

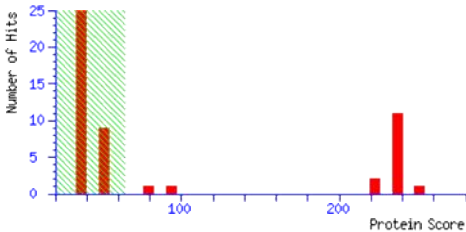
MATRIX SCIENCE

Mascot Search Results

User :
Email :
Search title : BAEDW\2020_3_5\2020_3_5\MSMS 14\N16
Database : Uniprot_bovine_bovine_20200316 (134392 sequences; 76244912 residues)
Timestamp : 31 Mar 2020 at 01:08:51 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 251 for Q693V9, Complement component 3d (Fragment) OS=Bos taurus OX=9913 PE=2 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.	Q693V9	34593	251	Complement component 3d (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1
2.	A0A4W2D408	180682	237	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
3.	A0A3Q1MGT0	183008	236	Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=1
4.	A0A3Q1M2B2	185169	235	Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=1
5.	A0A4W2D441	186349	233	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
6.	Q2UVX4	188675	232	Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=2
7.	A0A0F6QNP7	188604	232	Complement component 3 OS=Bos taurus OX=9913 GN=C3 PE=2 SV=1
8.	A0A3Q1MHV6	181738	231	Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=1
9.	A0A4W2D3Y9	185555	231	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
10.	A0A4W2EPV7	179159	231	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
11.	A0A4W2D406	186684	231	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
12.	A0A4W2D411	190190	230	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
13.	A0A4W2CZG6	192486	229	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
14.	A0A4W2EPT5	182918	229	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
15.	A0A4W2HFJ5	188690	98	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
16.	A0A4W2CZQ8	170639	79	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
17.	A0A4W2DYP9	31930	54	Phosphatidylinositol transfer protein beta OS=Bos indicus x Bos taurus OX=30522 GN=PITPNB PE=4 SV=1
18.	A0A4W2C513	31804	53	Phosphatidylinositol transfer protein beta OS=Bos indicus x Bos taurus OX=30522 GN=PITPNB PE=4 SV=1
19.	Q9TR36	31804	53	Phosphatidylinositol transfer protein beta isoform OS=Bos taurus OX=9913 GN=PITPNB PE=1 SV=3
20.	A0A4W2FGB2	205135	53	Poly [ADP-ribose] polymerase OS=Bos indicus x Bos taurus OX=30522 GN=PARP14 PE=4 SV=1
21.	A0A4W2EPF9	190854	50	Poly(ADP-ribose) polymerase family member 14 OS=Bos indicus x Bos taurus OX=30522 GN=PARP14 PE=4 SV=1
22.	F1ML90	204793	49	Poly [ADP-ribose] polymerase OS=Bos taurus OX=9913 GN=PARP14 PE=4 SV=3
23.	A0A4W2CYS7	190256	48	Poly(ADP-ribose) polymerase family member 14 OS=Bos indicus x Bos taurus OX=30522 GN=PARP14 PE=4 SV=1
24.	A0A3Q1MDH0	196044	44	Poly [ADP-ribose] polymerase OS=Bos taurus OX=9913 GN=PARP14 PE=4 SV=1
25.	A0A4W2E5T5	31943	44	Phosphatidylinositol transfer protein beta OS=Bos indicus x Bos taurus OX=30522 GN=PITPNB PE=4 SV=1
26.	A0A452DJF3	31845	43	Phosphatidylinositol transfer protein beta isoform OS=Bos taurus OX=9913 GN=PITPNB PE=4 SV=1
27.	A0A4W2DWE1	8549	41	CD3e molecule OS=Bos indicus x Bos taurus OX=30522 GN=CD3E PE=4 SV=1
28.	A0A3Q1MWW7	28595	40	Electron transfer flavoprotein subunit beta lysine methyltransferase OS=Bos taurus OX=9913 GN=ETFBKMT PE=4 SV=1
29.	A0A3Q1M1B1	29199	40	Phosphatidylinositol transfer protein beta isoform OS=Bos taurus OX=9913 GN=PITPNB PE=4 SV=1
30.	Q8MI17	4845	40	Insulin receptor (Fragment) OS=Bos taurus OX=9913 GN=ir-A PE=2 SV=1

Results List

1.	Q693V9	Mass: 34593	Score: 251	Expect: 1.1e-020	Matches: 20
Complement component 3d (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Tons Peptide
845.4012	844.3939	844.4191	-29.85	254 - 259	0 --- R.WLNEQR.Y
987.5186	986.5113	986.5396	-28.69	42 - 49	0 --- R.QESLELIR.K
1083.5225	1082.5152	1082.5509	-32.98	51 - 59	0 14 K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	51 - 59	0 --- K.GYTQQLAFR.Q
1143.6165	1142.6092	1142.6407	-27.57	41 - 49	1 --- K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	244 - 253	0 --- K.DYDTTPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	217 - 225	1 --- K.NRWEENQK.L
1211.6163	1210.6090	1210.6458	-30.41	50 - 59	1 --- R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	50 - 59	1 --- R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	171 - 180	0 40 K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	171 - 180	0 --- K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	243 - 253	1 --- R.KDYDTTPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	155 - 166	0 --- K.DICEAQVNSLGR.S
1790.9982	1789.9909	1790.0454	-30.45	184 - 200	0 --- R.RPYTVAIAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	184 - 200	0 --- R.RPYTVAIAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	226 - 242	0 --- K.LYNVEATSYALLALLAR.K

1880.9891 1879.9819 1880.0407 -31.29 226 - 242 0 80 K.LYNVEATSYALLALLAR.K
2506.2144 2505.2071 2505.2692 -24.80 62 - 83 0 --- K.SSAYAAFQYRPPSTWLTAYVVK.V
2506.2144 2505.2071 2505.2692 -24.79 62 - 83 0 --- K.SSAYAAFQYRPPSTWLTAYVVK.V
2598.2195 2597.2122 2597.2697 -22.12 111 - 133 0 --- K.QKPDGIFQEDGPIVHQEMIGGFR.D
No match to: 842.4847, 848.4952, 850.5135, 853.4918, 857.4026, 857.4026, 864.5186, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 996.5623, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1090.4995, 1107.5156, 1124.5784, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2157.0273, 2157.0273, 2179.9844, 2211.0493, 2283.1272

2. **A0A4W2D408** Mass: 180682 Score: 237 Expect: 2.7e-019 Matches: 28

Complement	C3	OS=Bos indicus	x	Bos taurus	OX=30522	GN=C3	PE=4	SV=1	
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
845.4012	844.3939	844.3927	1.50	477	- 484	0	---	R.TDPGEQAK.I	
848.4952	847.4879	847.4400	56.6	1368	- 1375	0	---	K.TLSTGVDR.Y	
850.5135	849.5062	849.4266	93.8	639	- 645	0	---	R.SVQLMEK.R + Oxidation (M)	
864.5186	863.5113	863.4939	20.2	758	- 764	0	---	K.LMNVFLK.D	
987.5186	986.5113	986.5396	-28.69	1011	- 1018	0	---	R.QESLELIR.K	
996.5623	995.5550	995.4672	88.2	650	- 658	0	---	K.AQYSSDLR.K	
1083.5225	1082.5152	1082.5509	-32.98	1020	- 1028	0	14	K.GYTQQLAFR.Q	
1083.5225	1082.5152	1082.5509	-32.94	1020	- 1028	0	---	K.GYTQQLAFR.Q	
1090.4995	1089.4922	1089.4873	4.50	590	- 600	0	---	K.ADIGCTPGSGR.N	
1124.5784	1123.5711	1123.5622	7.97	650	- 659	1	---	K.AQYSSDLRK.C	
1143.6165	1142.6092	1142.6407	-27.57	1010	- 1018	1	---	K.RQESLELIR.K	
1162.5488	1161.5415	1161.5666	-21.61	1213	- 1222	0	---	K.DYDTPPVVR.W	
1200.5436	1199.5363	1199.5683	-26.65	1186	- 1194	1	---	K.NRWEEPNQK.L	
1211.6163	1210.6090	1210.6458	-30.41	1019	- 1028	1	---	R.KGYTQQLAFR.Q	
1211.6163	1210.6091	1210.6458	-30.39	1019	- 1028	1	---	R.KGYTQQLAFR.Q	
1221.5270	1220.5197	1220.5574	-30.90	1140	- 1149	0	40	K.AGDFLENHYR.E	
1221.5270	1220.5197	1220.5574	-30.88	1140	- 1149	0	---	K.AGDFLENHYR.E	
1290.6333	1289.6260	1289.6616	-27.57	1212	- 1222	1	---	R.KDYDTPPVVR.W	
1361.6049	1360.5976	1360.6405	-31.51	1124	- 1135	0	---	K.DICEAQVNSLGR.S	
1790.9982	1789.9909	1790.0454	-30.45	1153	- 1169	0	---	R.RPYTVIAAAYALALLGK.L	
1790.9982	1789.9909	1790.0454	-30.43	1153	- 1169	0	---	R.RPYTVIAAAYALALLGK.L	
1880.9891	1879.9818	1880.0407	-31.31	1195	- 1211	0	---	K.LYNVEATSYALLALLAR.K	
1880.9891	1879.9819	1880.0407	-31.29	1195	- 1211	0	80	K.LYNVEATSYALLALLAR.K	
2157.0273	2156.0200	2156.0783	-27.04	948	- 967	0	---	K.ILLQGTTPVQMTEIDAIDGER.L	
2157.0273	2156.0201	2156.0783	-27.02	948	- 967	0	35	K.ILLQGTTPVQMTEIDAIDGER.L	
2506.2144	2505.2071	2505.2692	-24.80	1031	- 1052	0	---	K.SSAYAAFQYRPPSTWLTAYVVK.V	
2506.2144	2505.2071	2505.2692	-24.79	1031	- 1052	0	---	K.SSAYAAFQYRPPSTWLTAYVVK.V	
2598.2195	2597.2122	2597.2697	-22.12	1080	- 1102	0	---	K.QKPDGIFQEDGPIVHQEMIGGFR.D	
No match to: 842.4847, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272									

3. **A0A3Q1MGTO** Mass: 183008 Score: 236 Expect: 3.4e-019 Matches: 28

Complement	C3	OS=Bos taurus	OX=9913	GN=C3	PE=1	SV=1		
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
845.4012	844.3939	844.3927	1.50	477	- 484	0	---	R.TDPGEQAK.I
848.4952	847.4879	847.4400	56.6	1368	- 1375	0	---	K.TLSTGVDR.Y
850.5135	849.5062	849.4266	93.8	639	- 645	0	---	R.SVQLMEK.R + Oxidation (M)
864.5186	863.5113	863.4939	20.2	758	- 764	0	---	K.LMNVFLK.D
987.5186	986.5113	986.5396	-28.69	1011	- 1018	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	650	- 658	0	---	K.AGQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1020	- 1028	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1020	- 1028	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	590	- 600	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	650	- 659	1	---	K.AGQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1010	- 1018	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1213	- 1222	0	---	K.DYDTPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	1186	- 1194	1	---	K.NRWEEPNQK.L
1211.6163	1210.6090	1210.6458	-30.41	1019	- 1028	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1019	- 1028	1	---	R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	1140	- 1149	0	40	K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	1140	- 1149	0	---	K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	1212	- 1222	1	---	R.KDYDTPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	1124	- 1135	0	---	K.DICEAQVNSLGR.S
1790.9982	1789.9909	1790.0454	-30.45	1153	- 1169	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1153	- 1169	0	---	R.RPYTVIAAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	1195	- 1211	0	---	K.LYNVEATSYALLALLAR.K
1880.9891	1879.9819	1880.0407	-31.29	1195	- 1211	0	80	K.LYNVEATSYALLALLAR.K
2157.0273	2156.0200	2156.0783	-27.04	948	- 967	0	---	K.ILLQGTTPVQMTEIDAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	948	- 967	0	35	K.ILLQGTTPVQMTEIDAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1031	- 1052	0	---	K.SSAYAAFQYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1031	- 1052	0	---	K.SSAYAAFQYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.2697	-22.12	1080	- 1102	0	---	K.QKPDGIFQEDGPVIVHQEMIGGFR.D
No match to: 842.4847, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272								

4. **A0A3Q1M2B2** Mass: 185169 Score: 235 Expect: 4.2e-019 Matches: 28

Complement	C3	OS=Bos taurus	OX=9913	GN=C3	PE=1	SV=1			
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
845.4012	844.3939	844.3927	1.50	477	- 484	0	---	R.TDPGEQAK.I	
848.4952	847.4879	847.4400	56.6	1388	- 1395	0	---	K.TLSTGVDR.Y	
850.5135	849.5062	849.4266	93.8	639	- 645	0	---	R.SVQLMEK.R + Oxidation (M)	
864.5186	863.5113	863.4939	20.2	758	- 764	0	---	K.LMNVFLK.D	
987.5186	986.5113	986.5396	-28.69	1011	- 1018	0	---	R.QESLELIR.K	
996.5623	995.5550	995.4672	88.2	650	- 658	0	---	K.AQYSSDLR.K	

1083.5225	1082.5152	1082.5509	-32.98	1020	-	1028	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1020	-	1028	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	590	-	600	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	650	-	659	1	---	K.AGQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1010	-	1018	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1213	-	1222	0	---	K.DYDTPPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	1186	-	1194	1	---	K.NRWEENQK.L
1211.6163	1210.6090	1210.6458	-30.41	1019	-	1028	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1019	-	1028	1	---	R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	1140	-	1149	0	40	K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	1140	-	1149	0	---	K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	1212	-	1222	1	---	R.KDYDTPPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	1124	-	1135	0	---	K.DICEAQVNSLGR.S
1790.9982	1789.9909	1790.0454	-30.45	1153	-	1169	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1153	-	1169	0	---	R.RPYTVIAAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	1195	-	1211	0	---	K.LYNVEATSYALLALLAR.K
1880.9891	1879.9819	1880.0407	-31.29	1195	-	1211	0	80	K.LYNVEATSYALLALLAR.K
2157.0273	2156.0200	2156.0783	-27.04	948	-	967	0	---	K.ILLQGTTPVAQMTEDAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	948	-	967	0	35	K.ILLQGTTPVAQMTEDAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1031	-	1052	0	---	K.SSAYAAPQYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1031	-	1052	0	---	K.SSAYAAPQYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.2697	-22.12	1080	-	1102	0	---	K.QKPDGIFQEDGVPVIHQEMIGGFR.D
No match to: 842.4847, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272									

5. [A0A4W2D441](#) Mass: 186349 Score: 233 Expect: 6.7e-019 Matches: 28

Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
845.4012	844.3939	844.3927	1.50	477	-	484	0	---	R.TDPGEQAK.I
848.4952	847.4879	847.4400	56.6	1419	-	1426	0	---	K.TLSTGVDR.Y
850.5135	849.5062	849.4266	93.8	670	-	676	0	---	R.SVQLMEK.R + Oxidation (M)
864.5186	863.5113	863.4939	20.2	789	-	795	0	---	K.LMNVFLK.D
987.5186	986.5113	986.5396	-28.69	1042	-	1049	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	681	-	689	0	---	K.AGQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1051	-	1059	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1051	-	1059	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	621	-	631	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	681	-	690	1	---	K.AGQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1041	-	1049	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1244	-	1253	0	---	K.DYDTPPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	1217	-	1225	1	---	K.NRWEENQK.L
1211.6163	1210.6090	1210.6458	-30.41	1050	-	1059	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1050	-	1059	1	---	R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	1171	-	1180	0	40	K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	1171	-	1180	0	---	K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	1243	-	1253	1	---	R.KDYDTPPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	1155	-	1166	0	---	K.DICEAQVNSLGR.S
1790.9982	1789.9909	1790.0454	-30.45	1184	-	1200	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1184	-	1200	0	---	R.RPYTVIAAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	1226	-	1242	0	---	K.LYNVEATSYALLALLAR.K
1880.9891	1879.9819	1880.0407	-31.29	1226	-	1242	0	80	K.LYNVEATSYALLALLAR.K
2157.0273	2156.0200	2156.0783	-27.04	979	-	998	0	---	K.ILLQGTTPVAQMTEDAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	979	-	998	0	35	K.ILLQGTTPVAQMTEDAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1062	-	1083	0	---	K.SSAYAAPQYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1062	-	1083	0	---	K.SSAYAAPQYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.2697	-22.12	1111	-	1133	0	---	K.QKPDGIFQEDGVPVIHQEMIGGFR.D
No match to: 842.4847, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272									

6. [Q2UVX4](#) Mass: 188675 Score: 232 Expect: 8.5e-019 Matches: 28

Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=2									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
845.4012	844.3939	844.3927	1.50	477	-	484	0	---	R.TDPGEQAK.I
848.4952	847.4879	847.4400	56.6	1419	-	1426	0	---	K.TLSTGVDR.Y
850.5135	849.5062	849.4266	93.8	670	-	676	0	---	R.SVQLMEK.R + Oxidation (M)
864.5186	863.5113	863.4939	20.2	789	-	795	0	---	K.LMNVFLK.D
987.5186	986.5113	986.5396	-28.69	1042	-	1049	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	681	-	689	0	---	K.AGQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1051	-	1059	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1051	-	1059	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	621	-	631	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	681	-	690	1	---	K.AGQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1041	-	1049	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1244	-	1253	0	---	K.DYDTPPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	1217	-	1225	1	---	K.NRWEENQK.L
1211.6163	1210.6090	1210.6458	-30.41	1050	-	1059	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1050	-	1059	1	---	R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	1171	-	1180	0	40	K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	1171	-	1180	0	---	K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	1243	-	1253	1	---	R.KDYDTPPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	1155	-	1166	0	---	K.DICEAQVNSLGR.S
1790.9982	1789.9909	1790.0454	-30.45	1184	-	1200	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1184	-	1200	0	---	R.RPYTVIAAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	1226	-	1242	0	---	K.LYNVEATSYALLALLAR.K
1880.9891	1879.9819	1880.0407	-31.29	1226	-	1242	0	80	K.LYNVEATSYALLALLAR.K
2157.0273	2156.0200	2156.0783	-27.04	979	-	998	0	---	K.ILLQGTTPVAQMTEDAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	979	-	998	0	35	K.ILLQGTTPVAQMTEDAIDGER.L

2506.2144 2505.2071 2505.2692 -24.80 1062 - 1083 0 --- K.SSAYAAAFQYRPPSTWLTAYVVK.V
2506.2144 2505.2071 2505.2692 -24.79 1062 - 1083 0 --- K.SSAYAAAFQYRPPSTWLTAYVVK.V
2598.2195 2597.2122 2597.2697 -22.12 1111 - 1133 0 --- K.QKPDGIFQEDGVPVIHQEMIGGF.R.D
No match to: 842.4847, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272

7. [A0A0F6QNP7](#) Mass: 188604 Score: 232 Expect: 8.5e-019 Matches: 28

Complement component 3 OS=Bos taurus OX=9913 GN=C3 PE=2 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
845.4012	844.3939	844.3927	1.50	477	-	484	0	---	R.TDPGEQAK.I
848.4952	847.4879	847.4400	56.6	1419	-	1426	0	---	K.TLSTGVDR.Y
850.5135	849.5062	849.4266	93.8	670	-	676	0	---	R.SVQLMEK.R + Oxidation (M)
853.4918	852.4845	852.4779	7.76	789	-	795	0	---	K.LMSVFLK.D + Oxidation (M)
987.5186	986.5113	986.5396	-28.69	1042	-	1049	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	681	-	689	0	---	K.AGQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1051	-	1059	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1051	-	1059	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	621	-	631	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	681	-	690	1	---	K.AGQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1041	-	1049	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1244	-	1253	0	---	K.DYDTTPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	1217	-	1225	1	---	K.NRWEENPQK.L
1211.6163	1210.6090	1210.6458	-30.41	1050	-	1059	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1050	-	1059	1	---	R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	1171	-	1180	0	40	K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	1171	-	1180	0	---	K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	1243	-	1253	1	---	R.KDYDTTPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	1155	-	1166	0	---	K.DICEAQVNSLGR.S
1790.9982	1789.9909	1790.0454	-30.45	1184	-	1200	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1184	-	1200	0	---	R.RPYTVIAAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	1226	-	1242	0	---	K.LYNVEATSYALLALLAR.K
1880.9891	1879.9819	1880.0407	-31.29	1226	-	1242	0	80	K.LYNVEATSYALLALLAR.K
2157.0273	2156.0200	2156.0783	-27.04	979	-	998	0	---	K.ILLQGTTPVQMTEAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	979	-	998	0	35	K.ILLQGTTPVQMTEAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1062	-	1083	0	---	K.SSAYAAAFQYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1062	-	1083	0	---	K.SSAYAAAFQYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.2697	-22.12	1111	-	1133	0	---	K.QKPDGIFQEDGVPVIHQEMIGGF.R.D
No match to: 842.4847, 857.4026, 857.4026, 864.5186, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272									

8. [A0A3Q1MHV6](#) Mass: 181738 Score: 231 Expect: 1.1e-018 Matches: 27

Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
845.4012	844.3939	844.3927	1.50	477	-	484	0	---	R.TDPGEQAK.I
850.5135	849.5062	849.4266	93.8	639	-	645	0	---	R.SVQLMEK.R + Oxidation (M)
864.5186	863.5113	863.4939	20.2	758	-	764	0	---	K.LMNVFLK.D
987.5186	986.5113	986.5396	-28.69	1011	-	1018	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	650	-	658	0	---	K.AGQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1020	-	1028	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1020	-	1028	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	590	-	600	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	650	-	659	1	---	K.AGQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1010	-	1018	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1213	-	1222	0	---	K.DYDTTPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	1186	-	1194	1	---	K.NRWEENPQK.L
1211.6163	1210.6090	1210.6458	-30.41	1019	-	1028	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1019	-	1028	1	---	R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	1140	-	1149	0	40	K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	1140	-	1149	0	---	K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	1212	-	1222	1	---	R.KDYDTTPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	1124	-	1135	0	---	K.DICEAQVNSLGR.S
1790.9982	1789.9909	1790.0454	-30.45	1153	-	1169	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1153	-	1169	0	---	R.RPYTVIAAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	1195	-	1211	0	---	K.LYNVEATSYALLALLAR.K
1880.9891	1879.9819	1880.0407	-31.29	1195	-	1211	0	80	K.LYNVEATSYALLALLAR.K
2157.0273	2156.0200	2156.0783	-27.04	948	-	967	0	---	K.ILLQGTTPVQMTEAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	948	-	967	0	35	K.ILLQGTTPVQMTEAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1031	-	1052	0	---	K.SSAYAAAFQYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1031	-	1052	0	---	K.SSAYAAAFQYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.2697	-22.12	1080	-	1102	0	---	K.QKPDGIFQEDGVPVIHQEMIGGF.R.D
No match to: 842.4847, 848.4952, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272									

9. [A0A4W2D3Y9](#) Mass: 185555 Score: 231 Expect: 1.1e-018 Matches: 28

Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
845.4012	844.3939	844.3927	1.50	511	-	518	0	---	R.TDPGEQAK.I
848.4952	847.4879	847.4400	56.6	1422	-	1429	0	---	K.TLSTGVDR.Y
850.5135	849.5062	849.4266	93.8	673	-	679	0	---	R.SVQLMEK.R + Oxidation (M)
864.5186	863.5113	863.4939	20.2	792	-	798	0	---	K.LMNVFLK.D
987.5186	986.5113	986.5396	-28.69	1045	-	1052	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	684	-	692	0	---	K.AGQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1054	-	1062	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1054	-	1062	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	624	-	634	0	---	K.ADIGCTPGSGR.N



1124.5784	1123.5711	1123.5622	7.97	684	-	693	1	---	K.AGQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1044	-	1052	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1247	-	1256	0	---	K.DYDTPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	1220	-	1228	1	---	K.NRWEENPQK.L
1211.6163	1210.6090	1210.6458	-30.41	1053	-	1062	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1053	-	1062	1	---	R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	1174	-	1183	0	40	K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	1174	-	1183	0	---	K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	1246	-	1256	1	---	R.KDYDTPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	1158	-	1169	0	---	K.DICEAQVNSLGR.S
1790.9982	1789.9909	1790.0454	-30.45	1187	-	1203	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1187	-	1203	0	---	R.RPYTVIAAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	1229	-	1245	0	---	K.LYNVEATSYALLALLAR.K
1880.9891	1879.9819	1880.0407	-31.29	1229	-	1245	0	80	K.LYNVEATSYALLALLAR.K
2157.0273	2156.0200	2156.0783	-27.04	982	-	1001	0	---	K.ILLQGTTPVAQMTEDAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	982	-	1001	0	35	K.ILLQGTTPVAQMTEDAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1065	-	1086	0	---	K.SSAYAFAQYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1065	-	1086	0	---	K.SSAYAFAQYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.2697	-22.12	1114	-	1136	0	---	K.QKPDGIFQEDGPVIHQEMIGGFR.D
No match to: 842.4847, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272									

10. [A0A4W2EPV7](#) Mass: 179159 Score: 231 Expect: 1.1e-018 Matches: 27

Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
845.4012	844.3939	844.3927	1.50	477	-	484	0	---	R.TDPGEQAK.I
848.4952	847.4879	847.4400	56.6	1355	-	1362	0	---	K.TLSTGVDR.Y
850.5135	849.5062	849.4266	93.8	639	-	645	0	---	R.SVQLMEK.R + Oxidation (M)
864.5186	863.5113	863.4939	20.2	758	-	764	0	---	K.LMNVFLK.D
987.5186	986.5113	986.5396	-28.69	1011	-	1018	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	650	-	658	0	---	K.AGQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1020	-	1028	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1020	-	1028	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	590	-	600	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	650	-	659	1	---	K.AGQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1010	-	1018	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1180	-	1189	0	---	K.DYDTPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	1153	-	1161	1	---	K.NRWEENPQK.L
1211.6163	1210.6090	1210.6458	-30.41	1019	-	1028	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1019	-	1028	1	---	R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	1107	-	1116	0	40	K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	1107	-	1116	0	---	K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	1179	-	1189	1	---	R.KDYDTPPVVR.W
1790.9982	1789.9909	1790.0454	-30.45	1120	-	1136	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1120	-	1136	0	---	R.RPYTVIAAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	1162	-	1178	0	---	K.LYNVEATSYALLALLAR.K
1880.9891	1879.9819	1880.0407	-31.29	1162	-	1178	0	80	K.LYNVEATSYALLALLAR.K
2157.0273	2156.0200	2156.0783	-27.04	948	-	967	0	---	K.ILLQGTTPVAQMTEDAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	948	-	967	0	35	K.ILLQGTTPVAQMTEDAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1031	-	1052	0	---	K.SSAYAFAQYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1031	-	1052	0	---	K.SSAYAFAQYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.3085	-37.09	601	-	624	1	---	R.NYAGVFTDAGLTSLKTSQLETQQR.A
No match to: 842.4847, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1361.6049, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272									

11. [A0A4W2D406](#) Mass: 186684 Score: 231 Expect: 1.1e-018 Matches: 28

Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
845.4012	844.3939	844.3927	1.50	511	-	518	0	---	R.TDPGEQAK.I
848.4952	847.4879	847.4400	56.6	1422	-	1429	0	---	K.TLSTGVDR.Y
850.5135	849.5062	849.4266	93.8	673	-	679	0	---	R.SVQLMEK.R + Oxidation (M)
864.5186	863.5113	863.4939	20.2	792	-	798	0	---	K.LMNVFLK.D
987.5186	986.5113	986.5396	-28.69	1045	-	1052	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	684	-	692	0	---	K.AGQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1054	-	1062	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1054	-	1062	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	624	-	634	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	684	-	693	1	---	K.AGQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1044	-	1052	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1247	-	1256	0	---	K.DYDTPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	1220	-	1228	1	---	K.NRWEENPQK.L
1211.6163	1210.6090	1210.6458	-30.41	1053	-	1062	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1053	-	1062	1	---	R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	1174	-	1183	0	40	K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	1174	-	1183	0	---	K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	1246	-	1256	1	---	R.KDYDTPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	1158	-	1169	0	---	K.DICEAQVNSLGR.S
1790.9982	1789.9909	1790.0454	-30.45	1187	-	1203	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1187	-	1203	0	---	R.RPYTVIAAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	1229	-	1245	0	---	K.LYNVEATSYALLALLAR.K
1880.9891	1879.9819	1880.0407	-31.29	1229	-	1245	0	80	K.LYNVEATSYALLALLAR.K
2157.0273	2156.0200	2156.0783	-27.04	982	-	1001	0	---	K.ILLQGTTPVAQMTEDAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	982	-	1001	0	35	K.ILLQGTTPVAQMTEDAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1065	-	1086	0	---	K.SSAYAFAQYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1065	-	1086	0	---	K.SSAYAFAQYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.2697	-22.12	1114	-	1136	0	---	K.QKPDGIFQEDGPVIHQEMIGGFR.D

No match to: 842.4847, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272

12. A0A4W2D411 Mass: 190190 Score: 230 Expect: 1.3e-018 Matches: 28

Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Ions	Peptide
845.4012	844.3939	844.3927	1.50	511	518	0	---	R.TDPGEQAK.I
848.4952	847.4879	847.4400	56.6	1453	1460	0	---	K.TLSTGVDR.Y
850.5135	849.5062	849.4266	93.8	704	710	0	---	R.SVQLMEK.R + Oxidation (M)
864.5186	863.5113	863.4939	20.2	823	829	0	---	K.LMNVFLK.D
987.5186	986.5113	986.5396	-28.69	1076	1083	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	715	723	0	---	K.AGQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1085	1093	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1085	1093	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	655	665	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	715	724	1	---	K.AGQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1075	1083	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1278	1287	0	---	K.DYDTTPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	1251	1259	1	---	K.NRWEEPNQK.L
1211.6163	1210.6090	1210.6458	-30.41	1084	1093	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1084	1093	1	---	R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	1205	1214	0	40	K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	1205	1214	0	---	K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	1277	1287	1	---	R.KDYDTTPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	1189	1200	0	---	K.DICEAQNLSGR.S
1790.9982	1789.9909	1790.0454	-30.45	1218	1234	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1218	1234	0	---	R.RPYTVIAAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	1260	1276	0	---	K.LYNVEATSYALLALLAR.K
1880.9891	1879.9819	1880.0407	-31.29	1260	1276	0	80	K.LYNVEATSYALLALLAR.K
2157.0273	2156.0200	2156.0783	-27.04	1013	1032	0	---	K.ILLQGTTPVQMTEAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	1013	1032	0	35	K.ILLQGTTPVQMTEAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1096	1117	0	---	K.SSAYAAFPYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1096	1117	0	---	K.SSAYAAFPYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.2697	-22.12	1145	1167	0	---	K.QKPDGIFQEDGPVIHQEMIGGFR.D

No match to: 842.4847, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272

13. A0A4W2CZN6 Mass: 192486 Score: 229 Expect: 1.7e-018 Matches: 28

Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1

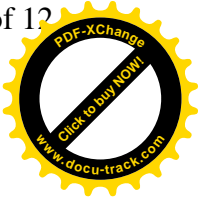
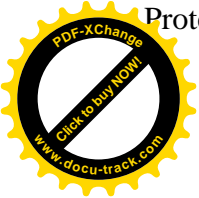
Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Ions	Peptide
845.4012	844.3939	844.3927	1.50	511	518	0	---	R.TDPGEQAK.I
848.4952	847.4879	847.4400	56.6	1453	1460	0	---	K.TLSTGVDR.Y
850.5135	849.5062	849.4266	93.8	704	710	0	---	R.SVQLMEK.R + Oxidation (M)
864.5186	863.5113	863.4939	20.2	823	829	0	---	K.LMNVFLK.D
987.5186	986.5113	986.5396	-28.69	1076	1083	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	715	723	0	---	K.AGQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1085	1093	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1085	1093	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	655	665	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	715	724	1	---	K.AGQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1075	1083	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1278	1287	0	---	K.DYDTTPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	1251	1259	1	---	K.NRWEEPNQK.L
1211.6163	1210.6090	1210.6458	-30.41	1084	1093	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1084	1093	1	---	R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	1205	1214	0	40	K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	1205	1214	0	---	K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	1277	1287	1	---	R.KDYDTTPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	1189	1200	0	---	K.DICEAQNLSGR.S
1790.9982	1789.9909	1790.0454	-30.45	1218	1234	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1218	1234	0	---	R.RPYTVIAAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	1260	1276	0	---	K.LYNVEATSYALLALLAR.K
1880.9891	1879.9819	1880.0407	-31.29	1260	1276	0	80	K.LYNVEATSYALLALLAR.K
2157.0273	2156.0200	2156.0783	-27.04	1013	1032	0	---	K.ILLQGTTPVQMTEAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	1013	1032	0	35	K.ILLQGTTPVQMTEAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1096	1117	0	---	K.SSAYAAFPYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1096	1117	0	---	K.SSAYAAFPYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.2697	-22.12	1145	1167	0	---	K.QKPDGIFQEDGPVIHQEMIGGFR.D

No match to: 842.4847, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272

14. A0A4W2EPI5 Mass: 182918 Score: 229 Expect: 1.7e-018 Matches: 27

Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Ions	Peptide
845.4012	844.3939	844.3927	1.50	477	484	0	---	R.TDPGEQAK.I
850.5135	849.5062	849.4266	93.8	670	676	0	---	R.SVQLMEK.R + Oxidation (M)
864.5186	863.5113	863.4939	20.2	789	795	0	---	K.LMNVFLK.D
987.5186	986.5113	986.5396	-28.69	1042	1049	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	681	689	0	---	K.AGQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1051	1059	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1051	1059	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	621	631	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	681	690	1	---	K.AGQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1041	1049	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1244	1253	0	---	K.DYDTTPPVVR.W



1200.5436	1199.5363	1199.5683	-26.65	1217	-	1225	1	---	K.NRWEENPK.L
1211.6163	1210.6090	1210.6458	-30.41	1050	-	1059	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1050	-	1059	1	---	R.KGYTQQLAFR.Q
1221.5270	1220.5197	1220.5574	-30.90	1171	-	1180	0	40	K.AGDFLENHYR.E
1221.5270	1220.5197	1220.5574	-30.88	1171	-	1180	0	---	K.AGDFLENHYR.E
1290.6333	1289.6260	1289.6616	-27.57	1243	-	1253	1	---	R.KDYDTTPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	1155	-	1166	0	---	K.DICEAQVNSLGR.S
1790.9982	1789.9909	1790.0454	-30.45	1184	-	1200	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1184	-	1200	0	---	R.RPYTVIAAAYALALLGK.L
1880.9891	1879.9818	1880.0407	-31.31	1226	-	1242	0	---	K.LYNVEATSYALLALLAR.K
1880.9891	1879.9819	1880.0407	-31.29	1226	-	1242	0	80	K.LYNVEATSYALLALLAR.K
2157.0273	2156.0200	2156.0783	-27.04	979	-	998	0	---	K.ILLQGTTPVAQMTEDAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	979	-	998	0	35	K.ILLQGTTPVAQMTEDAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1062	-	1083	0	---	K.SSAYAAFYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1062	-	1083	0	---	K.SSAYAAFYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.2697	-22.12	1111	-	1133	0	---	K.QKPDGIFQEDGPIHQEMIGGFR.D
No match to: 842.4847, 848.4952, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1107.5156, 1131.6732, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272									

15. A0A4W2HFJ5 Mass: 188690 Score: 98 Expect: 2.3e-005 Matches: 24

Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
845.4012	844.3939	844.3927	1.50	477	-	484	0	---	R.TDPGEQAK.I
848.4952	847.4879	847.4400	56.6	1419	-	1426	0	---	K.TLSTGVDR.Y
850.5135	849.5062	849.4266	93.8	670	-	676	0	---	R.SVQLMEK.R + Oxidation (M)
864.5186	863.5113	863.4939	20.2	789	-	795	0	---	K.LMNVFLK.D
987.5186	986.5113	986.5396	-28.69	1042	-	1049	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	681	-	689	0	---	K.AQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1051	-	1059	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1051	-	1059	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	621	-	631	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	681	-	690	1	---	K.AQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1041	-	1049	1	---	K.RQESLELIR.K
1162.5488	1161.5415	1161.5666	-21.61	1244	-	1253	0	---	K.DYDTTPPVVR.W
1200.5436	1199.5363	1199.5683	-26.65	1217	-	1225	1	---	K.NRWEENPK.L
1211.6163	1210.6090	1210.6458	-30.41	1050	-	1059	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1050	-	1059	1	---	R.KGYTQQLAFR.Q
1290.6333	1289.6260	1289.6616	-27.57	1243	-	1253	1	---	R.KDYDTTPPVVR.W
1361.6049	1360.5976	1360.6405	-31.51	1155	-	1166	0	---	K.DICEAQVNSLGR.S
1790.9982	1789.9909	1790.0454	-30.45	1184	-	1200	0	---	R.RPYTVIAAAYALALLGK.L
1790.9982	1789.9909	1790.0454	-30.43	1184	-	1200	0	---	R.RPYTVIAAAYALALLGK.L
2157.0273	2156.0200	2156.0783	-27.04	979	-	998	0	---	K.ILLQGTTPVAQMTEDAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	979	-	998	0	35	K.ILLQGTTPVAQMTEDAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1062	-	1083	0	---	K.SSAYAAFYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1062	-	1083	0	---	K.SSAYAAFYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.2697	-22.12	1111	-	1133	0	---	K.QKPDGIFQEDGPIHQEMIGGFR.D
No match to: 842.4847, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1221.5270, 1221.5270, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1808.9220, 1879.9926, 1880.9891, 1880.9891, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272									

16. A0A4W2CZQ8 Mass: 170639 Score: 79 Expect: 0.0019 Matches: 18

Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
845.4012	844.3939	844.3927	1.50	477	-	484	0	---	R.TDPGEQAK.I
848.4952	847.4879	847.4400	56.6	1281	-	1288	0	---	K.TLSTGVDR.Y
850.5135	849.5062	849.4266	93.8	639	-	645	0	---	R.SVQLMEK.R + Oxidation (M)
864.5186	863.5113	863.4939	20.2	758	-	764	0	---	K.LMNVFLK.D
987.5186	986.5113	986.5396	-28.69	1011	-	1018	0	---	R.QESLELIR.K
996.5623	995.5550	995.4672	88.2	650	-	658	0	---	K.AQYSSDLR.K
1083.5225	1082.5152	1082.5509	-32.98	1020	-	1028	0	14	K.GYTQQLAFR.Q
1083.5225	1082.5152	1082.5509	-32.94	1020	-	1028	0	---	K.GYTQQLAFR.Q
1090.4995	1089.4922	1089.4873	4.50	590	-	600	0	---	K.ADIGCTPGSGR.N
1124.5784	1123.5711	1123.5622	7.97	650	-	659	1	---	K.AQYSSDLRK.C
1143.6165	1142.6092	1142.6407	-27.57	1010	-	1018	1	---	K.RQESLELIR.K
1211.6163	1210.6090	1210.6458	-30.41	1019	-	1028	1	---	R.KGYTQQLAFR.Q
1211.6163	1210.6091	1210.6458	-30.39	1019	-	1028	1	---	R.KGYTQQLAFR.Q
2157.0273	2156.0200	2156.0783	-27.04	948	-	967	0	---	K.ILLQGTTPVAQMTEDAIDGER.L
2157.0273	2156.0201	2156.0783	-27.02	948	-	967	0	35	K.ILLQGTTPVAQMTEDAIDGER.L
2506.2144	2505.2071	2505.2692	-24.80	1031	-	1052	0	---	K.SSAYAAFYRPPSTWLTAYVVK.V
2506.2144	2505.2071	2505.2692	-24.79	1031	-	1052	0	---	K.SSAYAAFYRPPSTWLTAYVVK.V
2598.2195	2597.2122	2597.2697	-22.12	1080	-	1102	0	---	K.QKPDGIFQEDGPIHQEMIGGFR.D
No match to: 842.4847, 853.4918, 857.4026, 857.4026, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1162.5488, 1165.5533, 1165.7053, 1179.5667, 1200.5436, 1221.5270, 1221.5270, 1263.6616, 1277.6742, 1290.6333, 1300.8134, 1334.8459, 1334.8459, 1361.6049, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1790.9982, 1790.9982, 1808.9220, 1879.9926, 1880.9891, 1880.9891, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2211.0493, 2283.1272									

17. A0A4W2DYD9 Mass: 31930 Score: 54 Expect: 0.56 Matches: 12

Phosphatidylinositol transfer protein beta OS=Bos indicus x Bos taurus OX=30522 GN=PITPNB PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
848.4952	847.4879	847.5531	-76.92	195	-	201	1	---	K.LVTIKFK.W
868.5277	867.5204	867.4603	69.3	171	-	178	0	---	R.GPLGNPWK.K
996.5623	995.5550	995.5552	-0.21	171	-	179	1	---	R.GPLGNPWK.E
1036.5013	1035.4940	1035.4873	6.52	147	-	155	0	---	R.SQVEPADYK.A
1036.5013	1035.4941	1035.4873	6.56	147	-	155	0	---	R.SQVEPADYK.A
1051.6785	1050.6712	1050.5896	77.7	1	-	8	1	---	-.MVLKEFR.V + Oxidation (M)
1051.6785	1050.6712	1050.5896	77.7	1	-	8	1	---	-.MVLKEFR.V + Oxidation (M)
1090.4995	1089.4922	1089.5832	-83.49	219	-	226	1	---	K.RIFTNFHR.Q

1162.5488 1161.5415 1161.5414 0.07 51 - 60 1 --- K.DGEKGGQYTHK.I
1179.5667 1178.5594 1178.6237 -54.50 200 - 208 1 --- K.PKWWGLQSK.V
1200.5436 1199.5363 1199.5182 15.1 87 - 95 0 --- K.AWNAYPYCR.T
1879.9926 1878.9853 1878.9073 41.5 96 - 110 1 --- R.TIVTNEYMKDDFFIK.I + Oxidation (M)
No match to: 842.4847, 845.4012, 850.5135, 853.4918, 857.4026, 857.4026, 864.5186, 870.5200, 882.5434, 882.5434, 951.5951, 987.5186, 1017.6425, 1019.6487, 1033.6698, 1045.5382, 1083.5225, 1083.5225, 1107.5156, 1124.5784, 1131.6732, 1136.6610, 1143.6165, 1151.6952, 1165.5533, 1165.7053, 1211.6163, 1211.6163, 1221.5270, 1221.5270, 1263.6616, 1277.6742, 1290.6333, 1300.8134, 1334.8459, 1334.8459, 1361.6049, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1790.9982, 1790.9982, 1808.9220, 1880.9891, 1880.9891, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2157.0273, 2157.0273, 2179.9844, 2211.0493, 2283.1272, 2506.2144, 2506.2144, 2598.2195

18. [A0A4W2C513](#) Mass: 31804 Score: 53 Expect: 0.64 Matches: 12
Phosphatidylinositol transfer protein beta OS=Bos indicus x Bos taurus OX=30522 GN=PITPNB PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4952	847.4879	847.5531	-76.92	195	201	1	---	K.LVTIKFK.W
868.5277	867.5204	867.4603	69.3	171	178	0	---	R.GPLGPNWK.K
996.5623	995.5550	995.5552	-0.21	171	179	1	---	R.GPLGPNWK.K.E
1036.5013	1035.4940	1035.4873	6.52	147	155	0	---	R.SQVEPADYK.A
1036.5013	1035.4941	1035.4873	6.56	147	155	0	---	R.SQVEPADYK.A
1051.6785	1050.6712	1050.5896	77.7	1	8	1	---	-.MVLIKEFR.V + Oxidation (M)
1051.6785	1050.6712	1050.5896	77.7	1	8	1	---	-.MVLIKEFR.V + Oxidation (M)
1090.4995	1089.4922	1089.5832	-83.49	219	226	1	---	K.RIFTNFRH.Q
1162.5488	1161.5415	1161.5414	0.07	51	60	1	---	K.DGEKGGQYTHK.I
1179.5667	1178.5594	1178.6237	-54.50	200	208	1	---	K.PKWWGLQSK.V
1200.5436	1199.5363	1199.5182	15.1	87	95	0	---	K.AWNAYPYCR.T
1879.9926	1878.9853	1878.9073	41.5	96	110	1	---	R.TIVTNEYMKDDFFIK.I + Oxidation (M)
No match to: 842.4847, 845.4012, 850.5135, 853.4918, 857.4026, 857.4026, 864.5186, 870.5200, 882.5434, 882.5434, 951.5951, 987.5186, 1017.6425, 1019.6487, 1033.6698, 1045.5382, 1083.5225, 1083.5225, 1107.5156, 1124.5784, 1131.6732, 1136.6610, 1143.6165, 1151.6952, 1165.5533, 1165.7053, 1211.6163, 1211.6163, 1221.5270, 1221.5270, 1263.6616, 1277.6742, 1290.6333, 1300.8134, 1334.8459, 1334.8459, 1361.6049, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1790.9982, 1790.9982, 1808.9220, 1880.9891, 1880.9891, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2157.0273, 2157.0273, 2179.9844, 2211.0493, 2283.1272, 2506.2144, 2506.2144, 2598.2195								

19. [Q9TR36](#) Mass: 31804 Score: 53 Expect: 0.64 Matches: 12
Phosphatidylinositol transfer protein beta isoform OS=Bos taurus OX=9913 GN=PITPNB PE=1 SV=3

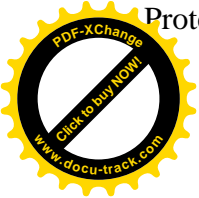
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4952	847.4879	847.5531	-76.92	195	201	1	---	K.LVTIKFK.W
868.5277	867.5204	867.4603	69.3	171	178	0	---	R.GPLGPNWK.K
996.5623	995.5550	995.5552	-0.21	171	179	1	---	R.GPLGPNWK.K.E
1036.5013	1035.4940	1035.4873	6.52	147	155	0	---	R.SQVEPADYK.A
1036.5013	1035.4941	1035.4873	6.56	147	155	0	---	R.SQVEPADYK.A
1051.6785	1050.6712	1050.5896	77.7	1	8	1	---	-.MVLIKEFR.V + Oxidation (M)
1051.6785	1050.6712	1050.5896	77.7	1	8	1	---	-.MVLIKEFR.V + Oxidation (M)
1090.4995	1089.4922	1089.5832	-83.49	219	226	1	---	K.RIFTNFRH.Q
1162.5488	1161.5415	1161.5414	0.07	51	60	1	---	K.DGEKGGQYTHK.I
1179.5667	1178.5594	1178.6237	-54.50	200	208	1	---	K.PKWWGLQSK.V
1200.5436	1199.5363	1199.5182	15.1	87	95	0	---	K.AWNAYPYCR.T
1879.9926	1878.9853	1878.9073	41.5	96	110	1	---	R.TIVTNEYMKDDFFIK.I + Oxidation (M)
No match to: 842.4847, 845.4012, 850.5135, 853.4918, 857.4026, 857.4026, 864.5186, 870.5200, 882.5434, 882.5434, 951.5951, 987.5186, 1017.6425, 1019.6487, 1033.6698, 1045.5382, 1083.5225, 1083.5225, 1107.5156, 1124.5784, 1131.6732, 1136.6610, 1143.6165, 1151.6952, 1165.5533, 1165.7053, 1211.6163, 1211.6163, 1221.5270, 1221.5270, 1263.6616, 1277.6742, 1290.6333, 1300.8134, 1334.8459, 1334.8459, 1361.6049, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1790.9982, 1790.9982, 1808.9220, 1880.9891, 1880.9891, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2157.0273, 2157.0273, 2179.9844, 2211.0493, 2283.1272, 2506.2144, 2506.2144, 2598.2195								

20. [A0A4W2FGB2](#) Mass: 205135 Score: 53 Expect: 0.67 Matches: 18
Poly [ADP-ribose] polymerase OS=Bos indicus x Bos taurus OX=30522 GN=PARP14 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.5135	849.5062	849.5324	-30.79	1752	1759	0	---	R.SLIVPPPK.D
882.5434	881.5361	881.4494	98.4	1580	1587	0	---	K.TYIATDAK.G
882.5434	881.5361	881.4494	98.4	1580	1587	0	---	K.TYIATDAK.G
996.5623	995.5550	995.5011	54.2	1734	1740	1	---	K.KHMYVVR.V
1124.5784	1123.5711	1123.5509	18.0	385	394	0	---	K.DASTLFSDIR.S
1143.6165	1142.6092	1142.6295	-17.75	1052	1061	1	---	K.AGQKLQEELK.T
1162.5488	1161.5415	1161.5699	-24.47	1549	1558	0	---	K.ITNMQLEDAK.K
1200.5436	1199.5363	1199.6121	-63.16	29	37	1	---	K.LQMYFQSRK.R
1211.6163	1210.6090	1210.5618	39.0	73	82	0	---	R.ESHELEWPGK.G
1211.6163	1210.6091	1210.5618	39.0	73	82	0	---	R.ESHELEWPGK.G
1290.6333	1289.6260	1289.6146	8.85	1264	1274	1	---	R.AGRNVEIECSR.Q
1407.6674	1406.6601	1406.7340	-52.53	1420	1431	1	---	K.KTELAVFQVGR.N
1434.8688	1433.8615	1433.8103	35.7	1295	1307	1	---	K.NIIHVIGGNDVKR.S
1880.9891	1879.9818	1879.9527	15.5	1237	1253	1	---	K.EEADVIVNSTSKSFNLK.A
1880.9891	1879.9819	1879.9527	15.5	1237	1253	1	---	K.EEADVIVNSTSKSFNLK.A
2157.0273	2156.0200	2156.1478	-59.24	83	101	1	---	K.GTFKLTQIPTVPDEVQER.K
2157.0273	2156.0201	2156.1478	-59.22	83	101	1	26	K.GTFKLTQIPTVPDEVQER.K
2211.0493	2210.0420	2210.2271	-83.72	1056	1076	1	---	K.LQEELKTAGQGVVVDVGTCLR.T
No match to: 842.4847, 845.4012, 848.4952, 853.4918, 857.4026, 857.4026, 864.5186, 868.5277, 870.5200, 951.5951, 987.5186, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1083.5225, 1083.5225, 1090.4995, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1221.5270, 1221.5270, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1361.6049, 1379.6898, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1790.9982, 1790.9982, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2283.1272, 2506.2144, 2506.2144, 2598.2195								

21. [A0A4W2EP89](#) Mass: 190854 Score: 50 Expect: 1.4 Matches: 17
Poly(ADP-ribose) polymerase family member 14 OS=Bos indicus x Bos taurus OX=30522 GN=PARP14 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
882.5434	881.5361	881.4494	98.4	1580	1587	0	---	K.TYIATDAK.G
882.5434	881.5361	881.4494	98.4	1580	1587	0	---	K.TYIATDAK.G
1124.5784	1123.5711	1123.5509	18.0	385	394	0	---	K.DASTLFSDIR.S
1143.6165	1142.6092	1142.6295	-17.75	1052	1061	1	---	K.AGQKLQEELK.T
1162.5488	1161.5415	1161.5699	-24.47	1549	1558	0	---	K.ITNMQLEDAK.K
1179.5667	1178.5594	1178.5689	-8.01	1663	1671	1	---	K.TVWMPRMAR.- + 2 Oxidation (M)
1200.5436	1199.5363	1199.6121	-63.16	29	37	1	---	K.LQMYFQSRK.R
1211.6163	1210.6090	1210.5618	39.0	73	82	0	---	R.ESHELEWPGK.G
1211.6163	1210.6091	1210.5618	39.0	73	82	0	---	R.ESHELEWPGK.G



1290.6333	1289.6260	1289.6146	8.85	1264	-	1274	1	---	R.AGRNVEIECSR.Q
1407.6674	1406.6601	1406.7340	-52.53	1420	-	1431	1	---	K.KTELAVFQVCGR.N
1434.8688	1433.8615	1433.8103	35.7	1295	-	1307	1	---	K.NIIHVIGGNDVKR.S
1880.9891	1879.9818	1879.9527	15.5	1237	-	1253	1	---	K.EEADVIVNSTKSFNLK.A
1880.9891	1879.9819	1879.9527	15.5	1237	-	1253	1	---	K.EEADVIVNSTKSFNLK.A
2157.0273	2156.0200	2156.1478	-59.24	83	-	101	1	---	K.GTFKLTQIPTVPDEVQER.K
2157.0273	2156.0201	2156.1478	-59.22	83	-	101	1	26	K.GTFKLTQIPTVPDEVQER.K
2211.0493	2210.0420	2210.2271	-83.72	1056	-	1076	1	---	K.LQEELKTAGQGVVVDVGTVLR.T
No match to: 842.4847, 845.4012, 848.4952, 850.5135, 853.4918, 857.4026, 857.4026, 864.5186, 868.5277, 870.5200, 951.5951, 987.5186, 996.5623, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1083.5225, 1083.5225, 1090.4995, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1221.5270, 1221.5270, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1361.6049, 1379.6898, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1790.9982, 1790.9982, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2283.1272, 2506.2144, 2506.2144, 2598.2195									

22. [F1ML90](#) Mass: 204793 Score: 49 Expect: 1.5 Matches: 17

Poly [ADP-ribose] polymerase OS=Bos taurus OX=9913 GN=PARP14 PE=4 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
882.5434	881.5361	881.4494	98.4	1578	- 1585	0	---	K.TYIATDAK.G
882.5434	881.5361	881.4494	98.4	1578	- 1585	0	---	K.TYIATDAK.G
996.5623	995.5550	995.5011	54.2	1732	- 1738	1	---	K.KHMYVVR.V
1124.5784	1123.5711	1123.5509	18.0	383	- 392	0	---	K.DASTLFSDIR.S
1143.6165	1142.6092	1142.6295	-17.75	1050	- 1059	1	---	K.AGQKLQEELK.T
1162.5488	1161.5415	1161.5699	-24.47	1547	- 1556	0	---	K.ITNMQLEDAK.K
1200.5436	1199.5363	1199.6121	-63.16	27	- 35	1	---	K.LQMYFQSRK.R
1211.6163	1210.6090	1210.5618	39.0	71	- 80	0	---	R.ESHELEWPGK.G
1211.6163	1210.6091	1210.5618	39.0	71	- 80	0	---	R.ESHELEWPGK.G
1290.6333	1289.6260	1289.6146	8.85	1262	- 1272	1	---	R.AGRNVEIECSR.Q
1407.6674	1406.6601	1406.7340	-52.53	1418	- 1429	1	---	K.KTELAVFQVCGR.N
1434.8688	1433.8615	1433.8103	35.7	1293	- 1305	1	---	K.NIIHVIGGNDVKR.S
1880.9891	1879.9818	1879.9527	15.5	1235	- 1251	1	---	K.EEADVIVNSTKSFNLK.A
1880.9891	1879.9819	1879.9527	15.5	1235	- 1251	1	---	K.EEADVIVNSTKSFNLK.A
2157.0273	2156.0200	2156.1478	-59.24	81	- 99	1	---	K.GTFKLTVQIPTVPDEVQER.K
2157.0273	2156.0201	2156.1478	-59.22	81	- 99	1	26	K.GTFKLTVQIPTVPDEVQER.K
2211.0493	2210.0420	2210.2271	-83.72	1054	- 1074	1	---	K.LQEELKTAGQGVVVDVGTVLR.T
No match to: 842.4847, 845.4012, 848.4952, 850.5135, 853.4918, 857.4026, 857.4026, 864.5186, 868.5277, 870.5200, 951.5951, 987.5186, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1083.5225, 1083.5225, 1090.4995, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1221.5270, 1221.5270, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1361.6049, 1379.6898, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1790.9982, 1790.9982, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2283.1272, 2506.2144, 2506.2144, 2598.2195								

23. [A0A4W2CYS7](#) Mass: 190256 Score: 48 Expect: 2 Matches: 16

Poly(ADP-ribose) polymerase family member 14 OS=Bos indicus x Bos taurus OX=30522 GN=PARP14 PE=4 SV=1

observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
882.5434	881.5361	881.4494	98.4	1580	- 1587	0	---	K.TYIATDAK.G
882.5434	881.5361	881.4494	98.4	1580	- 1587	0	---	K.TYIATDAK.G
1124.5784	1123.5711	1123.5509	18.0	385	- 394	0	---	K.DASTLFSDDR.S
1143.6165	1142.6092	1142.6295	-17.75	1052	- 1061	1	---	K.AGQKLQEELK.T
1162.5488	1161.5415	1161.5699	-24.47	1549	- 1558	0	---	K.ITNMQLEDAK.K
1200.5436	1199.5363	1199.6121	-63.16	29	- 37	1	---	K.LQMYFQSRK.R
1211.6163	1210.6090	1210.5618	39.0	73	- 82	0	---	R.ESHELEWPGK.G
1211.6163	1210.6091	1210.5618	39.0	73	- 82	0	---	R.ESHELEWPGK.G
1290.6333	1289.6260	1289.6146	8.85	1264	- 1274	1	---	R.AGRNVEIECSR.Q
1407.6674	1406.6601	1406.7340	-52.53	1420	- 1431	1	---	K.KTELAVFQVCGR.N
1434.8688	1433.8615	1433.8103	35.7	1295	- 1307	1	---	K.NIIHVIGGNDVKR.S
1880.9891	1879.9818	1879.9527	15.5	1237	- 1253	1	---	K.EEADVIVNSTKSFNLK.A
1880.9891	1879.9819	1879.9527	15.5	1237	- 1253	1	---	K.EEADVIVNSTKSFNLK.A
2157.0273	2156.0200	2156.1478	-59.24	83	- 101	1	---	K.GTFKLTQIPTVPDEVQER.K
2157.0273	2156.0201	2156.1478	-59.22	83	- 101	1	26	K.GTFKLTQIPTVPDEVQER.K
2211.0493	2210.0420	2210.2271	-83.72	1056	- 1076	1	---	K.LQEELKTAGQGVVVDVGTVLR.T
No match to: 842.4847, 845.4012, 848.4952, 850.5135, 853.4918, 857.4026, 857.4026, 864.5186, 868.5277, 870.5200, 951.5951, 987.5186, 996.5623, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1083.5225, 1083.5225, 1090.4995, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1221.5270, 1221.5270, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1361.6049, 1379.6898, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1790.9982, 1790.9982, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2283.1272, 2506.2144, 2506.2144, 2598.2195								

24. [A0A3Q1MDH0](#) Mass: 196044 Score: 44 Expect: 5.2 Matches: 17

Poly [ADP-ribose] polymerase OS=Bos taurus OX=9913 GN=PARP14 PE=4 SV=1

observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
882.5434	881.5361	881.4494	98.4	1501	- 1508	0	---	K.TYIATDAK.G
882.5434	881.5361	881.4494	98.4	1501	- 1508	0	---	K.TYIATDAK.G
996.5623	995.5550	995.5011	54.2	1655	- 1661	1	---	K.KHMYVVR.V
1124.5784	1123.5711	1123.5509	18.0	306	- 315	0	---	K.DASTLFSDIR.S
1143.6165	1142.6092	1142.6295	-17.75	973	- 982	1	---	K.AGQKLQELK.T
1162.5488	1161.5415	1161.5699	-24.47	1470	- 1479	0	---	K.ITNMQLEDAK.K
1200.5436	1199.5363	1199.6121	-63.16	29	- 37	1	---	K.LQMYFQSRK.R
1211.6163	1210.6090	1210.5618	39.0	73	- 82	0	---	R.ESHELEWPGK.G
1211.6163	1210.6091	1210.5618	39.0	73	- 82	0	---	R.ESHELEWPGK.G
1290.6333	1289.6260	1289.6146	8.85	1185	- 1195	1	---	R.AGRNVEIECSR.Q
1407.6674	1406.6601	1406.7340	-52.53	1341	- 1352	1	---	K.KTELAVFQVCGR.N
1434.8688	1433.8615	1433.8103	35.7	1216	- 1228	1	---	K.NIIHVIGGNDVKR.S
1880.9891	1879.9818	1879.9527	15.5	1158	- 1174	1	---	K.EEADVIVNSTKSFNLK.A
1880.9891	1879.9819	1879.9527	15.5	1158	- 1174	1	---	K.EEADVIVNSTKSFNLK.A
2157.0273	2156.0200	2156.1478	-59.24	83	- 101	1	---	K.GTFKLTVQIPTVPDEVQER.K
2157.0273	2156.0201	2156.1478	-59.22	83	- 101	1	26	K.GTFKLTVQIPTVPDEVQER.K
2211.0493	2210.0420	2210.2271	-83.72	977	- 997	1	---	K.LQEELKTAGQGVVVDGTVLR.T
No match to: 842.4847, 845.4012, 848.4952, 850.5135, 853.4918, 857.4026, 857.4026, 864.5186, 868.5277, 870.5200, 951.5951, 987.5186, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1083.5225, 1083.5225, 1090.4995, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1221.5270, 1221.5270, 1263.6616, 1277.6742, 1300.8134, 1334.8459, 1334.8459, 1361.6049, 1379.6898, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1790.9982, 1790.9982, 1808.9220, 1879.9926, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2179.9844, 2283.1272, 2506.2144, 2506.2144, 2598.2195								



A0A4W2E5T5 **Mass:** 31943 **Score:** 44 **Expect:** 5.6 **Matches:** 10

Phosphatidylinositol transfer protein beta OS=Bos indicus x Bos taurus OX=30522 GN=PITPNB PE=4 SV=1

[illegible]

26. [A0A452DJF3](#) Mass: 31845 Score: 43 Expect: 7.1 Matches: 11

Phosphatidylinositol transfer protein beta isoform OS=Bos taurus OX=9913 GN=PITPNB PE=4 SV=1

[illegible]

27. [A0A4W2DWE1](#) Mass: 8549 Score: 41 Expect: 10 Matches: 5

CD3e molecule OS=Bos indicus x Bos taurus OX=30522 GN=CD3E PE=4 SV=1

[illegible]

28. [A0A3Q1MWW7](#) Mass: 28595 Score: 40 Expect: 13 Matches: 7

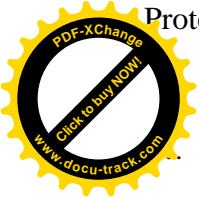
Electron transfer flavoprotein subunit beta lysine methyltransferase OS=Bos taurus OX=9913 GN=ETFBKMT PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Tons	Peptide
868.5277	867.5204	867.5654	-51.84	58	-	64	1 ---	R.LRLLTPR.C
870.5200	869.5127	869.4759	42.3	72	-	78	0 ---	R.ADLWPLR.D
1162.5488	1161.5415	1161.6064	-55.81	27	-	37	1 ---	R.GTGLSLDPPKMK.A + Oxidation (M)
1879.9926	1878.9853	1878.9053	42.6	79	-	94	0 ---	R.DPYWAIIYWPQGQALSR.Y
2157.0273	2156.0200	2156.0527	-15.15	9	-	26	1 ---	R.AVRSSGFFLPFWGHCPWR.G
2157.0273	2156.0201	2156.0527	-15.13	9	-	26	1 7	R.AVRSSGFFLPFWGHCPWR.G
2179.9844	2178.9771	2179.0644	-40.07	38	-	57	0 ---	K.AFLEENTEVTSSGSILTPEIR.L
No match to: 842.4847, 845.4012, 848.4952, 850.5135, 853.4918, 857.4026, 857.4026, 864.5186, 882.5434, 882.5434, 951.5951, 987.5186, 996.5623, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1083.5225, 1083.5225, 1090.4995, 1107.5156, 1124.5784, 1131.6732, 1136.6610, 1143.6165, 1151.6952, 1165.5533, 1165.7053, 1179.5667, 1200.5436, 1211.6163, 1211.6163, 1221.5270, 1221.5270, 1236.6616, 1277.6742, 1290.6333, 1300.8134, 1334.8459, 1334.8459, 1361.6049, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1790.9982, 1790.9982, 1808.9220, 1880.9891, 1880.9891, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2211.0493, 2283.1272.								
2506.2144.				2506.2144. 2598.2195				

29. [A0A3Q1M1B1](#) Mass: 29199 Score: 40 Expect: 14 Matches: 9

Phosphatidylinositol transfer protein beta isoform OS=Bos taurus OX=9913 GN=PITPNB PE=4 SV=1

[illegible]



Q8MII7 Mass: 4845 Score: 40 Expect: 15 Matches: 4

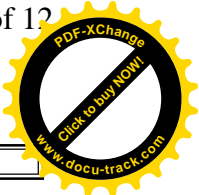
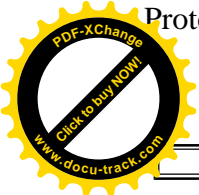
Insulin receptor (Fragment) OS=Bos taurus OX=9913 GN=ir-A PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
987.5186	986.5113	986.5033	8.15	32	-	42	0	R.ALGDVGNVTAA.-
996.5623	995.5550	995.4560	99.5	3	-	10	0	K.ELEESSFR.K
1124.5784	1123.5711	1123.5509	18.0	3	-	11	1	K.ELEESSFRK.T
1143.6165	1142.6092	1142.6044	4.24	31	-	42	1	R.RALGDVGNVTAA.-

No match to: 842.4847, 845.4012, 848.4952, 850.5135, 853.4918, 857.4026, 857.4026, 864.5186, 868.5277, 870.5200, 882.5434, 882.5434, 951.5951, 1017.6425, 1019.6487, 1033.6698, 1036.5013, 1036.5013, 1045.5382, 1051.6785, 1051.6785, 1083.5225, 1083.5225, 1090.4995, 1107.5156, 1131.6732, 1136.6610, 1151.6952, 1162.5488, 1165.5533, 1165.7053, 1179.5667, 1200.5436, 1211.6163, 1211.6163, 1221.5270, 1221.5270, 1263.6616, 1277.6742, 1290.6333, 1300.8134, 1334.8459, 1334.8459, 1361.6049, 1379.6898, 1407.6674, 1434.8688, 1448.8787, 1475.7053, 1479.7522, 1482.7051, 1567.6991, 1618.0178, 1732.0514, 1790.9982, 1790.9982, 1808.9220, 1879.9926, 1880.9891, 1880.9891, 1890.9176, 1901.2008, 1993.9156, 2064.0874, 2098.0544, 2157.0273, 2157.0273, 2179.9844, 2211.0493, 2283.1272, 2506.2144, 2506.2144, 2598.2195

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 (842.4847,1+): <no title>
Query2 (845.4012,1+): <no title>
Query3 (848.4952,1+): <no title>
Query4 (850.5135,1+): <no title>
Query5 (853.4918,1+): <no title>
Query6 (857.4026,1+): Locus:1..14.0.12
Query7 (857.4026,1+): <no title>
Query8 (864.5186,1+): <no title>
Query9 (868.5277,1+): <no title>
Query10 (870.5200,1+): <no title>
Query11 (882.5434,1+): <no title>
Query12 (882.5434,1+): Locus:1..14.0.9
Query13 (951.5951,1+): <no title>
Query14 (987.5186,1+): <no title>
Query15 (996.5623,1+): <no title>
Query16 (1017.6425,1+): <no title>
Query17 (1019.6487,1+): <no title>
Query18 (1033.6698,1+): <no title>
Query19 (1036.5013,1+): <no title>
Query20 (1036.5013,1+): Locus:1..14.0.10
Query21 (1045.5382,1+): <no title>
Query22 (1051.6785,1+): Locus:1..14.0.5
Query23 (1051.6785,1+): <no title>
Query24 (1083.5225,1+): Locus:1..14.0.3
Query25 (1083.5225,1+): <no title>
Query26 (1090.4995,1+): <no title>
Query27 (1107.5156,1+): <no title>
Query28 (1124.5784,1+): <no title>
Query29 (1131.6732,1+): <no title>
Query30 (1136.6610,1+): <no title>
Query31 (1143.6165,1+): <no title>
Query32 (1151.6952,1+): <no title>
Query33 (1162.5488,1+): <no title>
Query34 (1165.5533,1+): <no title>
Query35 (1165.7053,1+): <no title>
Query36 (1179.5667,1+): <no title>
Query37 (1200.5436,1+): <no title>
Query38 (1211.6163,1+): <no title>
Query39 (1211.6163,1+): Locus:1..14.0.11
Query40 (1221.5270,1+): Locus:1..14.0.4
Query41 (1221.5270,1+): <no title>
Query42 (1263.6616,1+): <no title>
Query43 (1277.6742,1+): <no title>
Query44 (1290.6333,1+): <no title>
Query45 (1300.8134,1+): <no title>
Query46 (1334.8459,1+): <no title>
Query47 (1334.8459,1+): Locus:1..14.0.8
Query48 (1361.6049,1+): <no title>
Query49 (1379.6898,1+): <no title>
Query50 (1407.6674,1+): <no title>
Query51 (1434.8688,1+): <no title>
Query52 (1448.8787,1+): <no title>
Query53 (1475.7053,1+): <no title>
Query54 (1479.7522,1+): <no title>
Query55 (1482.7051,1+): <no title>
Query56 (1567.6991,1+): <no title>
Query57 (1618.0178,1+): <no title>
Query58 (1732.0514,1+): <no title>
Query59 (1790.9982,1+): Locus:1..14.0.2
Query60 (1790.9982,1+): <no title>
Query61 (1808.9220,1+): <no title>
Query62 (1879.9926,1+): <no title>
Query63 (1880.9891,1+): <no title>
Query64 (1880.9891,1+): Locus:1..14.0.1
Query65 (1890.9176,1+): <no title>
Query66 (1901.2008,1+): <no title>
Query67 (1993.9156,1+): <no title>
Query68 (2064.0874,1+): <no title>
Query69 (2098.0544,1+): <no title>
Query70 (2157.0273,1+): <no title>
Query71 (2157.0273,1+): Locus:1..14.0.6
Query72 (2179.9844,1+): <no title>
Query73 (2211.0493,1+): <no title>
Query74 (2283.1272,1+): <no title>
Query75 (2506.2144,1+): Locus:1..14.0.7
Query76 (2506.2144,1+): <no title>
Query77 (2598.2195,1+): <no title>



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