-like protein 2 isoform X2 [Microcebus murinus]

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1610.8131	1609.8058	1609.8385	-20.31	143	-	155	1 ---	R.DLTDYLMKILTER.G
1622.8273	1621.8200	1621.8419	-13.48	272	-	285	1 ---	R.MQKEIITLAPSTMK.V + 2 Oxidation (M)
1638.8357	1637.8284	1637.8161	7.50	319	-	332	1 ---	K.QEYDEAGGPVHRK.C
1656.8834	1655.8761	1655.8267	29.8	156	-	169	1 ---	R.GYNFTTTAEREIVR.D
1790.8844	1789.8771	1789.8846	-4.19	198	-	213	0 ---	R.SYELPDGQVITIGNER.F
1790.8844	1789.8771	1789.8846	-4.19	198	-	213	0 60	R.SYELPDGQVITIGNER.F
1910.9115	1909.9042	1909.8398	33.8	2	-	19	0 ---	M.TDELSALVVDNGSGMCK.A
2345.1975	2344.1902	2344.1369	22.7	250	-	271	1 ---	R.KDLYANTVLSGGSTMYPGIADR.M + Oxidation (M)

No match to: 983.5242, 1128.5931, 1128.5931, 1237.6570, 1240.6102, 1264.6069, 1268.6627, 1300.6390, 1359.6914, 1359.6914, 1376.7162, 1410.7299, 1439.7598, 1515.7330, 1531.7305, 1535.7333, 1537.7397, 1553.7462, 1571.7726, 1581.7998, 1585.7614, 1642.7932, 1646.7865, 1655.8826, 1655.8826, 1670.8241, 1677.8427, 1698.8546, 1703.7977, 1733.8387, 1761.8594, 1770.8787, 1792.8848, 1818.9027, 1851.8911, 1894.9287, 1897.9340, 1922.9425, 1938.9855, 2012.0171, 2099.0762, 2107.0601, 2118.0129, 2121.0042, 2126.0940, 2133.0781, 2149.0737, 2180.0413, 2196.1062, 2219.0864, 2225.1675, 2229.1194, 2256.1023, 2282.1709, 2302.1433, 2308.1584, 2314.1497, 2633.3140, 2762.4597, 3154.6409, 3268.7122

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 : ± 80 ppm
 Fragment Mass Tolerance: ± 0.3 Da
 Max Missed Cleavages : 1
 Instrument type : MALDI-TOF-TOF
 Query1 (983.5242,1+) : <no title>
 Query2 (1128.5931,1+) : <no title>
 Query3 (1128.5931,1+) : MaldiWellID: 60697, SpectrumID: 127322,
 Query4 (1237.6570,1+) : <no title>
 Query5 (1240.6102,1+) : <no title>
 Query6 (1264.6069,1+) : <no title>
 Query7 (1268.6627,1+) : <no title>
 Query8 (1300.6390,1+) : <no title>
 Query9 (1359.6914,1+) : <no title>
 Query10 (1359.6914,1+) : MaldiWellID: 60697, SpectrumID: 127321,
 Query11 (1376.7162,1+) : <no title>
 Query12 (1410.7299,1+) : <no title>
 Query13 (1439.7598,1+) : <no title>
 Query14 (1515.7330,1+) : <no title>
 Query15 (1531.7305,1+) : <no title>
 Query16 (1535.7333,1+) : <no title>
 Query17 (1537.7397,1+) : <no title>
 Query18 (1553.7462,1+) : <no title>
 Query19 (1571.7726,1+) : <no title>
 Query20 (1581.7998,1+) : <no title>
 Query21 (1585.7614,1+) : <no title>
 Query22 (1610.8131,1+) : <no title>
 Query23 (1622.8273,1+) : <no title>
 Query24 (1638.8357,1+) : <no title>
 Query25 (1642.7932,1+) : <no title>
 Query26 (1646.7865,1+) : <no title>
 Query27 (1655.8826,1+) : <no title>
 Query28 (1655.8826,1+) : MaldiWellID: 60697, SpectrumID: 127320,
 Query29 (1656.8834,1+) : <no title>
 Query30 (1670.8241,1+) : <no title>
 Query31 (1677.8427,1+) : <no title>
 Query32 (1698.8546,1+) : <no title>
 Query33 (1703.7977,1+) : <no title>
 Query34 (1733.8387,1+) : <no title>
 Query35 (1761.8594,1+) : <no title>
 Query36 (1770.8787,1+) : <no title>
 Query37 (1790.8844,1+) : <no title>
 Query38 (1790.8844,1+) : MaldiWellID: 60697, SpectrumID: 127323,
 Query39 (1792.8848,1+) : <no title>
 Query40 (1818.9027,1+) : <no title>
 Query41 (1851.8911,1+) : <no title>
 Query42 (1894.9287,1+) : <no title>
 Query43 (1897.9340,1+) : <no title>
 Query44 (1910.9115,1+) : <no title>
 Query45 (1922.9425,1+) : <no title>
 Query46 (1938.9855,1+) : <no title>
 Query47 (2012.0171,1+) : <no title>
 Query48 (2099.0762,1+) : <no title>
 Query49 (2107.0601,1+) : <no title>
 Query50 (2118.0129,1+) : <no title>

Query51 (2121.0042,1+) : <no title>
Query52 (2126.0940,1+) : <no title>
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Query56 (2196.1062,1+) : <no title>
Query57 (2219.0864,1+) : <no title>
Query58 (2225.1675,1+) : <no title>
Query59 (2229.1194,1+) : <no title>
Query60 (2256.1023,1+) : <no title>
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Query63 (2308.1584,1+) : <no title>
Query64 (2314.1497,1+) : <no title>
Query65 (2345.1975,1+) : <no title>
Query66 (2633.3140,1+) : <no title>
Query67 (2762.4597,1+) : <no title>
Query68 (3154.6409,1+) : <no title>
Query69 (3268.7122,1+) : <no title>

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