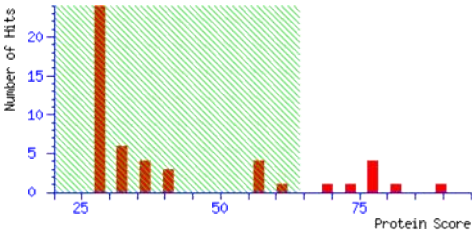


User :
Email :
Search title : BAEDW\2020_3_5\2020_3_5\MSMS 14\N11
Database : Uniprot_bovine bovine_20200316 (134392 sequences; 76244912 residues)
Timestamp : 31 Mar 2020 at 01:08:40 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 90 for R9QSM8, Alpha-2-macroglobulin OS=Bos taurus OX=9913 GN=A2M 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. R9QSM8	134613	90	Alpha-2-macroglobulin OS=Bos taurus OX=9913 GN=A2M PE=2 SV=1
2. K4JF16	102208	83	Alpha-2-macroglobulin variant 23 OS=Bos taurus OX=9913 GN=A2M PE=2 SV=1
3. K4JR88	78030	78	Alpha-2-macroglobulin variant 22 OS=Bos taurus OX=9913 GN=A2M PE=2 SV=1
4. A0A4W2E185	169075	78	Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1
5. Q7STH1	168953	78	Alpha-2-macroglobulin OS=Bos taurus OX=9913 GN=A2M PE=1 SV=2
6. A0A4W2CTC9	169552	78	Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1
7. K4JBR5	116087	75	Alpha-2-macroglobulin variant 1 OS=Bos taurus OX=9913 GN=A2M PE=2 SV=1
8. K4JDT2	99307	68	Alpha-2-macroglobulin variant 20 OS=Bos taurus OX=9913 GN=A2M PE=2 SV=1
9. A0A4W2FQH1	164938	59	Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1
10. A0A4W2FQJ3	166227	59	Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1
11. A0A4W2FCM6	168925	58	Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1
12. A0A4W2HMY5	168978	58	Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1
13. A0A4W2HM51	168906	58	Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1
14. A0A4W2BQ12	48807	41	Tripartite motif containing 77 OS=Bos indicus x Bos taurus OX=30522 GN=TRIM77 PE=4 SV=1
15. A0A4W2FVS5	48837	41	Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=LOC113885841 PE=4 SV=1
16. A0A1L7BC46	55660	39	NS5A (Fragment) OS=Bovine viral diarrhea virus OX=11099 PE=4 SV=1
17. A0A4W2FCR6	52833	36	Reverse transcriptase domain-containing protein OS=Bos indicus x Bos taurus OX=30522 PE=4 SV=1
18. A0A4W2HM23	53406	35	Glucosaminyl (N-acetyl) transferase 4 OS=Bos indicus x Bos taurus OX=30522 GN=GCNT4 PE=4 SV=1
19. A0A1L7BC66	56212	35	NS5A (Fragment) OS=Bovine viral diarrhea virus OX=11099 PE=4 SV=1
20. A0A3Q1MD56	430029	34	Lysosomal-trafficcking regulator OS=Bos taurus OX=9913 GN=LYST PE=4 SV=1
21. A0A4W2E9U7	76824	34	Nibrin OS=Bos indicus x Bos taurus OX=30522 GN=NBIN PE=4 SV=1
22. E1BNC9	124764	32	Ankyrin 3 OS=Bos taurus OX=9913 GN=ANK3 PE=4 SV=3
23. G8JVK3	11943	32	Glutaredoxin domain-containing protein OS=Bos taurus OX=9913 PE=4 SV=1
24. A0A4W2C8T2	11943	32	Glutaredoxin domain-containing protein OS=Bos indicus x Bos taurus OX=30522 PE=4 SV=1
25. A0A3Q1MUB2	54957	31	Glucosaminyl (N-acetyl) transferase 4 OS=Bos taurus OX=9913 GN=GCNT4 PE=4 SV=1
26. A0A3Q1M1F6	143195	30	Myomesin 3 OS=Bos taurus OX=9913 GN=MYOM3 PE=4 SV=1
27. Q9QAQ5	12971	30	Non-structural protein of 12.7 kDa OS=Bovine coronavirus (strain OK-0514) OX=231432 GN=5a PE=3 SV=1
28. Q6YPB4	16612	30	NOSIC domain-containing protein (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1
29. D8V071	35943	30	Phosphoprotein OS=Tibrogargan virus (strain CS132) OX=1559361 GN=P PE=3 SV=1
30. A0A4W2DGE8	25670	29	Peptidylprolyl isomerase OS=Bos indicus x Bos taurus OX=30522 GN=FKBP11 PE=4 SV=1

Results List

1.	R9QSM8	Mass: 134613	Score: 90	Expect: 0.00014	Matches: 20
Alpha-2-macroglobulin OS=Bos taurus OX=9913 GN=A2M PE=2 SV=1					
Observed	Mr (expnt)	Mr (calc)	ppm	Start	End Miss Ions Peptide
996.5488	995.5415	995.4607	81.2	1111 - 1118	1 --- K.QKSNGCFFR.S
1131.6523	1130.6450	1130.6295	13.7	1119 - 1129	0 --- R.STGTLLNNAIK.G
1250.6191	1249.6118	1249.6667	-43.88	350 - 360	0 --- K.LSFVTVDSNLR.R
1250.6191	1249.6119	1249.6667	-43.85	350 - 360	0 --- K.LSFVTVDSNLR.R
1287.6302	1286.6229	1286.6830	-46.71	777 - 789	0 --- R.DTGLGLSPTASLR.V
1302.6307	1301.6234	1301.6762	-40.52	587 - 598	0 --- R.VTASFPQSLCALR.A
1421.6768	1420.6695	1420.7350	-46.15	455 - 466	0 14 R.SNSFVYLEPLPR.E
1421.6768	1420.6695	1420.7350	-46.12	455 - 466	0 --- R.SNSFVYLEPLPR.E
1479.7271	1478.7198	1478.6422	52.5	667 - 678	0 --- K.DMYSFLQDMGLK.A + 2 Oxidation (M)
1491.6775	1490.6702	1490.7340	-42.81	82 - 93	0 --- K.DLFHCVSFTLPR.S
1523.7185	1522.7112	1522.7814	-46.06	983 - 997	0 --- R.ASFSVLGDILGSAMR.N
1707.8094	1706.8021	1706.8913	-52.25	94 - 108	0 --- R.SPTSQEVFMPLTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540 - 557	0 13 R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540 - 557	0 --- R.LLIYAILPDGEVVGDSAR.Y
1991.8297	1990.8224	1990.8909	-34.39	718 - 734	0 --- R.DFVHDDTSEPPTETVR.K

2001.9189	2000.9116	2000.9844	-36.36	210	-	228	0	---	K.GSGGTAEHPTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	-	586	0	---	K.VGLNFSPGQSFPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	-	586	0	---	K.VGLNFSPGQSFPASQAHLR.V
2073.0088	2072.0015	2072.0805	-38.12	790	-	806	0	---	R.VFQPPFFVELTMPYSVIR.G
2927.5508	2926.5435	2926.5837	-13.74	599	-	625	0	---	R.AVDQSVLLMRPEAELSAATVYNLLPVK.D
No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 2015.1936, 2044.9634, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156									

2. [K4JF16](#) Mass: 102208 Score: 83 Expect: 0.00071 Matches: 17

Alpha-2-macroglobulin variant 23 OS=Bos taurus OX=9913 GN=A2M PE=2 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1250.6191	1249.6118	1249.6667	-43.88	350	-	360	0	---	K.LSFVTVDNSNLR.R
1250.6191	1249.6119	1249.6667	-43.85	350	-	360	0	---	K.LSFVTVDNSNLR.R
1287.6302	1286.6229	1286.6830	-46.71	777	-	789	0	---	R.DTGLGLSPTASLR.V
1302.6307	1301.6234	1301.6762	-40.52	587	-	598	0	---	R.VTASPQSLCALR.A
1421.6768	1420.6695	1420.7350	-46.15	455	-	466	0	14	R.SNSFVYLEPLPR.E
1421.6768	1420.6695	1420.7350	-46.12	455	-	466	0	---	R.SNSFVYLEPLPR.E
1479.7271	1478.7198	1478.6422	52.5	667	-	678	0	---	K.DMYSFLQDMGLK.A + 2 Oxidation (M)
1491.6775	1490.6702	1490.7340	-42.81	82	-	93	0	---	K.DLFHCVSFTLPR.S
1707.8094	1706.8021	1706.8913	-52.25	94	-	108	0	---	R.SPTSQEVFMFLTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540	-	557	0	13	R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540	-	557	0	---	R.LLIYAILPDGEVVGDSAR.Y
1991.8297	1990.8224	1990.8909	-34.39	718	-	734	0	---	R.DFVHFDITSEPPETVTR.K
2001.9189	2000.9116	2000.9844	-36.36	210	-	228	0	---	K.GSGGTAEHPTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	-	586	0	---	K.VGLNFSPGQSFPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	-	586	0	---	K.VGLNFSPGQSFPASQAHLR.V
2073.0088	2072.0015	2072.0805	-38.12	790	-	806	0	---	R.VFQPPFFVELTMPYSVIR.G
2927.5508	2926.5435	2926.5837	-13.74	599	-	625	0	---	R.AVDQSVLLMRPEAELSAATVYNLLPVK.D
No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 996.5488, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1131.6523, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 2015.1936, 2044.9634, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156									

3. [K4JR88](#) Mass: 78030 Score: 78 Expect: 0.0021 Matches: 15

Alpha-2-macroglobulin variant 22 OS=Bos taurus OX=9913 GN=A2M PE=2 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1250.6191	1249.6118	1249.6667	-43.88	350	-	360	0	---	K.LSFVTVDNSNLR.R
1250.6191	1249.6119	1249.6667	-43.85	350	-	360	0	---	K.LSFVTVDNSNLR.R
1287.6302	1286.6229	1286.6983	-58.57	473	-	483	0	---	K.TQTQVAHYVLK.G
1302.6307	1301.6234	1301.6762	-40.52	587	-	598	0	---	R.VTASPQSLCALR.A
1421.6768	1420.6695	1420.7350	-46.15	455	-	466	0	14	R.SNSFVYLEPLPR.E
1421.6768	1420.6695	1420.7350	-46.12	455	-	466	0	---	R.SNSFVYLEPLPR.E
1479.7271	1478.7198	1478.6422	52.5	667	-	678	0	---	K.DMYSFLQDMGLK.A + 2 Oxidation (M)
1491.6775	1490.6702	1490.7340	-42.81	82	-	93	0	---	K.DLFHCVSFTLPR.S
1707.8094	1706.8021	1706.8913	-52.25	94	-	108	0	---	R.SPTSQEVFMFLTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540	-	557	0	13	R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540	-	557	0	---	R.LLIYAILPDGEVVGDSAR.Y
2001.9189	2000.9116	2000.9844	-36.36	210	-	228	0	---	K.GSGGTAEHPTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	-	586	0	---	K.VGLNFSPGQSFPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	-	586	0	---	K.VGLNFSPGQSFPASQAHLR.V
2927.5508	2926.5435	2926.5837	-13.74	599	-	625	0	---	R.AVDQSVLLMRPEAELSAATVYNLLPVK.D
No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 996.5488, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1131.6523, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1523.7185, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 1991.8297, 2015.1936, 2044.9634, 2073.0088, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156									

4. [A0A4W2E185](#) Mass: 169075 Score: 78 Expect: 0.0022 Matches: 20

Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
996.5488	995.5415	995.4607	81.2	1111	-	1118	1	---	K.QKSNCGCFR.S
1131.6523	1130.6450	1130.6295	13.7	1119	-	1129	0	---	R.STGTLLNNAIK.G
1250.6191	1249.6118	1249.6667	-43.88	350	-	360	0	---	K.LSFVTVDNSNLR.R
1250.6191	1249.6119	1249.6667	-43.85	350	-	360	0	---	K.LSFVTVDNSNLR.R
1287.6302	1286.6229	1286.6830	-46.71	777	-	789	0	---	R.DTGLGLSPTASLR.V
1302.6307	1301.6234	1301.6762	-40.52	587	-	598	0	---	R.VTASPQSLCALR.A
1421.6768	1420.6695	1420.7350	-46.15	455	-	466	0	14	R.SNSFVYLEPLPR.E
1421.6768	1420.6695	1420.7350	-46.12	455	-	466	0	---	R.SNSFVYLEPLPR.E
1479.7271	1478.7198	1478.6422	52.5	667	-	678	0	---	K.DMYSFLQDMGLK.A + 2 Oxidation (M)
1491.6775	1490.6702	1490.7340	-42.81	82	-	93	0	---	K.DLFHCVSFTLPR.S
1523.7185	1522.7112	1522.7814	-46.06	983	-	997	0	---	R.ASFVSLGDILGSAMR.N
1707.8094	1706.8021	1706.8913	-52.25	94	-	108	0	---	R.SPTSQEVFMFLTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540	-	557	0	13	R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540	-	557	0	---	R.LLIYAILPDGEVVGDSAR.Y
1991.8297	1990.8224	1990.8909	-34.39	718	-	734	0	---	R.DFVHFDITSEPPETVTR.K
2001.9189	2000.9116	2000.9844	-36.36	210	-	228	0	---	K.GSGGTAEHPTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	-	586	0	---	K.VGLNFSPGQSFPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	-	586	0	---	K.VGLNFSPGQSFPASQAHLR.V
2073.0088	2072.0015	2072.0805	-38.12	790	-	806	0	---	R.VFQPPFFVELTMPYSVIR.G
2927.5508	2926.5435	2926.5837	-13.74	599	-	625	0	---	R.AVDQSVLLMRPEAELSAATVYNLLPVK.D
No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 2015.1936, 2044.9634, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156									

5. [Q7SIHI](#) Mass: 168953 Score: 78 Expect: 0.0022 Matches: 20

Alpha-2-macroglobulin OS=Bos taurus OX=9913 GN=A2M PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
996.5488	995.5415	995.4607	81.2	1111	1118	1	---	K.QKSNGCFR.S
1131.6523	1130.6450	1130.6295	13.7	1119	1129	0	---	R.STGTLNNAIK.G
1250.6191	1249.6118	1249.6667	-43.88	350	360	0	---	K.LSFVTVDNSLR.R
1250.6191	1249.6119	1249.6667	-43.85	350	360	0	---	K.LSFVTVDNSLR.R
1287.6302	1286.6229	1286.6830	-46.71	777	789	0	---	R.DTGLGLSPTASLR.V
1302.6307	1301.6234	1301.6762	-40.52	587	598	0	---	R.VTASPSQLCALR.A
1421.6768	1420.6695	1420.7350	-46.15	455	466	0	14	R.SNSFVYLEPLPR.E
1421.6768	1420.6695	1420.7350	-46.12	455	466	0	---	R.SNSFVYLEPLPR.E
1479.7271	1478.7198	1478.6422	52.5	667	678	0	---	K.DMYSFLQDMGLK.A + 2 Oxidation (M)
1491.6775	1490.6702	1490.7340	-42.81	82	93	0	---	K.DLFHCVSFTLPR.S
1523.7185	1522.7112	1522.7814	-46.06	983	997	0	---	R.ASFVSLGDILGSAMR.N
1707.8094	1706.8021	1706.8913	-52.25	94	108	0	---	R.SPTSQEVFMFLTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540	557	0	13	R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540	557	0	---	R.LLIYAILPDGEVVGDSAR.Y
1991.8297	1990.8224	1990.8909	-34.39	718	734	0	---	R.DFVHFDTTSEPTTETVR.K
2001.9189	2000.9116	2000.9844	-36.36	210	228	0	---	K.GSGGTAEHPTTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	586	0	---	K.VGLNFSFGQSFSPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	586	0	---	K.VGLNFSFGQSFSPASQAHLR.V
2073.0088	2072.0015	2072.0805	-38.12	790	806	0	---	R.VFQPFVVELTMPYSVIR.G
2927.5508	2926.5435	2926.5837	-13.74	599	625	0	---	R.AVDQSVLLMRPEAELSAATVYNLLPVK.D
No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 2015.1936, 2044.9634, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156								

6. [A0A4W2CTC9](#) Mass: 169552 Score: 78 Expect: 0.0023 Matches: 20

Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
996.5488	995.5415	995.4607	81.2	1111	1118	1	---	K.QKSNGCFR.S
1131.6523	1130.6450	1130.6295	13.7	1119	1129	0	---	R.STGTLNNAIK.G
1250.6191	1249.6118	1249.6667	-43.88	350	360	0	---	K.LSFVTVDNSLR.R
1250.6191	1249.6119	1249.6667	-43.85	350	360	0	---	K.LSFVTVDNSLR.R
1287.6302	1286.6229	1286.6830	-46.71	777	789	0	---	R.DTGLGLSPTASLR.V
1302.6307	1301.6234	1301.6762	-40.52	587	598	0	---	R.VTASPSQLCALR.A
1421.6768	1420.6695	1420.7350	-46.15	455	466	0	14	R.SNSFVYLEPLPR.E
1421.6768	1420.6695	1420.7350	-46.12	455	466	0	---	R.SNSFVYLEPLPR.E
1479.7271	1478.7198	1478.6422	52.5	667	678	0	---	K.DMYSFLQDMGLK.A + 2 Oxidation (M)
1491.6775	1490.6702	1490.7340	-42.81	82	93	0	---	K.DLFHCVSFTLPR.S
1523.7185	1522.7112	1522.7814	-46.06	983	997	0	---	R.ASFVSLGDILGSAMR.N
1707.8094	1706.8021	1706.8913	-52.25	94	108	0	---	R.SPTSQEVFMFLTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540	557	0	13	R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540	557	0	---	R.LLIYAILPDGEVVGDSAR.Y
1991.8297	1990.8224	1990.8909	-34.39	718	734	0	---	R.DFVHFDTTSEPTTETVR.K
2001.9189	2000.9116	2000.9844	-36.36	210	228	0	---	K.GSGGTAEHPTTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	586	0	---	K.VGLNFSFGQSFSPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	586	0	---	K.VGLNFSFGQSFSPASQAHLR.V
2073.0088	2072.0015	2072.0805	-38.12	790	806	0	---	R.VFQPFVVELTMPYSVIR.G
2927.5508	2926.5435	2926.5837	-13.74	599	625	0	---	R.AVDQSVLLMRPEAELSAATVYNLLPVK.D
No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 2015.1936, 2044.9634, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156								

7. [K4JBR5](#) Mass: 116087 Score: 75 Expect: 0.0041 Matches: 16

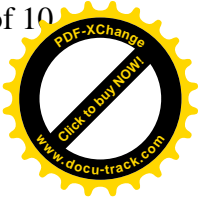
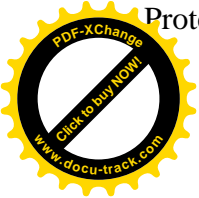
Alpha-2-macroglobulin variant 1 OS=Bos taurus OX=9913 GN=A2M PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1250.6191	1249.6118	1249.6667	-43.88	350	360	0	---	K.LSFVTVDNSLR.R
1250.6191	1249.6119	1249.6667	-43.85	350	360	0	---	K.LSFVTVDNSLR.R
1287.6302	1286.6229	1286.6830	-46.71	777	789	0	---	R.DTGLGLSPTASLR.V
1302.6307	1301.6234	1301.6762	-40.52	587	598	0	---	R.VTASPSQLCALR.A
1421.6768	1420.6695	1420.7350	-46.15	455	466	0	14	R.SNSFVYLEPLPR.E
1421.6768	1420.6695	1420.6367	23.1	667	678	0	---	K.DMYSFLQDMGLK.A + 2 Oxidation (M)
1491.6775	1490.6702	1490.7340	-42.81	82	93	0	---	K.DLFHCVSFTLPR.S
1707.8094	1706.8021	1706.8913	-52.25	94	108	0	---	R.SPTSQEVFMFLTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540	557	0	13	R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540	557	0	---	R.LLIYAILPDGEVVGDSAR.Y
1991.8297	1990.8224	1990.8909	-34.39	718	734	0	---	R.DFVHFDTTSEPTTETVR.K
2001.9189	2000.9116	2000.9844	-36.36	210	228	0	---	K.GSGGTAEHPTTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	586	0	---	K.VGLNFSFGQSFSPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	586	0	---	K.VGLNFSFGQSFSPASQAHLR.V
2073.0088	2072.0015	2072.0805	-38.12	790	806	0	---	R.VFQPFVVELTMPYSVIR.G
2927.5508	2926.5435	2926.5837	-13.74	599	625	0	---	R.AVDQSVLLMRPEAELSAATVYNLLPVK.D
No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 996.5488, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1131.6523, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 2015.1936, 2044.9634, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156								

8. [K4JDT2](#) Mass: 99307 Score: 68 Expect: 0.02 Matches: 15

Alpha-2-macroglobulin variant 20 OS=Bos taurus OX=9913 GN=A2M PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1250.6191	1249.6118	1249.6667	-43.88	350	360	0	---	K.LSFVTVDNSLR.R
1250.6191	1249.6119	1249.6667	-43.85	350	360	0	---	K.LSFVTVDNSLR.R
1287.6302	1286.6229	1286.6830	-46.71	777	789	0	---	R.DTGLGLSPTASLR.V
1421.6768	1420.6695	1420.7350	-46.15	455	466	0	14	R.SNSFVYLEPLPR.E
1421.6768	1420.6695	1420.7350	-46.12	455	466	0	---	R.SNSFVYLEPLPR.E
1479.7271	1478.7198	1478.6422	52.5	667	678	0	---	K.DMYSFLQDMGLK.A + 2 Oxidation (M)



1491.6775	1490.6702	1490.7340	-42.81	82	-	93	0	---	K.DLFHCVSFTLPR.S
1707.8094	1706.8021	1706.8913	-52.25	94	-	108	0	---	R.SPTSQEVFMFLTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540	-	557	0	13	R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540	-	557	0	---	R.LLIYAILPDGEVVGDSAR.Y
1991.8297	1990.8224	1990.8909	-34.39	718	-	734	0	---	R.DFVHFDDTSEPPTETVR.K
2001.9189	2000.9116	2000.9844	-36.36	210	-	228	0	---	K.GSGGTAEHFPTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	-	586	0	---	K.VGLNFSFGQSFPPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	-	586	0	---	K.VGLNFSFGQSFPPASQAHLR.V
2073.0088	2072.0015	2072.0805	-38.12	790	-	806	0	---	R.VFQPFVVELTMPYSVIR.G
No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 996.5488, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1131.6523, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1302.6307, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1523.7185, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 2015.1936, 2044.9634, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 2927.5508, 3337.7156									

9. [A0A4W2FQH1](#) Mass: 164938 Score: 59 Expect: 0.17 Matches: 18

Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
996.5488	995.5415	995.4607	81.2	1073	-	1080	1	---	K.QKSNCGCFR.S
1131.6523	1130.6450	1130.6295	13.7	1081	-	1091	0	---	R.STGTLLNNAIK.G
1250.6191	1249.6118	1249.6667	-43.88	350	-	360	0	---	K.LSFVTVDNSLR.R
1250.6191	1249.6119	1249.6667	-43.85	350	-	360	0	---	K.LSFVTVDNSLR.R
1287.6302	1286.6229	1286.6830	-46.71	775	-	787	0	---	R.DTGLGLSPTASLR.V
1302.6307	1301.6234	1301.6762	-40.52	587	-	598	0	---	R.VTASPSQLCALR.A
1479.7271	1478.7198	1478.6422	52.5	667	-	678	0	---	K.DMYSFLQDMGLK.A + 2 Oxidation (M)
1491.6775	1490.6702	1490.7340	-42.81	82	-	93	0	---	K.DLFHCVSFTLPR.S
1523.7185	1522.7112	1522.7814	-46.06	945	-	959	0	---	R.ASFVSLGDLGSAMR.N
1707.8094	1706.8021	1706.8913	-52.25	94	-	108	0	---	R.SPTSQEVFMFLTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540	-	557	0	13	R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540	-	557	0	---	R.LLIYAILPDGEVVGDSAR.Y
1991.8297	1990.8224	1990.8909	-34.39	716	-	732	0	---	R.DFVHFDDTSEPPTETVR.K
2001.9189	2000.9116	2000.9844	-36.36	210	-	228	0	---	K.GSGGTAEHFPTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	-	586	0	---	K.VGLNFSFGQSFPPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	-	586	0	---	K.VGLNFSFGQSFPPASQAHLR.V
2073.0088	2072.0015	2072.0805	-38.12	788	-	804	0	---	R.VFQPFVVELTMPYSVIR.G
2927.5508	2926.5435	2926.5837	-13.74	599	-	625	0	---	R.AVDQSLLMRPEAELSAATVYNLLPVK.D
No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 2015.1936, 2044.9634, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156									

10. [A0A4W2FQJ3](#) Mass: 166227 Score: 59 Expect: 0.19 Matches: 18

Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
996.5488	995.5415	995.4607	81.2	1111	-	1118	1	---	K.QKSNCGCFR.S
1131.6523	1130.6450	1130.6295	13.7	1119	-	1129	0	---	R.STGTLLNNAIK.G
1250.6191	1249.6118	1249.6667	-43.88	350	-	360	0	---	K.LSFVTVDNSLR.R
1250.6191	1249.6119	1249.6667	-43.85	350	-	360	0	---	K.LSFVTVDNSLR.R
1287.6302	1286.6229	1286.6830	-46.71	777	-	789	0	---	R.DTGLGLSPTASLR.V
1302.6307	1301.6234	1301.6762	-40.52	587	-	598	0	---	R.VTASPSQLCALR.A
1479.7271	1478.7198	1478.6422	52.5	667	-	678	0	---	K.DMYSFLQDMGLK.A + 2 Oxidation (M)
1491.6775	1490.6702	1490.7340	-42.81	82	-	93	0	---	K.DLFHCVSFTLPR.S
1523.7185	1522.7112	1522.7814	-46.06	983	-	997	0	---	R.ASFVSLGDLGSAMR.N
1707.8094	1706.8021	1706.8913	-52.25	94	-	108	0	---	R.SPTSQEVFMFLTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540	-	557	0	13	R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540	-	557	0	---	R.LLIYAILPDGEVVGDSAR.Y
1991.8297	1990.8224	1990.8909	-34.39	718	-	734	0	---	R.DFVHFDDTSEPPTETVR.K
2001.9189	2000.9116	2000.9844	-36.36	210	-	228	0	---	K.GSGGTAEHFPTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	-	586	0	---	K.VGLNFSFGQSFPPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	-	586	0	---	K.VGLNFSFGQSFPPASQAHLR.V
2073.0088	2072.0015	2072.0805	-38.12	790	-	806	0	---	R.VFQPFVVELTMPYSVIR.G
2927.5508	2926.5435	2926.5837	-13.74	599	-	625	0	---	R.AVDQSLLMRPEAELSAATVYNLLPVK.D
No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 2015.1936, 2044.9634, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156									

11. [A0A4W2FQM6](#) Mass: 168925 Score: 58 Expect: 0.22 Matches: 18

Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
996.5488	995.5415	995.4607	81.2	1111	-	1118	1	---	K.QKSNCGCFR.S
1131.6523	1130.6450	1130.6295	13.7	1119	-	1129	0	---	R.STGTLLNNAIK.G
1250.6191	1249.6118	1249.6667	-43.88	350	-	360	0	---	K.LSFVTVDNSLR.R
1250.6191	1249.6119	1249.6667	-43.85	350	-	360	0	---	K.LSFVTVDNSLR.R
1287.6302	1286.6229	1286.6830	-46.71	777	-	789	0	---	R.DTGLGLSPTASLR.V
1302.6307	1301.6234	1301.6762	-40.52	587	-	598	0	---	R.VTASPSQLCALR.A
1479.7271	1478.7198	1478.6422	52.5	667	-	678	0	---	K.DMYSFLQDMGLK.A + 2 Oxidation (M)
1491.6775	1490.6702	1490.7340	-42.81	82	-	93	0	---	K.DLFHCVSFTLPR.S
1523.7185	1522.7112	1522.7814	-46.06	983	-	997	0	---	R.ASFVSLGDLGSAMR.N
1707.8094	1706.8021	1706.8913	-52.25	94	-	108	0	---	R.SPTSQEVFMFLTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540	-	557	0	13	R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540	-	557	0	---	R.LLIYAILPDGEVVGDSAR.Y
1991.8297	1990.8224	1990.8909	-34.39	718	-	734	0	---	R.DFVHFDDTSEPPTETVR.K
2001.9189	2000.9116	2000.9844	-36.36	210	-	228	0	---	K.GSGGTAEHFPTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	-	586	0	---	K.VGLNFSFGQSFPPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	-	586	0	---	K.VGLNFSFGQSFPPASQAHLR.V
2073.0088	2072.0015	2072.0805	-38.12	790	-	806	0	---	R.VFQPFVVELTMPYSVIR.G
2927.5508	2926.5435	2926.5837	-13.74	599	-	625	0	---	R.AVDQSLLMRPEAELSAATVYNLLPVK.D

No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 2015.1936, 2044.9634, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156

12. A0A4W2HWM5 Mass: 168978 Score: 58 Expect: 0.22 Matches: 18

Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
996.5488	995.5415	995.4607	81.2	1111	1118	1	---	K.QKSNCGCFR.S
1131.6523	1130.6450	1130.6295	13.7	1119	1129	0	---	R.STGTLLNNAIK.G
1250.6191	1249.6118	1249.6667	-43.88	350	360	0	---	K.LSFVTVDNLR.R
1250.6191	1249.6119	1249.6667	-43.85	350	360	0	---	K.LSFVTVDNLR.R
1287.6302	1286.6229	1286.6830	-46.71	777	789	0	---	R.DTGLGLSPTASLR.V
1302.6307	1301.6234	1301.6762	-40.52	587	598	0	---	R.VTASPSQLCALR.A
1479.7271	1478.7198	1478.6422	52.5	667	678	0	---	K.DMYSFLQDMGLK.A + 2 Oxidation (M)
1491.6775	1490.6702	1490.7340	-42.81	82	93	0	---	K.DLFHCVSFTLPR.S
1523.7185	1522.7112	1522.7814	-46.06	983	997	0	---	R.ASFVSLGDLGSAKR.N
1707.8094	1706.8021	1706.8913	-52.25	94	108	0	---	R.SPTSQEVMLFTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540	557	0	13	R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540	557	0	---	R.LLIYAILPDGEVVGDSAR.Y
1991.8297	1990.8224	1990.8909	-34.39	718	734	0	---	R.DFVHFDSTSEPTETVR.K
2001.9189	2000.9116	2000.9844	-36.36	210	228	0	---	K.GSGGTAEHPTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	586	0	---	K.VGLNFSFGQSFPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	586	0	---	K.VGLNFSFGQSFPASQAHLR.V
2073.0088	2072.0015	2072.0805	-38.12	790	806	0	---	R.VFQPFVVELTMPYSVIR.G
2927.5508	2926.5435	2926.5837	-13.74	599	625	0	---	R.AVDQSLLMRPEALSAATVYNLLPVK.D

No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 2015.1936, 2044.9634, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156

13. A0A4W2HMS1 Mass: 168906 Score: 58 Expect: 0.22 Matches: 18

Alpha-2-macroglobulin OS=Bos indicus x Bos taurus OX=30522 GN=A2M PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
996.5488	995.5415	995.4607	81.2	1111	1118	1	---	K.QKSNCGCFR.S
1131.6523	1130.6450	1130.6295	13.7	1119	1129	0	---	R.STGTLLNNAIK.G
1250.6191	1249.6118	1249.6667	-43.88	350	360	0	---	K.LSFVTVDNLR.R
1250.6191	1249.6119	1249.6667	-43.85	350	360	0	---	K.LSFVTVDNLR.R
1287.6302	1286.6229	1286.6830	-46.71	777	789	0	---	R.DTGLGLSPTASLR.V
1302.6307	1301.6234	1301.6762	-40.52	587	598	0	---	R.VTASPSQLCALR.A
1479.7271	1478.7198	1478.6422	52.5	667	678	0	---	K.DMYSFLQDMGLK.A + 2 Oxidation (M)
1491.6775	1490.6702	1490.7340	-42.81	82	93	0	---	K.DLFHCVSFTLPR.S
1523.7185	1522.7112	1522.7814	-46.06	983	997	0	---	R.ASFVSLGDLGSAKR.N
1707.8094	1706.8021	1706.8913	-52.25	94	108	0	---	R.SPTSQEVMLFTIQVK.G
1900.9595	1899.9522	1900.0306	-41.25	540	557	0	13	R.LLIYAILPDGEVVGDSAR.Y
1900.9595	1899.9522	1900.0306	-41.23	540	557	0	---	R.LLIYAILPDGEVVGDSAR.Y
1991.8297	1990.8224	1990.8909	-34.39	718	734	0	---	R.DFVHFDSTSEPTETVR.K
2001.9189	2000.9116	2000.9844	-36.36	210	228	0	---	K.GSGGTAEHPTVEEFVLPK.F
2012.9465	2011.9392	2012.0228	-41.54	568	586	0	---	K.VGLNFSFGQSFPASQAHLR.V
2012.9465	2011.9393	2012.0228	-41.53	568	586	0	---	K.VGLNFSFGQSFPASQAHLR.V
2073.0088	2072.0015	2072.0805	-38.12	790	806	0	---	R.VFQPFVVELTMPYSVIR.G
2927.5508	2926.5435	2926.5837	-13.74	599	625	0	---	R.AVDQSLLMRPEALSAATVYNLLPVK.D

No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1518.6587, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1732.0206, 2015.1936, 2044.9634, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156

14. A0A4W2BQ12 Mass: 48807 Score: 41 Expect: 12 Matches: 11

Tripartite motif containing 77 OS=Bos indicus x Bos taurus OX=30522 GN=TRIM77 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4690	841.4617	841.4882	-31.47	212	218	1	---	R.LNRNVAR.M
1045.5168	1044.5095	1044.5096	-0.07	138	145	0	---	R.EHLLMQMK.S + Oxidation (M)
1136.6420	1135.6347	1135.5510	73.8	20	29	0	---	K.DTFTDPATIR.C
1300.7900	1299.7827	1299.6540	99.1	91	100	1	---	K.QMCRTHQVIK.L
1518.6587	1517.6514	1517.7508	-65.47	76	90	0	---	R.STGNSVICQLPGSAK.Q
1559.7947	1558.7874	1558.8000	-8.04	138	149	1	---	R.EHLLMQMKSIWK.K + Oxidation (M)
1567.6738	1566.6665	1566.6906	-15.35	240	253	0	---	K.ADVDMQLQGVEDTMK.R + Oxidation (M)
1707.8094	1706.8021	1706.7968	3.15	240	254	1	---	K.ADVDMQLQGVEDTMKR.S
2012.9465	2011.9392	2012.0877	-73.79	195	211	1	---	K.QKHLEMLAIEGTVIFQR.L
2012.9465	2011.9393	2012.0877	-73.77	195	211	1	---	K.QKHLEMLAIEGTVIFQR.L
2193.0256	2192.0183	2192.1333	-52.46	366	383	1	---	R.NDMLNSEDIFLLLCVKR.K

No match to: 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 956.5488, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1051.6565, 1051.6565, 1131.6523, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1250.6191, 1250.6191, 1287.6302, 1302.6307, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1479.7271, 1491.6775, 1523.7185, 1552.7145, 1617.9915, 1617.9915, 1732.0206, 1900.9595, 1900.9595, 1991.8297, 2001.9189, 2015.1936, 2044.9634, 2073.0088, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 2927.5508, 3337.7156

15. A0A4W2FVS5 Mass: 48837 Score: 41 Expect: 12 Matches: 11

Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=LOC113885841 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4690	841.4617	841.4882	-31.47	212	218	1	---	R.LNRNVAR.M
1045.5168	1044.5095	1044.5096	-0.07	138	145	0	---	R.EHLLMQMK.S + Oxidation (M)
1136.6420	1135.6347	1135.5510	73.8	20	29	0	---	K.DTFTDPATIR.C
1300.7900	1299.7827	1299.6540	99.1	91	100	1	---	K.QMCRTHQVIK.L
1518.6587	1517.6514	1517.7508	-65.47	76	90	0	---	R.STGNSVICQLPGSAK.Q
1559.7947	1558.7874	1558.8000	-8.04	138	149	1	---	R.EHLLMQMKSIWK.K + Oxidation (M)

1567.6738 1566.6665 1566.6906 -15.35 240 - 253 0 --- K.ADVDMQLQGVEDTMK.R + Oxidation (M)
1707.8094 1706.8021 1706.7968 3.15 240 - 254 1 --- K.ADVDMQLQGVEDTMKR.S
2012.9465 2011.9392 2012.0877 -73.79 195 - 211 1 --- K.QKHLEMLAIEGTVIFQR.L
2012.9465 2011.9393 2012.0877 -73.77 195 - 211 1 --- K.QKHLEMLAIEGTVIFQR.L
2193.0256 2192.0183 2192.1333 -52.46 366 - 383 1 --- R.NDMLLNSIEDIFLLLCVKR.K
No match to: 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 996.5488, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1051.6565, 1051.6565, 1131.6523, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1250.6191, 1250.6191, 1287.6302, 1302.6307, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1356.6021, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1479.7271, 1491.6775, 1523.7185, 1552.7145, 1617.9915, 1617.9915, 1732.0206, 1900.9595, 1900.9595, 1991.8297, 2001.9189, 2015.1936, 2044.9634, 2073.0088, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 2927.5508, 3337.7156

16. [A0A1L7BC46](#) Mass: 55660 Score: 39 Expect: 15 Matches: 10

NS5A (Fragment) OS=Bovine viral diarrhea virus OX=11099 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1033.6514	1032.6441	1032.5716	70.2	91	99	1	---	R.GPVNRYRVTK.Y
1045.5168	1044.5095	1044.5240	-13.88	459	467	0	---	K.YHLVGVDVK.V
1250.6191	1249.6118	1249.6779	-52.84	356	366	1	---	K.TARNINLYTGK.D
1250.6191	1249.6119	1249.6779	-52.81	356	366	1	---	K.TARNINLYTGK.D
1356.6021	1355.5948	1355.6036	-6.46	57	67	1	---	K.CPCGYEMKALK.N
1448.8531	1447.8458	1447.7671	54.4	45	56	1	---	R.LPTDNYLRVETK.C
1523.7185	1522.7112	1522.8256	-75.11	143	155	1	---	K.WEVEHGVVTRLAK.R
1552.7145	1551.7072	1551.7457	-24.78	387	399	0	---	R.DFNPELSELVDFK.G
2001.9189	2000.9116	2001.0935	-90.88	107	123	1	---	K.EIKPVAKLEGLVDHYK.G
2927.5508	2926.5435	2926.3945	50.9	298	326	1	---	K.TEPNADGGPSSIKIGLDEGSYPGGLQDR.T

No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 996.5488, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1051.6565, 1051.6565, 1131.6523, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1287.6302, 1300.7900, 1302.6307, 1316.8218, 1334.8221, 1334.8221, 1421.6768, 1421.6768, 1454.7075, 1475.6875, 1479.7271, 1491.6775, 1518.6587, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1707.8094, 1732.0206, 1900.9595, 1900.9595, 1991.8297, 2012.9465, 2012.9465, 2015.1936, 2044.9634, 2073.0088, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156

17. [A0A4W2FCR6](#) Mass: 52833 Score: 36 Expect: 36 Matches: 8

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4879	847.4806	847.4287	61.3	381	387	1	---	K.VKEESEK.V
864.5118	863.5045	863.5453	-47.26	440	446	1	---	K.RHLLLR.N
868.5078	867.5005	867.4888	13.5	376	382	1	---	K.SFLMKVK.E + Oxidation (M)
1131.6523	1130.6450	1130.5720	64.6	221	230	0	---	R.ELPDVQAGFR.K
1356.6021	1355.5948	1355.6642	-51.20	370	380	1	---	K.SEEELKSFLMK.V + Oxidation (M)
1479.7271	1478.7198	1478.6922	18.7	75	87	1	---	R.NGMDLTAEDIKK.R + Oxidation (M)
2283.0967	2282.0894	2282.0249	28.3	255	272	1	---	K.NICCFDIYAKTFDCVDHKK.L
2927.5508	2926.5435	2926.3767	57.0	99	123	1	---	K.GLRLDPDNHGMITNLEPDILEYEV.R + Oxidation (M)

No match to: 842.4690, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 865.9869, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 996.5488, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1250.6191, 1250.6191, 1287.6302, 1300.7900, 1302.6307, 1316.8218, 1334.8221, 1334.8221, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1491.6775, 1518.6587, 1523.7185, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1707.8094, 1732.0206, 1900.9595, 1900.9595, 1991.8297, 2001.9189, 2015.1936, 2044.9634, 2073.0088, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2284.0908, 2305.0867, 3337.7156

18. [A0A4W2HM23](#) Mass: 53406 Score: 35 Expect: 40 Matches: 10

Glucosaminyl (N-acetyl) transferase 4 OS=Bos indicus x Bos taurus OX=30522 GN=GCNT4 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
996.5488	995.5415	995.5651	-23.72	346	355	0	---	R.VPGIPGEISK.T
1033.6514	1032.6441	1032.5968	45.9	435	443	1	---	R.KWITLSSAK.L
1131.6523	1130.6450	1130.5760	61.0	315	323	0	---	K.YIFNNSFVK.D
1165.6849	1164.6776	1164.6026	64.4	236	245	0	---	K.SNFELVSELK.K
1165.6849	1164.6777	1164.6026	64.4	236	245	0	---	K.SNFELVSELK.K
1316.8218	1315.8145	1315.6884	95.8	193	203	0	---	K.LETVQYAHISR.L
1448.8531	1447.8458	1447.7267	82.3	356	368	1	---	K.TAQDVSDLQSKTR.L
1732.0206	1731.0133	1730.8873	72.8	247	262	0	---	K.LNGSNMLETVKPPSTK.T + Oxidation (M)
2012.9465	2011.9392	2011.9832	-21.87	315	330	1	---	K.YIFNNSFVKDFFAWSK.D
2012.9465	2011.9393	2011.9832	-21.86	315	330	1	---	K.YIFNNSFVKDFFAWSK.D

No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 996.5488, 1017.6209, 1017.6209, 1019.6330, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1147.6807, 1151.6740, 1250.6191, 1250.6191, 1287.6302, 1300.7900, 1302.6307, 1334.8221, 1334.8221, 1356.6021, 1421.6768, 1421.6768, 1454.7075, 1475.6875, 1479.7271, 1491.6775, 1518.6587, 1523.7185, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1707.8094, 1900.9595, 1900.9595, 1991.8297, 2001.9189, 2015.1936, 2044.9634, 2073.0088, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 2927.5508, 3337.7156

19. [A0A1L7BC66](#) Mass: 56212 Score: 35 Expect: 46 Matches: 11

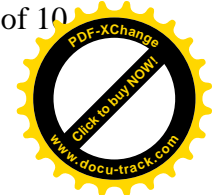
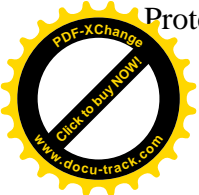
NS5A (Fragment) OS=Bovine viral diarrhea virus OX=11099 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
882.5228	881.5155	881.4494	75.0	129	135	1	---	K.IDYSKEK.T
882.5228	881.5155	881.4494	75.0	129	135	1	---	K.IDYSKEK.T
1033.6514	1032.6441	1032.5716	70.2	91	99	1	---	R.GPVNRYRVTK.Y
1131.6523	1130.6450	1130.5866	51.7	370	379	1	---	R.EIRDLMAAGR.M
1147.6807	1146.6734	1146.5815	80.2	370	379	1	---	R.EIRDLMAAGR.M + Oxidation (M)
1302.6307	1301.6234	1301.7303	-82.12	474	485	1	---	K.TLGATDQTRIVK.E
1518.6587	1517.6514	1517.8011	-98.62	284	297	0	---	R.ETLMTTGVTPVLEK.V
1523.7185	1522.7112	1522.6861	16.5	387	399	0	---	R.DVDPELSEMVDK.FK
1900.9595	1899.9522	1899.9538	-0.83	298	315	1	---	K.VEPDASNNQSSVKIGLDK.G
1900.9595	1899.9522	1899.9538	-0.81	298	315	1	---	K.VEPDASNNQSSVKIGLDK.G
2001.9189	2000.9116	2000.9990	-43.65	136	152	1	---	K.TLLATDKWEHGVMT.R + Oxidation (M)

No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 892.9686, 951.5814, 953.4899, 996.5488, 1017.6209, 1017.6209, 1019.6330, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1151.6740, 1165.6849, 1165.6849, 1250.6191, 1250.6191, 1287.6302, 1300.7900, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1479.7271, 1491.6775, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1707.8094, 1732.0206, 1991.8297, 2012.9465, 2012.9465, 2015.1936, 2044.9634, 2073.0088, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 2927.5508, 3337.7156

20. [A0A3Q1MD56](#) Mass: 430029 Score: 34 Expect: 48 Matches: 27

Lyosomal-trafficking regulator OS=Bos taurus OX=9913 GN=LYST PE=4 SV=1



Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4690	841.4617	841.4545	8.57	86	-	92	0	K.IPVQEEK.A
853.4743	852.4670	852.4164	59.4	2381	-	2387	0	K.NMGLFQK.W + Oxidation (M)
853.4743	852.4670	852.4164	59.4	2381	-	2387	0	K.NMGLFQK.W + Oxidation (M)
1017.6209	1016.6136	1016.5754	37.6	1034	-	1042	0	K.EDLLSLTVK.I
1017.6209	1016.6136	1016.5754	37.6	1034	-	1042	0	K.EDLLSLTVK.I
1019.6330	1018.6257	1018.5308	93.2	149	-	156	1	K.TTHRYSVR.D
1045.5168	1044.5095	1044.5175	-7.64	982	-	990	0	R.LGGFQVCHK.L
1250.6191	1249.6118	1249.5840	22.3	3234	-	3243	0	R.TFHSNTNTWR.L
1250.6191	1249.6119	1249.7044	-74.03	184	-	193	1	R.RSHVLQHFVK.Q
1300.7900	1299.7827	1299.6922	69.7	1043	-	1054	0	K.IDPTPTLSSLK.K
1302.6307	1301.6234	1301.6993	-58.27	3284	-	3294	0	R.VNHVNLPPWAR.N
1316.8218	1315.8145	1315.7724	32.0	2606	-	2616	1	R.LQRLTVFAVNR.I
1334.8221	1333.8148	1333.6911	92.7	1351	-	1361	0	R.TCSEELTLLR.I
1334.8221	1333.8149	1333.6911	92.8	1351	-	1361	0	R.TCSEELTLLR.I
1448.8531	1447.8458	1447.7168	89.1	2827	-	2838	0	K.TVNNNQSLFQR.L
1518.6587	1517.6514	1517.6966	-29.79	2575	-	2587	0	R.SVASDELHVMQR.R + Oxidation (M)
1523.7185	1522.7112	1522.8429	-86.45	2560	-	2572	1	R.KFLLAQTDSSLK.M + Oxidation (M)
1559.7947	1558.7874	1558.8541	-42.79	1617	-	1629	1	R.KPDVTLDFMLPRK.T
1707.8094	1706.8021	1706.7278	43.5	1011	-	1024	1	K.EGDRTMNEQDLNR.I + Oxidation (M)
1732.0206	1731.0133	1730.9607	30.4	3417	-	3431	1	K.EITYSPSLWIKGLK.W
1900.9595	1899.9522	1900.0088	-29.78	2983	-	3000	1	R.CISVAPSRETAGEALLGK.C
1900.9595	1899.9522	1900.0088	-29.76	2983	-	3000	1	R.CISVAPSRETAGEALLGK.C
2193.0256	2192.0183	2192.0406	-10.14	2767	-	2785	0	K.DELTEEELDTAELLMNALK.L + Oxidation (M)
2211.0200	2210.0127	2210.0098	1.33	2364	-	2380	1	K.YMCTLKFCIFDLEVDK.N
2230.1453	2229.1380	2229.1059	14.4	1015	-	1033	1	R.TMNEQDLNRISQPEITVK.E
2233.0505	2232.0432	2232.0595	-7.30	2370	-	2387	1	K.FECIFDLEVDK.NMGLFQK.W
2927.5508	2926.5435	2926.4600	28.5	2944	-	2969	1	K.SEDVVKKPLSYLFEDKTHSSFSSTVK.D
No match to: 848.4879, 850.0154, 850.4973, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 996.5488, 1033.6514, 1051.6565, 1051.6565, 1131.6523, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1287.6302, 1356.6021, 1421.6768, 1421.6768, 1454.7075, 1475.6875, 1479.7271, 1491.6775, 1552.7145, 1567.6738, 1617.9915, 1617.9915, 1991.8297, 2001.9189, 2012.9465, 2012.9465, 2015.1936, 2044.9634, 2073.0088, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 3337.7156								

21. [A0A4W2E9U7](#) Mass: 76824 Score: 34 Expect: 52 Matches: 12

Nibrin OS=Bos indicus x Bos taurus OX=30522 GN=NBEN PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.4973	849.4900	849.4232	78.6	547	-	553	0	K.ESLWSTK.E
951.5814	950.5741	950.5073	70.3	457	-	464	0	K.SLTENLK.S
1131.6523	1130.6450	1130.6118	29.4	1	-	10	0	-.MQNGLSQILK.S
1147.6807	1146.6734	1146.6067	58.2	1	-	10	0	-.MQNGLSQILK.S + Oxidation (M)
1316.8218	1315.8145	1315.6925	92.8	15	-	25	1	R.VTFGVFESKFR.V
1421.6768	1420.6695	1420.7344	-45.70	311	-	322	1	K.CRILSQETSTVK.K
1421.6768	1420.6695	1420.7344	-45.67	311	-	322	1	K.CRILSQETSTVK.K
1479.7271	1478.7198	1478.7518	-21.60	374	-	385	1	R.DYFQPLTSPQKR.E
1991.8297	1990.8224	1990.8612	-19.46	554	-	570	0	K.ELSNCELQDQDEMLPK.K
2012.9465	2011.9392	2011.9231	8.02	26	-	43	0	R.VEYEPVLVACSSCLDVSGK.T
2012.9465	2011.9393	2011.9231	8.04	26	-	43	0	R.VEYEPVLVACSSCLDVSGK.T
2211.0200	2210.0127	2210.0559	-19.53	402	-	420	0	R.METSCSLLEQTQPTTSLIR.K + Oxidation (M)
No match to: 842.4690, 848.4879, 850.0154, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 892.9686, 953.4899, 996.5488, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1136.6420, 1151.6740, 1165.6849, 1165.6849, 1250.6191, 1250.6191, 1287.6302, 1300.7900, 1302.6307, 1334.8221, 1334.8221, 1356.6021, 1448.8531, 1454.7075, 1475.6875, 1491.6775, 1518.6587, 1523.7185, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1707.8094, 1732.0206, 1900.9595, 1900.9595, 2001.9189, 2015.1936, 2044.9634, 2073.0088, 2193.0256, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 2927.5508, 3337.7156								

22. [E1BNC9](#) Mass: 124764 Score: 32 Expect: 77 Matches: 15

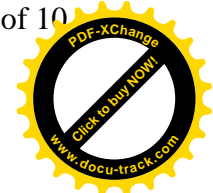
Ankyrin 3 OS=Bos taurus OX=9913 GN=ANK3 PE=4 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4690	841.4617	841.4004	72.9	1096	-	1102	1	K.GEAYKMK.T + Oxidation (M)
953.4899	952.4826	952.4410	43.7	156	-	163	1	R.GSRHHGMR.I + Oxidation (M)
996.5488	995.5415	995.5651	-23.71	861	-	869	0	K.DVKPAEPLK.Q
1302.6307	1301.6234	1301.6510	-21.19	1069	-	1080	1	K.MSRTSPADGKPR.L
1316.8218	1315.8145	1315.7136	76.7	354	-	365	0	K.ATFSPIVTVPEPR.R
1334.8221	1333.8148	1333.7089	79.4	692	-	704	0	K.NATTDALTSVLTK.I
1334.8221	1333.8149	1333.7089	79.4	692	-	704	0	K.NATTDALTSVLTK.I
1356.6021	1355.5948	1355.6140	-14.13	428	-	439	0	K.DCVSFTTNVSAR.F
1491.6775	1490.6702	1490.7360	-44.14	90	-	102	0	R.DSMIEELLVPSK.E
1518.6587	1517.6514	1517.7667	-75.96	536	-	548	0	K.GGQQQLVFNFYAFK.E
1523.7185	1522.7112	1522.7259	-9.61	90	-	102	0	R.DSMIEELLVPSK.E + 2 Oxidation (M)
1559.7947	1558.7874	1558.8005	-8.37	2	-	15	1	M.TGGAVFSPDRHIFR.K
2001.9189	2000.9116	2000.8608	25.4	617	-	633	0	R.YSYLTEPGMSPQSPCER.T
2012.9465	2011.9392	2011.9157	11.7	966	-	982	1	R.LDDSPDQCRDSITSYLK.G
2012.9465	2011.9393	2011.9157	11.7	966	-	982	1	R.LDDSPDQCRDSITSYLK.G
No match to: 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 892.9686, 951.5814, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1131.6523, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1250.6191, 1250.6191, 1287.6302, 1300.7900, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1479.7271, 1552.7145, 1567.6738, 1617.9915, 1617.9915, 1707.8094, 1732.0206, 1900.9595, 1900.9595, 1991.8297, 2015.1936, 2044.9634, 2073.0088, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 2927.5508, 3337.7156								

23. [G8JKV3](#) Mass: 11943 Score: 32 Expect: 91 Matches: 4

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
864.5118	863.5045	863.4501	63.0	2	-	9	0	M.AQAFVNSK.I
870.5034	869.4961	869.5334	-42.91	99	-	106	1	R.LKQIGALQ.-
1518.6587	1517.6514	1517.8024	-99.48	1	-	14	1	-.MAQAFVNSKIQPGK.V
2305.0867	2304.0794	2304.0627	7.25	73	-	92	0	R.VFIGQECIGGCTDLVNTHR.G
No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 865.9869, 868.5078, 876.9944, 881.9677, 882.5228, 892.9686, 951.5814, 953.4899, 996.5488, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1131.6523, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1250.6191, 1250.6191, 1287.6302, 1300.7900, 1302.6307, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1479.7271, 1491.6775, 1523.7185, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1707.8094, 1732.0206, 1900.9595,								



D8V071 Mass: 35943 Score: 30 Expect: 1.5e+002 Matches: 7
 Phosphoprotein OS=Tibrogargan virus (strain CS132) OX=1559361 GN=P PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
951.5814	950.5741	950.4933	85.0	52	-	58	1	R.ELNYRTR.A
996.5488	995.5415	995.5222	19.4	295	-	303	1	K.ASGIYRAMK.L
1250.6191	1249.6118	1249.6302	-14.74	42	-	51	1	K.QDLKEFLDSR.E
1250.6191	1249.6119	1249.6302	-14.71	42	-	51	1	K.QDLKEFLDSR.E
1518.6587	1517.6514	1517.7031	-34.08	85	-	97	1	K.MEESSLHDDKAIK.Q + Oxidation (M)
1523.7185	1522.7112	1522.7092	1.31	185	-	196	1	K.DNQGYFYPTKK.W
2044.9634	2043.9561	2044.0185	-30.51	111	-	130	1	R.SPNANSIGGQSVIKDVSSER.K

No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 953.4899, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1131.6523, 1136.6420, 1147.6807, 1151.6740, 1165.6849, 1165.6849, 1287.6302, 1300.7900, 1302.6307, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1479.7271, 1491.6775, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1707.8094, 1732.0206, 1900.9595, 1900.9595, 1991.8297, 2001.9189, 2012.9465, 2012.9465, 2015.1936, 2073.0088, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 2927.5508, 3337.7156

30. **A0A4W2DGE8** Mass: 25670 Score: 29 Expect: 1.5e+002 Matches: 7
 Peptidylprolyl isomerase OS=Bos indicus x Bos taurus OX=30522 GN=FKBP11 PE=4 SV=1

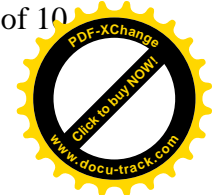
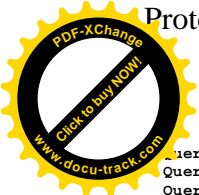
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1165.6849	1164.6776	1164.7343	-48.62	2	-	11	0	M.TLRPSLLPLR.L
1165.6849	1164.6777	1164.7343	-48.59	2	-	11	0	M.TLRPSLLPLR.L
1250.6191	1249.6118	1249.6891	-61.83	172	-	182	0	R.LSTHALRPEAR.R
1250.6191	1249.6119	1249.6891	-61.79	172	-	182	0	R.LSTHALRPEAR.R
1300.7900	1299.7827	1299.6717	85.4	138	-	148	1	R.NLCQGSQRLPK.V
1518.6587	1517.6514	1517.7020	-33.33	214	-	224	1	K.VMQYCHPHFRK.T + Oxidation (M)
2044.9634	2043.9561	2044.1205	-80.39	74	-	91	1	R.IFDTSLTRDPLVIELGQK.Q

No match to: 842.4690, 848.4879, 850.0154, 850.4973, 853.4743, 853.4743, 861.0195, 864.5118, 865.9869, 868.5078, 870.5034, 876.9944, 881.9677, 882.5228, 882.5228, 892.9686, 951.5814, 953.4899, 996.5488, 1017.6209, 1017.6209, 1019.6330, 1033.6514, 1045.5168, 1051.6565, 1051.6565, 1131.6523, 1136.6420, 1147.6807, 1151.6740, 1287.6302, 1302.6307, 1316.8218, 1334.8221, 1334.8221, 1356.6021, 1421.6768, 1421.6768, 1448.8531, 1454.7075, 1475.6875, 1479.7271, 1491.6775, 1523.7185, 1552.7145, 1559.7947, 1567.6738, 1617.9915, 1617.9915, 1707.8094, 1732.0206, 1900.9595, 1900.9595, 1991.8297, 2001.9189, 2012.9465, 2012.9465, 2015.1936, 2073.0088, 2193.0256, 2211.0200, 2230.1453, 2233.0505, 2239.0674, 2283.0967, 2284.0908, 2305.0867, 2927.5508, 3337.7156

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 (842.4690,1+): <no title>
 Query2 (848.4879,1+): <no title>
 Query3 (850.0154,1+): <no title>
 Query4 (850.4973,1+): <no title>
 Query5 (853.4743,1+): <no title>
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 Query7 (861.0195,1+): <no title>
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Query61 (2001.9189,1+): <no title>
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Query63 (2012.9465,1+): Locus:1..14.0.5
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Query70 (2233.0505,1+): <no title>
Query71 (2239.0674,1+): <no title>
Query72 (2283.0967,1+): <no title>
Query73 (2284.0908,1+): <no title>
Query74 (2305.0867,1+): <no title>
Query75 (2927.5508,1+): <no title>
Query76 (3337.7156,1+): <no title>

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