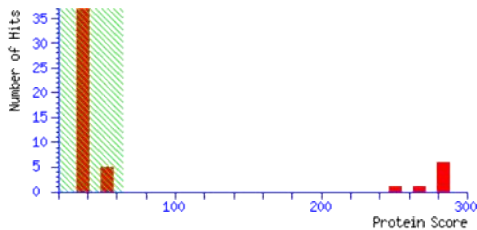


MATRIX SCIENCE Mascot Search Results

User :  
Email :  
Search title : BAEDW\2020\_3\_5\2020\_3\_5\MSMS 14\N20  
Database : Uniprot\_bovine bovine\_20200316 (134392 sequences; 76244912 residues)  
Timestamp : 31 Mar 2020 at 01:09:00 GMT  
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.  
Top Score : 283 for V6F7X3, Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=3 SV=1

Mascot Score Histogram

Protein score is  $-10 \cdot \log(P)$ , 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 ion scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

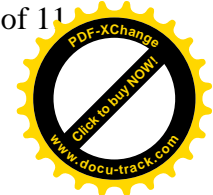
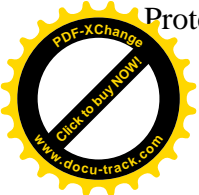
Format As Protein Summary (deprecated) [Help](#)  
Significance threshold  $p < 0.05$  Max. number of hits 30  
Preferred taxonomy All entries  
Re-Search All Search Unmatched

Index

Accession	Mass	Score	Description
1. <a href="#">V6F7X3</a>	42963	283	Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=3 SV=1
2. <a href="#">A0A4W2CCP9</a>	42963	283	Apolipoprotein A4 OS=Bos indicus x Bos taurus OX=30522 GN=APOA4 PE=3 SV=1
3. <a href="#">A0A3Q1M3N0</a>	43165	283	Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=3 SV=1
4. <a href="#">A0A3Q1MZJ9</a>	45782	282	Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=3 SV=1
5. <a href="#">A0A4W2GRG6</a>	43654	281	Apolipoprotein A4 OS=Bos indicus x Bos taurus OX=30522 GN=APOA4 PE=3 SV=1
6. <a href="#">A0A4W2GSL9</a>	46566	279	Apolipoprotein A4 OS=Bos indicus x Bos taurus OX=30522 GN=APOA4 PE=3 SV=1
7. <a href="#">F1N3Q7</a>	52487	271	Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=3 SV=2
8. <a href="#">Q32PJ2</a>	42991	248	Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=2 SV=1
9. <a href="#">F1N6W4</a>	145999	48	DENN domain containing 5A OS=Bos taurus OX=9913 GN=DENN5A PE=4 SV=3
10. <a href="#">A0A3Q1MUN3</a>	148571	48	DENN domain containing 5A OS=Bos taurus OX=9913 GN=DENN5A PE=4 SV=1
11. <a href="#">A0A4W2DBN8</a>	47465	46	Reverse transcriptase domain-containing protein OS=Bos indicus x Bos taurus OX=30522 PE=4 SV=1
12. <a href="#">A0A4W2FJP8</a>	473166	45	Dynein axonemal heavy chain 6 OS=Bos indicus x Bos taurus OX=30522 GN=DNAH6 PE=4 SV=1
13. <a href="#">A0A4W2HIT4</a>	478985	45	Dynein axonemal heavy chain 6 OS=Bos indicus x Bos taurus OX=30522 GN=DNAH6 PE=4 SV=1
14. <a href="#">A0A3Q1LWT9</a>	14058	44	Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1
15. <a href="#">A0A4W2DIE4</a>	14058	44	Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 PE=4 SV=1
16. <a href="#">A0A4W2EFU9</a>	24150	44	Hypoxanthine phosphoribosyltransferase OS=Bos indicus x Bos taurus OX=30522 PE=3 SV=1
17. <a href="#">E1BA06</a>	24150	44	Hypoxanthine phosphoribosyltransferase OS=Bos taurus OX=9913 PE=3 SV=2
18. <a href="#">A0A4W2HDP5</a>	60337	43	Zinc finger protein 382 OS=Bos indicus x Bos taurus OX=30522 GN=ZNF382 PE=4 SV=1
19. <a href="#">A0A4W2FFL4</a>	343058	43	Kalirin RhoGEF kinase OS=Bos indicus x Bos taurus OX=30522 GN=KALRN PE=4 SV=1
20. <a href="#">A0A4W2EN51</a>	85445	43	Cyclin and CBS domain divalent metal cation transport mediator 4 OS=Bos indicus x Bos taurus OX=30522 GN=
21. <a href="#">A0A4W2F426</a>	60709	42	Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 PE=4 SV=1
22. <a href="#">A0A4W2HZ94</a>	170798	42	Lysine demethylase 2B OS=Bos indicus x Bos taurus OX=30522 GN=KDM2B PE=4 SV=1
23. <a href="#">A0A3Q1MCG0</a>	472745	42	Dynein axonemal heavy chain 6 OS=Bos taurus OX=9913 GN=DNAH6 PE=4 SV=1
24. <a href="#">A0A4W2GJX2</a>	108528	40	Nebulette OS=Bos indicus x Bos taurus OX=30522 GN=NEBL PE=4 SV=1
25. <a href="#">A0A4W2EA29</a>	473215	40	Dynein axonemal heavy chain 6 OS=Bos indicus x Bos taurus OX=30522 GN=DNAH6 PE=4 SV=1
26. <a href="#">A0A4W2CJR0</a>	108457	40	Nebulette OS=Bos indicus x Bos taurus OX=30522 GN=NEBL PE=4 SV=1
27. <a href="#">A0A3Q1MXR2</a>	108457	40	Nebulette OS=Bos taurus OX=9913 GN=NEBL PE=4 SV=1
28. <a href="#">A0A4W2GHX5</a>	112926	40	Nebulette OS=Bos indicus x Bos taurus OX=30522 GN=NEBL PE=4 SV=1
29. <a href="#">A0A4W2CVR3</a>	479034	40	Dynein axonemal heavy chain 6 OS=Bos indicus x Bos taurus OX=30522 GN=DNAH6 PE=4 SV=1
30. <a href="#">A0A4W2I420</a>	167724	40	Lysine demethylase 2B OS=Bos indicus x Bos taurus OX=30522 GN=KDM2B PE=4 SV=1

Results List

1.	<a href="#">V6F7X3</a>	Mass: 42963	Score: 283	Expect: 6.7e-024	Matches: 24			
Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=3 SV=1								
Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Ions	Peptide
862.4257	861.4184	861.4556	-43.12	288	295	0	---	K.SLAELSSR.L
977.4595	976.4522	976.4978	-46.64	156	163	0	---	R.QLTPYAER.M
977.4595	976.4523	976.4978	-46.61	156	163	0	15	R.QLTPYAER.M
1047.4978	1046.4905	1046.5396	-46.92	135	143	0	---	R.LGPYAEELR.T
1047.4978	1046.4905	1046.5396	-46.92	135	143	0	20	R.LGPYAEELR.T
1133.5562	1132.5489	1132.5989	-44.10	155	163	1	---	R.RQLTPYAER.M
1149.5057	1148.4984	1148.5462	-41.60	296	304	0	---	R.LDQQVEDFR.R
1149.5057	1148.4985	1148.5462	-41.57	296	304	0	20	R.LDQQVEDFR.R
1174.5699	1173.5626	1173.6176	-46.83	317	326	0	---	K.AMVQQLDTLR.Q
1174.5700	1173.5627	1173.6176	-46.79	317	326	0	50	K.AMVQQLDTLR.Q
1190.5620	1189.5547	1189.6125	-48.57	317	326	0	---	K.AMVQQLDTLR.Q + Oxidation (M)
1212.5294	1211.5221	1211.5823	-49.63	306	316	0	---	R.TVGPYGETFNK.A
1277.6251	1276.6178	1276.6663	-37.98	201	211	0	---	R.LTPYADQLQTK.I
1287.6068	1286.5995	1286.6579	-45.36	144	154	0	---	R.TQVDTQAQQLR.R
1287.6068	1286.5995	1286.6579	-45.35	144	154	0	14	R.TQVDTQAQQLR.R
1305.5947	1304.5874	1304.6473	-45.90	296	305	1	---	R.LDQQVEDFRR.T



1311.6462 1310.6389 1310.6983 -45.28 80 - 90 0 --- K.LVPFATELHER.L  
 1311.6462 1310.6390 1310.6983 -45.25 80 - 90 0 14 K.LVPFATELHER.L  
 1439.7417 1438.7344 1438.7932 -40.87 79 - 90 1 --- K.KLVFPATELHER.L  
 1528.7235 1527.7162 1527.7868 -46.17 234 - 246 0 --- K.LNHQLEGLAFQMK.K  
 1664.7775 1663.7702 1663.8417 -42.96 52 - 65 0 --- K.SELTQQLNTLFPQDK.L  
 1839.8657 1838.8584 1838.9414 -45.13 329 - 345 0 --- K.LGPLAGDVEDHLSFLEK.D  
 2700.2822 2699.2749 2699.3514 -28.34 170 - 193 0 --- R.QNLDQLQASLAPYAEELQATVNQR.V  
 2700.2822 2699.2750 2699.3514 -28.33 170 - 193 0 36 R.QNLDQLQASLAPYAEELQATVNQR.V  
**No match to:** 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1051.6609, 1069.4803, 1131.6592, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1179.5543, 1182.6278, 1182.6278, 1194.5756, 1269.6084, 1300.7948, 1334.8268, 1425.6982, 1448.8599, 1475.6879, 1617.9976, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788

2. [A0A4W2CCP9](#) Mass: 42963 Score: 283 Expect: 6.7e-024 Matches: 24

Apolipoprotein A4 OS=Bos indicus x Bos taurus OX=30522 GN=APOA4 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
862.4257	861.4184	861.4556	-43.12	288	295	0	---	K.SLAELSSR.L
977.4595	976.4522	976.4978	-46.64	156	163	0	---	R.QLTPYAEER.M
977.4595	976.4523	976.4978	-46.61	156	163	0	15	R.QLTPYAEER.M
1047.4978	1046.4905	1046.5396	-46.92	135	143	0	---	R.LGPYAEELR.T
1047.4978	1046.4905	1046.5396	-46.92	135	143	0	20	R.LGPYAEELR.T
1133.5562	1132.5489	1132.5989	-44.10	155	163	1	---	R.RQLTPYAEER.M
1149.5057	1148.4984	1148.5462	-41.60	296	304	0	---	R.LDQQVEDFR.R
1149.5057	1148.4985	1148.5462	-41.57	296	304	0	20	R.LDQQVEDFR.R
1174.5699	1173.5626	1173.6176	-46.83	317	326	0	---	K.AMVQQLDTLR.Q
1174.5700	1173.5627	1173.6176	-46.79	317	326	0	50	K.AMVQQLDTLR.Q
1190.5620	1189.5547	1189.6125	-48.57	317	326	0	---	K.AMVQQLDTLR.Q + Oxidation (M)
1212.5294	1211.5221	1211.5823	-49.63	306	316	0	---	R.TVGPYGETFNK.A
1277.6251	1276.6178	1276.6663	-37.98	201	211	0	---	R.LTPYADQLQTK.I
1287.6068	1286.5995	1286.6579	-45.36	144	154	0	---	R.TQVDTQAQQLR.R
1287.6068	1286.5995	1286.6579	-45.35	144	154	0	14	R.TQVDTQAQQLR.R
1305.5947	1304.5874	1304.6473	-45.90	296	305	1	---	R.LDQQVEDFR.R
1311.6462	1310.6389	1310.6983	-45.28	80	90	0	---	K.LVPFATELHER.L
1311.6462	1310.6390	1310.6983	-45.25	80	90	0	14	K.LVPFATELHER.L
1439.7417	1438.7344	1438.7932	-40.87	79	90	1	---	K.KLVFPATELHER.L
1528.7235	1527.7162	1527.7868	-46.17	234	246	0	---	K.LNHQLEGLAFQMK.K
1664.7775	1663.7702	1663.8417	-42.96	52	65	0	---	K.SELTQQLNTLFPQDK.L
1839.8657	1838.8584	1838.9414	-45.13	329	345	0	---	K.LGPLAGDVEDHLSFLEK.D
2700.2822	2699.2749	2699.3514	-28.34	170	193	0	---	R.QNLDQLQASLAPYAEELQATVNQR.V
2700.2822	2699.2750	2699.3514	-28.33	170	193	0	36	R.QNLDQLQASLAPYAEELQATVNQR.V
<b>No match to:</b> 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1051.6609, 1069.4803, 1131.6592, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1179.5543, 1182.6278, 1182.6278, 1194.5756, 1269.6084, 1300.7948, 1334.8268, 1425.6982, 1448.8599, 1475.6879, 1617.9976, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788								

3. [A0A3Q1M3N0](#) Mass: 43165 Score: 283 Expect: 6.7e-024 Matches: 24

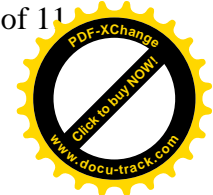
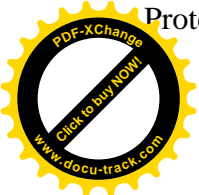
Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
862.4257	861.4184	861.4556	-43.12	313	320	0	---	K.SLAELSSR.L
977.4595	976.4522	976.4978	-46.64	181	188	0	---	R.QLTPYAEER.M
977.4595	976.4523	976.4978	-46.61	181	188	0	15	R.QLTPYAEER.M
1047.4978	1046.4905	1046.5396	-46.92	160	168	0	---	R.LGPYAEELR.T
1047.4978	1046.4905	1046.5396	-46.92	160	168	0	20	R.LGPYAEELR.T
1133.5562	1132.5489	1132.5989	-44.10	180	188	1	---	R.RQLTPYAEER.M
1149.5057	1148.4984	1148.5462	-41.60	321	329	0	---	R.LDQQVEDFR.R
1149.5057	1148.4985	1148.5462	-41.57	321	329	0	20	R.LDQQVEDFR.R
1174.5699	1173.5626	1173.6176	-46.83	342	351	0	---	K.AMVQQLDTLR.Q
1174.5700	1173.5627	1173.6176	-46.79	342	351	0	50	K.AMVQQLDTLR.Q
1190.5620	1189.5547	1189.6125	-48.57	342	351	0	---	K.AMVQQLDTLR.Q + Oxidation (M)
1212.5294	1211.5221	1211.5823	-49.63	331	341	0	---	R.TVGPYGETFNK.A
1277.6251	1276.6178	1276.6663	-37.98	226	236	0	---	R.LTPYADQLQTK.I
1287.6068	1286.5995	1286.6579	-45.36	169	179	0	---	R.TQVDTQAQQLR.R
1287.6068	1286.5995	1286.6579	-45.35	169	179	0	14	R.TQVDTQAQQLR.R
1305.5947	1304.5874	1304.6473	-45.90	321	330	1	---	R.LDQQVEDFR.R
1311.6462	1310.6389	1310.6983	-45.28	105	115	0	---	K.LVPFATELHER.L
1311.6462	1310.6390	1310.6983	-45.25	105	115	0	14	K.LVPFATELHER.L
1439.7417	1438.7344	1438.7932	-40.87	104	115	1	---	K.KLVFPATELHER.L
1528.7235	1527.7162	1527.7868	-46.17	259	271	0	---	K.LNHQLEGLAFQMK.K
1664.7775	1663.7702	1663.8417	-42.96	77	90	0	---	K.SELTQQLNTLFPQDK.L
1839.8657	1838.8584	1838.9414	-45.13	354	370	0	---	K.LGPLAGDVEDHLSFLEK.D
2700.2822	2699.2749	2699.3514	-28.34	195	218	0	---	R.QNLDQLQASLAPYAEELQATVNQR.V
2700.2822	2699.2750	2699.3514	-28.33	195	218	0	36	R.QNLDQLQASLAPYAEELQATVNQR.V
<b>No match to:</b> 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1051.6609, 1069.4803, 1131.6592, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1179.5543, 1182.6278, 1182.6278, 1194.5756, 1269.6084, 1300.7948, 1334.8268, 1425.6982, 1448.8599, 1475.6879, 1617.9976, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788								

4. [A0A3Q1MZJ9](#) Mass: 45782 Score: 282 Expect: 8.5e-024 Matches: 24

Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
862.4257	861.4184	861.4556	-43.12	339	346	0	---	K.SLAELSSR.L
977.4595	976.4522	976.4978	-46.64	207	214	0	---	R.QLTPYAEER.M
977.4595	976.4523	976.4978	-46.61	207	214	0	15	R.QLTPYAEER.M
1047.4978	1046.4905	1046.5396	-46.92	186	194	0	---	R.LGPYAEELR.T
1047.4978	1046.4905	1046.5396	-46.92	186	194	0	20	R.LGPYAEELR.T
1133.5562	1132.5489	1132.5989	-44.10	206	214	1	---	R.RQLTPYAEER.M
1149.5057	1148.4984	1148.5462	-41.60	347	355	0	---	R.LDQQVEDFR.R
1149.5057	1148.4985	1148.5462	-41.57	347	355	0	20	R.LDQQVEDFR.R
1174.5699	1173.5626	1173.6176	-46.83	368	377	0	---	K.AMVQQLDTLR.Q
1174.5700	1173.5627	1173.6176	-46.79	368	377	0	50	K.AMVQQLDTLR.Q
1190.5620	1189.5547	1189.6125	-48.57	368	377	0	---	K.AMVQQLDTLR.Q + Oxidation (M)



1212.5294	1211.5221	1211.5823	-49.63	357	-	367	0	---	R.TVGPYGETFNK.A
1277.6251	1276.6178	1276.6663	-37.98	252	-	262	0	---	R.LTPYADQLQTK.I
1287.6068	1286.5995	1286.6579	-45.36	195	-	205	0	---	R.TQVDTQAQQLR.R
1287.6068	1286.5995	1286.6579	-45.35	195	-	205	0	14	R.TQVDTQAQQLR.R
1305.5947	1304.5874	1304.6473	-45.90	347	-	356	1	---	R.LDQQVEDFRR.T
1311.6462	1310.6389	1310.6983	-45.28	131	-	141	0	---	K.LVPFATELHER.L
1311.6462	1310.6390	1310.6983	-45.25	131	-	141	0	14	K.LVPFATELHER.L
1439.7417	1438.7344	1438.7932	-40.87	130	-	141	1	---	K.KLVFPATELHER.L
1528.7235	1527.7162	1527.7868	-46.17	285	-	297	0	---	K.LNHQLEGLAFQMK.K
1664.7775	1663.7702	1663.8417	-42.96	103	-	116	0	---	K.SELTQQLNTLFQDK.L
1839.8657	1838.8584	1838.9414	-45.13	380	-	396	0	---	K.LGPLAGDVEDHLSFLEK.D
2700.2822	2699.2749	2699.3514	-28.34	221	-	244	0	---	R.QNLDQLQASLAPYAEELQATVNQR.V
2700.2822	2699.2750	2699.3514	-28.33	221	-	244	0	36	R.QNLDQLQASLAPYAEELQATVNQR.V

**No match to:** 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1051.6609, 1069.4803, 1131.6592, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1179.5543, 1182.6278, 1182.6278, 1194.5756, 1269.6084, 1300.7948, 1334.8268, 1425.6982, 1448.8599, 1475.6879, 1617.9976, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788

5. [A0A4W2GRG6](#) Mass: 43654 Score: 281 Expect: 1.1e-023 Matches: 24

Apolipoprotein A4 OS=Bos indicus x Bos taurus OX=30522 GN=APOA4 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
862.4257	861.4184	861.4556	-43.12	318	-	325	0	---	K.SLAELSSR.L
977.4595	976.4522	976.4978	-46.64	186	-	193	0	---	R.QLTPYAER.M
977.4595	976.4523	976.4978	-46.61	186	-	193	0	15	R.QLTPYAER.M
1047.4978	1046.4905	1046.5396	-46.92	165	-	173	0	---	R.LGPYAEELR.T
1047.4978	1046.4905	1046.5396	-46.92	165	-	173	0	20	R.LGPYAEELR.T
1133.5562	1132.5489	1132.5989	-44.10	185	-	193	1	---	R.RQLTPYAER.M
1149.5057	1148.4984	1148.5462	-41.60	326	-	334	0	---	R.LDQQVEDFR.R
1149.5057	1148.4985	1148.5462	-41.57	326	-	334	0	20	R.LDQQVEDFR.R
1174.5699	1173.5626	1173.6176	-46.83	347	-	356	0	---	K.AMVQQLDTRL.Q
1174.5700	1173.5627	1173.6176	-46.79	347	-	356	0	50	K.AMVQQLDTRL.Q
1190.5620	1189.5547	1189.6125	-48.57	347	-	356	0	---	K.AMVQQLDTRL.Q + Oxidation (M)
1212.5294	1211.5221	1211.5823	-49.63	336	-	346	0	---	R.TVGPYGETFNK.A
1277.6251	1276.6178	1276.6663	-37.98	231	-	241	0	---	R.LTPYADQLQTK.I
1287.6068	1286.5995	1286.6579	-45.36	174	-	184	0	---	R.TQVDTQAQQLR.R
1287.6068	1286.5995	1286.6579	-45.35	174	-	184	0	14	R.TQVDTQAQQLR.R
1305.5947	1304.5874	1304.6473	-45.90	326	-	335	1	---	R.LDQQVEDFRR.T
1311.6462	1310.6389	1310.6983	-45.28	110	-	120	0	---	K.LVPFATELHER.L
1311.6462	1310.6390	1310.6983	-45.25	110	-	120	0	14	K.LVPFATELHER.L
1439.7417	1438.7344	1438.7932	-40.87	109	-	120	1	---	K.KLVFPATELHER.L
1528.7235	1527.7162	1527.7868	-46.17	264	-	276	0	---	K.LNHQLEGLAFQMK.K
1664.7775	1663.7702	1663.8417	-42.96	82	-	95	0	---	K.SELTQQLNTLFQDK.L
1839.8657	1838.8584	1838.9414	-45.13	359	-	375	0	---	K.LGPLAGDVEDHLSFLEK.D
2700.2822	2699.2749	2699.3514	-28.34	200	-	223	0	---	R.QNLDQLQASLAPYAEELQATVNQR.V
2700.2822	2699.2750	2699.3514	-28.33	200	-	223	0	36	R.QNLDQLQASLAPYAEELQATVNQR.V

**No match to:** 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1051.6609, 1069.4803, 1131.6592, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1179.5543, 1182.6278, 1182.6278, 1194.5756, 1269.6084, 1300.7948, 1334.8268, 1425.6982, 1448.8599, 1475.6879, 1617.9976, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788

6. [A0A4W2GSL9](#) Mass: 46566 Score: 279 Expect: 1.7e-023 Matches: 24

Apolipoprotein A4 OS=Bos indicus x Bos taurus OX=30522 GN=APOA4 PE=3 SV=1

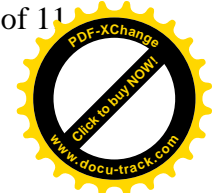
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
862.4257	861.4184	861.4556	-43.12	318	-	325	0	---	K.SLAELSSR.L
977.4595	976.4522	976.4978	-46.64	186	-	193	0	---	R.QLTPYAER.M
977.4595	976.4523	976.4978	-46.61	186	-	193	0	15	R.QLTPYAER.M
1047.4978	1046.4905	1046.5396	-46.92	165	-	173	0	---	R.LGPYAEELR.T
1047.4978	1046.4905	1046.5396	-46.92	165	-	173	0	20	R.LGPYAEELR.T
1133.5562	1132.5489	1132.5989	-44.10	185	-	193	1	---	R.RQLTPYAER.M
1149.5057	1148.4984	1148.5462	-41.60	326	-	334	0	---	R.LDQQVEDFR.R
1149.5057	1148.4985	1148.5462	-41.57	326	-	334	0	20	R.LDQQVEDFR.R
1174.5699	1173.5626	1173.6176	-46.83	347	-	356	0	---	K.AMVQQLDTRL.Q
1174.5700	1173.5627	1173.6176	-46.79	347	-	356	0	50	K.AMVQQLDTRL.Q
1190.5620	1189.5547	1189.6125	-48.57	347	-	356	0	---	K.AMVQQLDTRL.Q + Oxidation (M)
1212.5294	1211.5221	1211.5823	-49.63	336	-	346	0	---	R.TVGPYGETFNK.A
1277.6251	1276.6178	1276.6663	-37.98	231	-	241	0	---	R.LTPYADQLQTK.I
1287.6068	1286.5995	1286.6579	-45.36	174	-	184	0	---	R.TQVDTQAQQLR.R
1287.6068	1286.5995	1286.6579	-45.35	174	-	184	0	14	R.TQVDTQAQQLR.R
1305.5947	1304.5874	1304.6473	-45.90	326	-	335	1	---	R.LDQQVEDFRR.T
1311.6462	1310.6389	1310.6983	-45.28	110	-	120	0	---	K.LVPFATELHER.L
1311.6462	1310.6390	1310.6983	-45.25	110	-	120	0	14	K.LVPFATELHER.L
1439.7417	1438.7344	1438.7932	-40.87	109	-	120	1	---	K.KLVFPATELHER.L
1528.7235	1527.7162	1527.7868	-46.17	264	-	276	0	---	K.LNHQLEGLAFQMK.K
1664.7775	1663.7702	1663.8417	-42.96	82	-	95	0	---	K.SELTQQLNTLFQDK.L
1839.8657	1838.8584	1838.9414	-45.13	359	-	375	0	---	K.LGPLAGDVEDHLSFLEK.D
2700.2822	2699.2749	2699.3514	-28.34	200	-	223	0	---	R.QNLDQLQASLAPYAEELQATVNQR.V
2700.2822	2699.2750	2699.3514	-28.33	200	-	223	0	36	R.QNLDQLQASLAPYAEELQATVNQR.V

**No match to:** 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1051.6609, 1069.4803, 1131.6592, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1179.5543, 1182.6278, 1182.6278, 1194.5756, 1269.6084, 1300.7948, 1334.8268, 1425.6982, 1448.8599, 1475.6879, 1617.9976, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788

7. [F1N3Q7](#) Mass: 52487 Score: 271 Expect: 1.1e-022 Matches: 24

Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
862.4257	861.4184	861.4556	-43.12	373	-	380	0	---	K.SLAELSSR.L
977.4595	976.4522	976.4978	-46.64	241	-	248	0	---	R.QLTPYAER.M
977.4595	976.4523	976.4978	-46.61	241	-	248	0	15	R.QLTPYAER.M
1047.4978	1046.4905	1046.5396	-46.92	220	-	228	0	---	R.LGPYAEELR.T
1047.4978	1046.4905	1046.5396	-46.92	220	-	228	0	20	R.LGPYAEELR.T
1133.5562	1132.5489	1132.5989	-44.10	240	-	248	1	---	R.RQLTPYAER.M



1149.5057	1148.4984	1148.5462	-41.60	381	-	389	0	---	R.LDQQVEDFR.R
1149.5057	1148.4985	1148.5462	-41.57	381	-	389	0	20	R.LDQQVEDFR.R
1174.5699	1173.5626	1173.6176	-46.83	402	-	411	0	---	K.AMVQQLDTRLR.Q
1174.5700	1173.5627	1173.6176	-46.79	402	-	411	0	50	K.AMVQQLDTRLR.Q
1190.5620	1189.5547	1189.6125	-48.57	402	-	411	0	---	K.AMVQQLDTRLR.Q + Oxidation (M)
1212.5294	1211.5221	1211.5823	-49.63	391	-	401	0	---	R.TVGPYGETFNK.A
1277.6251	1276.6178	1276.6663	-37.98	286	-	296	0	---	R.LTPYADQLQTK.I
1287.6068	1286.5995	1286.6579	-45.36	229	-	239	0	---	R.TQVDTQAQQLR.R
1287.6068	1286.5995	1286.6579	-45.35	229	-	239	0	14	R.TQVDTQAQQLR.R
1305.5947	1304.5874	1304.6473	-45.90	381	-	390	1	---	R.LDQQVEDFRR.T
1311.6462	1310.6389	1310.6983	-45.28	165	-	175	0	---	K.LVPFATELHER.L
1311.6462	1310.6390	1310.6983	-45.25	165	-	175	0	14	K.LVPFATELHER.L
1439.7417	1438.7344	1438.7932	-40.87	164	-	175	1	---	K.KLVPFATELHER.L
1528.7235	1527.7162	1527.7868	-46.17	319	-	331	0	---	K.LNHQLEGLAFQMK.K
1664.7775	1663.7702	1663.8417	-42.96	137	-	150	0	---	K.SELTQQLNTLTFQDK.L
1839.8657	1838.8584	1838.9414	-45.13	414	-	430	0	---	K.LGPLAGDVEDHLSFLEK.D
2700.2822	2699.2749	2699.3514	-28.34	255	-	278	0	---	R.QNLDDLQASLAPYAEELQATVNQR.V
2700.2822	2699.2750	2699.3514	-28.33	255	-	278	0	36	R.QNLDDLQASLAPYAEELQATVNQR.V

**No match to:** 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1051.6609, 1069.4803, 1131.6592, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1179.5543, 1182.6278, 1182.6278, 1182.6278, 1194.5756, 1269.6084, 1300.7948, 1334.8268, 1425.6982, 1448.8599, 1475.6879, 1617.9976, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788

8. [Q32PJ2](#) Mass: 42991 Score: 248 Expect: 2.1e-020 Matches: 21

Apolipoprotein A-IV OS=Bos taurus OX=9913 GN=APOA4 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
862.4257	861.4184	861.4556	-43.12	288	-	295	0	---	K.SLAELSSR.L
1047.4978	1046.4905	1046.5396	-46.92	135	-	143	0	---	R.LGPIYAEELR.T
1047.4978	1046.4905	1046.5396	-46.92	135	-	143	0	20	R.LGPIYAEELR.T
1149.5057	1148.4984	1148.5462	-41.60	296	-	304	0	---	R.LDQQVEDFR.R
1149.5057	1148.4985	1148.5462	-41.57	296	-	304	0	20	R.LDQQVEDFR.R
1174.5699	1173.5626	1173.6176	-46.83	317	-	326	0	---	K.AMVQQLDTRLR.Q
1174.5700	1173.5627	1173.6176	-46.79	317	-	326	0	50	K.AMVQQLDTRLR.Q
1190.5620	1189.5547	1189.6125	-48.57	317	-	326	0	---	K.AMVQQLDTRLR.Q + Oxidation (M)
1212.5294	1211.5221	1211.5823	-49.63	306	-	316	0	---	R.TVGPYGETFNK.A
1277.6251	1276.6178	1276.6663	-37.98	201	-	211	0	---	R.LTPYADQLQTK.I
1287.6068	1286.5995	1286.6579	-45.36	144	-	154	0	---	R.TQVDTQAQQLR.R
1287.6068	1286.5995	1286.6579	-45.35	144	-	154	0	14	R.TQVDTQAQQLR.R
1305.5947	1304.5874	1304.6473	-45.90	296	-	305	1	---	R.LDQQVEDFRR.T
1311.6462	1310.6389	1310.6983	-45.28	80	-	90	0	---	K.LVPFATELHER.L
1311.6462	1310.6390	1310.6983	-45.25	80	-	90	0	14	K.LVPFATELHER.L
1439.7417	1438.7344	1438.7932	-40.87	79	-	90	1	---	K.KLVPFATELHER.L
1528.7235	1527.7162	1527.7868	-46.17	234	-	246	0	---	K.LNHQLEGLAFQMK.K
1664.7775	1663.7702	1663.8417	-42.96	52	-	65	0	---	K.SELTQQLNTLTFQDK.L
1839.8657	1838.8584	1838.9414	-45.13	329	-	345	0	---	K.LGPLAGDVEDHLSFLEK.D
2700.2822	2699.2749	2699.3514	-28.34	170	-	193	0	---	R.QNLDDLQASLAPYAEELQATVNQR.V
2700.2822	2699.2750	2699.3514	-28.33	170	-	193	0	36	R.QNLDDLQASLAPYAEELQATVNQR.V

**No match to:** 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 977.4595, 977.4595, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1051.6609, 1069.4803, 1131.6592, 1133.5562, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1179.5543, 1182.6278, 1182.6278, 1194.5756, 1269.6084, 1300.7948, 1334.8268, 1425.6982, 1448.8599, 1475.6879, 1617.9976, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788

9. [F1N6W4](#) Mass: 145999 Score: 48 Expect: 2 Matches: 12

DENN domain containing 5A OS=Bos taurus OX=9913 GN=DENN5A PE=4 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
842.4698	841.4625	841.4195	51.2	670	-	676	0	---	R.NAPAQWR.R
848.4878	847.4805	847.4287	61.2	419	-	426	0	---	R.ASELVSDK.R
1051.6609	1050.6536	1050.5822	68.0	849	-	857	0	---	R.HIQNIGIEIK.T
1131.6592	1130.6519	1130.5866	57.8	704	-	713	1	---	R.NMGSTIRQPK.L
1174.5699	1173.5626	1173.5123	42.9	2	-	17	0	---	M.SGGGGGGGGGSAPS.R
1174.5700	1173.5627	1173.5123	42.9	2	-	17	0	8	M.SGGGGGGGGGSAPS.R
1182.6278	1181.6205	1181.7244	-87.92	592	-	601	1	---	R.LLNVRTPTLR.T
1182.6278	1181.6205	1181.7244	-87.92	592	-	601	1	24	R.LLNVRTPTLR.T
1194.5756	1193.5683	1193.6049	-30.66	1197	-	1206	0	---	K.FQMLVCLGAR.D
1305.5947	1304.5874	1304.5528	26.5	1	-	17	0	---	-MSGGGGGGGGSAPS.R
1311.6462	1310.6389	1310.7194	-61.39	882	-	892	1	---	K.QLLSDHELTKK.L
1311.6462	1310.6390	1310.7194	-61.36	882	-	892	1	---	K.QLLSDHELTKK.L

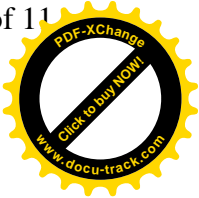
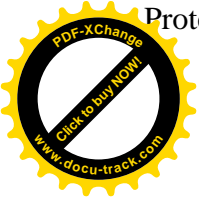
**No match to:** 834.4748, 850.0129, 850.4987, 853.4788, 862.4257, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 977.4595, 977.4595, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1047.4978, 1047.4978, 1069.4803, 1133.5562, 1149.5057, 1149.5057, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1179.5543, 1190.5620, 1212.5294, 1269.6084, 1277.6251, 1287.6068, 1287.6068, 1300.7948, 1334.8268, 1425.6982, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788, 2700.2822, 2700.2822

10. [A0A3Q1MUN3](#) Mass: 148571 Score: 48 Expect: 2.2 Matches: 12

DENN domain containing 5A OS=Bos taurus OX=9913 GN=DENN5A PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
842.4698	841.4625	841.4195	51.2	694	-	700	0	---	R.NAPAQWR.R
848.4878	847.4805	847.4287	61.2	443	-	450	0	---	R.ASELVSDK.R
1051.6609	1050.6536	1050.5822	68.0	873	-	881	0	---	R.HIQNIGIEIK.T
1131.6592	1130.6519	1130.5866	57.8	728	-	737	1	---	R.NMGSTIRQPK.L
1174.5699	1173.5626	1173.5123	42.9	2	-	17	0	---	M.SGGGGGGGGGSAPS.R
1174.5700	1173.5627	1173.5123	42.9	2	-	17	0	8	M.SGGGGGGGGGSAPS.R
1182.6278	1181.6205	1181.7244	-87.92	616	-	625	1	---	R.LLNVRTPTLR.T
1182.6278	1181.6205	1181.7244	-87.92	616	-	625	1	24	R.LLNVRTPTLR.T
1194.5756	1193.5683	1193.6049	-30.66	1221	-	1230	0	---	K.FQMLVCLGAR.D
1305.5947	1304.5874	1304.5528	26.5	1	-	17	0	---	-MSGGGGGGGGSAPS.R
1311.6462	1310.6389	1310.7194	-61.39	906	-	916	1	---	K.QLLSDHELTKK.L
1311.6462	1310.6390	1310.7194	-61.36	906	-	916	1	---	K.QLLSDHELTKK.L

**No match to:** 834.4748, 850.0129, 850.4987, 853.4788, 862.4257, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 977.4595, 977.4595, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1047.4978, 1047.4978, 1069.4803, 1133.5562, 1149.5057, 1149.5057, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1179.5543,



1190.5620, 1212.5294, 1269.6084, 1277.6251, 1287.6068, 1287.6068, 1300.7948, 1334.8268, 1425.6982, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788, 2700.2822, 2700.2822

11. [A0A4W2DBN8](#) Mass: 47465 Score: 46 Expect: 3.2 Matches: 14

Reverse transcriptase domain-containing protein OS=Bos indicus x Bos taurus OX=30522 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
834.4748	833.4675	833.5044	-44.29	305	311	1	---	K.SLLMKVK.E + Oxidation (M)
848.4878	847.4805	847.4287	61.2	310	316	1	---	K.VKEESEK.V
882.5245	881.5172	881.4607	64.2	387	393	1	---	K.SRDITYK.G
882.5245	881.5173	881.4607	64.2	387	393	1	---	K.SRDITYK.G
1131.6592	1130.6519	1130.5720	70.7	148	157	0	---	R.ELPDVQAGFR.K
1133.5562	1132.5489	1132.6162	-59.38	377	386	0	---	K.VMTNLSILK.S
1149.5057	1148.4984	1148.6111	-98.10	377	386	0	---	K.VMTNLSILK.S + Oxidation (M)
1149.5057	1148.4985	1148.6111	-98.06	377	386	0	---	K.VMTNLSILK.S + Oxidation (M)
1269.6084	1268.6011	1268.7101	-85.93	279	288	1	---	K.IAWRNINLNR.Y
1277.6251	1276.6178	1276.7061	-69.11	376	386	1	---	R.KVMTNLSILK.S + Oxidation (M)
1287.6068	1286.5995	1286.6731	-57.20	147	157	1	---	K.RELPDVQAGFR.K
1287.6068	1286.5995	1286.6731	-57.20	147	157	1	---	K.RELPDVQAGFR.K
1702.7892	1701.7819	1701.7570	14.7	394	409	1	---	K.GPSSQGYGFSSGRVWM.-
2683.2788	2682.2715	2682.2644	2.65	245	266	0	---	K.GVCSQGYILSPCLFNLYAEYIMR.N + Oxidation (M)

No match to: 842.4698, 850.0129, 850.4987, 853.4788, 862.4257, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 892.9658, 951.5779, 960.4399, 977.4595, 977.4595, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1047.4978, 1047.4978, 1051.6609, 1069.4803, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1174.5699, 1174.5700, 1179.5543, 1182.6278, 1182.6278, 1190.5620, 1194.5756, 1212.5294, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1425.6982, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2700.2822, 2700.2822

12. [A0A4W2FJP8](#) Mass: 473166 Score: 45 Expect: 4.1 Matches: 30

Dynein axonemal heavy chain 6 OS=Bos indicus x Bos taurus OX=30522 GN=DNAH6 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
834.4748	833.4675	833.4647	3.40	1784	1790	0	---	K.TYVLNPK.S
848.4878	847.4805	847.4334	55.6	2431	2436	1	---	R.MIRQER.G + Oxidation (M)
864.5128	863.5055	863.4753	35.0	925	931	0	---	K.FVTQLEK.G
868.5118	867.5045	867.4464	67.1	649	654	1	---	K.YHRQHK.D
960.4399	959.4326	959.4672	-36.05	2545	2553	0	---	K.EVGISEGNNR.D
977.4595	976.4522	976.5012	-50.11	1810	1818	0	---	K.DGLMALSVR.A + Oxidation (M)
977.4595	976.4523	976.5012	-50.08	1810	1818	0	---	K.DGLMALSVR.A + Oxidation (M)
1045.5190	1044.5117	1044.5451	-31.97	3977	3986	0	---	R.DQATVIEAAK.T
1131.6592	1130.6519	1130.5608	80.6	232	240	1	---	K.NDYTTISKK.A
1149.5057	1148.4984	1148.4855	11.2	2320	2327	0	---	R.LFCHECQR.V
1149.5057	1148.4985	1148.4855	11.3	2320	2327	0	---	R.LFCHECQR.V
1156.5675	1155.5602	1155.5746	-12.48	1551	1559	1	---	R.FMFEGREIK.L
1182.6278	1181.6205	1181.5750	38.5	1280	1289	0	---	K.VEEAMFTSLR.R
1182.6278	1181.6205	1181.5750	38.5	1280	1289	0	5	K.VEEAMFTSLR.R
1287.6068	1286.5995	1286.7207	-94.20	1205	1215	1	---	R.NPQAVQPHLRK.C
1287.6068	1286.5995	1286.7207	-94.19	1205	1215	1	---	R.NPQAVQPHLRK.C
1425.6982	1424.6909	1424.7088	-12.57	3334	3344	0	---	R.LTEAEWNFFLR.G
1439.7417	1438.7344	1438.6472	60.6	1889	1900	0	---	R.CGMVFVDPEELK.W + Oxidation (M)
1448.8599	1447.8526	1447.9238	-49.18	1355	1368	1	---	R.LNALAAIVRGILPK.L
1475.6879	1474.6806	1474.7701	-60.67	2856	2869	0	---	R.AAQALDITMATLK.E
1528.7235	1527.7162	1527.8046	-57.81	1030	1042	1	---	K.TTEFVVLPHRDSK.D
1617.9976	1616.9903	1616.8596	80.9	1119	1132	1	---	R.QLPAEAKMFLQVSK.S
1664.7775	1663.7702	1663.9185	-89.12	3454	3468	0	---	K.VVFALTDVFVNLGK.A
1691.7629	1690.7556	1690.8414	-50.71	907	921	0	---	K.FDSLDPPELLNSQVSK.Y
1880.9835	1879.9762	1879.9138	33.2	4092	4107	1	---	K.DYWIAKGALLCQLNE.-
1901.1722	1900.1649	1900.0319	70.0	2415	2430	1	---	K.LVFFQDAIEHVSRIAR.M
1904.9435	1903.9362	1903.9778	-21.86	3818	3834	0	---	R.VPEILETENASESLFVK.D
2211.0264	2210.0191	2210.0677	-22.00	1271	1289	1	---	R.GNVEEWLKGVEEAMFTSLR.R + Oxidation (M)
2682.3079	2681.3006	2681.3871	-32.27	3145	3167	1	---	K.SGLEDQLLSDVVRLEKPELEEQR.I
2683.2788	2682.2715	2682.3725	-37.66	2999	3022	1	---	R.QWNTDGLPRDLISTENGILVTQGR.R

No match to: 842.4698, 850.0129, 850.4987, 853.4788, 862.4257, 865.9851, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 977.4595, 977.4595, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1047.4978, 1047.4978, 1051.6609, 1069.4803, 1133.5562, 1151.6812, 1165.6880, 1165.6880, 1174.5699, 1174.5700, 1179.5543, 1190.5620, 1194.5756, 1212.5294, 1269.6084, 1277.6251, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 2015.2070, 2283.1013, 2700.2822, 2700.2822

13. [A0A4W2HIT4](#) Mass: 478985 Score: 45 Expect: 4.3 Matches: 30

Dynein axonemal heavy chain 6 OS=Bos indicus x Bos taurus OX=30522 GN=DNAH6 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
834.4748	833.4675	833.4647	3.40	1784	1790	0	---	K.TYVLNPK.S
848.4878	847.4805	847.4334	55.6	2431	2436	1	---	R.MIRQER.G + Oxidation (M)
864.5128	863.5055	863.4753	35.0	925	931	0	---	K.FVTQLEK.G
868.5118	867.5045	867.4464	67.1	649	654	1	---	K.YHRQHK.D
960.4399	959.4326	959.4672	-36.05	2545	2553	0	---	K.EVGISEGNNR.D
977.4595	976.4522	976.5012	-50.11	1810	1818	0	---	K.DGLMALSVR.A + Oxidation (M)
977.4595	976.4523	976.5012	-50.08	1810	1818	0	---	K.DGLMALSVR.A + Oxidation (M)
1045.5190	1044.5117	1044.5451	-31.97	4024	4033	0	---	R.DQATVIEAAK.T
1131.6592	1130.6519	1130.5608	80.6	232	240	1	---	K.NDYTTISKK.A
1149.5057	1148.4984	1148.4855	11.2	2320	2327	0	---	R.LFCHECQR.V
1149.5057	1148.4985	1148.4855	11.3	2320	2327	0	---	R.LFCHECQR.V
1156.5675	1155.5602	1155.5746	-12.48	1551	1559	1	---	R.FMFEGREIK.L
1182.6278	1181.6205	1181.5750	38.5	1280	1289	0	---	K.VEEAMFTSLR.R
1182.6278	1181.6205	1181.5750	38.5	1280	1289	0	5	K.VEEAMFTSLR.R
1287.6068	1286.5995	1286.7207	-94.20	1205	1215	1	---	R.NPQAVQPHLRK.C
1287.6068	1286.5995	1286.7207	-94.19	1205	1215	1	---	R.NPQAVQPHLRK.C
1425.6982	1424.6909	1424.7088	-12.57	3381	3391	0	---	R.LTEAEWNFFLR.G
1439.7417	1438.7344	1438.6472	60.6	1889	1900	0	---	R.CGMVFVDPEELK.W + Oxidation (M)
1448.8599	1447.8526	1447.9238	-49.18	1355	1368	1	---	R.LNALAAIVRGILPK.L
1475.6879	1474.6806	1474.7701	-60.67	2903	2916	0	---	R.AAQALDITMATLK.E
1528.7235	1527.7162	1527.8046	-57.81	1030	1042	1	---	K.TTEFVVLPHRDSK.D
1617.9976	1616.9903	1616.8596	80.9	1119	1132	1	---	R.QLPAEAKMFLQVSK.S
1664.7775	1663.7702	1663.9185	-89.12	3501	3515	0	---	K.VVFALTDVFVNLGK.A
1691.7629	1690.7556	1690.8414	-50.71	907	921	0	---	K.FDSLDPPELLNSQVSK.Y



1880.9835	1879.9762	1879.9138	33.2	4139	-	4154	1	---	K.DYWIAKGSALLCQLNE.-
1901.1722	1900.1649	1900.0319	70.0	2415	-	2430	1	---	K.LVFFQDAIEHVSRIAR.M
1904.9435	1903.9362	1903.9778	-21.86	3865	-	3881	0	---	R.VPEILETENASESLFVK.D
2211.0264	2210.0191	2210.0677	-22.00	1271	-	1289	1	---	R.GNVEEWLGKVEAMFTSLR.R + Oxidation (M)
2682.3079	2681.3006	2681.3871	-32.27	3192	-	3214	1	---	K.SGLEDQLLSDVVRLEKPELEEQR.I
2683.2788	2682.2715	2682.3725	-37.66	3046	-	3069	1	---	R.QWNTDGLPRDLISTENGILVTQGR.R
<b>No match to:</b> 842.4698, 850.0129, 850.4987, 853.4788, 862.4257, 865.9851, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1047.4978, 1047.4978, 1051.6609, 1069.4803, 1133.5562, 1151.6812, 1165.6880, 1165.6880, 1174.5699, 1174.5699, 1174.5700, 1179.5543, 1190.5620, 1194.5756, 1212.5294, 1269.6084, 1300.7948, 1305.5947, 1311.6462, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1425.6982, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 2015.2070, 2283.1013, 2700.2822, 2700.2822									

14. [A0A3Q1LWT9](#) Mass: 14058 Score: 44 Expect: 5.4 Matches: 7

Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
862.4257	861.4184	861.4416	-26.96	96	-	104	1	---	R.GASASSRAR.V
977.4595	976.4522	976.4839	-32.39	94	-	102	1	---	R.WRGASASSR.A
977.4595	976.4523	976.4839	-32.36	94	-	102	1	15	R.WRGASASSR.A
1149.5057	1148.4984	1148.5682	-60.73	30	-	39	0	---	R.LDTAQMAMIR.Y
1149.5057	1148.4985	1148.5682	-60.69	30	-	39	0	2	R.LDTAQMAMIR.Y
1287.6068	1286.5995	1286.5739	20.0	18	-	29	0	---	R.SAVYSSSESTNR.L
1287.6068	1286.5995	1286.5739	20.0	18	-	29	0	---	R.SAVYSSSESTNR.L
<b>No match to:</b> 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1047.4978, 1047.4978, 1051.6609, 1069.4803, 1131.6592, 1133.5562, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1174.5699, 1174.5700, 1179.5543, 1182.6278, 1182.6278, 1190.5620, 1194.5756, 1212.5294, 1269.6084, 1277.6251, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1425.6982, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788, 2700.2822, 2700.2822									

15. [A0A4W2DIE4](#) Mass: 14058 Score: 44 Expect: 5.4 Matches: 7

Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
862.4257	861.4184	861.4416	-26.96	96	-	104	1	---	R.GASASSRAR.V
977.4595	976.4522	976.4839	-32.39	94	-	102	1	---	R.WRGASASSR.A
977.4595	976.4523	976.4839	-32.36	94	-	102	1	15	R.WRGASASSR.A
1149.5057	1148.4984	1148.5682	-60.73	30	-	39	0	---	R.LDTAQMAMIR.Y
1149.5057	1148.4985	1148.5682	-60.69	30	-	39	0	2	R.LDTAQMAMIR.Y
1287.6068	1286.5995	1286.5739	20.0	18	-	29	0	---	R.SAVYSSSESTNR.L
1287.6068	1286.5995	1286.5739	20.0	18	-	29	0	---	R.SAVYSSSESTNR.L
<b>No match to:</b> 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1047.4978, 1047.4978, 1051.6609, 1069.4803, 1131.6592, 1133.5562, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1174.5699, 1174.5700, 1179.5543, 1182.6278, 1182.6278, 1190.5620, 1194.5756, 1212.5294, 1269.6084, 1277.6251, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1425.6982, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788, 2700.2822, 2700.2822									

16. [A0A4W2EFU9](#) Mass: 24150 Score: 44 Expect: 5.5 Matches: 9

Hypoxanthine phosphoribosyltransferase OS=Bos indicus x Bos taurus OX=30522 PE=3 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
848.4878	847.4805	847.4586	25.9	49	-	55	1	---	R.LARDVMK.E + Oxidation (M)
882.5245	881.5172	881.4395	88.1	74	-	80	0	---	K.FFADLNR.N
882.5245	881.5173	881.4395	88.2	74	-	80	0	---	K.FFADLNR.N
1133.5562	1132.5489	1132.6526	-91.51	135	-	144	0	---	K.TMQTLLSLVK.K
1194.5756	1193.5683	1193.6115	-36.13	85	-	94	0	---	K.SIPMTVDFIR.L + Oxidation (M)
1277.6251	1276.6178	1276.7424	-97.61	135	-	145	1	---	K.TMQTLLSLVKK.H + Oxidation (M)
1287.6068	1286.5995	1286.6408	-32.05	70	-	80	1	---	K.GGYKFFADLNR.N
1287.6068	1286.5995	1286.6408	-32.04	70	-	80	1	---	K.GGYKFFADLNR.N
2682.3079	2681.3006	2681.1738	47.3	1	-	24	0	---	-.MAAHSFSVVNSNDEPGYDLDFCK.T + Oxidation (M)
<b>No match to:</b> 834.4748, 842.4698, 850.0129, 850.4987, 853.4788, 862.4257, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 892.9658, 951.5779, 960.4399, 977.4595, 977.4595, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1047.4978, 1047.4978, 1051.6609, 1069.4803, 1131.6592, 1149.5057, 1149.5057, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1174.5699, 1174.5700, 1179.5543, 1182.6278, 1182.6278, 1190.5620, 1212.5294, 1269.6084, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1425.6982, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2683.2788, 2700.2822, 2700.2822									

17. [E1BA06](#) Mass: 24150 Score: 44 Expect: 5.5 Matches: 9

Hypoxanthine phosphoribosyltransferase OS=Bos taurus OX=9913 PE=3 SV=2									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
848.4878	847.4805	847.4586	25.9	49	-	55	1	---	R.LARDVMK.E + Oxidation (M)
882.5245	881.5172	881.4395	88.1	74	-	80	0	---	K.FFADLNR.N
882.5245	881.5173	881.4395	88.2	74	-	80	0	---	K.FFADLNR.N
1133.5562	1132.5489	1132.6526	-91.51	135	-	144	0	---	K.TMQTLLSLVK.K
1194.5756	1193.5683	1193.6115	-36.13	85	-	94	0	---	K.SIPMTVDFIR.L + Oxidation (M)
1277.6251	1276.6178	1276.7424	-97.61	135	-	145	1	---	K.TMQTLLSLVKK.H + Oxidation (M)
1287.6068	1286.5995	1286.6408	-32.05	70	-	80	1	---	K.GGYKFFADLNR.N
1287.6068	1286.5995	1286.6408	-32.04	70	-	80	1	---	K.GGYKFFADLNR.N
2682.3079	2681.3006	2681.1738	47.3	1	-	24	0	---	-.MAAHSFSVVNSNDEPGYDLDFCK.T + Oxidation (M)
<b>No match to:</b> 834.4748, 842.4698, 850.0129, 850.4987, 853.4788, 862.4257, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 892.9658, 951.5779, 960.4399, 977.4595, 977.4595, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1047.4978, 1047.4978, 1051.6609, 1069.4803, 1131.6592, 1149.5057, 1149.5057, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1174.5699, 1174.5700, 1179.5543, 1182.6278, 1182.6278, 1190.5620, 1212.5294, 1269.6084, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1425.6982, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2683.2788, 2700.2822, 2700.2822									

18. [A0A4W2HDP5](#) Mass: 60337 Score: 43 Expect: 6.6 Matches: 8

Zinc finger protein 382 OS=Bos indicus x Bos taurus OX=30522 GN=ZNF382 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1045.5190	1044.5117	1044.5352	-22.49	262	-	269	0	---	K.SYLIEHQR.I
1047.4978	1046.4905	1046.5331	-40.71	234	-	241	0	---	K.SIFIMHQR.S + Oxidation (M)
1047.4978	1046.4905	1046.5331	-40.71	234	-	241	0	---	K.SIFIMHQR.S + Oxidation (M)
1051.6609	1050.6536	1050.5934	57.3	150	-	157	1	---	K.QLIQHRK.V
1151.6812	1150.6739	1150.5838	78.3	1	-	9	1	---	-.MTKPD MIRK.L + 2 Oxidation (M)
1182.6278	1181.6205	1181.6880	-57.13	78	-	87	1	---	K.NHIISKTTLR.E
1182.6278	1181.6205	1181.6880	-57.12	78	-	87	1	24	K.NHIISKTTLR.E

1194.5756 1193.5683 1193.6193 -42.69 219 - 228 1 --- K.KPHSYSKYGK.F  
**No match to:** 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 862.4257, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 977.4595, 977.4595, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1069.4803, 1131.6592, 1133.5562, 1149.5057, 1149.5057, 1156.5675, 1165.6880, 1165.6880, 1174.5699, 1174.5700, 1179.5543, 1190.5620, 1212.5294, 1269.6084, 1277.6251, 1287.6068, 1287.6068, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1425.6982, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788, 2700.2822, 2700.2822

19. [AOA4W2FFL4](#) Mass: 343058 Score: 43 Expect: 6.9 Matches: 21

Kalirin RhoGEF kinase OS=Bos indicus x Bos taurus OX=30522 GN=KALRN PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
834.4748	833.4675	833.3879	95.5	723	-	730	0 ---	R.DSAVSNK.T
848.4878	847.4805	847.4440	43.1	1212	-	1218	0 ---	K.WVTTVDK.H
951.5779	950.5706	950.5410	31.2	618	-	625	1 ---	K.AARHLEVR.I
996.5483	995.5410	995.5036	37.6	138	-	146	1 ---	K.QKTNFGSSK.F
1017.6229	1016.6156	1016.6019	13.5	765	-	772	0 ---	K.LDIFLQLR.I
1017.6229	1016.6156	1016.6019	13.6	765	-	772	0 ---	K.LDIFLQLR.I
1033.6520	1032.6447	1032.5465	95.2	1202	-	1210	0 ---	K.GHIHATEIR.K
1051.6609	1050.6536	1050.5532	95.6	93	-	101	0 ---	R.GPTVIIDMR.G
1156.5675	1155.5602	1155.6360	-65.56	1574	-	1582	1 ---	K.NIREVIQER.I
1174.5699	1173.5626	1173.5713	-7.40	2400	-	2408	1 ---	K.KSCSWHTLR.M
1174.5700	1173.5627	1173.5713	-7.35	2400	-	2408	1 16	K.KSCSWHTLR.M
1269.6084	1268.6011	1268.6765	-59.39	2279	-	2290	0 ---	K.GSSYNPLPLK.I
1448.8599	1447.8526	1447.7493	71.3	411	-	423	0 ---	R.STILAMSAVFHQK.A + Oxidation (M)
1664.7775	1663.7702	1663.8682	-58.88	2914	-	2926	1 ---	R.DFINVILQEDFRR.R
1702.7892	1701.7819	1701.9274	-85.49	2566	-	2581	0 ---	K.VQGVPAAPNRPIAQER.S
1839.8657	1838.8584	1838.8291	15.9	1900	-	1916	0 ---	K.DPTGCLNEGMPPTPPR.N
1880.9835	1879.9762	1879.8337	75.8	2291	-	2308	0 ---	K.ISTNNGSPGFDYHQAGDK.F
1904.9435	1903.9362	1903.9879	-27.15	2014	-	2027	1 ---	R.KLHIYVWYQCNKPR.S
2683.2788	2682.2715	2682.2781	-2.47	2177	-	2198	1 ---	K.MNYLVLEENVNDNPKFALLNR.E + Oxidation (M)
2700.2822	2699.2749	2699.3303	-20.52	1378	-	1400	0 ---	K.NKPDSNQLILEHAGTFFDEIQQR.H
2700.2822	2699.2750	2699.3303	-20.51	1378	-	1400	0 0	K.NKPDSNQLILEHAGTFFDEIQQR.H
<b>No match to:</b> 842.4698, 850.0129, 850.4987, 853.4788, 862.4257, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 960.4399, 977.4595, 977.4595, 1019.6358, 1045.5190, 1047.4978, 1047.4978, 1069.4803, 1131.6592, 1133.5562, 1149.5057, 1149.5057, 1151.6812, 1165.6880, 1165.6880, 1179.5543, 1182.6278, 1182.6278, 1190.5620, 1194.5756, 1212.5294, 1277.6251, 1287.6068, 1287.6068, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1425.6982, 1439.7417, 1475.6879, 1528.7235, 1617.9976, 1691.7629, 1695.6990, 1732.0278, 1901.1722, 2015.2070, 2211.0264, 2283.1013, 2682.3079								

20. [AOA4W2EN51](#) Mass: 85445 Score: 43 Expect: 7.2 Matches: 8

Cyclin and CBS domain divalent metal cation transport mediator 4 OS=Bos indicus x Bos taurus OX=30522 GN=CNM4 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1047.4978	1046.4905	1046.5179	-26.14	216	-	224	0 ---	R.IVQNCGTQK.E
1047.4978	1046.4905	1046.5179	-26.14	216	-	224	0 ---	R.IVQNCGTQK.E
1174.5699	1173.5626	1173.5989	-30.94	710	-	721	0 ---	R.SLAAAEGADTLR.A
1174.5700	1173.5627	1173.5989	-30.90	710	-	721	0 31	R.SLAAAEGADTLR.A
1287.6068	1286.5995	1286.6520	-40.77	601	-	610	0 ---	R.LASHHYLYQR.S
1287.6068	1286.5995	1286.6520	-40.76	601	-	610	0 ---	R.LASHHYLYQR.S
1439.7417	1438.7344	1438.7099	17.0	1	-	16	0 ---	-.MAPVGGGGRPGSGPAR.G + Oxidation (M)
1904.9435	1903.9362	1904.0401	-54.56	120	-	137	1 ---	K.LVINVRGDTSGMLVLT.K + Oxidation (M)
<b>No match to:</b> 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 862.4257, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 977.4595, 977.4595, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1051.6609, 1069.4803, 1131.6592, 1133.5562, 1149.5057, 1149.5057, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1179.5543, 1182.6278, 1182.6278, 1190.5620, 1194.5756, 1212.5294, 1269.6084, 1277.6251, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1425.6982, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788, 2700.2822, 2700.2822								

21. [AOA4W2F4Z6](#) Mass: 60709 Score: 42 Expect: 8.1 Matches: 14

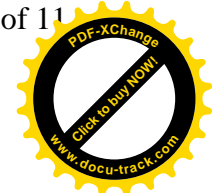
Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4878	847.4805	847.4188	72.8	521	-	528	1 ---	K.SRSSFPFA.-
862.4257	861.4184	861.4742	-64.76	411	-	417	1 ---	K.MQKTQVK.C
1017.6229	1016.6156	1016.5729	42.1	162	-	170	0 ---	K.TLLMPFAPK.E
1017.6229	1016.6156	1016.5729	42.1	162	-	170	0 ---	K.TLLMPFAPK.E
1033.6520	1032.6447	1032.5678	74.5	162	-	170	0 ---	K.TLLMPFAPK.E + Oxidation (M)
1045.5190	1044.5117	1044.5280	-15.61	381	-	389	0 ---	R.SFYSGFGLK.S
1156.5675	1155.5602	1155.5812	-18.13	357	-	365	0 ---	R.EEVTFTYQK.L
1174.5699	1173.5626	1173.5414	18.1	171	-	180	0 ---	K.EEGHYLSPSR.S
1174.5700	1173.5627	1173.5414	18.1	171	-	180	0 ---	K.EEGHYLSPSR.S
1182.6278	1181.6205	1181.5057	97.2	224	-	233	0 ---	K.STSMIPDCQK.L + Oxidation (M)
1182.6278	1181.6205	1181.5057	97.2	224	-	233	0 ---	K.STSMIPDCQK.L + Oxidation (M)
1311.6462	1310.6389	1310.6367	1.66	291	-	301	1 ---	K.EGHKWDVVEGR.Q
1311.6462	1310.6390	1310.6295	7.20	92	-	101	0 ---	K.TLEYTFHWSK.D
1425.6982	1424.6909	1424.7663	-52.93	357	-	367	1 ---	R.EEVTFTYQKLR.E
<b>No match to:</b> 834.4748, 842.4698, 850.0129, 850.4987, 853.4788, 864.5128, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 977.4595, 977.4595, 996.5483, 1019.6358, 1047.4978, 1047.4978, 1051.6609, 1069.4803, 1131.6592, 1133.5562, 1149.5057, 1149.5057, 1151.6812, 1165.6880, 1165.6880, 1179.5543, 1190.5620, 1194.5756, 1212.5294, 1269.6084, 1277.6251, 1287.6068, 1287.6068, 1300.7948, 1305.5947, 1334.8268, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788, 2700.2822, 2700.2822								

22. [AOA4W2HZ94](#) Mass: 170798 Score: 42 Expect: 8.5 Matches: 22

Lysine demethylase 2B OS=Bos indicus x Bos taurus OX=30522 GN=KDM2B PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4698	841.4625	841.4698	-8.61	18	-	24	0 ---	R.LPVEWAK.L
868.5118	867.5045	867.4199	97.6	925	-	931	1 ---	R.RSDEHPK.K
977.4595	976.4522	976.3920	61.7	916	-	923	0 ---	R.SCEEAAPR.R
977.4595	976.4523	976.3920	61.7	916	-	923	0 9	R.SCEEAAPR.R
1047.4978	1046.4905	1046.5066	-15.38	471	-	479	0 ---	R.ESMLIDAPR.K + Oxidation (M)
1047.4978	1046.4905	1046.5066	-15.38	471	-	479	0 0	R.ESMLIDAPR.K + Oxidation (M)
1069.4803	1068.4730	1068.4878	-13.85	730	-	737	1 ---	R.MKQSCIMR.Q + Oxidation (M)
1133.5562	1132.5489	1132.4931	49.3	916	-	924	1 ---	R.SCEEAAPRR.R
1156.5675	1155.5602	1155.5196	35.1	243	-	251	0 ---	R.YYETPEAQR.D
1165.6880	1164.6807	1164.6437	31.7	109	-	118	0 ---	R.RPPVPIMSR.A + Oxidation (M)



1165.6880 1164.6807 1164.6437 31.8 109 - 118 0 --- R.RPPVPPIMSR.A + Oxidation (M)  
 1194.5756 1193.5683 1193.6040 -29.91 425 - 433 1 --- R.IYEIEDRTR.V  
 1277.6251 1276.6178 1276.6333 -12.14 221 - 231 0 --- R.LVDVMDVNTQK.G + Oxidation (M)  
 1287.6068 1286.5995 1286.6871 -68.03 1325 - 1335 0 --- R.TLDVQWVEGLK.D  
 1287.6068 1286.5995 1286.6871 -68.02 1325 - 1335 0 --- R.TLDVQWVEGLK.D  
 1300.7948 1299.7875 1299.7584 22.4 1260 - 1271 0 --- K.SITPLMLSGIIR.R  
 1311.6462 1310.6389 1310.7129 -56.44 83 - 95 1 --- K.VAPVPKVGCTGAR.G  
 1311.6462 1310.6390 1310.7129 -56.41 83 - 95 1 --- K.VAPVPKVGCTGAR.G  
 1334.8268 1333.8195 1333.6990 90.4 954 - 964 1 --- K.YEKPQELSGRK.R  
 1702.7892 1701.7819 1701.8111 -17.11 175 - 187 1 --- K.DFNYYVQREALR.V  
 1904.9435 1903.9362 1903.9462 -5.24 1325 - 1340 1 --- R.TLDVQWVEGLKDAQMR.D + Oxidation (M)  
 2683.2788 2682.2715 2682.4817 -78.36 819 - 846 0 --- K.VSAGLQVPGVSPGGVDLGLARPSLSPPR.R  
**No match to:** 834.4748, 848.4878, 850.0129, 850.4987, 853.4788, 862.4257, 864.5128, 865.9851, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1051.6609, 1131.6592, 1149.5057, 1149.5057, 1151.6812, 1174.5699, 1174.5700, 1179.5543, 1182.6278, 1182.6278, 1190.5620, 1212.5294, 1269.6084, 1305.5947, 1425.6982, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2700.2822, 2700.2822

23. **A0A3Q1MCG0** Mass: 472745 Score: 42 Expect: 9.5 Matches: 29

Dynein axonemal heavy chain 6 OS=Bos taurus OX=9913 GN=DNAH6 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
834.4748	833.4675	833.4647	3.40	1732	-	1738	0	K.TYVLNPK.S
848.4878	847.4805	847.4334	55.6	2379	-	2384	1	R.MIRQER.G + Oxidation (M)
864.5128	863.5055	863.4753	35.0	925	-	931	0	K.FVTQLEK.G
868.5118	867.5045	867.4464	67.1	649	-	654	1	K.YHRQHK.D
960.4399	959.4326	959.4672	-36.05	2493	-	2501	0	K.EVGISEGNNR.D
977.4595	976.4522	976.5012	-50.11	1758	-	1766	0	K.DGLMALSVR.A + Oxidation (M)
977.4595	976.4523	976.5012	-50.08	1758	-	1766	0	K.DGLMALSVR.A + Oxidation (M)
1045.5190	1044.5117	1044.5451	-31.97	3972	-	3981	0	R.DQATVIEAAK.T
1131.6592	1130.6519	1130.5608	80.6	232	-	240	1	K.NDYITISK.K.A
1149.5057	1148.4984	1148.4855	11.2	2268	-	2275	0	R.LFCHCEQR.V
1149.5057	1148.4985	1148.4855	11.3	2268	-	2275	0	R.LFCHCEQR.V
1156.5675	1155.5602	1155.5746	-12.48	1499	-	1507	1	R.FMFEGREIK.L
1182.6278	1181.6205	1181.5750	38.5	1280	-	1289	0	K.VEEAMFTSLR.R
1182.6278	1181.6205	1181.5750	38.5	1280	-	1289	0	K.VEEAMFTSLR.R
1287.6068	1286.5995	1286.7207	-94.20	1205	-	1215	1	R.NPQAVQPHLRK.C
1287.6068	1286.5995	1286.7207	-94.19	1205	-	1215	1	R.NPQAVQPHLRK.C
1425.6982	1424.6909	1424.7088	-12.57	3329	-	3339	0	R.LTEAEWNFFLR.G
1439.7417	1438.7344	1438.6472	60.6	1837	-	1848	0	R.CGMVFVDPEELK.W + Oxidation (M)
1448.8599	1447.8526	1447.9238	-49.18	1355	-	1368	1	R.LNALAAIVRGILPK.L
1475.6879	1474.6806	1474.7701	-60.67	2851	-	2864	0	R.AAQAEIDITMATLK.E
1528.7235	1527.7162	1527.8046	-57.81	1030	-	1042	1	K.TTEFVVLPHRDSK.D
1617.9976	1616.9903	1616.8596	80.9	1119	-	1132	1	R.QLPAEAKMFLQVSK.S
1664.7775	1663.7702	1663.9185	-89.12	3449	-	3463	0	K.VVFALTDVFVLENLKG.A
1691.7629	1690.7556	1690.8414	-50.71	907	-	921	0	K.FDSLDPPELLNSQVSK.Y
1880.9835	1879.9762	1879.9138	33.2	4087	-	4102	1	K.DYWIAKGSALLCQLNE.-
1901.1722	1900.1649	1900.0319	70.0	2363	-	2378	1	K.LVFFQDAIEHVSRIAR.M
2211.0264	2210.0191	2210.0677	-22.00	1271	-	1289	1	R.GNVEEWLGKVEEAMFTSLR.R + Oxidation (M)
2682.3079	2681.3006	2681.3871	-32.27	3140	-	3162	1	K.SGLEDDQLSDVVRLEKPELEEQR.I
2683.2788	2682.2715	2682.3725	-37.66	2994	-	3017	1	R.QWNTDGLPRDLISTENGILVTQGR.R
<b>No match to:</b> 842.4698, 850.0129, 850.4987, 853.4788, 862.4257, 865.9851, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1047.4978, 1047.4978, 1051.6609, 1069.4803, 1133.5562, 1151.6812, 1165.6880, 1165.6880, 1174.5699, 1174.5700, 1179.5543, 1190.5620, 1194.5756, 1212.5294, 1269.6084, 1277.6251, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 1904.9435, 2015.2070, 2283.1013, 2700.2822, 2700.2822								

24. **A0A4W2GJX2** Mass: 108528 Score: 40 Expect: 12 Matches: 17

Nebulette OS=Bos indicus x Bos taurus OX=30522 GN=NEBL PE=4 SV=1

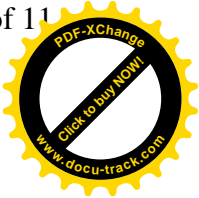
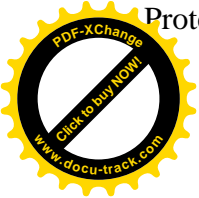
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
864.5128	863.5055	863.5116	-7.07	329	-	335	0	K.YITNLLK.E
960.4399	959.4326	959.4746	-43.74	792	-	799	0	R.SLHMLSEK.A + Oxidation (M)
996.5483	995.5410	995.4923	48.9	825	-	832	0	K.SEISEIYR.S
1017.6229	1016.6156	1016.5251	89.1	544	-	552	0	K.NQQNISSVK.Y
1017.6229	1016.6156	1016.5251	89.1	544	-	552	0	K.NQQNISSVK.Y
1045.5190	1044.5117	1044.5451	-31.96	453	-	461	1	K.DLENEIKGK.G
1069.4803	1068.4730	1068.5134	-37.83	876	-	884	0	R.SMOHSPNLR.T
1179.5543	1178.5470	1178.4575	76.0	18	-	27	0	K.TGEEENEEDK.V
1269.6084	1268.6011	1268.6612	-47.36	621	-	632	0	K.QATAISDPPELK.R
1287.6068	1286.5995	1286.5812	14.2	441	-	451	1	K.ASEMASQKEYK.K + Oxidation (M)
1287.6068	1286.5995	1286.5812	14.2	441	-	451	1	K.ASEMASQKEYK.K + Oxidation (M)
1305.5947	1304.5874	1304.6296	-32.30	750	-	760	0	K.GVHPHIVEMDR.R + Oxidation (M)
1425.6982	1424.6909	1424.7623	-50.11	621	-	633	1	K.QATAISDPPELKR.V
1664.7775	1663.7702	1663.8199	-29.88	423	-	437	1	R.GKGMQVSTDTLDIQR.A + Oxidation (M)
1691.7629	1690.7556	1690.8204	-38.34	462	-	476	1	K.GMQVSMIDPMLRAK.R
1702.7892	1701.7819	1701.8719	-52.89	351	-	365	1	K.GMELNSEVLDIQRAK.R
2682.3079	2681.3006	2681.3231	-8.40	200	-	224	1	K.GQGVNMKEPAVIGRPDFEHAASK.L + Oxidation (M)
<b>No match to:</b> 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 862.4257, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 977.4595, 977.4595, 977.4595, 1019.6358, 1033.6520, 1047.4978, 1047.4978, 1051.6609, 1131.6592, 1133.5562, 1149.5057, 1149.5057, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1174.5699, 1174.5700, 1182.6278, 1182.6278, 1190.5620, 1194.5756, 1212.5294, 1277.6251, 1300.7948, 1311.6462, 1311.6462, 1334.8268, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1695.6990, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2683.2788, 2700.2822, 2700.2822								

25. **A0A4W2EAZ9** Mass: 473215 Score: 40 Expect: 13 Matches: 29

Dynein axonemal heavy chain 6 OS=Bos indicus x Bos taurus OX=30522 GN=DNAH6 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
834.4748	833.4675	833.4647	3.40	1784	-	1790	0	K.TYVLNPK.S
848.4878	847.4805	847.4334	55.6	2431	-	2436	1	R.MIRQER.G + Oxidation (M)
864.5128	863.5055	863.4753	35.0	925	-	931	0	K.FVTQLEK.G
868.5118	867.5045	867.4464	67.1	649	-	654	1	K.YHRQHK.D
960.4399	959.4326	959.4672	-36.05	2545	-	2553	0	K.EVGISEGNNR.D
977.4595	976.4522	976.5012	-50.11	1810	-	1818	0	K.DGLMALSVR.A + Oxidation (M)
977.4595	976.4523	976.5012	-50.08	1810	-	1818	0	K.DGLMALSVR.A + Oxidation (M)
1045.5190	1044.5117	1044.5451	-31.97	3977	-	3986	0	R.DQATVIEAAK.T





1131.6592	1130.6519	1130.5608	80.6	232	-	240	1	---	K.NDYITISKK.A
1149.5057	1148.4984	1148.4855	11.2	2320	-	2327	0	---	R.LFCHQCQR.V
1149.5057	1148.4985	1148.4855	11.3	2320	-	2327	0	---	R.LFCHQCQR.V
1156.5675	1155.5602	1155.5746	-12.48	1551	-	1559	1	---	R.FMFEGREIK.L
1182.6278	1181.6205	1181.5750	38.5	1280	-	1289	0	---	K.VEEAMFTSLR.R
1182.6278	1181.6205	1181.5750	38.5	1280	-	1289	0	5	K.VEEAMFTSLR.R
1287.6068	1286.5995	1286.7207	-94.20	1205	-	1215	1	---	R.NPQAVQPHLRK.C
1287.6068	1286.5995	1286.7207	-94.19	1205	-	1215	1	---	R.NPQAVQPHLRK.C
1425.6982	1424.6909	1424.7088	-12.57	3334	-	3344	0	---	R.LTAEAWNFFLR.G
1439.7417	1438.7344	1438.6472	60.6	1889	-	1900	0	---	R.CGMVFVDPEELK.W + Oxidation (M)
1448.8599	1447.8526	1447.9238	-49.18	1355	-	1368	1	---	R.LNALAAIVRGILPK.L
1475.6879	1474.6806	1474.7701	-60.67	2856	-	2869	0	---	R.AAQAELEDITMATLK.E
1528.7235	1527.7162	1527.8046	-57.81	1030	-	1042	1	---	K.TTEFVVLPHRDSK.D
1617.9976	1616.9903	1616.8596	80.9	1119	-	1132	1	---	R.QLPAEAKMFLQVDK.S
1664.7775	1663.7702	1663.9185	-89.12	3454	-	3468	0	---	K.VVFALTDVFVIENTLKG.A
1691.7629	1690.7556	1690.8414	-50.71	907	-	921	0	---	K.FDSLDPPELLNSQVSK.Y
1880.9835	1879.9762	1879.9138	33.2	4092	-	4107	1	---	K.DYWIAKGSALLCQLNE.-
1901.1722	1900.1649	1900.0319	70.0	2415	-	2430	1	---	K.LVFFQDAIEHVSRIAR.M
2211.0264	2210.0191	2210.0677	-22.00	1271	-	1289	1	---	R.GNVEEVLGKVEEAMFTSLR.R + Oxidation (M)
2682.3079	2681.3006	2681.3871	-32.27	3145	-	3167	1	---	K.SGLEDDLSDVVRLEKPELEEQR.I
2683.2788	2682.2715	2682.3725	-37.66	2999	-	3022	1	---	R.QWNTDGLPRDLISTENGILVTQGR.R
No match to: 842.4698, 850.0129, 850.4987, 853.4788, 862.4257, 865.9851, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 996.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1047.4978, 1047.4978, 1051.6609, 1069.4803, 1133.5562, 1151.6812, 1165.6880, 1174.5699, 1174.5700, 1179.5543, 1190.5620, 1194.5756, 1212.5294, 1269.6084, 1277.6251, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 1904.9435, 2015.2070, 2283.1013, 2700.2822, 2700.2822									

26.	<a href="#">A0A4W2CJRO</a>	Mass: 108457	Score: 40	Expect: 13	Matches: 17
Nebulette OS=Bos indicus x Bos taurus OX=30522 GN=NEBL PE=4 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
864.5128	863.5055	863.5116	-7.07	329	- 335 0 --- K.YITNLLK.E
960.4399	959.4326	959.4746	-43.74	792	- 799 0 --- R.SLHMLSEK.A + Oxidation (M)
996.5483	995.5410	995.4923	48.9	825	- 832 0 --- K.SEISEIYR.S
1017.6229	1016.6156	1016.5251	89.1	544	- 552 0 --- K.NQONISSVK.Y
1017.6229	1016.6156	1016.5251	89.1	544	- 552 0 --- K.NQONISSVK.Y
1045.5190	1044.5117	1044.5451	-31.96	453	- 461 1 --- K.DLENEIKGK.G
1069.4803	1068.4730	1068.5134	-37.83	876	- 884 0 --- R.SMQHSPNLR.T
1179.5543	1178.5470	1178.4575	76.0	18	- 27 0 --- K.TGEEENEEDK.V
1269.6084	1268.6011	1268.6612	-47.36	621	- 632 0 --- K.QATAISDPPELK.R
1287.6068	1286.5995	1286.5812	14.2	441	- 451 1 --- K.ASEMASQKEYK.K + Oxidation (M)
1287.6068	1286.5995	1286.5812	14.2	441	- 451 1 --- K.ASEMASQKEYK.K + Oxidation (M)
1305.5947	1304.5874	1304.6296	-32.30	750	- 760 0 --- K.GVHPHIVEMDR.R + Oxidation (M)
1425.6982	1424.6909	1424.7623	-50.11	621	- 633 1 --- K.QATAISDPPELK.R.V
1664.7775	1663.7702	1663.8199	-29.88	423	- 437 1 --- R.GKGQMVSTDTLTIQR.A + Oxidation (M)
1691.7629	1690.7556	1690.8204	-38.34	462	- 476 1 --- K.GMQVSMIDIPDMLRAK.R
1702.7892	1701.7819	1701.8719	-52.89	351	- 365 1 --- K.GMELNSEVLDIQR.AK.R
2682.3079	2681.3006	2681.3231	-8.40	200	- 224 1 --- K.GQGVMNKEPAVIGRPDPEHAVEASK.L + Oxidation (M)
No match to: 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 862.4257, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 977.4595, 977.4595, 1019.6358, 1033.6520, 1047.4978, 1047.4978, 1051.6609, 1131.6592, 1133.5562, 1149.5057, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1174.5699, 1174.5700, 1182.6278, 1182.6278, 1190.5620, 1194.5756, 1212.5294, 1277.6251, 1300.7948, 1311.6462, 1311.6462, 1334.8268, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1695.6990, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2683.2788, 2700.2822, 2700.2822					

27.	<a href="#">A0A3Q1MXR2</a>	Mass: 108457	Score: 40	Expect: 13	Matches: 17
Nebulette OS=Bos taurus OX=9913 GN=NEBL PE=4 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
864.5128	863.5055	863.5116	-7.07	329	- 335 0 --- K.YITNLLK.E
960.4399	959.4326	959.4746	-43.74	792	- 799 0 --- R.SLHMLSEK.A + Oxidation (M)
996.5483	995.5410	995.4923	48.9	825	- 832 0 --- K.SEISEIYR.S
1017.6229	1016.6156	1016.5251	89.1	544	- 552 0 --- K.NQONISSVK.Y
1017.6229	1016.6156	1016.5251	89.1	544	- 552 0 --- K.NQONISSVK.Y
1045.5190	1044.5117	1044.5451	-31.96	453	- 461 1 --- K.DLENEIKGK.G
1069.4803	1068.4730	1068.5134	-37.83	876	- 884 0 --- R.SMQHSPNLR.T
1179.5543	1178.5470	1178.4575	76.0	18	- 27 0 --- K.TGEEENEEDK.V
1269.6084	1268.6011	1268.6612	-47.36	621	- 632 0 --- K.QATAISDPPELK.R
1287.6068	1286.5995	1286.5812	14.2	441	- 451 1 --- K.ASEMASQKEYK.K + Oxidation (M)
1287.6068	1286.5995	1286.5812	14.2	441	- 451 1 --- K.ASEMASQKEYK.K + Oxidation (M)
1305.5947	1304.5874	1304.6296	-32.30	750	- 760 0 --- K.GVHPHIVEMDR.R + Oxidation (M)
1425.6982	1424.6909	1424.7623	-50.11	621	- 633 1 --- K.QATAISDPPELK.R.V
1664.7775	1663.7702	1663.8199	-29.88	423	- 437 1 --- R.GKGQMVSTDTLTIQR.A + Oxidation (M)
1691.7629	1690.7556	1690.8204	-38.34	462	- 476 1 --- K.GMQVSMIDIPDMLRAK.R
1702.7892	1701.7819	1701.8719	-52.89	351	- 365 1 --- K.GMELNSEVLDIQR.AK.R
2682.3079	2681.3006	2681.3231	-8.40	200	- 224 1 --- K.GQGVMNKEPAVIGRPDPEHAVEASK.L + Oxidation (M)
No match to: 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 862.4257, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 977.4595, 977.4595, 1019.6358, 1033.6520, 1047.4978, 1047.4978, 1051.6609, 1131.6592, 1133.5562, 1149.5057, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1174.5699, 1174.5700, 1182.6278, 1182.6278, 1190.5620, 1194.5756, 1212.5294, 1277.6251, 1300.7948, 1311.6462, 1311.6462, 1334.8268, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1695.6990, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2683.2788, 2700.2822, 2700.2822					

28.	<a href="#">A0A4W2GHX5</a>	Mass: 112926	Score: 40	Expect: 14	Matches: 17
Nebulette OS=Bos indicus x Bos taurus OX=30522 GN=NEBL PE=4 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
864.5128	863.5055	863.5116	-7.07	367	- 373 0 --- K.YITNLLK.E
960.4399	959.4326	959.4746	-43.74	830	- 837 0 --- R.SLHMLSEK.A + Oxidation (M)
996.5483	995.5410	995.4923	48.9	863	- 870 0 --- K.SEISEIYR.S
1017.6229	1016.6156	1016.5251	89.1	582	- 590 0 --- K.NQONISSVK.Y
1017.6229	1016.6156	1016.5251	89.1	582	- 590 0 --- K.NQONISSVK.Y
1045.5190	1044.5117	1044.5451	-31.96	491	- 499 1 --- K.DLENEIKGK.G
1069.4803	1068.4730	1068.5134	-37.83	914	- 922 0 --- R.SMQHSPNLR.T
1179.5543	1178.5470	1178.4575	76.0	18	- 27 0 --- K.TGEEENEEDK.V
1269.6084	1268.6011	1268.6612	-47.36	659	- 670 0 --- K.QATAISDPPELK.R
1287.6068	1286.5995	1286.5812	14.2	479	- 489 1 --- K.ASEMASQKEYK.K + Oxidation (M)



1287.6068 1286.5995 1286.5812 14.2 479 - 489 1 --- K.ASEMASQKEYK.K + Oxidation (M)  
1305.5947 1304.5874 1304.6296 -32.30 788 - 798 0 --- K.GVHPHIVEMDR.R + Oxidation (M)  
1425.6982 1424.6909 1424.7623 -50.11 659 - 671 1 --- K.QATAISDPPELKR.V  
1664.7775 1663.7702 1663.8199 -29.88 461 - 475 1 --- R.GKGMQVSTDTLTDIQR.A + Oxidation (M)  
1691.7629 1690.7556 1690.8204 -38.34 500 - 514 1 --- K.GMQVSMIDIPMLRAK.R  
1702.7892 1701.7819 1701.8719 -52.89 389 - 403 1 --- K.GMELNSEVLDIQR.AK.R  
2682.3079 2681.3006 2681.3231 -8.40 200 - 224 1 --- K.GQGVNMKEPAVIGRPDPEHAVEASK.L + Oxidation (M)  
**No match to:** 834.4748, 842.4698, 848.4878, 850.0129, 850.4987, 853.4788, 862.4257, 865.9851, 868.5118, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 977.4595, 977.4595, 1019.6358, 1033.6520, 1047.4978, 1047.4978, 1051.6609, 1131.6592, 1133.5562, 1149.5057, 1149.5057, 1151.6812, 1156.5675, 1165.6880, 1165.6880, 1174.5699, 1174.5699, 1182.6278, 1182.6278, 1190.5620, 1194.5756, 1212.5294, 1277.6251, 1300.7948, 1311.6462, 1311.6462, 1334.8268, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1695.6990, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 1904.9435, 2015.2070, 2211.0264, 2283.1013, 2683.2788, 2700.2822, 2700.2822

29. [A0A4W2CVR3](#) Mass: 479034 Score: 40 Expect: 14 Matches: 29

Dynein axonemal heavy chain 6 OS=Bos indicus x Bos taurus OX=30522 GN=DNAH6 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
834.4748	833.4675	833.4647	3.40	1784	1790	0	---	K.TYVLNPK.S
848.4878	847.4805	847.4334	55.6	2431	2436	1	---	R.MIRQER.G + Oxidation (M)
864.5128	863.5055	863.4753	35.0	925	931	0	---	K.FVTQLEK.G
868.5118	867.5045	867.4464	67.1	649	654	1	---	K.YHRQHK.D
960.4399	959.4326	959.4672	-36.05	2545	2553	0	---	K.EVGISEGNNR.D
977.4595	976.4522	976.5012	-50.11	1810	1818	0	---	K.DGLMALSVR.A + Oxidation (M)
977.4595	976.4523	976.5012	-50.08	1810	1818	0	---	K.DGLMALSVR.A + Oxidation (M)
1045.5190	1044.5117	1044.5451	-31.97	4024	4033	0	---	R.DQATVIEAAK.T
1131.6592	1130.6519	1130.5608	80.6	232	240	1	---	K.NDYITISK.K
1149.5057	1148.4984	1148.4855	11.2	2320	2327	0	---	R.LFCHCQR.V
1149.5057	1148.4985	1148.4855	11.3	2320	2327	0	---	R.LFCHCQR.V
1156.5675	1155.5602	1155.5746	-12.48	1551	1559	1	---	R.FMFEGREIK.L
1182.6278	1181.6205	1181.5750	38.5	1280	1289	0	---	K.VEEAMFTSLR.R
1182.6278	1181.6205	1181.5750	38.5	1280	1289	0	5	K.VEEAMFTSLR.R
1287.6068	1286.5995	1286.7207	-94.20	1205	1215	1	---	R.NPQAVQPHLRK.C
1287.6068	1286.5995	1286.7207	-94.19	1205	1215	1	---	R.NPQAVQPHLRK.C
1425.6982	1424.6909	1424.7088	-12.57	3381	3391	0	---	R.LTEAEWNFFLR.G
1439.7417	1438.7344	1438.6472	60.6	1889	1900	0	---	R.CGMVFVDPEELK.W + Oxidation (M)
1448.8599	1447.8526	1447.9238	-49.18	1355	1368	1	---	R.LNALAAIVRGILPK.L
1475.6879	1474.6806	1474.7701	-60.67	2903	2916	0	---	R.AAQAEIDITMATLK.E
1528.7235	1527.7162	1527.8046	-57.81	1030	1042	1	---	K.TTEFVVLPHRDSK.D
1617.9976	1616.9903	1616.8596	80.9	1119	1132	1	---	R.QLPAEAKMFLQVDK.S
1664.7775	1663.7702	1663.9185	-89.12	3501	3515	0	---	K.VVFALTDVFVIENTLKG.A
1691.7629	1690.7556	1690.8414	-50.71	907	921	0	---	K.FDSLDPPELLNSQVSK.Y
1880.9835	1879.9762	1879.9138	33.2	4139	4154	1	---	K.DYWIAGKSALLCOLNE.-
1901.1722	1900.1649	1900.0319	70.0	2415	2430	1	---	K.LVFFQDAIEHVSRIAR.M
2211.0264	2210.0191	2210.0677	-22.00	1271	1289	1	---	R.GNVEEWLKGVEEAMFTSLR.R + Oxidation (M)
2682.3079	2681.3006	2681.3871	-32.27	3192	3214	1	---	K.SGLEDDLQSDVVRLEKPELEEQR.I
2683.2788	2682.2715	2682.3725	-37.66	3046	3069	1	---	R.QWNTDGLPRDLISTENGILVTQGR.R
<b>No match to:</b> 842.4698, 850.0129, 850.4987, 853.4788, 862.4257, 865.9851, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 966.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1047.4978, 1047.4978, 1051.6609, 1069.4803, 1133.5562, 1151.6812, 1165.6880, 1165.6880, 1174.5699, 1174.5700, 1179.5543, 1190.5620, 1194.5756, 1212.5294, 1269.6084, 1277.6251, 1300.7948, 1305.5947, 1311.6462, 1311.6462, 1334.8268, 1695.6990, 1702.7892, 1732.0278, 1839.8657, 1904.9435, 2015.2070, 2283.1013, 2700.2822, 2700.2822								

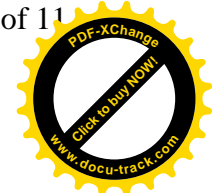
30. [A0A4W2I420](#) Mass: 167724 Score: 40 Expect: 14 Matches: 21

Lysine demethylase 2B OS=Bos indicus x Bos taurus OX=30522 GN=KDM2B PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4698	841.4625	841.4698	-8.61	18	24	0	---	R.LPVEWAK.L
868.5118	867.5045	867.4199	97.6	896	902	1	---	R.RSDEHPK.K
977.4595	976.4522	976.3920	61.7	887	894	0	---	R.SCEEAAPR.R
977.4595	976.4523	976.3920	61.7	887	894	0	9	R.SCEEAAPR.R
1047.4978	1046.4905	1046.5066	-15.38	471	479	0	---	R.ESMLIDAPR.K + Oxidation (M)
1047.4978	1046.4905	1046.5066	-15.38	471	479	0	0	R.ESMLIDAPR.K + Oxidation (M)
1069.4803	1068.4730	1068.4878	-13.85	730	737	1	---	R.MKQSCIMR.Q + Oxidation (M)
1133.5562	1132.5489	1132.4931	49.3	887	895	1	---	R.SCEEAAPR.R
1156.5675	1155.5602	1155.5196	35.1	243	251	0	---	R.YYETPEAQR.D
1165.6880	1164.6807	1164.6437	31.7	109	118	0	---	R.RPPVPPIMSR.A + Oxidation (M)
1165.6880	1164.6807	1164.6437	31.8	109	118	0	---	R.RPPVPPIMSR.A + Oxidation (M)
1194.5756	1193.5683	1193.6040	-29.91	425	433	1	---	R.IYEIEDRTR.V
1277.6251	1276.6178	1276.6333	-12.14	221	231	0	---	R.LVDVMDVNTQK.G + Oxidation (M)
1287.6068	1286.5995	1286.6871	-68.03	1296	1306	0	---	R.TLDVQWVEGLK.D
1287.6068	1286.5995	1286.6871	-68.02	1296	1306	0	---	R.TLDVQWVEGLK.D
1300.7948	1299.7875	1299.7584	22.4	1231	1242	0	---	K.SITPLMLSGIIR.R
1311.6462	1310.6389	1310.7129	-56.44	83	95	1	---	K.VAPVPKVGCTGAR.G
1311.6462	1310.6390	1310.7129	-56.41	83	95	1	---	K.VAPVPKVGCTGAR.G
1334.8268	1333.8195	1333.6990	90.4	925	935	1	---	K.YEKPQELSGRK.R
1702.7892	1701.7819	1701.8111	-17.11	175	187	1	---	K.DFNYYVQREALR.V
1904.9435	1903.9362	1903.9462	-5.24	1296	1311	1	---	R.TLDVQWVEGLKDAQMR.D + Oxidation (M)
<b>No match to:</b> 834.4748, 848.4878, 850.0129, 850.4987, 853.4788, 862.4257, 864.5128, 865.9851, 870.5065, 876.9959, 882.5245, 882.5245, 892.9658, 951.5779, 960.4399, 966.5483, 1017.6229, 1017.6229, 1019.6358, 1033.6520, 1045.5190, 1051.6609, 1131.6592, 1149.5057, 1149.5057, 1151.6812, 1174.5699, 1174.5700, 1179.5543, 1182.6278, 1182.6278, 1190.5620, 1212.5294, 1269.6084, 1305.5947, 1425.6982, 1439.7417, 1448.8599, 1475.6879, 1528.7235, 1617.9976, 1664.7775, 1691.7629, 1695.6990, 1732.0278, 1839.8657, 1880.9835, 1901.1722, 2015.2070, 2211.0264, 2283.1013, 2682.3079, 2683.2788, 2700.2822, 2700.2822								

## Search Parameters

Type of search : Sequence Query  
Enzyme : Trypsin  
Fixed modifications : [Carbamidomethyl \(C\)](#)  
Variable modifications : [Oxidation \(M\)](#)  
Mass values : Monoisotopic  
Protein Mass : Unrestricted  
Peptide Mass Tolerance :  $\pm 100$  ppm  
Fragment Mass Tolerance :  $\pm 0.3$  Da  
Max Missed Cleavages : 1  
Instrument type : MALDI-TOF-TOF



Query1 (834.4748,1+): <no title>  
Query2 (842.4698,1+): <no title>  
Query3 (848.4878,1+): <no title>  
Query4 (850.0129,1+): <no title>  
Query5 (850.4987,1+): <no title>  
Query6 (853.4788,1+): <no title>  
Query7 (862.4257,1+): <no title>  
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Query9 (865.9851,1+): <no title>  
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Query12 (876.9959,1+): <no title>  
Query13 (882.5245,1+): <no title>  
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