

MASCOT Search Results

User :
 Email :
 Search title : BAEDW\2020_3_5\2020_3_5\MSMS 14\N19
 Database : Uniprot_bovine bovine_20200316 (134392 sequences; 76244912 residues)
 Timestamp : 31 Mar 2020 at 01:08:58 GMT
 Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
 Top Score : 98 for Q2KJF1, Alpha-1B-glycoprotein OS=Bos taurus OX=9913 GN=ALBG PE=1 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 ions scores as a non-probabilistic basis for ranking protein hits.

Error: try setting browser cache to automatic.

Protein Summary Report

Format As Protein Summary (deprecated) [Help](#)

Significance threshold $p < 0.05$ Max. number of hits 30

Preferred taxonomy All entries

Index

	Accession	Mass	Score	Description
1.	Q2KJF1	54091	98	Alpha-1B-glycoprotein OS=Bos taurus OX=9913 GN=ALBG PE=1 SV=1
2.	A0A4W2GYB4	54132	97	Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1
3.	A0A4W2E798	54147	97	Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1
4.	A0A4W2IFR5	54987	97	Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1
5.	A0A4W2EBB7	55003	97	Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1
6.	A0A4W2H1C4	60879	94	Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1
7.	A0A3Q1MJT2	62948	93	Alpha-1B-glycoprotein OS=Bos taurus OX=9913 GN=ALBG PE=1 SV=1
8.	A0A4W2EKQ3	63006	93	Alpha-1-B glycoprotein OS=Bos indicus x Bos taurus OX=30522 GN=ALBG PE=4 SV=1
9.	A0A4W2IGA3	80257	50	Kinesin-like protein OS=Bos indicus x Bos taurus OX=30522 GN=KIF3B PE=3 SV=1
10.	A0A3Q1MG81	80257	50	Kinesin-like protein OS=Bos taurus OX=9913 GN=KIF3B PE=3 SV=1
11.	A0A4W2H2X1	84971	49	Kinesin-like protein OS=Bos indicus x Bos taurus OX=30522 GN=KIF3B PE=3 SV=1
12.	F1N020	84971	49	Kinesin-like protein OS=Bos taurus OX=9913 GN=KIF3B PE=3 SV=2
13.	A0A4W2F5Q7	26142	41	Peroxisomal protein 2A OS=Bos indicus x Bos taurus OX=30522 GN=PRXL2A PE=4 SV=1
14.	A0A3Q1LNN7	68022	41	Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=4 SV=1
15.	A0A452DI98	15508	41	U6 snRNA-associated Sm-like protein LSM4 OS=Bos taurus OX=9913 GN=LSM4 PE=3 SV=1
16.	A0A4W2FGN9	123016	40	Coiled-coil domain containing 150 OS=Bos indicus x Bos taurus OX=30522 GN=CCDC150 PE=4 SV=1
17.	A0A4W2I014	105104	40	Protein phosphatase 1 regulatory subunit 21 OS=Bos indicus x Bos taurus OX=30522 GN=PPP1R21 PE=4 SV=1
18.	A0A4W2CGR1	105032	40	Protein phosphatase 1 regulatory subunit 21 OS=Bos indicus x Bos taurus OX=30522 GN=PPP1R21 PE=4 SV=1
19.	A0A4W2DDL5	70207	40	Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1
20.	A0A140T897	71274	40	Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=4 SV=1
21.	A0A4W2EVR9	71453	40	Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1
22.	A0A4W2DGX3	13967	40	U6 snRNA-associated Sm-like protein LSM4 OS=Bos indicus x Bos taurus OX=30522 GN=LSM4 PE=3 SV=1
23.	A0A4W2HT62	15511	39	U6 snRNA-associated Sm-like protein LSM4 OS=Bos indicus x Bos taurus OX=30522 GN=LSM4 PE=3 SV=1
24.	Q3ZBK6	15511	39	U6 snRNA-associated Sm-like protein LSM4 OS=Bos taurus OX=9913 GN=LSM4 PE=2 SV=1
25.	A0A4W2EW60	76020	39	Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1
26.	A0A4W2D8T3	76089	39	Albumin OS=Bos indicus x Bos taurus OX=30522 GN=ALB PE=4 SV=1
27.	A0A4W2HAU5	24454	38	Peroxisomal protein 2A OS=Bos indicus x Bos taurus OX=30522 GN=PRXL2A PE=4 SV=1
28.	Q3ZBK2	24454	38	Peroxisomal protein 2A OS=Bos taurus OX=9913 GN=PRXL2A PE=2 SV=1
29.	A0A4W2H5Z2	33370	37	Ketohexokinase OS=Bos indicus x Bos taurus OX=30522 GN=KHK PE=4 SV=1
30.	P02769	71244	36	Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4

Results List

1.	Q2KJF1	Mass: 54091	Score: 98	Expect: 2.4e-005	Matches: 12
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
805.4537	804.4464	804.4858	-48.92	148 - 154	0 --- R.GVTFLLR.L
919.4136	918.4063	918.4559	-53.98	288 - 295	0 --- R.SELAAWSR.D
1142.5725	1141.5652	1141.6244	-51.83	415 - 425	0 --- R.ALWTGALTPGR.D
1142.5725	1141.5652	1141.6244	-51.82	415 - 425	0 --- R.ALWTGALTPGR.D
1175.5778	1174.5705	1174.6346	-54.59	81 - 91	0 --- R.FPLGPVTSFTR.G
1457.7133	1456.7060	1456.7773	-48.93	487 - 499	0 --- R.SLLSELSDPVELR.V
1498.6241	1497.6168	1497.6882	-47.65	269 - 283	0 --- R.LSALAAGDGSYGTCR.Y
1513.7238	1512.7165	1512.7936	-51.00	357 - 370	0 27 R.VLSPAGPEAQFELR.G
1513.7238	1512.7165	1512.7936	-50.97	357 - 370	0 --- R.VLSPAGPEAQFELR.G
1647.7585	1646.7512	1646.8338	-50.13	431 - 444	0 --- R.CEAEPVDVSFLLLR.A
1647.7585	1646.7513	1646.8338	-50.11	431 - 444	0 27 R.CEAEPVDVSFLLLR.A
2530.2642	2529.2569	2529.3374	-31.80	224 - 247	0 --- K.VLRPGSSASLTCVAPLSGVDFQLR.R
No match to: 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1194.5631,					

1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806

2.

AOA4W2GYB4

Mass: 54132

Score: 97

Expect: 2.4e-005

Matches: 12

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
805.4537	804.4464	804.4858	-48.92	142	148	0	---	R.GVTFLLR.L
919.4136	918.4063	918.4559	-53.98	282	289	0	---	R.SELAAWSR.D
1142.5725	1141.5652	1141.6244	-51.83	417	427	0	---	R.ALWTGALTPGR.D
1142.5725	1141.5652	1141.6244	-51.82	417	427	0	---	R.ALWTGALTPGR.D
1175.5778	1174.5705	1174.6346	-54.59	75	85	0	---	R.FPLGPVTSTTR.G
1457.7133	1456.7060	1456.7773	-48.93	489	501	0	---	R.SLLSELSDPVELR.V
1498.6241	1497.6168	1497.6882	-47.65	263	277	0	---	R.LSALAAGDGSGYTCR.Y
1513.7238	1512.7165	1512.7936	-51.00	351	364	0	27	R.VLSPAGPEAQFELR.G
1513.7238	1512.7165	1512.7936	-50.97	351	364	0	---	R.VLSPAGPEAQFELR.G
1647.7585	1646.7512	1646.8338	-50.13	433	446	0	---	R.CEAEVPDVSFLLLR.A
1647.7585	1646.7513	1646.8338	-50.11	433	446	0	27	R.CEAEVPDVSFLLLR.A
2530.2642	2529.2569	2529.3374	-31.80	218	241	0	---	K.VLRPGSSASLTCVAPLSGVDFQLR.R

No match to: 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806

3.

AOA4W2E798

Mass: 54147

Score: 97

Expect: 2.4e-005

Matches: 12

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
805.4537	804.4464	804.4858	-48.92	142	148	0	---	R.GVTFLLR.L
919.4136	918.4063	918.4559	-53.98	282	289	0	---	R.SELAAWSR.D
1142.5725	1141.5652	1141.6244	-51.83	417	427	0	---	R.ALWTGALTPGR.D
1142.5725	1141.5652	1141.6244	-51.82	417	427	0	---	R.ALWTGALTPGR.D
1175.5778	1174.5705	1174.6346	-54.59	75	85	0	---	R.FPLGPVTSTTR.G
1457.7133	1456.7060	1456.7773	-48.93	489	501	0	---	R.SLLSELSDPVELR.V
1498.6241	1497.6168	1497.6882	-47.65	263	277	0	---	R.LSALAAGDGSGYTCR.Y
1513.7238	1512.7165	1512.7936	-51.00	351	364	0	27	R.VLSPAGPEAQFELR.G
1513.7238	1512.7165	1512.7936	-50.97	351	364	0	---	R.VLSPAGPEAQFELR.G
1647.7585	1646.7512	1646.8338	-50.13	433	446	0	---	R.CEAEVPDVSFLLLR.A
1647.7585	1646.7513	1646.8338	-50.11	433	446	0	27	R.CEAEVPDVSFLLLR.A
2530.2642	2529.2569	2529.3374	-31.80	218	241	0	---	K.VLRPGSSASLTCVAPLSGVDFQLR.R

No match to: 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806

4.

AOA4W2IFR5

Mass: 54987

Score: 97

Expect: 2.6e-005

Matches: 12

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
805.4537	804.4464	804.4858	-48.92	148	154	0	---	R.GVTFLLR.L
919.4136	918.4063	918.4559	-53.98	288	295	0	---	R.SELAAWSR.D
1142.5725	1141.5652	1141.6244	-51.83	423	433	0	---	R.ALWTGALTPGR.D
1142.5725	1141.5652	1141.6244	-51.82	423	433	0	---	R.ALWTGALTPGR.D
1175.5778	1174.5705	1174.6346	-54.59	81	91	0	---	R.FPLGPVTSTTR.G
1457.7133	1456.7060	1456.7773	-48.93	495	507	0	---	R.SLLSELSDPVELR.V
1498.6241	1497.6168	1497.6882	-47.65	269	283	0	---	R.LSALAAGDGSGYTCR.Y
1513.7238	1512.7165	1512.7936	-51.00	357	370	0	27	R.VLSPAGPEAQFELR.G
1513.7238	1512.7165	1512.7936	-50.97	357	370	0	---	R.VLSPAGPEAQFELR.G
1647.7585	1646.7512	1646.8338	-50.13	439	452	0	---	R.CEAEVPDVSFLLLR.A
1647.7585	1646.7513	1646.8338	-50.11	439	452	0	27	R.CEAEVPDVSFLLLR.A
2530.2642	2529.2569	2529.3374	-31.80	224	247	0	---	K.VLRPGSSASLTCVAPLSGVDFQLR.R

No match to: 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806

5.

AOA4W2E8B7

Mass: 55003

Score: 97

Expect: 2.6e-005

Matches: 12

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
805.4537	804.4464	804.4858	-48.92	148	154	0	---	R.GVTFLLR.L
919.4136	918.4063	918.4559	-53.98	288	295	0	---	R.SELAAWSR.D
1142.5725	1141.5652	1141.6244	-51.83	423	433	0	---	R.ALWTGALTPGR.D
1142.5725	1141.5652	1141.6244	-51.82	423	433	0	---	R.ALWTGALTPGR.D
1175.5778	1174.5705	1174.6346	-54.59	81	91	0	---	R.FPLGPVTSTTR.G
1457.7133	1456.7060	1456.7773	-48.93	495	507	0	---	R.SLLSELSDPVELR.V
1498.6241	1497.6168	1497.6882	-47.65	269	283	0	---	R.LSALAAGDGSGYTCR.Y
1513.7238	1512.7165	1512.7936	-51.00	357	370	0	27	R.VLSPAGPEAQFELR.G
1513.7238	1512.7165	1512.7936	-50.97	357	370	0	---	R.VLSPAGPEAQFELR.G
1647.7585	1646.7512	1646.8338	-50.13	439	452	0	---	R.CEAEVPDVSFLLLR.A
1647.7585	1646.7513	1646.8338	-50.11	439	452	0	27	R.CEAEVPDVSFLLLR.A
2530.2642	2529.2569	2529.3374	-31.80	224	247	0	---	K.VLRPGSSASLTCVAPLSGVDFQLR.R

No match to: 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806

6.

AOA4W2H1C4

Mass: 60879

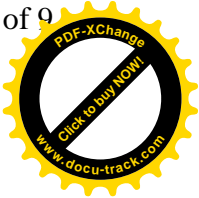
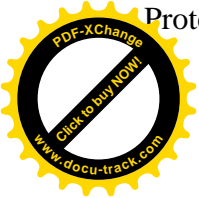
Score: 94

Expect: 5.6e-005

Matches: 12

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

http://203.255.41.217/mascot/cgi/master_results.pl?file=../data/20200330/F002155.da... 2021-01-19



Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
805.4537	804.4464	804.4858	-48.92	148	-	154	0 ---	R.GVTFLLR.L
919.4136	918.4063	918.4559	-53.98	288	-	295	0 ---	R.SELAAWSR.D
1142.5725	1141.5652	1141.6244	-51.83	415	-	425	0 ---	R.ALWTGALTPGR.D
1142.5725	1141.5652	1141.6244	-51.82	415	-	425	0 ---	R.ALWTGALTPGR.D
1175.5778	1174.5705	1174.6346	-54.59	81	-	91	0 ---	R.FPLGPGVTSTTR.G
1457.7133	1456.7060	1456.7773	-48.93	487	-	499	0 ---	R.SLLSELSDPVELR.V
1498.6241	1497.6168	1497.6882	-47.65	269	-	283	0 ---	R.LSALAAGDGSQYTCR.Y
1513.7238	1512.7165	1512.7936	-51.00	357	-	370	0 27	R.VLSPAGPEAQFELR.G
1513.7238	1512.7165	1512.7936	-50.97	357	-	370	0 ---	R.VLSPAGPEAQFELR.G
1647.7585	1646.7512	1646.8338	-50.13	431	-	444	0 ---	R.CEAEVPDVSFLLLR.A
1647.7585	1646.7513	1646.8338	-50.11	431	-	444	0 27	R.CEAEVPDVSFLLLR.A
2530.2642	2529.2569	2529.3374	-31.80	224	-	247	0 ---	K.VLRPGSSASLTCVAPLSGVDFQLR.R
No match to: 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806								

7. [A0A3Q1MJT2](#) Mass: 62948 Score: 93 Expect: 7.1e-005 Matches: 12

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
805.4537	804.4464	804.4858	-48.92	148	-	154	0 ---	R.GVTFLLR.L
919.4136	918.4063	918.4559	-53.98	288	-	295	0 ---	R.SELAAWSR.D
1142.5725	1141.5652	1141.6244	-51.83	415	-	425	0 ---	R.ALWTGALTPGR.D
1142.5725	1141.5652	1141.6244	-51.82	415	-	425	0 ---	R.ALWTGALTPGR.D
1175.5778	1174.5705	1174.6346	-54.59	81	-	91	0 ---	R.FPLGPGVTSTTR.G
1457.7133	1456.7060	1456.7773	-48.93	487	-	499	0 ---	R.SLLSELSDPVELR.V
1498.6241	1497.6168	1497.6882	-47.65	269	-	283	0 ---	R.LSALAAGDGSQYTCR.Y
1513.7238	1512.7165	1512.7936	-51.00	357	-	370	0 27	R.VLSPAGPEAQFELR.G
1513.7238	1512.7165	1512.7936	-50.97	357	-	370	0 ---	R.VLSPAGPEAQFELR.G
1647.7585	1646.7512	1646.8338	-50.13	431	-	444	0 ---	R.CEAEVPDVSFLLLR.A
1647.7585	1646.7513	1646.8338	-50.11	431	-	444	0 27	R.CEAEVPDVSFLLLR.A
2530.2642	2529.2569	2529.3374	-31.80	224	-	247	0 ---	K.VLRPGSSASLTCVAPLSGVDFQLR.R
No match to: 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806								

8. [A0A4W2EKQ3](#) Mass: 63006 Score: 93 Expect: 7.1e-005 Matches: 12

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
805.4537	804.4464	804.4858	-48.92	148	-	154	0 ---	R.GVTFLLR.L
919.4136	918.4063	918.4559	-53.98	288	-	295	0 ---	R.SELAAWSR.D
1142.5725	1141.5652	1141.6244	-51.83	415	-	425	0 ---	R.ALWTGALTPGR.D
1142.5725	1141.5652	1141.6244	-51.82	415	-	425	0 ---	R.ALWTGALTPGR.D
1175.5778	1174.5705	1174.6346	-54.59	81	-	91	0 ---	R.FPLGPGVTSTTR.G
1457.7133	1456.7060	1456.7773	-48.93	487	-	499	0 ---	R.SLLSELSDPVELR.V
1498.6241	1497.6168	1497.6882	-47.65	269	-	283	0 ---	R.LSALAAGDGSQYTCR.Y
1513.7238	1512.7165	1512.7936	-51.00	357	-	370	0 27	R.VLSPAGPEAQFELR.G
1513.7238	1512.7165	1512.7936	-50.97	357	-	370	0 ---	R.VLSPAGPEAQFELR.G
1647.7585	1646.7512	1646.8338	-50.13	431	-	444	0 ---	R.CEAEVPDVSFLLLR.A
1647.7585	1646.7513	1646.8338	-50.11	431	-	444	0 27	R.CEAEVPDVSFLLLR.A
2530.2642	2529.2569	2529.3374	-31.80	224	-	247	0 ---	K.VLRPGSSASLTCVAPLSGVDFQLR.R
No match to: 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806								

9. [A0A4W2IGA3](#) Mass: 80257 Score: 50 Expect: 1.4 Matches: 8

Kinesin-like protein OS=Bos indicus x Bos taurus OX=30522 GN=KIF3B PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
868.4995	867.4922	867.4273	74.9	48	-	55	0 ---	K.GVAHEMPK.T
1033.6417	1032.6344	1032.6331	1.24	540	-	548	1 ---	K.LFSKLQAVK.A
1045.5149	1044.5076	1044.5312	-22.57	252	-	261	1 ---	R.QAKTGAQGER.L
1498.6241	1497.6168	1497.6770	-40.15	103	-	115	1 ---	K.TYTMGVGRDPEK.R + Oxidation (M)
1513.7238	1512.7165	1512.7460	-19.50	142	-	153	0 9	R.ASYLEIYQEEIR.D
1513.7238	1512.7165	1512.7460	-19.47	142	-	153	0 ---	R.ASYLEIYQEEIR.D
1647.7585	1646.7512	1646.8007	-30.06	615	-	628	0 ---	R.AENIMLLELDMPK.R + Oxidation (M)
1647.7585	1646.7513	1646.8007	-30.04	615	-	628	0 27	R.AENIMLLELDMPK.R + Oxidation (M)
No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1457.7133, 1475.6820, 1479.7203, 1479.7203, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642								

10. [A0A3Q1MG81](#) Mass: 80257 Score: 50 Expect: 1.4 Matches: 8

Kinesin-like protein OS=Bos taurus OX=9913 GN=KIF3B PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
868.4995	867.4922	867.4273	74.9	48	-	55	0 ---	K.GVAHEMPK.T
1033.6417	1032.6344	1032.6331	1.24	540	-	548	1 ---	K.LFSKLQAVK.A
1045.5149	1044.5076	1044.5312	-22.57	252	-	261	1 ---	R.QAKTGAQGER.L
1498.6241	1497.6168	1497.6770	-40.15	103	-	115	1 ---	K.TYTMGVGRDPEK.R + Oxidation (M)
1513.7238	1512.7165	1512.7460	-19.50	142	-	153	0 9	R.ASYLEIYQEEIR.D
1513.7238	1512.7165	1512.7460	-19.47	142	-	153	0 ---	R.ASYLEIYQEEIR.D
1647.7585	1646.7512	1646.8007	-30.06	615	-	628	0 ---	R.AENIMLLELDMPK.R + Oxidation (M)
1647.7585	1646.7513	1646.8007	-30.04	615	-	628	0 27	R.AENIMLLELDMPK.R + Oxidation (M)

No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1479.7203, 1479.7203, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642

11. [A0A4W2H2X1](#) Mass: 84971 Score: 49 Expect: 1.7 Matches: 8

Kinesin-like protein OS=Bos indicus x Bos taurus OX=30522 GN=KIF3B PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
868.4995	867.4922	867.4273	74.9	48	55	0	---	K.GVAHEMPK.T
1033.6417	1032.6344	1032.6331	1.24	540	548	1	---	K.LFSKQLQAVK.A
1045.5149	1044.5076	1044.5312	-22.57	252	261	1	---	R.QAKTGAQGER.L
1498.6241	1497.6168	1497.6770	-40.15	103	115	1	---	K.TYTMGVGRGDPEK.R + Oxidation (M)
1513.7238	1512.7165	1512.7460	-19.50	142	153	0	9	R.ASYLEIYQEEIR.D
1513.7238	1512.7165	1512.7460	-19.47	142	153	0	---	R.ASYLEIYQEEIR.D
1647.7585	1646.7512	1646.8007	-30.06	653	666	0	---	R.AENIMLLELDMPSR.T + Oxidation (M)
1647.7585	1646.7513	1646.8007	-30.04	653	666	0	27	R.AENIMLLELDMPSR.T + Oxidation (M)

No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1479.7203, 1479.7203, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642

12. [F1N020](#) Mass: 84971 Score: 49 Expect: 1.7 Matches: 8

Kinesin-like protein OS=Bos taurus OX=9913 GN=KIF3B PE=3 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
868.4995	867.4922	867.4273	74.9	48	55	0	---	K.GVAHEMPK.T
1033.6417	1032.6344	1032.6331	1.24	540	548	1	---	K.LFSKQLQAVK.A
1045.5149	1044.5076	1044.5312	-22.57	252	261	1	---	R.QAKTGAQGER.L
1498.6241	1497.6168	1497.6770	-40.15	103	115	1	---	K.TYTMGVGRGDPEK.R + Oxidation (M)
1513.7238	1512.7165	1512.7460	-19.50	142	153	0	9	R.ASYLEIYQEEIR.D
1513.7238	1512.7165	1512.7460	-19.47	142	153	0	---	R.ASYLEIYQEEIR.D
1647.7585	1646.7512	1646.8007	-30.06	653	666	0	---	R.AENIMLLELDMPSR.T + Oxidation (M)
1647.7585	1646.7513	1646.8007	-30.04	653	666	0	27	R.AENIMLLELDMPSR.T + Oxidation (M)

No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1479.7203, 1479.7203, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642

13. [A0A4W2F5Q7](#) Mass: 26142 Score: 41 Expect: 10 Matches: 7

Peroxiredoxin like 2A OS=Bos indicus x Bos taurus OX=30522 GN=PRXL2A PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
996.5410	995.5337	995.5400	-6.27	119	126	1	---	K.EHIKNVEK.D
1065.5970	1064.5897	1064.5008	83.5	86	93	0	---	R.RPGCFCLCR.E
1151.6641	1150.6568	1150.6234	29.1	60	69	1	---	K.TLEKDAVTFK.A
1194.5631	1193.5558	1193.5396	13.6	151	159	1	---	R.KMMFMGFVLR.L + 3 Oxidation (M)
1300.7844	1299.7771	1299.7510	20.1	211	222	1	---	K.VNLTSVLEAARK.I
1414.8141	1413.8068	1413.6929	80.6	123	133	1	---	K.NEVKDFQPFYK.G
1557.7402	1556.7329	1556.8497	-75.00	72	85	1	---	K.ALWENKNGAVIMAVR.R

No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 927.4397, 951.5660, 982.5261, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1165.6772, 1165.6773, 1175.5778, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1479.7203, 1479.7203, 1498.6241, 1513.7238, 1513.7238, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642

14. [A0A3Q1LNN7](#) Mass: 68022 Score: 41 Expect: 11 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
927.4397	926.4324	926.4861	-57.97	161	167	0	---	K.YLYEIAR.R
1017.6141	1016.6068	1016.5727	33.6	212	220	1	---	K.VLTSSARQR.L
1017.6141	1016.6068	1016.5727	33.6	212	220	1	---	K.VLTSSARQR.L
1479.7203	1478.7130	1478.7881	-50.80	421	433	0	---	K.LGEYGFQNALIVR.Y
1479.7203	1478.7131	1478.7881	-50.77	421	433	0	---	K.LGEYGFQNALIVR.Y
1567.6654	1566.6581	1566.7354	-49.35	347	359	0	---	K.DAFLGSLFYEYSR.R
1567.6654	1566.6581	1566.7354	-49.34	347	359	0	22	K.DAFLGSLFYEYSR.R
1724.7576	1723.7503	1723.8273	-44.65	469	482	0	---	R.MPCTEDYLSLILNR.L
2044.9374	2043.9301	2044.0206	-44.28	168	183	1	---	R.RHPFYAPPELLYYANK.Y

No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 927.4397, 951.5660, 982.5261, 996.5410, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1732.0159, 1901.1652, 2015.1964, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642

15. [A0A452DI98](#) Mass: 15508 Score: 41 Expect: 12 Matches: 8

U6 snRNA-associated Sm-like protein LSm4 OS=Bos taurus OX=9913 GN=LSM4 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
805.4537	804.4464	804.4355	13.6	110	117	1	---	R.GVFGGRGR.G
864.5048	863.4975	863.4171	93.1	42	48	0	---	R.EVICTSR.D
927.4397	926.4324	926.5046	-77.93	116	125	1	---	R.GRGGIPGTGR.G
996.5410	995.5337	995.5512	-17.56	126	134	1	---	R.GQPEKKPGR.Q
1142.5725	1141.5652	1141.6204	-48.30	91	100	1	---	R.GGLQQKQKQK.G
1142.5725	1141.5652	1141.6204	-48.29	91	100	1	---	R.GGLQQKQKQK.G
1194.5631	1193.5558	1193.5724	-13.89	103	115	1	---	R.GMGGAGRGVFGGR.G + Oxidation (M)
1457.7133	1456.7060	1456.6744	21.7	53	62	1	---	K.FWRMPECYIR.G

No match to: 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 951.5660, 982.5261, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642

16. [A0A4W2FGN9](#) Mass: 123016 Score: 40 Expect: 12 Matches: 19

Coiled-coil domain containing 150 OS=Bos indicus x Bos taurus OX=30522 GN=CCDC150 PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Ions	Peptide
805.4537	804.4464	804.4341	15.3	548	554	1	---	K.ITDSKNK.L
848.4779	847.4706	847.4664	4.95	642	648	1	---	K.KVGNFQR.Q
864.5048	863.4975	863.4422	64.0	826	832	1	---	R.EVTEMKK.A
868.4995	867.4922	867.4450	54.4	766	772	0	---	K.LDHVQEK.L
919.4136	918.4063	918.4043	2.24	1010	1016	1	---	R.EEDQDKR.H
927.4397	926.4324	926.4094	24.9	941	948	0	---	R.SQYDTSAR.N
1147.6736	1146.6663	1146.6067	52.0	893	901	1	---	R.MKQIETELR.Q
1300.7844	1299.7771	1299.7510	20.1	441	451	1	---	K.ELLESTIARLR.G
1448.8483	1447.8410	1447.7453	66.1	30	41	1	---	R.MRIVEEQTSSLR.D
1448.8483	1447.8410	1447.7453	66.1	30	41	1	---	R.MRIVEEQTSSLR.D
1475.6820	1474.6747	1474.6535	14.4	163	174	1	---	K.EEEDKAQDEVQR.L
1479.7203	1478.7130	1478.7551	-28.48	985	996	1	---	K.CRFDGLQLELTK.N
1479.7203	1478.7131	1478.7551	-28.46	985	996	1	---	K.CRFDGLQLELTK.N
1498.6241	1497.6168	1497.6639	-31.43	90	100	1	---	K.NCEFLVNRMC.R
1557.7402	1556.7329	1556.8232	-58.00	660	673	0	---	K.VTIMLENVLASHSK.M + Oxidation (M)
1630.7391	1629.7318	1629.8759	-88.43	895	907	1	---	K.QIETELRQELIK.D
2184.3481	2183.3408	2183.1368	93.4	747	765	1	---	R.KLAMSLQALQTNHLQTK.L + Oxidation (M)
2211.0227	2210.0154	2210.0498	-15.54	964	981	1	---	R.QELENRCQITANLEEAHR.W
2283.0957	2282.0884	2282.1324	-19.29	359	377	1	---	K.MENTRIADHQAILQEEQK.M + Oxidation (M)

No match to: 842.4627, 850.0055, 850.4871, 853.4691, 865.9789, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1457.7133, 1513.7238, 1513.7238, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2305.0806, 2530.2642

17. [A0A4W2I014](#) Mass: 105104 Score: 40 Expect: 12 Matches: 16

Protein phosphatase 1 regulatory subunit 21 OS=Bos indicus x Bos taurus OX=30522 GN=PPP1R21 PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Ions	Peptide
842.4627	841.4554	841.4480	8.84	49	56	0	---	K.MAPLAPSR.G
853.4691	852.4618	852.4453	19.3	286	292	0	---	K.HVEAELR.S
1033.6417	1032.6344	1032.5451	86.5	334	342	1	---	K.SQTLEKAK.E
1131.6476	1130.6403	1130.5931	41.7	910	918	1	---	K.QREEIDTLK.M
1147.6736	1146.6663	1146.6357	26.7	700	709	1	---	R.RVLLSSTESR.E
1165.6772	1164.6699	1164.5696	86.2	860	869	1	---	K.SKEALTEEMK.V
1165.6773	1164.6700	1164.5696	86.2	860	869	1	---	K.SKEALTEEMK.V
1457.7133	1456.7060	1456.7522	-31.66	710	722	0	---	R.EGLAQVQVQSLEK.I
1567.6654	1566.6581	1566.7613	-65.84	840	852	1	---	K.SVHFYACRALS.K.R
1567.6654	1566.6581	1566.7613	-65.83	840	852	1	---	K.SVHFYACRALS.K.R
1617.9894	1616.9821	1616.8734	67.3	755	770	1	---	K.LKSTSSGQVVGVAQEK.A
1617.9894	1616.9821	1616.8734	67.3	755	770	1	---	K.LKSTSSGQVVGVAQEK.A
1633.7523	1632.7450	1632.8592	-69.94	42	56	1	---	R.HLGPCVKMAPLAPSR.G
1697.8313	1696.8240	1696.8090	8.86	148	163	1	---	R.AGEAMASAEQGGYQK.L + Oxidation (M)
2015.1964	2014.1891	2014.0346	76.7	490	505	1	---	K.LKTFSEHLTSYICFLR.K
2184.3481	2183.3408	2183.2201	55.3	549	568	0	---	K.LQTYTALLALPSTPDGLLR.T

No match to: 805.4537, 848.4779, 850.0055, 850.4871, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1019.6234, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1151.6641, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1583.9542, 1615.7332, 1630.7391, 1647.7585, 1647.7585, 1724.7576, 1732.0159, 1901.1652, 2044.9374, 2211.0227, 2283.0957, 2305.0806, 2530.2642

18. [A0A4W2CGR1](#) Mass: 105032 Score: 40 Expect: 12 Matches: 16

Protein phosphatase 1 regulatory subunit 21 OS=Bos indicus x Bos taurus OX=30522 GN=PPP1R21 PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Ions	Peptide
842.4627	841.4554	841.4480	8.84	49	56	0	---	K.MAPLAPSR.G
853.4691	852.4618	852.4453	19.3	286	292	0	---	K.HVEAELR.S
1033.6417	1032.6344	1032.5451	86.5	334	342	1	---	K.SQTLEKAK.E
1131.6476	1130.6403	1130.5931	41.7	910	918	1	---	K.QREEIDTLK.M
1147.6736	1146.6663	1146.6357	26.7	700	709	1	---	R.RVLLSSTESR.E
1165.6772	1164.6699	1164.5696	86.2	860	869	1	---	K.SKEALTEEMK.V
1165.6773	1164.6700	1164.5696	86.2	860	869	1	---	K.SKEALTEEMK.V
1457.7133	1456.7060	1456.7522	-31.66	710	722	0	---	R.EGLAQVQVQSLEK.I
1567.6654	1566.6581	1566.7613	-65.84	840	852	1	---	K.SVHFYACRALS.K.R
1567.6654	1566.6581	1566.7613	-65.83	840	852	1	---	K.SVHFYACRALS.K.R
1617.9894	1616.9821	1616.8734	67.3	755	770	1	---	K.LKSTSSGQVVGVAQEK.A
1617.9894	1616.9821	1616.8734	67.3	755	770	1	---	K.LKSTSSGQVVGVAQEK.A
1633.7523	1632.7450	1632.8592	-69.94	42	56	1	---	R.HLGPCVKMAPLAPSR.G
1697.8313	1696.8240	1696.8090	8.86	148	163	1	---	R.AGEAMASAEQGGYQK.L + Oxidation (M)
2015.1964	2014.1891	2014.0346	76.7	490	505	1	---	K.LKTFSEHLTSYICFLR.K
2184.3481	2183.3408	2183.2201	55.3	549	568	0	---	K.LQTYTALLALPSTPDGLLR.T

No match to: 805.4537, 848.4779, 850.0055, 850.4871, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1019.6234, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1151.6641, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1583.9542, 1615.7332, 1630.7391, 1647.7585, 1647.7585, 1724.7576, 1732.0159, 1901.1652, 2044.9374, 2211.0227, 2283.0957, 2305.0806, 2530.2642

19. [A0A4W2DDL5](#) Mass: 70207 Score: 40 Expect: 13 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
927.4397	926.4324	926.4861	-57.97	152	158	0	---	K.YLYEIAR.R
1017.6141	1016.6068	1016.5727	33.6	203	211	1	---	K.VLTSSARQR.L

1017.6141	1016.6068	1016.5727	33.6	203	-	211	1	---	K.VLTSSARQR.L
1479.7203	1478.7130	1478.7881	-50.80	412	-	424	0	---	K.LGEYGFQNALIVR.Y
1479.7203	1478.7131	1478.7881	-50.77	412	-	424	0	---	K.LGEYGFQNALIVR.Y
1567.6654	1566.6581	1566.7354	-49.35	338	-	350	0	---	K.DAFLGSFLYEYSR.R
1567.6654	1566.6581	1566.7354	-49.34	338	-	350	0	22	K.DAFLGSFLYEYSR.R
1724.7576	1723.7503	1723.8273	-44.65	460	-	473	0	---	R.MPCTEDYLSLILNR.L
2044.9374	2043.9301	2044.0206	-44.28	159	-	174	1	---	R.RHPYFYAPELLYYANK.Y
No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 951.5660, 982.5261, 996.5410, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1732.0159, 1901.1652, 2015.1964, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642									

20. [A0A140T897](#) Mass: 71274 Score: 40 Expect: 13 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	
927.4397	926.4324	926.4861	-57.97	161	-	167	0	---	K.YLYEIAR.R
1017.6141	1016.6068	1016.5727	33.6	212	-	220	1	---	K.VLTSSARQR.L
1017.6141	1016.6068	1016.5727	33.6	212	-	220	1	---	K.VLTSSARQR.L
1479.7203	1478.7130	1478.7881	-50.80	421	-	433	0	---	K.LGEYGFQNALIVR.Y
1479.7203	1478.7131	1478.7881	-50.77	421	-	433	0	---	K.LGEYGFQNALIVR.Y
1567.6654	1566.6581	1566.7354	-49.35	347	-	359	0	---	K.DAFLGSFLYEYSR.R
1567.6654	1566.6581	1566.7354	-49.34	347	-	359	0	22	K.DAFLGSFLYEYSR.R
1724.7576	1723.7503	1723.8273	-44.65	469	-	482	0	---	R.MPCTEDYLSLILNR.L
2044.9374	2043.9301	2044.0206	-44.28	168	-	183	1	---	R.RHPYFYAPELLYYANK.Y
No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 951.5660, 982.5261, 996.5410, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1732.0159, 1901.1652, 2015.1964, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642									

21. [A0A4W2EVR9](#) Mass: 71453 Score: 40 Expect: 13 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	
927.4397	926.4324	926.4861	-57.97	161	-	167	0	---	K.YLYEIAR.R
1017.6141	1016.6068	1016.5727	33.6	212	-	220	1	---	K.VLTSSARQR.L
1017.6141	1016.6068	1016.5727	33.6	212	-	220	1	---	K.VLTSSARQR.L
1479.7203	1478.7130	1478.7881	-50.80	421	-	433	0	---	K.LGEYGFQNALIVR.Y
1479.7203	1478.7131	1478.7881	-50.77	421	-	433	0	---	K.LGEYGFQNALIVR.Y
1567.6654	1566.6581	1566.7354	-49.35	347	-	359	0	---	K.DAFLGSFLYEYSR.R
1567.6654	1566.6581	1566.7354	-49.34	347	-	359	0	22	K.DAFLGSFLYEYSR.R
1724.7576	1723.7503	1723.8273	-44.65	469	-	482	0	---	R.MPCTEDYLSLILNR.L
2044.9374	2043.9301	2044.0206	-44.28	168	-	183	1	---	R.RHPYFYAPELLYYANK.Y
No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 951.5660, 982.5261, 996.5410, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1732.0159, 1901.1652, 2015.1964, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642									

22. [A0A4W2DGX3](#) Mass: 13967 Score: 40 Expect: 14 Matches: 8

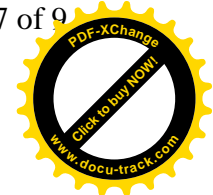
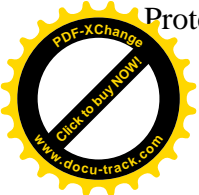
U6 snRNA-associated Sm-like protein LSM4 OS=Bos indicus x Bos taurus OX=30522 GN=LSM4 PE=3 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
805.4537	804.4464	804.4355	13.6	96	-	103	1	---	R.GVFGGRGR.G
864.5048	863.4975	863.4171	93.1	28	-	34	0	---	R.EVICTSR.D
927.4397	926.4324	926.5046	-77.93	102	-	111	1	---	R.GRGGIPGTGR.G
996.5410	995.5337	995.5512	-17.56	112	-	120	1	---	R.GQPEKKPGR.Q
1142.5725	1141.5652	1141.6204	-48.30	77	-	86	1	---	R.GGLQQQKQK.G
1142.5725	1141.5652	1141.6204	-48.29	77	-	86	1	---	R.GGLQQQKQK.G
1194.5631	1193.5558	1193.5724	-13.89	89	-	101	1	---	R.GMGAGRGVFGGR.G + Oxidation (M)
1457.7133	1456.7060	1456.6744	21.7	39	-	48	1	---	K.FWRMPECYIR.G
No match to: 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 951.5660, 982.5261, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642									

23. [A0A4W2HT62](#) Mass: 15511 Score: 39 Expect: 16 Matches: 8

U6 snRNA-associated Sm-like protein LSM4 OS=Bos indicus x Bos taurus OX=30522 GN=LSM4 PE=3 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
805.4537	804.4464	804.4355	13.6	110	-	117	1	---	R.GVFGGRGR.G
864.5048	863.4975	863.4171	93.1	42	-	48	0	---	R.EVICTSR.D
927.4397	926.4324	926.5046	-77.93	116	-	125	1	---	R.GRGGIPGTGR.G
996.5410	995.5337	995.5512	-17.56	126	-	134	1	---	R.GQPEKKPGR.Q
1142.5725	1141.5652	1141.6204	-48.30	91	-	100	1	---	R.GGLQQQKQK.G
1142.5725	1141.5652	1141.6204	-48.29	91	-	100	1	---	R.GGLQQQKQK.G
1194.5631	1193.5558	1193.5724	-13.89	103	-	115	1	---	R.GMGAGRGVFGGR.G + Oxidation (M)
1457.7133	1456.7060	1456.6744	21.7	53	-	62	1	---	K.FWRMPECYIR.G
No match to: 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 951.5660, 982.5261, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642									

24. [Q3ZBK6](#) Mass: 15511 Score: 39 Expect: 16 Matches: 8

U6 snRNA-associated Sm-like protein LSM4 OS=Bos taurus OX=9913 GN=LSM4 PE=2 SV=1									
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Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
805.4537	804.4464	804.4355	13.6	110	- 117	1	---	R.GVFGGRGR.G
864.5048	863.4975	863.4171	93.1	42	- 48	0	---	R.EVICTSR.D
927.4397	926.4324	926.5046	-77.93	116	- 125	1	---	R.GRGGIPGTGR.G
996.5410	995.5337	995.5512	-17.56	126	- 134	1	---	R.GQPEKKPGR.Q
1142.5725	1141.5652	1141.6204	-48.30	91	- 100	1	---	R.GGLQQKQKQK.G
1142.5725	1141.5652	1141.6204	-48.29	91	- 100	1	---	R.GGLQQKQKQK.G
1194.5631	1193.5558	1193.5724	-13.89	103	- 115	1	---	R.GMGGAGRGVFGGR.G + Oxidation (M)
1457.7133	1456.7060	1456.6744	21.7	53	- 62	1	---	K.FWRMPECYIR.G

No match to: 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 951.5660, 982.5261, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1475.6820, 1479.7203, 1479.7203, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642

25. [A0A4W2EW60](#) Mass: 76020 Score: 39 Expect: 17 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
927.4397	926.4324	926.4861	-57.97	161	- 167	0	---	K.YLYEIAR.R
1017.6141	1016.6068	1016.5727	33.6	212	- 220	1	---	K.VLTSSARQR.L
1017.6141	1016.6068	1016.5727	33.6	212	- 220	1	---	K.VLTSSARQR.L
1479.7203	1478.7130	1478.7881	-50.80	421	- 433	0	---	K.LGEYGFQNALIVR.Y
1479.7203	1478.7131	1478.7881	-50.77	421	- 433	0	---	K.LGEYGFQNALIVR.Y
1567.6654	1566.6581	1566.7354	-49.35	347	- 359	0	---	K.DAFLGSFLYEYSR.R
1567.6654	1566.6581	1566.7354	-49.34	347	- 359	0	22	K.DAFLGSFLYEYSR.R
1724.7576	1723.7503	1723.8273	-44.65	469	- 482	0	---	R.MPCTEDYLSLILNR.L
2044.9374	2043.9301	2044.0206	-44.28	168	- 183	1	---	R.RHPYFYAPPELLYYANK.Y

No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 951.5660, 982.5261, 996.5410, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1732.0159, 1901.1652, 2015.1964, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642

26. [A0A4W2D8T3](#) Mass: 76089 Score: 39 Expect: 18 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
927.4397	926.4324	926.4861	-57.97	209	- 215	0	---	K.YLYEIAR.R
1017.6141	1016.6068	1016.5727	33.6	260	- 268	1	---	K.VLTSSARQR.L
1017.6141	1016.6068	1016.5727	33.6	260	- 268	1	---	K.VLTSSARQR.L
1479.7203	1478.7130	1478.7881	-50.80	469	- 481	0	---	K.LGEYGFQNALIVR.Y
1479.7203	1478.7131	1478.7881	-50.77	469	- 481	0	---	K.LGEYGFQNALIVR.Y
1567.6654	1566.6581	1566.7354	-49.35	395	- 407	0	---	K.DAFLGSFLYEYSR.R
1567.6654	1566.6581	1566.7354	-49.34	395	- 407	0	22	K.DAFLGSFLYEYSR.R
1724.7576	1723.7503	1723.8273	-44.65	517	- 530	0	---	R.MPCTEDYLSLILNR.L
2044.9374	2043.9301	2044.0206	-44.28	216	- 231	1	---	R.RHPYFYAPPELLYYANK.Y

No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 951.5660, 982.5261, 996.5410, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1732.0159, 1901.1652, 2015.1964, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642

27. [A0A4W2HAU5](#) Mass: 24454 Score: 38 Expect: 21 Matches: 7

Peroxioredoxin like 2A OS=Bos indicus x Bos taurus OX=30522 GN=PRXL2A PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
996.5410	995.5337	995.5400	-6.27	104	- 111	1	---	K.EHIKNEVK.D
1065.5970	1064.5897	1064.5008	83.5	71	- 78	0	---	R.RPGCFPCR.E
1151.6641	1150.6568	1150.6234	29.1	45	- 54	1	---	K.TLEKDAVTFK.A
1194.5631	1193.5558	1193.5396	13.6	136	- 144	1	---	R.KMMFMGFVR.L + 3 Oxidation (M)
1300.7844	1299.7771	1299.7510	20.1	196	- 207	1	---	K.VNLTSLVLEAARK.I
1414.8141	1413.8068	1413.6929	80.6	108	- 118	1	---	K.NEVKDFQPYFK.G
1557.7402	1556.7329	1556.8497	-75.00	57	- 70	1	---	K.ALWEKNGAVIMAVR.R

No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 927.4397, 951.5660, 982.5261, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1165.6772, 1165.6773, 1175.5778, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1479.7203, 1479.7203, 1498.6241, 1513.7238, 1513.7238, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642

28. [Q3ZBK2](#) Mass: 24454 Score: 38 Expect: 21 Matches: 7

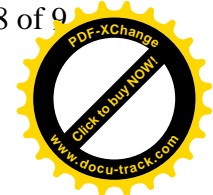
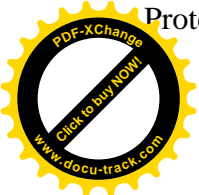
Peroxioredoxin-like 2A OS=Bos taurus OX=9913 GN=PRXL2A PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
996.5410	995.5337	995.5400	-6.27	104	- 111	1	---	K.EHIKNEVK.D
1065.5970	1064.5897	1064.5008	83.5	71	- 78	0	---	R.RPGCFPCR.E
1151.6641	1150.6568	1150.6234	29.1	45	- 54	1	---	K.TLEKDAVTFK.A
1194.5631	1193.5558	1193.5396	13.6	136	- 144	1	---	R.KMMFMGFVR.L + 3 Oxidation (M)
1300.7844	1299.7771	1299.7510	20.1	196	- 207	1	---	K.VNLTSLVLEAARK.I
1414.8141	1413.8068	1413.6929	80.6	108	- 118	1	---	K.NEVKDFQPYFK.G
1557.7402	1556.7329	1556.8497	-75.00	57	- 70	1	---	K.ALWEKNGAVIMAVR.R

No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 927.4397, 951.5660, 982.5261, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1165.6772, 1165.6773, 1175.5778, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1479.7203, 1479.7203, 1498.6241, 1513.7238, 1513.7238, 1567.6654, 1567.6654, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1630.7391, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642

29. [A0A4W2H5Z2](#) Mass: 33370 Score: 37 Expect: 26 Matches: 7

Ketohexokinase OS=Bos indicus x Bos taurus OX=30522 GN=KHK PE=4 SV=1



Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.4871	849.4798	849.4821	-2.65	210	-	216	1 ---	R.GLYSRVR.K
1065.5970	1064.5897	1064.4961	87.9	289	-	298	0 ---	K.CGLQGFGDGIV.-
1133.6560	1132.6487	1132.5560	81.9	32	-	39	1 ---	R.CLSQRWQR.G
1136.6389	1135.6316	1135.5873	39.0	124	-	132	1 ---	K.DFEKVELTR.F
1615.7332	1614.7259	1614.8227	-59.91	78	-	91	1 ---	R.QRGVDVSQVANQSR.G
1630.7391	1629.7318	1629.8376	-64.89	66	-	79	1 ---	R.GHVADFLVADFRQR.G
1697.8313	1696.8240	1696.8025	12.7	273	-	287	1 ---	K.SMQEALRFGCQVAGK.K + Oxidation (M)
No match to: 805.4537, 842.4627, 848.4779, 850.0055, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 927.4397, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1131.6476, 1142.5725, 1142.5725, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1479.7203, 1479.7203, 1498.6241, 1513.7238, 1513.7238, 1557.7402, 1567.6654, 1567.6654, 1583.9542, 1617.9894, 1617.9894, 1633.7523, 1647.7585, 1647.7585, 1724.7576, 1732.0159, 1901.1652, 2015.1964, 2044.9374, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642								

30. [P02769](#) Mass: 71244 Score: 36 Expect: 37 Matches: 7

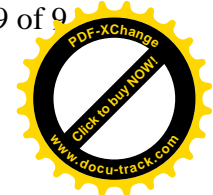
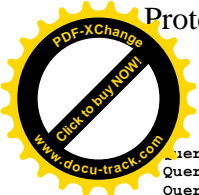
Serum albumin OS=Bos taurus OX=9913 GN=ALB PE=1 SV=4

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
927.4397	926.4324	926.4861	-57.97	161	-	167	0 ---	K.YLYEIR.R
1479.7203	1478.7130	1478.7881	-50.80	421	-	433	0 ---	K.LGEYGFQNALIVR.Y
1479.7203	1478.7131	1478.7881	-50.77	421	-	433	0 ---	K.LGEYGFQNALIVR.Y
1567.6654	1566.6581	1566.7354	-49.35	347	-	359	0 ---	K.DAFLGSLYEYSR.R
1567.6654	1566.6581	1566.7354	-49.34	347	-	359	0 22	K.DAFLGSLYEYSR.R
1724.7576	1723.7503	1723.8273	-44.65	469	-	482	0 ---	R.MPCTEDYLSLILNR.L
2044.9374	2043.9301	2044.0206	-44.28	168	-	183	1 ---	R.RHVFYAPPELLYANK.Y
No match to: 805.4537, 842.4627, 848.4779, 850.0055, 850.4871, 853.4691, 864.5048, 865.9789, 868.4995, 870.5005, 876.9857, 882.5121, 882.5121, 892.9567, 919.4136, 951.5660, 982.5261, 996.5410, 1017.6141, 1017.6141, 1019.6234, 1033.6417, 1045.5149, 1051.6498, 1051.6498, 1065.5970, 1131.6476, 1133.6560, 1136.6389, 1142.5725, 1142.5725, 1147.6736, 1151.6641, 1165.6772, 1165.6773, 1175.5778, 1194.5631, 1300.7844, 1302.7943, 1316.8119, 1334.8163, 1334.8163, 1351.5889, 1414.8141, 1434.8339, 1448.8483, 1448.8483, 1457.7133, 1475.6820, 1498.6241, 1513.7238, 1557.7402, 1583.9542, 1615.7332, 1617.9894, 1617.9894, 1633.7523, 1647.7585, 1647.7585, 1697.8313, 1732.0159, 1901.1652, 2015.1964, 2184.3481, 2211.0227, 2283.0957, 2305.0806, 2530.2642								

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 (805.4537,1+): <no title>
 Query2 (842.4627,1+): <no title>
 Query3 (848.4779,1+): <no title>
 Query4 (850.0055,1+): <no title>
 Query5 (850.4871,1+): <no title>
 Query6 (853.4691,1+): <no title>
 Query7 (864.5048,1+): <no title>
 Query8 (865.9789,1+): <no title>
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Query58 (1567.6654,1+): Locus:1..14.0.4
Query59 (1583.9542,1+): <no title>
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Query72 (2044.9374,1+): <no title>
Query73 (2184.3481,1+): <no title>
Query74 (2211.0227,1+): <no title>
Query75 (2283.0957,1+): <no title>
Query76 (2305.0806,1+): <no title>
Query77 (2530.2642,1+): <no title>

Mascot: <http://www.matrixscience.com/>