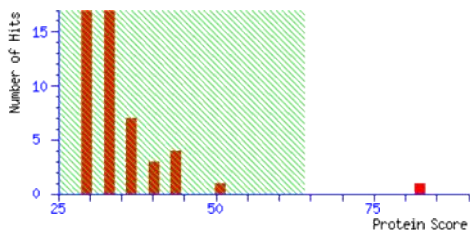


MATRIX SCIENCE Mascot Search Results

User :
Email :
Search title : BAEDW\2020_3_5\2020_3_5\MSMS 14\M20
Database : Uniprot_bovine bovine_20200316 (134392 sequences; 76244912 residues)
Timestamp : 31 Mar 2020 at 01:08:06 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 82 for A0A3Q1M3L6, Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=1

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 64 are significant (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

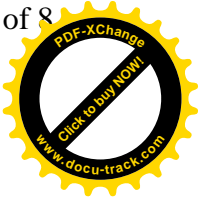
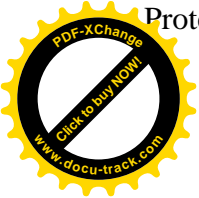
Format As Protein Summary (deprecated) [Help](#)
Significance threshold p< Max. number of hits
Preferred taxonomy All entries

Index

Accession	Mass	Score	Description
1. A0A3Q1M3L6	41077	82	Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=1
2. Q3SYZ4	57456	51	Aspartate--tRNA ligase, cytoplasmic OS=Bos taurus OX=9913 GN=DARS1 PE=2 SV=1
3. A0A4W2CKQ7	47880	45	Sorting nexin OS=Bos indicus x Bos taurus OX=30522 GN=SNX5 PE=3 SV=1
4. A0A4W2DFG4	53946	44	Aspartyl-tRNA synthetase OS=Bos indicus x Bos taurus OX=30522 GN=DARS PE=3 SV=1
5. A0A4W2HFK9	43131	44	PX domain-containing protein OS=Bos indicus x Bos taurus OX=30522 GN=SNX5 PE=4 SV=1
6. A0A4W2DFC3	57472	42	Aspartyl-tRNA synthetase OS=Bos indicus x Bos taurus OX=30522 GN=DARS PE=3 SV=1
7. A0A4W2FGA1	47047	42	Sorting nexin OS=Bos indicus x Bos taurus OX=30522 GN=SNX5 PE=3 SV=1
8. Q3ZBM5	47075	42	Sorting nexin-5 OS=Bos taurus OX=9913 GN=SNX5 PE=2 SV=1
9. P46166	4698	39	Beta-defensin 8 OS=Bos taurus OX=9913 GN=DEFB8 PE=1 SV=1
10. A0A3Q1MFP5	136327	37	Phospholipase OS=Bos taurus OX=9913 GN=PLD1 PE=3 SV=1
11. A0A4W2FRG9	61477	36	Transmembrane protein 200C OS=Bos indicus x Bos taurus OX=30522 GN=TMEM200C PE=4 SV=1
12. A0A1R3UGP4	28249	36	Kallikrein G OS=Bos taurus OX=9913 GN=KLNG PE=3 SV=1
13. A0A4W2F0S3	54184	36	Aspartyl-tRNA synthetase OS=Bos indicus x Bos taurus OX=30522 GN=DARS PE=3 SV=1
14. A0A4W2HLP0	45410	36	Secernin 1 OS=Bos indicus x Bos taurus OX=30522 GN=SCRN1 PE=4 SV=1
15. A0A3Q1LXT8	59645	35	Aspartate--tRNA ligase, cytoplasmic OS=Bos taurus OX=9913 GN=DARS1 PE=3 SV=1
16. A0A4W2C922	39936	35	N(alpha)-acetyltransferase 40, NatD catalytic subunit OS=Bos indicus x Bos taurus OX=30522 GN=NAA40 PE=
17. A0A4W2ETY0	130578	34	Phospholipase OS=Bos indicus x Bos taurus OX=30522 GN=PLD1 PE=3 SV=1
18. F1MTX7	57472	34	Aspartate--tRNA ligase, cytoplasmic OS=Bos taurus OX=9913 GN=DARS1 PE=3 SV=1
19. A0A4W2H2Q0	21512	34	Methionine sulfoxide reductase A OS=Bos indicus x Bos taurus OX=30522 GN=MSRA PE=3 SV=1
20. E1BKP4	84228	33	TANK binding kinase 1 OS=Bos taurus OX=9913 GN=TBK1 PE=4 SV=2
21. A0A4W2CVJ0	84228	33	TANK binding kinase 1 OS=Bos indicus x Bos taurus OX=30522 GN=TBK1 PE=4 SV=1
22. A0A4W2HQ46	39881	33	N(alpha)-acetyltransferase 40, NatD catalytic subunit OS=Bos indicus x Bos taurus OX=30522 GN=NAA40 PE=
23. A5PKK1	27850	33	N(alpha)-acetyltransferase 40, NatD catalytic subunit OS=Bos taurus OX=9913 GN=NAA40 PE=2 SV=1
24. A0A3Q1M909	23483	32	Mitochondrial peptide methionine sulfoxide reductase OS=Bos taurus OX=9913 GN=MSRA PE=1 SV=1
25. A0A4W2H5U8	23483	32	Methionine sulfoxide reductase A OS=Bos indicus x Bos taurus OX=30522 GN=MSRA PE=3 SV=1
26. A0A3Q1LVV9	13591	32	RNA_pol_L_2 domain-containing protein OS=Bos taurus OX=9913 PE=4 SV=1
27. A0A4W2E767	68716	32	Acyl-CoA dehydrogenase very long chain OS=Bos indicus x Bos taurus OX=30522 GN=ACADVL PE=3 SV=1
28. A0A4W2GRX4	68688	32	Acyl-CoA dehydrogenase very long chain OS=Bos indicus x Bos taurus OX=30522 GN=ACADVL PE=3 SV=1
29. A0A3Q1LG54	89438	32	Protein phosphatase 1 regulatory subunit 21 OS=Bos taurus OX=9913 GN=PPP1R21 PE=4 SV=1
30. A5D7H6	88869	32	KLRAQ1 protein OS=Bos taurus OX=9913 GN=PPP1R21 PE=2 SV=1

Results List

1.	A0A3Q1M3L6	Mass: 41077	Score: 82	Expect: 0.00079	Matches: 9
Uncharacterized protein OS=Bos taurus OX=9913 PE=1 SV=1					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Ions Peptide
	1019.6312	1018.6239	1018.5560	66.7	353 - 360 1 --- K.RTIVPDYR.N
	1169.5049	1168.4976	1168.5625	-55.54	156 - 165 0 --- R.IQHQQDTGGK.E
	1301.6583	1300.6510	1300.7252	-57.00	171 - 182 0 --- K.VHNEGLPAPIVR.T
	1301.6583	1300.6511	1300.7252	-56.97	171 - 182 0 --- K.VHNEGLPAPIVR.T
	1363.6659	1362.6586	1362.7660	-78.76	343 - 353 1 --- K.WIFSSVVLKLR.T
	1826.8557	1825.8484	1825.9462	-53.52	193 - 208 0 --- R.EPQVYVLAPPQEELSK.S
	2111.9341	2110.9268	2111.0324	-50.02	123 - 140 0 46 K.FSWFVDDVEVNTATTTPR.E
	2111.9341	2110.9268	2111.0324	-50.01	123 - 140 0 --- K.FSWFVDDVEVNTATTTPR.E
	2753.2139	2752.2066	2752.2877	-29.45	209 - 231 0 --- K.STVSLTCMVTSTFPYDIAVEWQR.N
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1179.5454, 1201.5295, 1334.8121, 1334.8121, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2351.1042, 3337.6887					
2.	Q3SYZ4	Mass: 57456	Score: 51	Expect: 1.1	Matches: 11



Aspartate--tRNA ligase, cytoplasmic OS=Bos taurus OX=9913 GN=DARS1 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1201.5295	1200.5222	1200.6350	-93.95	111	121	0	---	K.ESIVDVEGVVR.K
1301.6583	1300.6510	1300.5250	96.9	255	264	0	---	K.QMCICADFEK.V
1301.6583	1300.6511	1300.5250	96.9	255	264	0	---	K.QMCICADFEK.V
1363.6659	1362.6586	1362.7256	-49.12	320	330	1	---	K.RFQTEIQTVVK.Q
1838.8295	1837.8222	1837.9185	-52.39	394	408	0	---	K.YPLAVRPFYTMPDPR.N + Oxidation (M)
1901.1566	1900.1493	1899.9625	98.3	198	213	1	---	R.LQSGICHPFRETTLN.K
1939.9556	1938.9483	1938.9912	-22.10	82	99	0	---	R.QQQFNQALVAVGDHASK.Q
2004.8711	2003.8638	2003.9636	-49.79	265	281	1	---	K.VFCIGPVFRAEDSNTHR.H
2210.9976	2209.9903	2210.1114	-54.77	123	141	1	---	K.VNQKIGSCTQQDVELHVQK.I
2321.0444	2320.0371	2320.2288	-82.59	432	451	1	---	R.IHDPQLVTERALHHGIDLEK.I
2351.1042	2350.0969	2350.0318	27.7	412	431	1	---	K.QSNSYDMFMERGEILSGAQR.I + 2 Oxidation (M)
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 892.5198, 892.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1334.8121, 1334.8121, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1848.8546, 1873.8428, 1893.8798, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2233.0032, 2283.0698, 2305.0757, 2753.2139, 3337.6887								

3. A0A4W2CKQ7 Mass: 47880 Score: 45 Expect: 4.1 Matches: 12

Sorting nexin OS=Bos indicus x Bos taurus OX=30522 GN=SNX5 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
882.5198	881.5125	881.4317	91.7	119	125	1	---	K.EEFAKMK.Q
882.5198	881.5125	881.4317	91.7	119	125	1	---	K.EEFAKMK.Q
951.5755	950.5682	950.5371	32.7	264	270	1	---	K.KIVYICR.Y
1151.6693	1150.6620	1150.5870	65.2	193	203	0	---	K.SADEVLFSGVK.E
1334.8121	1333.8048	1333.6799	93.7	381	391	0	---	K.NLIEMSELEIK.H + Oxidation (M)
1334.8121	1333.8049	1333.6799	93.7	381	391	0	---	K.NLIEMSELEIK.H + Oxidation (M)
1363.6659	1362.6586	1362.6627	-2.97	285	296	1	---	K.VESRVSSDEDLK.L
1439.6532	1438.6459	1438.7344	-61.47	126	137	0	---	K.QELEAEYLAIVFK.K
1593.7277	1592.7204	1592.8046	-52.82	321	334	1	---	K.ALIDYENSINKALDK.A
1617.9797	1616.9724	1616.8621	68.2	289	302	1	---	R.VSSDEDLKLTELLR.Y
1826.8557	1825.8484	1825.9170	-37.54	2	17	1	---	M.AAVPEVLQQEEDRSK.L
2015.1777	2014.1704	2014.0418	63.9	392	408	1	---	K.HARNNVSLQSCIDLFK.N
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 892.5198, 892.9673, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1417.6385, 1433.6392, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1597.6893, 1597.6893, 1673.7250, 1690.7394, 1732.0092, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2351.1042, 2753.2139, 3337.6887								

4. A0A4W2DFG4 Mass: 53946 Score: 44 Expect: 5.2 Matches: 10

Aspartyl-tRNA synthetase OS=Bos indicus x Bos taurus OX=30522 GN=DARS PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1201.5295	1200.5222	1200.6350	-93.95	80	90	0	---	K.ESIVDVEGVVR.K
1301.6583	1300.6510	1300.5250	96.9	224	233	0	---	K.QMCICADFEK.V
1301.6583	1300.6511	1300.5250	96.9	224	233	0	---	K.QMCICADFEK.V
1363.6659	1362.6586	1362.7256	-49.12	289	299	1	---	K.RFQTEIQTVVK.Q
1838.8295	1837.8222	1837.9185	-52.39	363	377	0	---	K.YPLAVRPFYTMPDPR.N + Oxidation (M)
1939.9556	1938.9483	1938.9469	0.73	27	43	1	---	K.ERYGVSSMIQSQEKGK.Q + Oxidation (M)
2004.8711	2003.8638	2003.9636	-49.79	234	250	1	---	K.VFCIGPVFRAEDSNTHR.H
2210.9976	2209.9903	2210.1114	-54.77	92	110	1	---	K.VNQKIGSCTQQDVELHVQK.I
2321.0444	2320.0371	2320.2288	-82.59	401	420	1	---	R.IHDPQLVTERALHHGIDLEK.I
2351.1042	2350.0969	2350.0318	27.7	381	400	1	---	K.QSNSYDMFMERGEILSGAQR.I + 2 Oxidation (M)
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 892.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1417.6385, 1433.6392, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1597.6893, 1597.6893, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2233.0032, 2283.0698, 2305.0757, 2753.2139, 3337.6887								

5. A0A4W2HFK9 Mass: 43131 Score: 44 Expect: 5.4 Matches: 11

PX domain-containing protein OS=Bos indicus x Bos taurus OX=30522 GN=SNX5 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
882.5198	881.5125	881.4317	91.7	84	90	1	---	K.EEFAKMK.Q
882.5198	881.5125	881.4317	91.7	84	90	1	---	K.EEFAKMK.Q
1151.6693	1150.6620	1150.5870	65.2	158	168	0	---	K.SADEVLFSGVK.E
1334.8121	1333.8048	1333.6799	93.7	340	350	0	---	K.NLIEMSELEIK.H + Oxidation (M)
1334.8121	1333.8049	1333.6799	93.7	340	350	0	---	K.NLIEMSELEIK.H + Oxidation (M)
1363.6659	1362.6586	1362.6627	-2.97	244	255	1	---	K.VESRVSSDEDLK.L
1439.6532	1438.6459	1438.7344	-61.47	91	102	0	---	K.QELEAEYLAIVFK.K
1593.7277	1592.7204	1592.8046	-52.82	280	293	1	---	K.ALIDYENSINKALDK.A
1617.9797	1616.9724	1616.8621	68.2	248	261	1	---	R.VSSDEDLKLTELLR.Y
1826.8557	1825.8484	1825.9170	-37.54	2	17	1	---	M.AAVPEVLQQEEDRSK.T
2015.1777	2014.1704	2014.0418	63.9	351	367	1	---	K.HARNNVSLQSCIDLFK.N
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 892.5198, 892.9673, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1417.6385, 1433.6392, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1597.6893, 1597.6893, 1673.7250, 1690.7394, 1732.0092, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2351.1042, 2753.2139, 3337.6887								

6. A0A4W2DFC3 Mass: 57472 Score: 42 Expect: 7.9 Matches: 10

Aspartyl-tRNA synthetase OS=Bos indicus x Bos taurus OX=30522 GN=DARS PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1201.5295	1200.5222	1200.6350	-93.95	111	121	0	---	K.ESIVDVEGVVR.K
1301.6583	1300.6510	1300.5250	96.9	255	264	0	---	K.QMCICADFEK.V
1301.6583	1300.6511	1300.5250	96.9	255	264	0	---	K.QMCICADFEK.V
1363.6659	1362.6586	1362.7256	-49.12	320	330	1	---	K.RFQTEIQTVVK.Q
1838.8295	1837.8222	1837.9185	-52.39	394	408	0	---	K.YPLAVRPFYTMPDPR.N + Oxidation (M)
1939.9556	1938.9483	1938.9912	-22.10	82	99	0	---	R.QQQFNQALVAVGDHASK.Q
2004.8711	2003.8638	2003.9636	-49.79	265	281	1	---	K.VFCIGPVFRAEDSNTHR.H
2210.9976	2209.9903	2210.1114	-54.77	123	141	1	---	K.VNQKIGSCTQQDVELHVQK.I
2321.0444	2320.0371	2320.2288	-82.59	432	451	1	---	R.IHDPQLVTERALHHGIDLEK.I

2351.1042 2350.0969 2350.0318 27.7 412 - 431 1 --- K.QSNSYDMFMFGEEILSGAQR.I + 2 Oxidation (M)
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1169.5049, 1179.5454, 1334.8121, 1334.8121, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2233.0032, 2283.0698, 2305.0757, 2753.2139, 3337.6887

7. [A0A4W2FGA1](#) Mass: 47047 Score: 42 Expect: 9.1 Matches: 11
Sorting nexin OS=Bos indicus x Bos taurus OX=30522 GN=SNX5 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
882.5198	881.5125	881.4317	91.7	119	- 125	1	---	K.EEFAKMK.Q
882.5198	881.5125	881.4317	91.7	119	- 125	1	---	K.EEFAKMK.Q
1151.6693	1150.6620	1150.5870	65.2	193	- 203	0	---	K.SADEVLVFGVKE
1334.8121	1333.8048	1333.6799	93.7	375	- 385	0	---	K.NLIEMSELEIK.H + Oxidation (M)
1334.8121	1333.8049	1333.6799	93.7	375	- 385	0	---	K.NLIEMSELEIK.H + Oxidation (M)
1363.6659	1362.6586	1362.6627	-2.97	279	- 290	1	---	K.VESRVSSDEDLK.L
1439.6532	1438.6459	1438.7344	-61.47	126	- 137	0	---	K.QELEAEYLAIVFK.K
1593.7277	1592.7204	1592.8046	-52.82	315	- 328	1	---	K.ALIDYENSINKALDK.A
1617.9797	1616.9724	1616.8621	68.2	283	- 296	1	---	R.VSSDEDLKLTELLR.Y
1826.8557	1825.8484	1825.9170	-37.54	2	- 17	1	---	M.AAVPEVLQQEEDRSK.L
2015.1777	2014.1704	2014.0418	63.9	386	- 402	1	---	K.HARNNVSLQSCIDLPK.N
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1417.6385, 1433.6392, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1597.6893, 1597.6893, 1673.7250, 1690.7394, 1732.0092, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2351.1042, 2753.2139, 3337.6887								

8. [Q3ZBM5](#) Mass: 47075 Score: 42 Expect: 9.1 Matches: 11
Sorting nexin-5 OS=Bos taurus OX=9913 GN=SNX5 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
882.5198	881.5125	881.4317	91.7	119	- 125	1	---	K.EEFAKMK.Q
882.5198	881.5125	881.4317	91.7	119	- 125	1	---	K.EEFAKMK.Q
1151.6693	1150.6620	1150.5870	65.2	193	- 203	0	---	K.SADEVLVFGVKE
1334.8121	1333.8048	1333.6799	93.7	375	- 385	0	---	K.NLIEMSELEIK.H + Oxidation (M)
1334.8121	1333.8049	1333.6799	93.7	375	- 385	0	---	K.NLIEMSELEIK.H + Oxidation (M)
1363.6659	1362.6586	1362.6627	-2.97	279	- 290	1	---	K.VESRVSSDEDLK.L
1439.6532	1438.6459	1438.7344	-61.47	126	- 137	0	---	K.QELEAEYLAIVFK.K
1593.7277	1592.7204	1592.8046	-52.82	315	- 328	1	---	K.ALIDYENSINKALDK.A
1617.9797	1616.9724	1616.8621	68.2	283	- 296	1	---	R.VSSDEDLKLTELLR.Y
1826.8557	1825.8484	1825.9170	-37.54	2	- 17	1	---	M.AAVPEVLQQEEDRSK.L
2015.1777	2014.1704	2014.0418	63.9	386	- 402	1	---	K.HARNNVSLQSCIDLPK.N
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1417.6385, 1433.6392, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1597.6893, 1597.6893, 1673.7250, 1690.7394, 1732.0092, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2351.1042, 2753.2139, 3337.6887								

9. [P46166](#) Mass: 4698 Score: 39 Expect: 17 Matches: 5
Beta-defensin 8 OS=Bos taurus OX=9913 GN=DEFB8 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4858	847.4785	847.4375	48.5	12	- 18	0	---	R.GFCVPIR.C
1051.6508	1050.6435	1050.5393	99.2	1	- 8	1	---	-VRNFVTCR.I
1051.6508	1050.6435	1050.5393	99.2	1	- 8	1	---	-VRNFVTCR.I
1179.5454	1178.5381	1178.5979	-50.68	3	- 11	1	---	R.NFVTCRINR.G
1690.7394	1689.7321	1689.8113	-46.86	25	- 38	1	---	R.QIGTCLGPQIKCCR.-
No match to: 842.4648, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1597.6893, 1597.6893, 1673.7250, 1690.7394, 1732.0092, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2351.1042, 2753.2139, 3337.6887								

10. [A0A3Q1MFP5](#) Mass: 136327 Score: 37 Expect: 26 Matches: 13
Phospholipase OS=Bos taurus OX=9913 GN=PLD1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
951.5755	950.5682	950.5371	32.7	806	- 812	1	---	K.IMPKPYR.C + Oxidation (M)
1051.6508	1050.6435	1050.5718	68.2	291	- 298	1	---	K.LLKMPMYR.N
1051.6508	1050.6435	1050.5718	68.3	291	- 298	1	---	K.LLKMPMYR.N
1131.6466	1130.6393	1130.6699	-27.06	1118	- 1127	0	---	R.DFISKPIIAK.E
1363.6659	1362.6586	1362.7758	-86.01	283	- 293	1	---	K.QLEDYLTKLLK.M
1448.8452	1447.8379	1447.7030	93.2	776	- 788	0	---	R.MPWHDIASAVHGK.A
1848.8546	1847.8473	1847.9278	-43.56	438	- 454	1	---	R.DHRFGSYAAIQGNTLAK.W
1873.8428	1872.8355	1872.8312	2.31	266	- 280	0	---	R.TSENMIQQEQFFSR.R
2233.0032	2231.9959	2232.1613	-74.07	813	- 831	1	---	R.CLSYPFLLPKSQTAAHELK.Y
2283.0698	2282.0625	2282.0294	14.5	1024	- 1044	0	---	R.DSEMAVIVQDTETVPSVMDGK.E + 2 Oxidation (M)
2351.1042	2350.0969	2350.0576	16.8	455	- 474	1	---	K.WYVNAKGYFEDVANAMEEAK.E + Oxidation (M)
2753.2139	2752.2066	2752.3259	-43.34	604	- 629	1	---	R.VVGGPSLGSLSLTAEETSMESLCLRDKN + Oxidation (M)
3337.6887	3336.6814	3336.6455	10.8	31	- 61	1	---	K.EGNASQACLQVHSLPHSTSLGGYSLMPR.Q
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1417.6385, 1433.6392, 1439.6532, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1838.8295, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2305.0757, 2321.0444								

11. [A0A4W2FRG9](#) Mass: 61477 Score: 36 Expect: 31 Matches: 10
Transmembrane protein 200C OS=Bos indicus x Bos taurus OX=30522 GN=TMEM200C PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
870.5018	869.4945	869.4620	37.4	412	- 419	1	---	R.GGARWAPR.E
1147.6801	1146.6728	1146.5629	95.8	100	- 111	0	---	R.VPSVTSSSGGNR.N
1151.6693	1150.6620	1150.5731	77.3	449	- 458	1	---	R.RSTSGLPDYR.A
1201.5295	1200.5222	1200.5887	-55.41	88	- 99	0	---	K.QPPPPGDSGSPR.V

1417.6385	1416.6312	1416.7070	-53.46	100	-	113	1	---	R.VPSVTSSSGGNRRN.S
1479.7141	1478.7068	1478.7266	-13.36	416	-	428	1	---	R.WAPREPEEPAAAR.T
1479.7141	1478.7068	1478.7266	-13.35	416	-	428	1	---	R.WAPREPEEPAAAR.T
1838.8295	1837.8222	1837.8932	-38.60	375	-	392	1	---	R.DGAAGAASRGWQRPPGER.G
2233.0032	2231.9959	2232.1360	-62.73	284	-	307	1	---	R.SGGGGGTPGAASPDLVSSPRRPR.E
2321.0444	2320.0371	2320.1005	-27.31	571	-	592	1	---	K.LYMISRSHASGVDEGELESAGI.-
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2283.0698, 2305.0757, 2351.1042, 2753.2139, 3337.6887									

12. [A0A1R3UGP4](#) Mass: 28249 Score: 36 Expect: 32 Matches: 7

Kallikrein G OS=Bos taurus OX=9913 GN=KLNG PE=3 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
848.4858	847.4785	847.4473	36.8	109	-	115	0	---	R.NDIMLVK.M + Oxidation (M)
951.5755	950.5682	950.4862	86.3	239	-	245	0	---	K.YVDWIQK.T
1179.5454	1178.5381	1178.6482	-93.36	229	-	238	1	---	K.KPGVYTKVCK.Y
2015.1777	2014.1704	2013.9908	89.2	88	-	105	1	---	R.TATKSFPHDPFNNSLPNK.D
2283.0698	2282.0625	2282.0975	-15.31	68	-	87	1	---	R.YVVLHAHSLGRQDGCQTR.T
2305.0757	2304.0684	2304.1793	-48.10	1	-	21	0	---	-.MMTLQLIMFALVTGHVGGETR.I
2321.0444	2320.0371	2320.1742	-59.07	1	-	21	0	---	-.MMTLQLIMFALVTGHVGGETR.I + Oxidation (M)
No match to: 842.4648, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2351.1042, 2753.2139, 3337.6887									

13. [A0A4W2F0S3](#) Mass: 54184 Score: 36 Expect: 34 Matches: 9

Aspartyl-tRNA synthetase OS=Bos indicus x Bos taurus OX=30522 GN=DARS PE=3 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1201.5295	1200.5222	1200.6350	-93.95	111	-	121	0	---	K.ESIVDVEGVVR.K
1301.6583	1300.6510	1300.5250	96.9	255	-	264	0	---	K.QMCICADFEK.V
1301.6583	1300.6511	1300.5250	96.9	255	-	264	0	---	K.QMCICADFEK.V
1363.6659	1362.6586	1362.7256	-49.12	320	-	330	1	---	K.RFQTEIQTVVK.Q
1939.9556	1938.9483	1938.9912	-22.10	82	-	99	0	---	R.QQQFNQALVAVGDHASK.Q
2004.8711	2003.8638	2003.9636	-49.79	265	-	281	1	---	K.VFCIGPVFRAEDSNTHR.H
2210.9976	2209.9903	2210.1114	-54.77	123	-	141	1	---	K.VNQKIGSCTQQDVELHVQK.I
2321.0444	2320.0371	2320.2288	-82.59	405	-	424	1	---	R.IHDPQLVTERALHHGIDLEK.I
2351.1042	2350.0969	2350.0318	27.7	385	-	404	1	---	K.QSNSYDMFMRGEEILSGAQR.I + 2 Oxidation (M)
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1334.8121, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2233.0032, 2283.0698, 2305.0757, 2753.2139, 3337.6887									

14. [A0A4W2HLP0](#) Mass: 45410 Score: 36 Expect: 36 Matches: 8

Secernin 1 OS=Bos indicus x Bos taurus OX=30522 GN=SCRNL PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1301.6583	1300.6510	1300.6524	-1.04	320	-	329	1	---	K.EPRFQEKPD.R
1301.6583	1300.6511	1300.6524	-1.01	320	-	329	1	---	K.EPRFQEKPD.R
1417.6385	1416.6312	1416.7296	-69.44	2	-	13	0	---	M.LSLLPHDLCHGR.S
1439.6532	1438.6459	1438.7105	-44.91	331	-	341	1	---	R.HELKKAHEWAR.A
2004.8711	2003.8638	2004.0197	-77.80	231	-	247	1	---	K.QEESITVQTMIDVLRDK.A
2210.9976	2209.9903	2210.1261	-61.45	32	-	50	0	---	R.VLGSLMLMCTYISINQVPR.T + Oxidation (M)
2283.0698	2282.0625	2282.1940	-57.60	85	-	105	1	---	R.EPAATEALLGMDLVRLGLER.G
2351.1042	2350.0969	2350.2323	-57.61	31	-	50	1	---	R.RVLGSLMLMCTYISINQVPR.T
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1334.8121, 1334.8121, 1363.6659, 1433.6392, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2233.0032, 2305.0757, 2321.0444, 2753.2139, 3337.6887									

15. [A0A3QLXT8](#) Mass: 59645 Score: 35 Expect: 41 Matches: 9

Aspartate--tRNA ligase, cytoplasmic OS=Bos taurus OX=9913 GN=DARS1 PE=3 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1201.5295	1200.5222	1200.6350	-93.95	114	-	124	0	---	K.ESIVDVEGVVR.K
1301.6583	1300.6510	1300.5250	96.9	258	-	267	0	---	K.QMCICADFEK.V
1301.6583	1300.6511	1300.5250	96.9	258	-	267	0	---	K.QMCICADFEK.V
1363.6659	1362.6586	1362.7256	-49.12	323	-	333	1	---	K.RFQTEIQTVVK.Q
1838.8295	1837.8222	1837.9185	-52.39	397	-	411	0	---	K.YPLAVRPFFYTMPDPR.N + Oxidation (M)
1939.9556	1938.9483	1938.9912	-22.10	85	-	102	0	---	R.QQQFNQALVAVGDHASK.Q
2004.8711	2003.8638	2003.9636	-49.79	268	-	284	1	---	K.VFCIGPVFRAEDSNTHR.H
2210.9976	2209.9903	2210.1114	-54.77	126	-	144	1	---	K.VNQKIGSCTQQDVELHVQK.I
2351.1042	2350.0969	2350.0318	27.7	415	-	434	1	---	K.QSNSYDMFMRGEEILSGAQR.I + 2 Oxidation (M)
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1334.8121, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2753.2139, 3337.6887									

16. [A0A4W2C922](#) Mass: 39936 Score: 35 Expect: 42 Matches: 9

N(alpha)-acetyltransferase 40, NatD catalytic subunit OS=Bos indicus x Bos taurus OX=30522 GN=NAA40 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
853.4749	852.4676	852.4779	-12.08	279	-	285	0	---	K.VMLTVFK.H + Oxidation (M)
1479.7141	1478.7068	1478.6857	14.3	124	-	136	1	---	R.LEERAAMDAVCAK.V + Oxidation (M)
1479.7141	1478.7068	1478.6857	14.3	124	-	136	1	---	R.LEERAAMDAVCAK.V + Oxidation (M)
1567.6675	1566.6602	1566.7460	-54.76	156	-	168	1	---	K.YDRNGLNVSIECK.R
1597.6893	1596.6820	1596.8089	-79.47	72	-	85	1	---	R.GACAVRGRRPPLQCR.R

1597.6893 1596.6821 1596.8089 -79.46 72 - 85 1 --- R.GACAVRGRPPQLQCR.R
1848.8546 1847.8473 1847.9305 -45.03 170 - 186 0 --- R.VSGLEPATVDWAFDLTK.T
2004.8711 2003.8638 2004.0316 -83.74 169 - 186 1 --- K.RVSGLEPATVDWAFDLTK.T
2351.1042 2350.0969 2350.1528 -23.79 1 - 21 1 --- -.MAIDTAWREGGPPWLTSFLAR.H + Oxidation (M)
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1593.7277, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1838.8295, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2753.2139, 3337.6887

17. [A0A4W2ETY0](#) Mass: 130578 Score: 34 Expect: 50 Matches: 12

Phospholipase OS=Bos indicus x Bos taurus OX=30522 GN=PLD1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
951.5755	950.5682	950.5371	32.7	806	-	812	1	K.IMKPKYR.C + Oxidation (M)
1051.6508	1050.6435	1050.5718	68.2	291	-	298	1	K.LLKMPMYR.N
1051.6508	1050.6435	1050.5718	68.3	291	-	298	1	K.LLKMPMYR.N
1363.6659	1362.6586	1362.7758	-86.01	283	-	293	1	K.QLEDYLTLLK.LM
1448.8452	1447.8379	1447.7030	93.2	776	-	788	0	R.MPWHDIASAVHGK.A
1848.8546	1847.8473	1847.9278	-43.56	438	-	454	1	R.DHRFGSYAAIQGNLAK.W
1873.8428	1872.8355	1872.8312	2.31	266	-	280	0	R.TSENMIQQEQFFSR.R
2233.0032	2231.9959	2232.1613	-74.07	813	-	831	1	R.CLSYPFLLPKSQTTAHELK.Y
2283.0698	2282.0625	2282.0294	14.5	1024	-	1044	0	R.DSEMAVIVQDTETVPSVMDGK.E + 2 Oxidation (M)
2351.1042	2350.0969	2350.0576	16.8	455	-	474	1	K.WYVNAKGYFEDVANAMEEAK.E + Oxidation (M)
2753.2139	2752.2066	2752.3259	-43.34	604	-	629	1	R.VVGGPSLGS�TAEETTESMESLCLRDK.N + Oxidation (M)
3337.6887	3336.6814	3336.6455	10.8	31	-	61	1	K.EGNASQACLRQVHSLPHSTALGGYSLMPR.Q
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1417.6385, 1433.6392, 1439.6532, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1838.8295, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2305.0757, 2321.0444								

18. [F1MTX7](#) Mass: 57472 Score: 34 Expect: 51 Matches: 9

Aspartate--tRNA ligase, cytoplasmic OS=Bos taurus OX=9913 GN=DARS1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1201.5295	1200.5222	1200.6350	-93.95	111	-	121	0	K.ESIVDVEGVVR.K
1301.6583	1300.6510	1300.5250	96.9	255	-	264	0	K.QMCICADFEK.V
1301.6583	1300.6511	1300.5250	96.9	255	-	264	0	K.QMCICADFEK.V
1363.6659	1362.6586	1362.7256	-49.12	320	-	330	1	K.RFQTEIQTVVK.Q
1838.8295	1837.8222	1837.9185	-52.39	394	-	408	0	K.YPLAVRPFYTMPDPR.N + Oxidation (M)
1939.9556	1938.9483	1938.9912	-22.10	82	-	99	0	R.QQQFNQVQALVAVGDHASK.Q
2004.8711	2003.8638	2003.9636	-49.79	265	-	281	1	K.VFCIGPVFRAEDSNTHR.H
2210.9976	2209.9903	2210.1114	-54.77	123	-	141	1	K.VNQKIGSCSTQQDVELHVQK.I
2351.1042	2350.0969	2350.0318	27.7	412	-	431	1	K.QSNSYDMFMERGEIILSGAQR.I + 2 Oxidation (M)
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2753.2139, 3337.6887								

19. [A0A4W2H2Q0](#) Mass: 21512 Score: 34 Expect: 57 Matches: 6

Methionine sulfoxide reductase A OS=Bos indicus x Bos taurus OX=30522 GN=MSRA PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.4961	849.4888	849.4491	46.8	1	-	7	1	-.MLSATRR.A + Oxidation (M)
868.5096	867.5023	867.4563	53.1	71	-	78	0	K.TGHAEEVVR.V
1826.8557	1825.8484	1825.9356	-47.75	21	-	38	1	R.MGDSAAKIVSPQALPGR.K
2150.9111	2149.9038	2150.0137	-51.08	173	-	193	1	K.DPDGYCGLGGTGVSCPLGIKK.-
2150.9111	2149.9039	2150.0137	-51.07	173	-	193	1	K.DPDGYCGLGGTGVSCPLGIKK.-
2321.0444	2320.0371	2320.1699	-57.24	135	-	154	1	K.EDYQKVLSEHGFLITTDIR.E
No match to: 842.4648, 848.4858, 850.0170, 853.4749, 861.0225, 864.5088, 865.9901, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2351.1042, 2753.2139, 3337.6887								

20. [E1BKP4](#) Mass: 84228 Score: 33 Expect: 64 Matches: 11

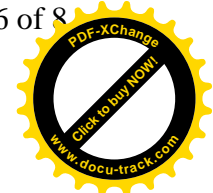
TANK binding kinase 1 OS=Bos taurus OX=9913 GN=TBK1 PE=4 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.4961	849.4888	849.4345	64.0	155	-	162	0	K.LTDFGAAR.E
864.5088	863.5015	863.4753	30.4	31	-	38	0	K.TGDLFAIK.V
927.4315	926.4242	926.4531	-31.20	230	-	236	1	R.NKEVMYK.I + Oxidation (M)
1151.6693	1150.6620	1150.6135	42.2	588	-	596	1	K.QKLYYHATK.A
1169.5049	1168.4976	1168.5547	-48.82	714	-	724	0	R.FGSLTMDGGLR.N + Oxidation (M)
1201.5295	1200.5222	1200.4969	21.1	406	-	416	0	R.YDLGDGASMAK.A + Oxidation (M)
1593.7277	1592.7204	1592.8596	-87.39	461	-	473	1	K.KTEVVITLDFCIR.N
1690.7394	1689.7321	1689.7781	-27.19	402	-	416	1	K.VHPRYDLGDGASMAK.A + Oxidation (M)
1848.8546	1847.8473	1847.9788	-71.15	128	-	143	1	R.ENGIVHRDIKPGNIMR.V
1901.1566	1900.1493	1900.0921	30.1	385	-	401	1	R.EPLSTIGLIYEKKSILPK.V
2305.0757	2304.0684	2304.2172	-64.58	505	-	525	1	K.LLRLLSSQGTIETSLQDIESK.L
No match to: 842.4648, 848.4858, 850.0170, 853.4749, 861.0225, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1165.6774, 1165.6774, 1179.5454, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1732.0092, 1826.8557, 1838.8295, 1873.8428, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2321.0444, 2351.1042, 2753.2139, 3337.6887								

21. [A0A4W2CVJ0](#) Mass: 84228 Score: 33 Expect: 64 Matches: 11

TANK binding kinase 1 OS=Bos indicus x Bos taurus OX=30522 GN=TBK1 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.4961	849.4888	849.4345	64.0	155	-	162	0	K.LTDFGAAR.E
864.5088	863.5015	863.4753	30.4	31	-	38	0	K.TGDLFAIK.V
927.4315	926.4242	926.4531	-31.20	230	-	236	1	R.NKEVMYK.I + Oxidation (M)



1151.6693 1150.6620 1150.6135 42.2 588 - 596 1 --- K.QKLYYHATK.A
 1169.5049 1168.4976 1168.5547 -48.82 714 - 724 0 --- R.FGSLTMDGGLR.N + Oxidation (M)
 1201.5295 1200.5222 1200.4969 21.1 406 - 416 0 --- R.YDLGDGDSMAK.A + Oxidation (M)
 1593.7277 1592.7204 1592.8596 -87.39 461 - 473 1 --- K.KTEVVITLDFCIR.N
 1690.7394 1689.7321 1689.7781 -27.19 402 - 416 1 --- K.VHPRYDLGDGDSMAK.A + Oxidation (M)
 1848.8546 1847.8473 1847.9788 -71.15 128 - 143 1 --- R.ENGIVHRDIKPGNIMR.V
 1901.1566 1900.1493 1900.0921 30.1 385 - 401 1 --- R.EPLSTIGLIYEKISLKP.V
 2305.0757 2304.0684 2304.2172 -64.58 505 - 525 1 --- K.LLRSLSSQGTIETSLQDIESK.L
No match to: 842.4648, 848.4858, 850.0170, 853.4749, 861.0225, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1165.6774, 1165.6774, 1179.5454, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1732.0092, 1826.8557, 1838.8295, 1873.8428, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2321.0444, 2351.1042, 2753.2139, 3337.6887

22. A0A4W2HQ46 Mass: 39881 Score: 33 Expect: 71 Matches: 9

N(alpha)-acetyltransferase 40, NatD catalytic subunit OS=Bos indicus x Bos taurus OX=30522 GN=NAA40 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.4749	852.4676	852.4779	-12.08	279	285	0	---	K.VMLTVFK.H + Oxidation (M)
1479.7141	1478.7068	1478.6857	14.3	124	136	1	---	R.LEERAAMDAVCAK.V + Oxidation (M)
1479.7141	1478.7068	1478.6857	14.3	124	136	1	---	R.LEERAAMDAVCAK.V + Oxidation (M)
1567.6675	1566.6602	1566.7460	-54.76	156	168	1	---	K.YDRNGLNLSIECK.R
1597.6893	1596.6820	1596.8089	-79.47	72	85	1	---	R.GACAVRGRPLQCR.R
1597.6893	1596.6821	1596.8089	-79.46	72	85	1	---	R.GACAVRGRPLQCR.R
1848.8546	1847.8473	1847.9305	-45.03	170	186	0	---	R.VSGLEPATVDWAFDLTK.T
2004.8711	2003.8638	2004.0316	-83.74	169	186	1	---	K.RVSGLEPATVDWAFDLTK.T
2351.1042	2350.0969	2350.1627	-28.00	170	190	1	---	R.VSGLEPATVDWAFDLTKTNMR.T
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1593.7277, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1838.8295, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2753.2139, 3337.6887								

23. A5PKK1 Mass: 27850 Score: 33 Expect: 72 Matches: 7

N(alpha)-acetyltransferase 40, NatD catalytic subunit OS=Bos taurus OX=9913 GN=NAA40 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.4749	852.4676	852.4779	-12.08	171	177	0	---	K.VMLTVFK.H + Oxidation (M)
1479.7141	1478.7068	1478.6857	14.3	16	28	1	---	R.LEERAAMDAVCAK.V + Oxidation (M)
1479.7141	1478.7068	1478.6857	14.3	16	28	1	---	R.LEERAAMDAVCAK.V + Oxidation (M)
1567.6675	1566.6602	1566.7460	-54.76	48	60	1	---	K.YDRNGLNLSIECK.R
1848.8546	1847.8473	1847.9305	-45.03	62	78	0	---	R.VSGLEPATVDWAFDLTK.T
2004.8711	2003.8638	2004.0316	-83.74	61	78	1	---	K.RVSGLEPATVDWAFDLTK.T
2351.1042	2350.0969	2350.1627	-28.00	62	82	1	---	R.VSGLEPATVDWAFDLTKTNMR.T
No match to: 842.4648, 848.4858, 850.0170, 850.4961, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1838.8295, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2753.2139, 3337.6887								

24. A0A3Q1M909 Mass: 23483 Score: 32 Expect: 81 Matches: 6

Mitochondrial peptide methionine sulfoxide reductase OS=Bos taurus OX=9913 GN=MSRA PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.4961	849.4888	849.4491	46.8	1	7	1	---	-MLSATRR.A + Oxidation (M)
868.5096	867.5023	867.4563	53.1	88	95	0	---	K.TGHAEEVVR.V
1826.8557	1825.8484	1825.9356	-47.75	21	38	1	---	R.MGDSAAKIVSQEALPGR.K
2150.9111	2149.9038	2150.0137	-51.08	190	210	1	---	K.DPDGYCGLGGTGVSCPLGIKK.-
2150.9111	2149.9039	2150.0137	-51.07	190	210	1	---	K.DPDGYCGLGGTGVSCPLGIKK.-
2321.0444	2320.0371	2320.1699	-57.24	152	171	1	---	K.EDYQKVLSEHGFLITTDIR.E
No match to: 842.4648, 848.4858, 850.0170, 853.4749, 861.0225, 864.5088, 865.9901, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2351.1042, 2753.2139, 3337.6887								

25. A0A4W2HSU8 Mass: 23483 Score: 32 Expect: 81 Matches: 6

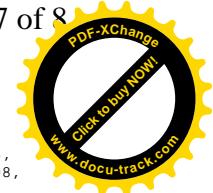
Methionine sulfoxide reductase A OS=Bos indicus x Bos taurus OX=30522 GN=MSRA PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.4961	849.4888	849.4491	46.8	1	7	1	---	-MLSATRR.A + Oxidation (M)
868.5096	867.5023	867.4563	53.1	88	95	0	---	K.TGHAEEVVR.V
1826.8557	1825.8484	1825.9356	-47.75	21	38	1	---	R.MGDSAAKIVSQEALPGR.K
2150.9111	2149.9038	2150.0137	-51.08	190	210	1	---	K.DPDGYCGLGGTGVSCPLGIKK.-
2150.9111	2149.9039	2150.0137	-51.07	190	210	1	---	K.DPDGYCGLGGTGVSCPLGIKK.-
2321.0444	2320.0371	2320.1699	-57.24	152	171	1	---	K.EDYQKVLSEHGFLITTDIR.E
No match to: 842.4648, 848.4858, 850.0170, 853.4749, 861.0225, 864.5088, 865.9901, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2351.1042, 2753.2139, 3337.6887								

26. A0A3Q1LVV9 Mass: 13591 Score: 32 Expect: 85 Matches: 6

RNA_pol_L_2 domain-containing protein OS=Bos taurus OX=9913 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1033.6478	1032.6405	1032.6305	9.74	57	64	1	---	K.VRRPLQHK.T
1045.5127	1044.5054	1044.5426	-35.62	110	119	0	---	K.MSGGLHLALF.-
1334.8121	1333.8048	1333.7466	43.6	79	90	1	---	R.RLPPVPSQTSR.N
1334.8121	1333.8049	1333.7466	43.7	79	90	1	---	R.RLPPVPSQTSR.N
1363.6659	1362.6586	1362.7408	-60.31	47	58	1	---	K.APQVQFAGYKVR.R
1690.7394	1689.7321	1689.8798	-87.39	32	46	0	---	K.ENHTLGNISHSQLLK.A



No match to: 842.4648, 848.4858, 850.0170, 850.4961, 853.4749, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1151.6693, 1165.6774, 1165.6774, 1169.5049, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1417.6385, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1593.7277, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1732.0092, 1826.8557, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2351.1042, 2753.2139, 3337.6887

27. [A0A4W2E767](#) Mass: 68716 Score: 32 Expect: 85 Matches: 9

Acyl-CoA dehydrogenase very long chain OS=Bos indicus x Bos taurus OX=30522 GN=ACADVL PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4858	847.4785	847.5167	-45.09	166	-	173	0	K.GILLFGTK.A
853.4749	852.4676	852.4202	55.6	337	-	344	0	K.AVDHAANR.T
870.5018	869.4945	869.4971	-2.93	82	-	89	0	K.ELVGPVTR.F
1151.6693	1150.6620	1150.5540	93.9	106	-	115	0	R.VEETTMQGLK.E + Oxidation (M)
1169.5049	1168.4976	1168.5400	-36.30	90	-	99	0	R.FFEEVNDAAK.N
1417.6385	1416.6312	1416.7460	-81.04	243	-	256	1	K.TPVTDTATGAVKEK.I
1593.7277	1592.7204	1592.8675	-92.31	435	-	447	1	R.IFRIFEGTNDILR.L
1848.8546	1847.8473	1847.7926	29.6	407	-	422	0	K.VTDECIQIMGGMGFMK.E + 2 Oxidation (M)
1873.8428	1872.8355	1872.9040	-36.56	278	-	294	1	K.MGIKASNTAEVYFDGVR.V + Oxidation (M)

No match to: 842.4648, 850.0170, 850.4961, 861.0225, 864.5088, 865.9901, 868.5096, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1165.6774, 1165.6774, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1838.8295, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2351.1042, 2753.2139, 3337.6887

28. [A0A4W2GRX4](#) Mass: 68688 Score: 32 Expect: 85 Matches: 9

Acyl-CoA dehydrogenase very long chain OS=Bos indicus x Bos taurus OX=30522 GN=ACADVL PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4858	847.4785	847.5167	-45.09	166	-	173	0	K.GILLFGTK.A
853.4749	852.4676	852.4202	55.6	337	-	344	0	K.AVDHAANR.T
870.5018	869.4945	869.4971	-2.93	82	-	89	0	K.ELVGPVTR.F
1151.6693	1150.6620	1150.5540	93.9	106	-	115	0	R.VEETTMQGLK.E + Oxidation (M)
1169.5049	1168.4976	1168.5400	-36.30	90	-	99	0	R.FFEEVNDAAK.N
1417.6385	1416.6312	1416.7460	-81.04	243	-	256	1	K.TPVTDTATGAVKEK.I
1593.7277	1592.7204	1592.8675	-92.31	435	-	447	1	R.IFRIFEGTNDILR.L
1848.8546	1847.8473	1847.7926	29.6	407	-	422	0	K.VTDECIQIMGGMGFMK.E + 2 Oxidation (M)
1873.8428	1872.8355	1872.9040	-36.56	278	-	294	1	K.MGIKASNTAEVYFDGVR.V + Oxidation (M)

No match to: 842.4648, 850.0170, 850.4961, 861.0225, 864.5088, 865.9901, 868.5096, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1033.6478, 1045.5127, 1051.6508, 1051.6508, 1131.6466, 1147.6801, 1165.6774, 1165.6774, 1179.5454, 1201.5295, 1301.6583, 1301.6583, 1334.8121, 1334.8121, 1363.6659, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1567.6675, 1597.6893, 1597.6893, 1617.9797, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1838.8295, 1901.1566, 1939.9556, 1993.8798, 2004.8711, 2015.1777, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2351.1042, 2753.2139, 3337.6887

29. [A0A3Q1LG54](#) Mass: 89438 Score: 32 Expect: 91 Matches: 14

Protein phosphatase 1 regulatory subunit 21 OS=Bos taurus OX=9913 GN=PPP1R21 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4648	841.4575	841.5134	-66.34	70	-	76	1	R.NLQLAKR.V
853.4749	852.4676	852.4453	26.1	139	-	145	0	K.HVEAELR.S
1033.6478	1032.6405	1032.5451	92.4	187	-	195	1	K.SQTLEKEAK.E
1131.6466	1130.6393	1130.5931	40.9	763	-	771	1	K.QREEIDTLK.M
1147.6801	1146.6728	1146.6357	32.4	553	-	562	1	R.RVLLSSTESR.E
1165.6774	1164.6701	1164.5696	86.3	713	-	722	1	K.SKEALTEEMK.V
1165.6774	1164.6701	1164.5696	86.3	713	-	722	1	K.SKEALTEEMK.V
1301.6583	1300.6510	1300.6623	-8.65	34	-	46	0	K.GVVDEQANSALK.E
1301.6583	1300.6511	1300.6623	-8.63	34	-	46	0	K.GVVDEQANSALK.E
1417.6385	1416.6312	1416.7395	-76.41	199	-	209	1	R.LRTEECQLQLK.N
1567.6675	1566.6602	1566.7613	-64.50	693	-	705	1	K.SVHFYAEACRLSK.R
1617.9797	1616.9724	1616.8734	61.3	608	-	623	1	K.LKSTSSGQVVGVAQEK.A
2004.8711	2003.8638	2003.9332	-34.64	508	-	525	0	K.TGSGFISPLSAECMLQYK.K + Oxidation (M)
2015.1777	2014.1704	2014.0346	67.4	343	-	358	1	K.LKTFSEHLTSYICFLR.K

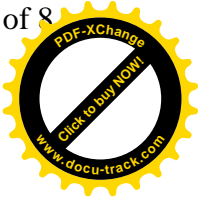
No match to: 848.4858, 850.0170, 850.4961, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1045.5127, 1051.6508, 1051.6508, 1151.6693, 1169.5049, 1179.5454, 1201.5295, 1334.8121, 1334.8121, 1363.6659, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1593.7277, 1597.6893, 1597.6893, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2351.1042, 2753.2139, 3337.6887

30. [A5D7H6](#) Mass: 88869 Score: 32 Expect: 95 Matches: 14

KLRAQ1 protein OS=Bos taurus OX=9913 GN=PPP1R21 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4648	841.4575	841.5134	-66.34	66	-	72	1	R.NLQLAKR.V
853.4749	852.4676	852.4453	26.1	135	-	141	0	K.HVEAELR.S
1033.6478	1032.6405	1032.5451	92.4	183	-	191	1	K.SQTLEKEAK.E
1131.6466	1130.6393	1130.5931	40.9	759	-	767	1	K.QREEIDTLK.M
1147.6801	1146.6728	1146.6357	32.4	549	-	558	1	R.RVLLSSTESR.E
1165.6774	1164.6701	1164.5696	86.3	709	-	718	1	K.SKEALTEEMK.V
1165.6774	1164.6701	1164.5696	86.3	709	-	718	1	K.SKEALTEEMK.V
1301.6583	1300.6510	1300.6623	-8.65	30	-	42	0	K.GVVDEQANSALK.E
1301.6583	1300.6511	1300.6623	-8.63	30	-	42	0	K.GVVDEQANSALK.E
1417.6385	1416.6312	1416.7395	-76.41	195	-	205	1	R.LRTEECQLQLK.N
1567.6675	1566.6602	1566.7613	-64.50	689	-	701	1	K.SVHFYAEACRLSK.R
1617.9797	1616.9724	1616.8734	61.3	604	-	619	1	K.LKSTSSGQVVGVAQEK.A
2004.8711	2003.8638	2003.9332	-34.64	504	-	521	0	K.TGSGFISPLSAECMLQYK.K + Oxidation (M)
2015.1777	2014.1704	2014.0346	67.4	339	-	354	1	K.LKTFSEHLTSYICFLR.K

No match to: 848.4858, 850.0170, 850.4961, 861.0225, 864.5088, 865.9901, 868.5096, 870.5018, 876.9943, 881.9693, 882.5198, 882.5198, 892.9673, 892.9674, 908.9358, 927.4315, 951.5755, 1017.6181, 1017.6181, 1019.6312, 1045.5127, 1051.6508, 1051.6508, 1151.6693, 1169.5049, 1179.5454, 1201.5295, 1334.8121, 1334.8121, 1363.6659, 1433.6392, 1439.6532, 1448.8452, 1475.6703, 1479.7141, 1479.7141, 1593.7277, 1597.6893, 1597.6893, 1673.7250, 1690.7394, 1732.0092, 1826.8557, 1838.8295, 1848.8546, 1873.8428, 1901.1566, 1939.9556, 1993.8798, 2093.9248, 2111.9341, 2111.9341, 2150.9111, 2150.9111, 2210.9976, 2233.0032, 2283.0698, 2305.0757, 2321.0444, 2351.1042, 2753.2139, 3337.6887



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 : ± 100 ppm
Fragment Mass Tolerance : ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF

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