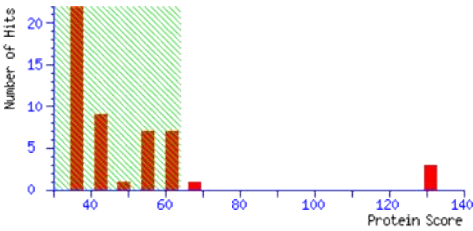


User :
Email :
Search title : BAEDW\2020_3_5\2020_3_5\MSMS 14\N24
Database : Uniprot_bovine_bovine_20200316 (134392 sequences; 76244912 residues)
Timestamp : 31 Mar 2020 at 01:09:09 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 131 for A0A3Q1MU98, Complement component C9 OS=Bos taurus OX=9913 GN=C9 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< 0.05 Max. number of hits 30

Preferred taxonomy All entries

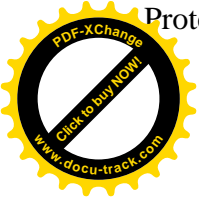
Re-Search All Search Unmatched

Index

Accession	Mass	Score	Description
1. A0A3Q1MU98	58618	131	Complement component C9 OS=Bos taurus OX=9913 GN=C9 PE=1 SV=1
2. A0A4W2FBY7	63327	128	Complement C9 OS=Bos indicus x Bos taurus OX=30522 GN=C9 PE=4 SV=1
3. Q3MHN2	63327	128	Complement component C9 OS=Bos taurus OX=9913 GN=C9 PE=2 SV=1
4. Q2KJF1	54091	68	Alpha-1B-glycoprotein OS=Bos taurus OX=9913 GN=ALBG PE=1 SV=1
5. A0A4W2H1C4	60879	64	Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1
6. A0A3Q1MJT2	62948	63	Alpha-1B-glycoprotein OS=Bos taurus OX=9913 GN=ALBG PE=1 SV=1
7. A0A4W2EKQ3	63006	63	Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1
8. A0A4W2GYB4	54132	61	Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1
9. A0A4W2E7Y8	54147	61	Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1
10. A0A4W2IFR5	54987	60	Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1
11. A0A4W2E8B7	55003	60	Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1
12. A0A3Q1LNN7	68022	57	Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=4 SV=1
13. A0A4W2DDL5	70207	56	Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1
14. A0A4W2D8T3	76089	56	Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1
15. A0A140T897	71274	56	Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=4 SV=1
16. A0A4W2EVR9	71453	56	Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1
17. A0A4W2EW60	76020	55	Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1
18. P02769	71244	55	Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4
19. C1J945	56189	48	Nonstructural protein 5A (Fragment) OS=Bovine viral diarrhea virus OX=11099 PE=4 SV=1
20. A0A4W2EGF3	97654	46	Dynamin 3 OS=Bos indicus x Bos taurus OX=30522 GN=DNM3 PE=3 SV=1
21. A0A4W2MDN4	96034	45	Uncharacterized protein OS=Bos taurus OX=9913 GN=DNM3 PE=3 SV=1
22. A0A4W2ET53	63308	44	Dynamin 3 OS=Bos indicus x Bos taurus OX=30522 GN=DNM3 PE=3 SV=1
23. A0A4W2LJA6	101091	43	Family with sequence similarity 111 member B OS=Bos indicus x Bos taurus OX=30522 GN=FAM111B PE=4 SV=1
24. A0A4W2BDJ6	52578	42	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 OS=Bos indicus x Bos taurus OX=30522 GN=PFKFB1 PE=
25. A0A3Q1LXK0	52578	42	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 OS=Bos taurus OX=9913 GN=PFKFB1 PE=4 SV=1
26. A0A4W2EAD9	72734	40	Dynamin 3 OS=Bos indicus x Bos taurus OX=30522 GN=DNM3 PE=3 SV=1
27. A0A4W2GWR3	70119	40	Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1
28. B0JYQ0	71244	40	ALB protein OS=Bos taurus OX=9913 GN=ALB PE=2 SV=1
29. A0A4W2D9L2	98304	39	Dynamin 3 OS=Bos indicus x Bos taurus OX=30522 GN=DNM3 PE=3 SV=1
30. A0A4W2IKT9	75992	39	Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1

Results List

1.	A0A3Q1MU98	Mass: 58618	Score: 131	Expect: 1.1e-008	Matches: 12
Complement component C9 OS=Bos taurus OX=9913 GN=C9 PE=1 SV=1					
	Observed	Mr(expt)	Mr(calcd)	ppm	Start End Miss Ions Peptide
	842.4471	841.4398	841.4480	-9.70	447 - 453 1 --- K.MKDAHLK.K
	868.4844	867.4771	867.4702	8.03	287 - 294 0 --- R.LLSSYSAK.Q
	1156.5005	1155.4932	1155.5706	-67.00	33 - 42 0 --- R.QGTPLPIDCR.M
	1175.5602	1174.5529	1174.6169	-54.42	295 - 303 1 --- K.QEKMFHLVK.G + Oxidation (M)
	1267.5582	1266.5509	1266.6357	-66.92	64 - 74 0 --- R.SIEIFGQFNGR.K
	1267.5582	1266.5510	1266.6357	-66.89	64 - 74 0 29 R.SIEIFGQFNGR.K
	1387.5682	1386.5609	1386.6568	-69.15	182 - 192 0 --- R.VWDGNTLTYYR.R
	1387.5682	1386.5610	1386.6568	-69.12	182 - 192 0 18 R.VWDGNTLTYYR.R
	1455.6167	1454.6094	1454.7041	-65.10	460 - 471 0 --- R.AIEDYINEFSVR.K
	1455.6167	1454.6094	1454.7041	-65.10	460 - 471 0 57 R.AIEDYINEFSVR.K
	1550.6960	1549.6887	1549.7889	-64.62	193 - 205 0 --- R.RPWNVASLTYDTK.A
	1550.6960	1549.6888	1549.7889	-64.60	193 - 205 0 --- R.RPWNVASLTYDTK.A
No match to: 805.4406, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 927.4218, 951.5530, 953.4604, 996.5237, 998.4718, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1165.6569, 1165.6569, 1184.6132, 1189.4962, 1247.6283, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938,					



1396.6301, 1439.7159, 1448.8251, 1475.6594, 1479.6964, 1479.6964, 1498.6063, 1513.6995, 1513.6995, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552

2. [A0A4W2FBY7](#) Mass: 63327 Score: 128 Expect: 2.1e-008 Matches: 12

Complement C9 OS=Bos indicus x Bos taurus OX=30522 GN=C9 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4471	841.4398	841.4480	-9.70	489	-	495	1	--- K.MKDAHLK.K
868.4844	867.4771	867.4702	8.03	287	-	294	0	--- R.LLSSYSAK.Q
1156.5005	1155.4932	1155.5706	-67.00	33	-	42	0	--- R.QGTPLPIDCR.M
1175.5602	1174.5529	1174.6169	-54.42	295	-	303	1	--- K.QEKMFLHVK.G + Oxidation (M)
1267.5582	1266.5509	1266.6357	-66.92	64	-	74	0	--- R.SIEIFGQFNGR.K
1267.5582	1266.5510	1266.6357	-66.89	64	-	74	0	29 R.SIEIFGQFNGR.K
1387.5682	1386.5609	1386.6568	-69.15	182	-	192	0	--- R.VWDGNILTYR.R
1387.5682	1386.5610	1386.6568	-69.12	182	-	192	0	18 R.VWDGNILTYR.R
1455.6167	1454.6094	1454.7041	-65.10	502	-	513	0	--- R.AIEDYINEFSVR.K
1455.6167	1454.6094	1454.7041	-65.10	502	-	513	0	57 R.AIEDYINEFSVR.K
1550.6960	1549.6887	1549.7889	-64.62	193	-	205	0	--- R.RPWNVASLTYDTK.A
1550.6960	1549.6888	1549.7889	-64.60	193	-	205	0	--- R.RPWNVASLTYDTK.A

No match to: 805.4406, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 927.4218, 951.5530, 953.4604, 996.5237, 998.4718, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1165.6569, 1165.6569, 1184.6132, 1189.4962, 1247.6283, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1396.6301, 1439.7159, 1448.8251, 1475.6594, 1479.6964, 1479.6964, 1498.6063, 1513.6995, 1513.6995, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552

3. [Q3MHN2](#) Mass: 63327 Score: 128 Expect: 2.1e-008 Matches: 12

Complement component C9 OS=Bos taurus OX=9913 GN=C9 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4471	841.4398	841.4480	-9.70	489	-	495	1	--- K.MKDAHLK.K
868.4844	867.4771	867.4702	8.03	287	-	294	0	--- R.LLSSYSAK.Q
1156.5005	1155.4932	1155.5706	-67.00	33	-	42	0	--- R.QGTPLPIDCR.M
1175.5602	1174.5529	1174.6169	-54.42	295	-	303	1	--- K.QEKMFLHVK.G + Oxidation (M)
1267.5582	1266.5509	1266.6357	-66.92	64	-	74	0	--- R.SIEIFGQFNGR.K
1267.5582	1266.5510	1266.6357	-66.89	64	-	74	0	29 R.SIEIFGQFNGR.K
1387.5682	1386.5609	1386.6568	-69.15	182	-	192	0	--- R.VWDGNILTYR.R
1387.5682	1386.5610	1386.6568	-69.12	182	-	192	0	18 R.VWDGNILTYR.R
1455.6167	1454.6094	1454.7041	-65.10	502	-	513	0	--- R.AIEDYINEFSVR.K
1455.6167	1454.6094	1454.7041	-65.10	502	-	513	0	57 R.AIEDYINEFSVR.K
1550.6960	1549.6887	1549.7889	-64.62	193	-	205	0	--- R.RPWNVASLTYDTK.A
1550.6960	1549.6888	1549.7889	-64.60	193	-	205	0	--- R.RPWNVASLTYDTK.A

No match to: 805.4406, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 927.4218, 951.5530, 953.4604, 996.5237, 998.4718, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1165.6569, 1165.6569, 1184.6132, 1189.4962, 1247.6283, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1396.6301, 1439.7159, 1448.8251, 1475.6594, 1479.6964, 1479.6964, 1498.6063, 1513.6995, 1513.6995, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552

4. [Q2KJF1](#) Mass: 54091 Score: 68 Expect: 0.022 Matches: 11

Alpha-1B-glycoprotein OS=Bos taurus OX=9913 GN=ALBG PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
805.4406	804.4333	804.4858	-65.20	148	-	154	0	--- R.GVTFLLR.L
919.3989	918.3916	918.4559	-69.98	288	-	295	0	--- R.SELAASR.D
998.4718	997.4645	997.5192	-54.85	249	-	257	0	--- R.GAEQLVPR.A
1142.5555	1141.5482	1141.6244	-66.72	415	-	425	0	--- R.ALWTGALTPGR.D
1142.5555	1141.5483	1141.6244	-66.68	415	-	425	0	--- R.ALWTGALTPGR.D
1175.5602	1174.5529	1174.6346	-69.57	81	-	91	0	--- R.FPLGPVTSTTR.G
1247.6283	1246.6210	1246.7146	-75.06	404	-	414	0	--- R.VDGPLPRPQLR.A
1498.6063	1497.5990	1497.6882	-59.53	269	-	283	0	--- R.LSALAAGDGSYTCR.Y
1513.6995	1512.6922	1512.7936	-67.06	357	-	370	0	27 R.VLSPAGPEAQFELR.G
1513.6995	1512.6922	1512.7936	-67.03	357	-	370	0	--- R.VLSPAGPEAQFELR.G
1647.7349	1646.7276	1646.8338	-64.46	431	-	444	0	--- R.CEAEVDPVSFLLLR.A

No match to: 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 927.4218, 951.5530, 953.4604, 996.5237, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1184.6132, 1189.4962, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1550.6960, 1550.6960, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552

5. [A0A4W2H1C4](#) Mass: 60879 Score: 64 Expect: 0.05 Matches: 11

Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
805.4406	804.4333	804.4858	-65.20	148	-	154	0	--- R.GVTFLLR.L
919.3989	918.3916	918.4559	-69.98	288	-	295	0	--- R.SELAASR.D
998.4718	997.4645	997.5192	-54.85	249	-	257	0	--- R.GAEQLVPR.A
1142.5555	1141.5482	1141.6244	-66.72	415	-	425	0	--- R.ALWTGALTPGR.D
1142.5555	1141.5483	1141.6244	-66.68	415	-	425	0	--- R.ALWTGALTPGR.D
1175.5602	1174.5529	1174.6346	-69.57	81	-	91	0	--- R.FPLGPVTSTTR.G
1247.6283	1246.6210	1246.7146	-75.06	404	-	414	0	--- R.VDGPLPRPQLR.A
1498.6063	1497.5990	1497.6882	-59.53	269	-	283	0	--- R.LSALAAGDGSYTCR.Y
1513.6995	1512.6922	1512.7936	-67.06	357	-	370	0	27 R.VLSPAGPEAQFELR.G
1513.6995	1512.6922	1512.7936	-67.03	357	-	370	0	--- R.VLSPAGPEAQFELR.G
1647.7349	1646.7276	1646.8338	-64.46	431	-	444	0	--- R.CEAEVDPVSFLLLR.A

No match to: 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 927.4218, 951.5530, 953.4604, 996.5237, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1184.6132, 1189.4962, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1550.6960, 1550.6960, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552

6. [A0A3Q1MJT2](#) Mass: 62948 Score: 63 Expect: 0.063 Matches: 11

Alpha-1B-glycoprotein OS=Bos taurus OX=9913 GN=ALBG PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
805.4406	804.4333	804.4858	-65.20	148	-	154	0	--- R.GVTFLLR.L
919.3989	918.3916	918.4559	-69.98	288	-	295	0	--- R.SELAASR.D
998.4718	997.4645	997.5192	-54.85	249	-	257	0	--- R.GAEQLVPR.A

1142.5555 1141.5482 1141.6244 -66.72 415 - 425 0 --- R.ALWTGALTTPGR.D
1142.5555 1141.5483 1141.6244 -66.68 415 - 425 0 --- R.ALWTGALTTPGR.D
1175.5602 1174.5529 1174.6346 -69.57 81 - 91 0 --- R.FPLGPVTSTTR.G
1247.6283 1246.6210 1246.7146 -75.06 404 - 414 0 --- R.VDGLPRPQLR.A
1498.6063 1497.5990 1497.6882 -59.53 269 - 283 0 --- R.LSALAAGDGSYTCR.Y
1513.6995 1512.6922 1512.7936 -67.06 357 - 370 0 27 R.VLSPAGPEAQFELR.G
1513.6995 1512.6922 1512.7936 -67.03 357 - 370 0 --- R.VLSPAGPEAQFELR.G
1647.7349 1646.7276 1646.8338 -64.46 431 - 444 0 --- R.CEAEPDVSFLLLR.A
No match to: 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 927.4218, 951.5530, 953.4604, 996.5237, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1184.6132, 1189.4962, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1550.6960, 1550.6960, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552

7. [A0A4W2EKQ3](#) Mass: 63006 Score: 63 Expect: 0.063 Matches: 11
Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
805.4406	804.4333	804.4858	-65.20	148	- 154	0	---	R.GVTFLLR.L
919.3989	918.3916	918.4559	-69.98	288	- 295	0	---	R.SELAASR.D
998.4718	997.4645	997.5192	-54.85	249	- 257	0	---	R.GAEEQLVPR.A
1142.5555	1141.5482	1141.6244	-66.72	415	- 425	0	---	R.ALWTGALTTPGR.D
1142.5555	1141.5483	1141.6244	-66.68	415	- 425	0	---	R.ALWTGALTTPGR.D
1175.5602	1174.5529	1174.6346	-69.57	81	- 91	0	---	R.FPLGPVTSTTR.G
1247.6283	1246.6210	1246.7146	-75.06	404	- 414	0	---	R.VDGLPRPQLR.A
1498.6063	1497.5990	1497.6882	-59.53	269	- 283	0	---	R.LSALAAGDGSYTCR.Y
1513.6995	1512.6922	1512.7936	-67.06	357	- 370	0	27	R.VLSPAGPEAQFELR.G
1513.6995	1512.6922	1512.7936	-67.03	357	- 370	0	---	R.VLSPAGPEAQFELR.G
1647.7349	1646.7276	1646.8338	-64.46	431	- 444	0	---	R.CEAEPDVSFLLLR.A

No match to: 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 927.4218, 951.5530, 953.4604, 996.5237, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1184.6132, 1189.4962, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1550.6960, 1550.6960, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552

8. [A0A4W2GYB4](#) Mass: 54132 Score: 61 Expect: 0.11 Matches: 10
Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
805.4406	804.4333	804.4858	-65.20	142	- 148	0	---	R.GVTFLLR.L
919.3989	918.3916	918.4559	-69.98	282	- 289	0	---	R.SELAASR.D
998.4718	997.4645	997.5192	-54.85	243	- 251	0	---	R.GAEEQLVPR.A
1142.5555	1141.5482	1141.6244	-66.72	417	- 427	0	---	R.ALWTGALTTPGR.D
1142.5555	1141.5483	1141.6244	-66.68	417	- 427	0	---	R.ALWTGALTTPGR.D
1175.5602	1174.5529	1174.6346	-69.57	75	- 85	0	---	R.FPLGPVTSTTR.G
1498.6063	1497.5990	1497.6882	-59.53	263	- 277	0	---	R.LSALAAGDGSYTCR.Y
1513.6995	1512.6922	1512.7936	-67.06	351	- 364	0	27	R.VLSPAGPEAQFELR.G
1513.6995	1512.6922	1512.7936	-67.03	351	- 364	0	---	R.VLSPAGPEAQFELR.G
1647.7349	1646.7276	1646.8338	-64.46	433	- 446	0	---	R.CEAEPDVSFLLLR.A

No match to: 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 927.4218, 951.5530, 953.4604, 996.5237, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1550.6960, 1550.6960, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552

9. [A0A4W2E798](#) Mass: 54147 Score: 61 Expect: 0.11 Matches: 10
Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1

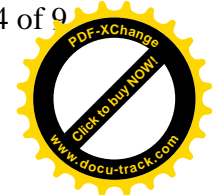
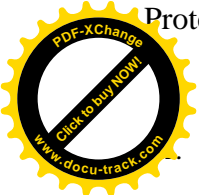
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
805.4406	804.4333	804.4858	-65.20	142	- 148	0	---	R.GVTFLLR.L
919.3989	918.3916	918.4559	-69.98	282	- 289	0	---	R.SELAASR.D
998.4718	997.4645	997.5192	-54.85	243	- 251	0	---	R.GAEEQLVPR.A
1142.5555	1141.5482	1141.6244	-66.72	417	- 427	0	---	R.ALWTGALTTPGR.D
1142.5555	1141.5483	1141.6244	-66.68	417	- 427	0	---	R.ALWTGALTTPGR.D
1175.5602	1174.5529	1174.6346	-69.57	75	- 85	0	---	R.FPLGPVTSTTR.G
1498.6063	1497.5990	1497.6882	-59.53	263	- 277	0	---	R.LSALAAGDGSYTCR.Y
1513.6995	1512.6922	1512.7936	-67.06	351	- 364	0	27	R.VLSPAGPEAQFELR.G
1513.6995	1512.6922	1512.7936	-67.03	351	- 364	0	---	R.VLSPAGPEAQFELR.G
1647.7349	1646.7276	1646.8338	-64.46	433	- 446	0	---	R.CEAEPDVSFLLLR.A

No match to: 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 927.4218, 951.5530, 953.4604, 996.5237, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1550.6960, 1550.6960, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552

10. [A0A4W2IFR5](#) Mass: 54987 Score: 60 Expect: 0.12 Matches: 10
Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
805.4406	804.4333	804.4858	-65.20	148	- 154	0	---	R.GVTFLLR.L
919.3989	918.3916	918.4559	-69.98	288	- 295	0	---	R.SELAASR.D
998.4718	997.4645	997.5192	-54.85	249	- 257	0	---	R.GAEEQLVPR.A
1142.5555	1141.5482	1141.6244	-66.72	423	- 433	0	---	R.ALWTGALTTPGR.D
1142.5555	1141.5483	1141.6244	-66.68	423	- 433	0	---	R.ALWTGALTTPGR.D
1175.5602	1174.5529	1174.6346	-69.57	81	- 91	0	---	R.FPLGPVTSTTR.G
1498.6063	1497.5990	1497.6882	-59.53	269	- 283	0	---	R.LSALAAGDGSYTCR.Y
1513.6995	1512.6922	1512.7936	-67.06	357	- 370	0	27	R.VLSPAGPEAQFELR.G
1513.6995	1512.6922	1512.7936	-67.03	357	- 370	0	---	R.VLSPAGPEAQFELR.G
1647.7349	1646.7276	1646.8338	-64.46	439	- 452	0	---	R.CEAEPDVSFLLLR.A

No match to: 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 927.4218, 951.5530, 953.4604, 996.5237, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1550.6960, 1550.6960, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552



A0A4W2E8B7 Mass: 55003 Score: 60 Expect: 0.12 Matches: 10

Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
805.4406	804.4333	804.4858	-65.20	148	154	0	---	R.GVTFLLR.L
919.3989	918.3916	918.4559	-69.98	288	295	0	---	R.SELAAWSR.D
998.4718	997.4645	997.5192	-54.85	249	257	0	---	R.GAEQLVPR.A
1142.5555	1141.5482	1141.6244	-66.72	423	433	0	---	R.ALWTGALTPGR.D
1142.5555	1141.5483	1141.6244	-66.68	423	433	0	---	R.ALWTGALTPGR.D
1175.5602	1174.5529	1174.6346	-69.57	81	91	0	---	R.FPLGPVSTTR.G
1498.6063	1497.5990	1497.6882	-59.53	269	283	0	---	R.LSALAAGDGSQYTCR.Y
1513.6995	1512.6922	1512.7936	-67.06	357	370	0	27	R.VLSPAGPEAQFELR.G
1513.6995	1512.6922	1512.7936	-67.03	357	370	0	---	R.VLSPAGPEAQFELR.G
1647.7349	1646.7276	1646.8338	-64.46	439	452	0	---	R.CEAEVDPVSFLLLR.A
No match to: 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 927.4218, 951.5530, 953.4604, 996.5237, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1550.6960, 1550.6960, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552								

12. **A0A3Q1LNN7** Mass: 68022 Score: 57 Expect: 0.25 Matches: 9

Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4861	-77.29	161	167	0	---	K.YLYEIAR.R
1017.5948	1016.5875	1016.5727	14.6	212	220	1	---	K.VLTSSARQR.L
1439.7159	1438.7086	1438.8045	-66.61	360	371	1	---	R.RHPEYAVSVLLR.L
1479.6964	1478.6891	1478.7881	-66.96	421	433	0	---	K.LGEYGFQNALIVR.Y
1479.6964	1478.6891	1478.7881	-66.96	421	433	0	10	K.LGEYGFQNALIVR.Y
1567.6414	1566.6341	1566.7354	-64.69	347	359	0	27	K.DAFLGSLFLEYYSR.R
1567.6414	1566.6341	1566.7354	-64.67	347	359	0	---	K.DAFLGSLFLEYYSR.R
1724.7261	1723.7188	1723.8273	-62.93	469	482	0	---	R.MPCTEDYLSLILNR.L
2044.9095	2043.9022	2044.0206	-57.93	168	183	1	---	R.RHPYFYAPELLEYANK.Y
No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1731.9867, 1901.1331, 2210.9834, 2283.0552								

13. **A0A4W2DDL5** Mass: 70207 Score: 56 Expect: 0.31 Matches: 9

Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4861	-77.29	152	158	0	---	K.YLYEIAR.R
1017.5948	1016.5875	1016.5727	14.6	203	211	1	---	K.VLTSSARQR.L
1439.7159	1438.7086	1438.8045	-66.61	351	362	1	---	R.RHPEYAVSVLLR.L
1479.6964	1478.6891	1478.7881	-66.96	412	424	0	---	K.LGEYGFQNALIVR.Y
1479.6964	1478.6891	1478.7881	-66.96	412	424	0	10	K.LGEYGFQNALIVR.Y
1567.6414	1566.6341	1566.7354	-64.69	338	350	0	27	K.DAFLGSLFLEYYSR.R
1567.6414	1566.6341	1566.7354	-64.67	338	350	0	---	K.DAFLGSLFLEYYSR.R
1724.7261	1723.7188	1723.8273	-62.93	460	473	0	---	R.MPCTEDYLSLILNR.L
2044.9095	2043.9022	2044.0206	-57.93	159	174	1	---	R.RHPYFYAPELLEYANK.Y
No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1731.9867, 1901.1331, 2210.9834, 2283.0552								

14. **A0A4W2D8T3** Mass: 76089 Score: 56 Expect: 0.33 Matches: 9

Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4861	-77.29	209	215	0	---	K.YLYEIAR.R
1017.5948	1016.5875	1016.5727	14.6	260	268	1	---	K.VLTSSARQR.L
1439.7159	1438.7086	1438.8045	-66.61	408	419	1	---	R.RHPEYAVSVLLR.L
1479.6964	1478.6891	1478.7881	-66.96	469	481	0	---	K.LGEYGFQNALIVR.Y
1479.6964	1478.6891	1478.7881	-66.96	469	481	0	10	K.LGEYGFQNALIVR.Y
1567.6414	1566.6341	1566.7354	-64.69	395	407	0	27	K.DAFLGSLFLEYYSR.R
1567.6414	1566.6341	1566.7354	-64.67	395	407	0	---	K.DAFLGSLFLEYYSR.R
1724.7261	1723.7188	1723.8273	-62.93	517	530	0	---	R.MPCTEDYLSLILNR.L
2044.9095	2043.9022	2044.0206	-57.93	216	231	1	---	R.RHPYFYAPELLEYANK.Y
No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1731.9867, 1901.1331, 2210.9834, 2283.0552								

15. **A0A140T897** Mass: 71274 Score: 56 Expect: 0.37 Matches: 9

Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4861	-77.29	161	167	0	---	K.YLYEIAR.R
1017.5948	1016.5875	1016.5727	14.6	212	220	1	---	K.VLTSSARQR.L
1439.7159	1438.7086	1438.8045	-66.61	360	371	1	---	R.RHPEYAVSVLLR.L
1479.6964	1478.6891	1478.7881	-66.96	421	433	0	---	K.LGEYGFQNALIVR.Y
1479.6964	1478.6891	1478.7881	-66.96	421	433	0	10	K.LGEYGFQNALIVR.Y
1567.6414	1566.6341	1566.7354	-64.69	347	359	0	27	K.DAFLGSLFLEYYSR.R
1567.6414	1566.6341	1566.7354	-64.67	347	359	0	---	K.DAFLGSLFLEYYSR.R
1724.7261	1723.7188	1723.8273	-62.93	469	482	0	---	R.MPCTEDYLSLILNR.L
2044.9095	2043.9022	2044.0206	-57.93	168	183	1	---	R.RHPYFYAPELLEYANK.Y
No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1731.9867, 1901.1331, 2210.9834, 2283.0552								

1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1731.9867, 1901.1331, 2210.9834, 2283.0552

16. A0A4W2EVR9 Mass: 71453 Score: 56 Expect: 0.37 Matches: 9

Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4861	-77.29	161	167	0	---	K.YLYEIAR.R
1017.5948	1016.5875	1016.5727	14.6	212	220	1	---	K.VLTSSARQR.L
1439.7159	1438.7086	1438.8045	-66.61	360	371	1	---	R.RHPEYAVSVLLR.L
1479.6964	1478.6891	1478.7881	-66.96	421	433	0	---	K.LGEYGFQNALIVR.Y
1479.6964	1478.6891	1478.7881	-66.96	421	433	0	10	K.LGEYGFQNALIVR.Y
1567.6414	1566.6341	1566.7354	-64.69	347	359	0	27	K.DAFLGSFLYEYSR.R
1567.6414	1566.6341	1566.7354	-64.67	347	359	0	---	K.DAFLGSFLYEYSR.R
1724.7261	1723.7188	1723.8273	-62.93	469	482	0	---	R.MPCTEDYLSLILNLR.L
2044.9095	2043.9022	2044.0206	-57.93	168	183	1	---	R.RHPYFYAPELLEYANK.Y

No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1731.9867, 1901.1331, 2210.9834, 2283.0552

17. A0A4W2EW60 Mass: 76020 Score: 55 Expect: 0.43 Matches: 9

Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4861	-77.29	161	167	0	---	K.YLYEIAR.R
1017.5948	1016.5875	1016.5727	14.6	212	220	1	---	K.VLTSSARQR.L
1439.7159	1438.7086	1438.8045	-66.61	360	371	1	---	R.RHPEYAVSVLLR.L
1479.6964	1478.6891	1478.7881	-66.96	421	433	0	---	K.LGEYGFQNALIVR.Y
1479.6964	1478.6891	1478.7881	-66.96	421	433	0	10	K.LGEYGFQNALIVR.Y
1567.6414	1566.6341	1566.7354	-64.69	347	359	0	27	K.DAFLGSFLYEYSR.R
1567.6414	1566.6341	1566.7354	-64.67	347	359	0	---	K.DAFLGSFLYEYSR.R
1724.7261	1723.7188	1723.8273	-62.93	469	482	0	---	R.MPCTEDYLSLILNLR.L
2044.9095	2043.9022	2044.0206	-57.93	168	183	1	---	R.RHPYFYAPELLEYANK.Y

No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1731.9867, 1901.1331, 2210.9834, 2283.0552

18. P02769 Mass: 71244 Score: 55 Expect: 0.46 Matches: 8

Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4861	-77.29	161	167	0	---	K.YLYEIAR.R
1439.7159	1438.7086	1438.8045	-66.61	360	371	1	---	R.RHPEYAVSVLLR.L
1479.6964	1478.6891	1478.7881	-66.96	421	433	0	---	K.LGEYGFQNALIVR.Y
1479.6964	1478.6891	1478.7881	-66.96	421	433	0	10	K.LGEYGFQNALIVR.Y
1567.6414	1566.6341	1566.7354	-64.69	347	359	0	27	K.DAFLGSFLYEYSR.R
1567.6414	1566.6341	1566.7354	-64.67	347	359	0	---	K.DAFLGSFLYEYSR.R
1724.7261	1723.7188	1723.8273	-62.93	469	482	0	---	R.MPCTEDYLSLILNLR.L
2044.9095	2043.9022	2044.0206	-57.93	168	183	1	---	R.RHPYFYAPELLEYANK.Y

No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1475.6594, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1731.9867, 1901.1331, 2210.9834, 2283.0552

19. C1J945 Mass: 56189 Score: 48 Expect: 2.1 Matches: 12

Nonstructural protein 5A (Fragment) OS=Bovine viral diarrhea virus OX=11099 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
805.4406	804.4333	804.4341	-1.00	68	75	0	---	R.NVSGSLTK.V
927.4218	926.4145	926.4974	-89.46	156	163	1	---	K.RYTGVPFK.G
1033.6263	1032.6190	1032.5716	45.9	91	99	1	---	R.GPVNRYRVTK.Y
1133.6357	1132.6284	1132.6427	-12.59	338	347	0	---	R.RPFVMVLGSK.T
1189.4962	1188.4889	1188.5921	-86.78	370	379	1	---	R.EIRDLMAEGR.M
1287.5924	1286.5851	1286.6507	-50.94	459	469	0	---	K.YHLVGDVVEVK.R
1557.7151	1556.7078	1556.7769	-44.40	143	155	1	---	K.WEVEHGVVTRMAK.R + Oxidation (M)
1567.6414	1566.6341	1566.7453	-71.01	387	399	0	---	R.EFDPPELSELVDFK.G
1567.6414	1566.6341	1566.7453	-70.99	387	399	0	---	R.EFDPPELSELVDFK.G
1724.7261	1723.7188	1723.8781	-92.37	100	113	1	---	K.YYDDDLKEIKPVAR.L
1731.9867	1730.9794	1730.8298	86.5	197	211	0	---	K.GCAFTYDYLTLNLNR.L
2044.9095	2043.9022	2044.0741	-84.11	107	123	1	---	K.EIKPVARLEGQVDHYYK.G

No match to: 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1017.5948, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1617.9590, 1647.7349, 1901.1331, 2210.9834, 2283.0552

20. A0A4W2EGF3 Mass: 97654 Score: 46 Expect: 3.8 Matches: 13

Dynamin 3 OS=Bos indicus x Bos taurus OX=30522 GN=DNM3 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4644	-53.82	272	279	0	---	R.MGTPHLQK.V + Oxidation (M)
1019.6071	1018.5998	1018.5672	32.0	229	237	1	---	R.RGYVGVVNR.S
1133.6357	1132.6284	1132.5910	33.0	247	256	1	---	K.DIKAAMLAER.K + Oxidation (M)
1136.6206	1135.6133	1135.6098	3.10	762	771	0	---	R.RPPSPPTQR.R
1142.5555	1141.5482	1141.6567	-95.05	510	519	1	---	K.NTIGNQVIRK.G
1142.5555	1141.5483	1141.6567	-95.01	509	518	1	---	K.KNTIGNQVIRK.K
1156.5005	1155.4932	1155.5560	-54.37	90	98	1	---	K.KFTDFDEV.R.H
1184.6132	1183.6059	1183.5729	27.9	158	166	0	---	R.EMIMQFITR.E + Oxidation (M)

1267.5582	1266.5509	1266.5703	-15.28	78	-	87	0	---	K.AEYAEFLHCK.G
1267.5582	1266.5510	1266.5703	-15.26	78	-	87	0	---	K.AEYAEFLHCK.G
1396.6301	1395.6228	1395.7068	-60.15	658	-	669	0	---	R.NLVDSYMISINK.C
1513.6995	1512.6922	1512.8412	-98.51	387	-	399	1	18	R.EISYAIKNIHGIR.T
1513.6995	1512.6922	1512.8412	-98.49	387	-	399	1	---	R.EISYAIKNIHGIR.T
No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1017.5948, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1139.4833, 1151.6481, 1165.6569, 1165.6569, 1175.5602, 1189.4962, 1247.6283, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1498.6063, 1550.6960, 1550.6960, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552									

21. [A0A3Q1MDN4](#) Mass: 96034 Score: 45 Expect: 4.1 Matches: 13

Uncharacterized protein OS=Bos taurus OX=9913 GN=DNM3 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4644	-53.82	272	- 279	0	---	R.MGTPHLQK.V + Oxidation (M)
1019.6071	1018.5998	1018.5672	32.0	229	- 237	1	---	R.RGYGVGVNR.S
1131.6298	1130.6225	1130.7063	-74.10	839	- 849	0	---	R.LPQGLPLALLP.-
1133.6357	1132.6284	1132.5910	33.0	247	- 256	1	---	K.DIKAAMLAER.K + Oxidation (M)
1142.5555	1141.5482	1141.6567	-95.05	510	- 519	1	---	K.NTIGNQVIRK.G
1142.5555	1141.5483	1141.6567	-95.01	509	- 518	1	---	K.KNTIGNQVIR.K
1156.5005	1155.4932	1155.5560	-54.37	90	- 98	1	---	K.KFTDFDEV.R.H
1184.6132	1183.6059	1183.5729	27.9	158	- 166	0	---	R.EMIMQFITR.E + Oxidation (M)
1267.5582	1266.5509	1266.5703	-15.28	78	- 87	0	---	K.AEYAEFLHCK.G
1267.5582	1266.5510	1266.5703	-15.26	78	- 87	0	---	K.AEYAEFLHCK.G
1396.6301	1395.6228	1395.7068	-60.15	654	- 665	0	---	R.NLVDSYMSINK.C
1513.6995	1512.6922	1512.8412	-98.51	387	- 399	1	18	R.EISYAIKNIHGIR.T
1513.6995	1512.6922	1512.8412	-98.49	387	- 399	1	---	R.EISYAIKNIHGIR.T
No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1017.5948, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1136.6206, 1139.4833, 1151.6481, 1165.6569, 1165.6569, 1175.5602, 1189.4962, 1247.6283, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1498.6063, 1550.6960, 1550.6960, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552								

22. [A0A4W2EI53](#) Mass: 63308 Score: 44 Expect: 5.7 Matches: 11

Dynamitin 3 OS=Bos indicus x Bos taurus OX=30522 GN=DNM3 PE=3 SV=1

observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4644	-53.82	272	-	279	0 ---	R.MGTPHLQK.V + Oxidation (M)
1019.6071	1018.5998	1018.5672	32.0	229	-	237	1 ---	R.RGYVGVVNR.S
1133.6357	1132.6284	1132.5910	33.0	247	-	256	1 ---	K.DIKAAMLAER.K + Oxidation (M)
1142.5555	1141.5482	1141.6567	-95.05	510	-	519	1 ---	K.NTIGNQVIRK.G
1142.5555	1141.5483	1141.6567	-95.01	509	-	518	1 ---	K.KNTIGNQVIR.K
1156.5005	1155.4932	1155.5560	-54.37	90	-	98	1 ---	K.KFTDFDEVR.H
1184.6132	1183.6059	1183.5729	27.9	158	-	166	0 ---	R.EMIMQFITR.E + Oxidation (M)
1267.5582	1266.5509	1266.5703	-15.28	78	-	87	0 ---	K.AEYAEFLHCK.G
1267.5582	1266.5510	1266.5703	-15.26	78	-	87	0 ---	K.AEYAEFLHCK.G
1513.6995	1512.6922	1512.8412	-98.51	387	-	399	1 18	R.EISYAIKNIHGIR.T
1513.6995	1512.6922	1512.8412	-98.49	387	-	399	1 ---	R.EISYAIKNIHGIR.T
No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1017.5948, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1136.6206, 1139.4833, 1151.6481, 1165.6569, 1165.6569, 1175.5602, 1189.4962, 1247.6283, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1498.6063, 1550.6960, 1550.6960, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552								

23. [A0A4W2IJA6](#) Mass: 101091 Score: 43 Expect: 7.1 Matches: 14

Family with sequence similarity 111 member B OS=Bos indicus x Bos taurus OX=30522 GN=FAM11B PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4471	841.4398	841.5021	-74.03	528	-	534	0 ---	K.NLQILNK.V
998.4718	997.4645	997.5015	-37.06	289	-	297	0 ---	R.CLPSGSHLK.I
1017.5948	1016.5875	1016.5363	50.4	88	-	96	1 ---	R.NLDRGSLSR.H
1045.4912	1044.4839	1044.5815	-93.44	391	-	400	0 ---	K.QSIVDIVSGK.V
1136.6206	1135.6133	1135.5305	72.9	32	-	41	1 ---	R.RCPHDAPGAR.L
1156.5005	1155.4932	1155.5309	-32.56	553	-	560	1 ---	K.YFQEERER.M
1247.6283	1246.6210	1246.6094	9.31	486	-	494	1 ---	R.YYNNILYKR.L
1305.5656	1304.5583	1304.6435	-65.27	642	-	652	0 ---	K.SWPDIISTCVK.V
1396.6301	1395.6228	1395.6743	-36.85	3	-	15	0 ---	K.GQDGLKPDPEQGR.G
1475.6594	1474.6521	1474.7892	-92.97	628	-	640	0 ---	R.HVLHLIVGESTDR.K
1557.7151	1556.7078	1556.6703	24.1	449	-	461	1 ---	K.DGETEDVEHNREK.I
1567.6414	1566.6341	1566.7402	-67.71	800	-	812	0 7	K.LVAMHSFGHFYSR.V + Oxidation (M)
1567.6414	1566.6341	1566.7402	-67.69	800	-	812	0 ---	K.LVAMHSFGHFYSR.V + Oxidation (M)
2044.9095	2043.9022	2044.0340	-64.45	642	-	658	1 ---	K.SWPDIISTCVKVTFITYK.E
No match to: 805.4406, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 927.4218, 951.5530, 953.4604, 996.5237, 1019.6071, 1033.6263, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1479.6964, 1479.6964, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2210.9834, 2283.0552								

24. [A0A4W2ED96](#) Mass: 52578 Score: 42 Expect: 7.7 Matches: 13

6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1 OS=Bos indicus x Bos taurus OX=30522 GN=PFKFB1 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.4734	849.4661	849.4014	76.2	1	-	7	1	--- -.MEEKASR.R
996.5237	995.5164	995.5189	-2.45	52	-	59	0	--- K.VFNLGQYR.R
1019.6071	1018.5998	1018.5811	18.4	166	-	173	1	--- K.VLEDFLKR.I
1051.6328	1050.6255	1050.5233	97.3	385	-	393	0	--- K.SSDELPYLK.C
1051.6328	1050.6255	1050.5233	97.3	385	-	393	0	--- K.SSDELPYLK.C
1142.5555	1141.5482	1141.5842	-31.47	376	-	384	0	--- R.CLLAYFLDK.S
1142.5555	1141.5483	1141.5842	-31.44	376	-	384	0	--- R.CLLAYFLDK.S
1267.5582	1266.5509	1266.6429	-72.59	236	-	246	1	--- R.HGESENLNRGR.I
1267.5582	1266.5510	1266.6429	-72.57	236	-	246	1	13 R.HGESENLNRGR.I
1479.6964	1478.6891	1478.7478	-39.65	104	-	116	1	--- R.VAVFDATNTTTRER.R
1479.6964	1478.6891	1478.7478	-39.64	104	-	116	1	--- R.VAVFDATNTTTRER.R
1567.6414	1566.6341	1566.6984	-41.06	153	-	165	1	--- K.LGSPDYIDCDREK.V

1567.6414 1566.6341 1566.6984 -41.03 153 - 165 1 --- K.LGSPDYIDCDREK.V
No match to: 805.4406, 842.4471, 848.4654, 849.9925, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 927.4218, 951.5530, 953.4604, 998.4718, 1017.5948, 1033.6263, 1045.4912, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552

25. [A0A3Q1LXR0](#) Mass: 52578 Score: 42 Expect: 7.7 Matches: 13
6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 OS=Bos taurus OX=9913 GN=PFKFB1 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.4734	849.4661	849.4014	76.2	1	-	7	1	--MEEKASR.R
996.5237	995.5164	995.5189	-2.45	52	-	59	0	--K.VFNLGQYR.R
1019.6071	1018.5998	1018.5811	18.4	166	-	173	1	--K.VLEDFLKR.I
1051.6328	1050.6255	1050.5233	97.3	385	-	393	0	--K.SSDELPYLK.C
1051.6328	1050.6255	1050.5233	97.3	385	-	393	0	--K.SSDELPYLK.C
1142.5555	1141.5482	1141.5842	-31.47	376	-	384	0	--R.CLLAYFLDK.S
1142.5555	1141.5483	1141.5842	-31.44	376	-	384	0	--R.CLLAYFLDK.S
1267.5582	1266.5509	1266.6429	-72.59	236	-	246	1	--R.HGESENLNRGR.I
1267.5582	1266.5510	1266.6429	-72.57	236	-	246	1	13 R.HGESENLNRGR.I
1479.6964	1478.6891	1478.7478	-39.65	104	-	116	1	--R.VAVFDATNTTTRER.R
1479.6964	1478.6891	1478.7478	-39.64	104	-	116	1	--R.VAVFDATNTTTRER.R
1567.6414	1566.6341	1566.6984	-41.06	153	-	165	1	--K.LGSPDYIDCDREK.V
1567.6414	1566.6341	1566.6984	-41.03	153	-	165	1	--K.LGSPDYIDCDREK.V
No match to: 805.4406, 842.4471, 848.4654, 849.9925, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 927.4218, 951.5530, 953.4604, 998.4718, 1017.5948, 1033.6263, 1045.4912, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552								

26. [A0A4W2EAW9](#) Mass: 72734 Score: 40 Expect: 13 Matches: 11
Dynamilin 3 OS=Bos indicus x Bos taurus OX=30522 GN=DNM3 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4644	-53.82	272	-	279	0	--R.MGTPHLQK.V + Oxidation (M)
1019.6071	1018.5998	1018.5672	32.0	229	-	237	1	--R.RGVYGVVNR.S
1133.6357	1132.6284	1132.5910	33.0	247	-	256	1	--K.DIKAAMLAER.K + Oxidation (M)
1142.5555	1141.5482	1141.6567	-95.05	510	-	519	1	--K.NTIGNQVIRK.G
1142.5555	1141.5483	1141.6567	-95.01	509	-	518	1	--K.NTIGNQVIRK.G
1156.5005	1155.4932	1155.5560	-54.37	90	-	98	1	--K.KFTDFDEVR.H
1184.6132	1183.6059	1183.5729	27.9	158	-	166	0	--R.EMIMQFTR.E + Oxidation (M)
1267.5582	1266.5509	1266.5703	-15.28	78	-	87	0	--K.AEYAEFLHCK.G
1267.5582	1266.5510	1266.5703	-15.26	78	-	87	0	--K.AEYAEFLHCK.G
1513.6995	1512.6922	1512.8412	-98.51	387	-	399	1	18 R.EISYAIKNIHGIR.T
1513.6995	1512.6922	1512.8412	-98.49	387	-	399	1	--R.EISYAIKNIHGIR.T
No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1017.5948, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1136.6206, 1139.4833, 1151.6481, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552								

27. [A0A4W2GW83](#) Mass: 70119 Score: 40 Expect: 13 Matches: 6
Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1

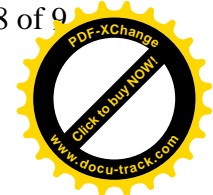
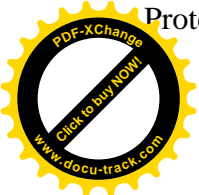
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4861	-77.29	152	-	158	0	--K.YLYEIAER.R
1017.5948	1016.5875	1016.5727	14.6	203	-	211	1	--K.VLTSSARQR.L
1439.7159	1438.7086	1438.8045	-66.61	351	-	362	1	--R.RHPEYAVSVLLR.L
1567.6414	1566.6341	1566.7354	-64.69	338	-	350	0	27 K.DAFLGSFLYEYSR.R
1567.6414	1566.6341	1566.7354	-64.67	338	-	350	0	--K.DAFLGSFLYEYSR.R
2044.9095	2043.9022	2044.0206	-57.93	159	-	174	1	--R.RHPYFYAPELLYYANK.Y
No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2210.9834, 2283.0552								

28. [B0JYQ0](#) Mass: 71244 Score: 40 Expect: 14 Matches: 6
ALB protein OS=Bos taurus OX=9913 GN=ALB PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4861	-77.29	161	-	167	0	--K.YLYEIAER.R
1017.5948	1016.5875	1016.5727	14.6	212	-	220	1	--K.VLTSSARQR.L
1439.7159	1438.7086	1438.8045	-66.61	360	-	371	1	--R.RHPEYAVSVLLR.L
1567.6414	1566.6341	1566.7354	-64.69	347	-	359	0	27 K.DAFLGSFLYEYSR.R
1567.6414	1566.6341	1566.7354	-64.67	347	-	359	0	--K.DAFLGSFLYEYSR.R
2044.9095	2043.9022	2044.0206	-57.93	168	-	183	1	--R.RHPYFYAPELLYYANK.Y
No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2210.9834, 2283.0552								

29. [A0A4W2D9L2](#) Mass: 98304 Score: 39 Expect: 16 Matches: 11
Dynamilin 3 OS=Bos indicus x Bos taurus OX=30522 GN=DNM3 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4644	-53.82	272	-	279	0	--R.MGTPHLQK.V + Oxidation (M)
1019.6071	1018.5998	1018.5672	32.0	229	-	237	1	--R.RGVYGVVNR.S
1133.6357	1132.6284	1132.5910	33.0	247	-	256	1	--K.DIKAAMLAER.K + Oxidation (M)
1136.6206	1135.6133	1135.6098	3.10	768	-	777	0	--R.RPPSPPTTQR.R
1156.5005	1155.4932	1155.5560	-54.37	90	-	98	1	--K.KFTDFDEVR.H
1184.6132	1183.6059	1183.5729	27.9	158	-	166	0	--R.EMIMQFTR.E + Oxidation (M)
1267.5582	1266.5509	1266.5703	-15.28	78	-	87	0	--K.AEYAEFLHCK.G



1267.5582 1266.5510 1266.5703 -15.26 78 - 87 0 --- K.AEYAEFLHCK.G
 1396.6301 1395.6228 1395.7068 -60.15 664 - 675 0 --- R.NLVDSYMSIINK.C
 1513.6995 1512.6922 1512.8412 -98.51 387 - 399 1 18 R.EISYAIKNIHGIR.T
 1513.6995 1512.6922 1512.8412 -98.49 387 - 399 1 --- R.EISYAIKNIHGIR.T

No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1017.5948, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1165.6569, 1165.6569, 1175.5602, 1189.4962, 1247.6283, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1439.7159, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1498.6063, 1550.6960, 1550.6960, 1557.7151, 1567.6414, 1567.6414, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2044.9095, 2210.9834, 2283.0552

30. A0A4W2IKT9 Mass: 75992 Score: 39 Expect: 17 Matches: 6

Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1

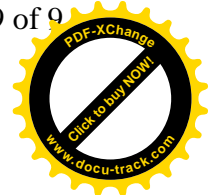
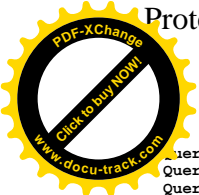
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4218	926.4145	926.4861	-77.29	161	-	167	0	--- K.YLYEIAR.R
1017.5948	1016.5875	1016.5727	14.6	212	-	220	1	--- K.VLTSSARQR.L
1439.7159	1438.7086	1438.8045	-66.61	360	-	371	1	--- R.RHPEYAVSVLLR.L
1567.6414	1566.6341	1566.7354	-64.69	347	-	359	0	27 K.DAFLGSFLYEYSR.R
1567.6414	1566.6341	1566.7354	-64.67	347	-	359	0	--- K.DAFLGSFLYEYSR.R
2044.9095	2043.9022	2044.0206	-57.93	168	-	183	1	--- R.RHPFYFAPELLYYANK.Y

No match to: 805.4406, 842.4471, 848.4654, 849.9925, 850.4734, 853.4557, 864.4832, 865.9639, 868.4844, 870.4808, 876.9719, 882.5003, 882.5003, 892.9417, 908.9123, 919.3989, 951.5530, 953.4604, 996.5237, 998.4718, 1019.6071, 1033.6263, 1045.4912, 1051.6328, 1051.6328, 1065.5367, 1131.6298, 1133.6357, 1136.6206, 1139.4833, 1142.5555, 1142.5555, 1151.6481, 1156.5005, 1165.6569, 1165.6569, 1175.5602, 1184.6132, 1189.4962, 1247.6283, 1267.5582, 1267.5582, 1268.5472, 1287.5924, 1300.7646, 1305.5656, 1311.6147, 1334.7938, 1334.7938, 1387.5682, 1387.5682, 1396.6301, 1448.8251, 1455.6167, 1455.6167, 1475.6594, 1479.6964, 1479.6964, 1498.6063, 1513.6995, 1513.6995, 1550.6960, 1550.6960, 1557.7151, 1617.9590, 1647.7349, 1724.7261, 1731.9867, 1901.1331, 2210.9834, 2283.0552

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

Query1 (805.4406,1+): <no title>
 Query2 (842.4471,1+): <no title>
 Query3 (848.4654,1+): <no title>
 Query4 (849.9925,1+): <no title>
 Query5 (850.4734,1+): <no title>
 Query6 (853.4557,1+): <no title>
 Query7 (864.4832,1+): <no title>
 Query8 (865.9639,1+): <no title>
 Query9 (868.4844,1+): <no title>
 Query10 (870.4808,1+): <no title>
 Query11 (876.9719,1+): <no title>
 Query12 (882.5003,1+): <no title>
 Query13 (882.5003,1+): Locus:1..14.0.7
 Query14 (892.9417,1+): <no title>
 Query15 (908.9123,1+): <no title>
 Query16 (919.3989,1+): <no title>
 Query17 (927.4218,1+): <no title>
 Query18 (951.5530,1+): <no title>
 Query19 (953.4604,1+): <no title>
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 Query21 (998.4718,1+): <no title>
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 Query23 (1019.6071,1+): <no title>
 Query24 (1033.6263,1+): <no title>
 Query25 (1045.4912,1+): <no title>
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 Query30 (1133.6357,1+): <no title>
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 Query43 (1267.5582,1+): <no title>
 Query44 (1267.5582,1+): Locus:1..14.0.2
 Query45 (1268.5472,1+): <no title>
 Query46 (1287.5924,1+): <no title>
 Query47 (1300.7646,1+): <no title>
 Query48 (1305.5656,1+): <no title>
 Query49 (1311.6147,1+): <no title>
 Query50 (1334.7938,1+): <no title>
 Query51 (1334.7938,1+): Locus:1..14.0.9
 Query52 (1387.5682,1+): <no title>
 Query53 (1387.5682,1+): Locus:1..14.0.3
 Query54 (1396.6301,1+): <no title>
 Query55 (1439.7159,1+): <no title>
 Query56 (1448.8251,1+): <no title>
 Query57 (1455.6167,1+): <no title>
 Query58 (1455.6167,1+): Locus:1..14.0.1
 Query59 (1475.6594,1+): <no title>
 Query60 (1479.6964,1+): <no title>
 Query61 (1479.6964,1+): Locus:1..14.0.5
 Query62 (1498.6063,1+): <no title>
 Query63 (1513.6995,1+): Locus:1..14.0.4



Query64 (1513.6995,1+): <no title>
Query65 (1550.6960,1+): <no title>
Query66 (1550.6960,1+): Locus:1..14.0.11
Query67 (1557.7151,1+): <no title>
Query68 (1567.6414,1+): Locus:1..14.0.8
Query69 (1567.6414,1+): <no title>
Query70 (1617.9590,1+): <no title>
Query71 (1647.7349,1+): <no title>
Query72 (1724.7261,1+): <no title>
Query73 (1731.9867,1+): <no title>
Query74 (1901.1331,1+): <no title>
Query75 (2044.9095,1+): <no title>
Query76 (2210.9834,1+): <no title>
Query77 (2283.0552,1+): <no title>

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