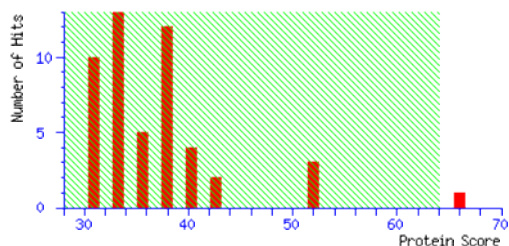


MATRIX SCIENCE Mascot Search Results

User :
Email :
Search title : BAEDW\2020_3_5\2020_3_5\MSMS 14\N22
Database : Uniprot_bovine bovine_20200316 (134392 sequences; 76244912 residues)
Timestamp : 31 Mar 2020 at 01:09:04 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 66 for A0A1R3UGP4, Kallikrein G OS=Bos taurus OX=9913 GN=KLNG PE=3 SV=1

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 64 are significant ($p < 0.05$).
Protein scores are derived from 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. A0A1R3UGP4	28249	66	Kallikrein G OS=Bos taurus OX=9913 GN=KLNG PE=3 SV=1
2. F1N376	69563	53	Tyrosine-protein phosphatase non-receptor type OS=Bos taurus OX=9913 GN=LOC526769 PE=3 SV=3
3. A0A4W2FSQ5	66334	52	Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=LOC113906723 PE=4 SV=1
4. A0A4W2CKS5	66352	52	Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 PE=4 SV=1
5. A0A4W2F3Q5	49802	43	Dihydrolipoamide dehydrogenase OS=Bos indicus x Bos taurus OX=30522 GN=DLD PE=3 SV=1
6. A0A4W2F4W9	52206	42	Dihydrolipoamide dehydrogenase OS=Bos indicus x Bos taurus OX=30522 GN=DLD PE=3 SV=1
7. A0A4W2G1C7	31863	41	Kallikrein related peptidase 11 OS=Bos indicus x Bos taurus OX=30522 GN=KLK11 PE=3 SV=1
8. A0A4W2G501	23018	40	TMEM9 domain family member B OS=Bos indicus x Bos taurus OX=30522 GN=TMEM9B PE=4 SV=1
9. Q3ZCD6	23018	40	TMEM9 domain family member B OS=Bos taurus OX=9913 GN=TMEM9B PE=2 SV=1
10. A0A4W2DBF5	25092	39	Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 PE=4 SV=1
11. F1N206	54723	39	Dihydrolipoamide dehydrogenase OS=Bos taurus OX=9913 GN=DLD PE=1 SV=2
12. A0A4W2H686	54723	39	Dihydrolipoamide dehydrogenase OS=Bos indicus x Bos taurus OX=30522 GN=DLD PE=3 SV=1
13. A0A4W2H5Z2	33370	38	Ketohexokinase OS=Bos indicus x Bos taurus OX=30522 GN=KHK PE=4 SV=1
14. A0A3Q1N4Y2	25122	38	Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1
15. F6PSE2	92262	38	Nibrin OS=Bos taurus OX=9913 GN=NBIN PE=4 SV=2
16. A0A4W2CAE8	92262	38	Nibrin OS=Bos indicus x Bos taurus OX=30522 GN=NBIN PE=4 SV=1
17. A0A4W2BNU6	41726	38	Dehydrogenase/reductase 12 OS=Bos indicus x Bos taurus OX=30522 GN=DHRS12 PE=4 SV=1
18. A0A4Q1M3R6	41726	38	Dehydrogenase/reductase SDR family member 12 OS=Bos taurus OX=9913 GN=DHRS12 PE=4 SV=1
19. A0A4W2E9U7	76824	38	Nibrin OS=Bos indicus x Bos taurus OX=30522 GN=NBIN PE=4 SV=1
20. A0A4W2E4S5	35275	38	Kallikrein related peptidase 11 OS=Bos indicus x Bos taurus OX=30522 GN=KLK11 PE=3 SV=1
21. Q5EA35	33326	37	Ketohexokinase OS=Bos taurus OX=9913 GN=KHK PE=2 SV=1
22. Q0I175	38414	37	Ketohexokinase OS=Bos taurus OX=9913 GN=KHK PE=1 SV=1
23. A0A4W2EMU6	31365	36	Ketohexokinase OS=Bos indicus x Bos taurus OX=30522 GN=KHK PE=4 SV=1
24. A0A4W2G3Z2	37905	36	Kallikrein related peptidase 11 OS=Bos indicus x Bos taurus OX=30522 GN=KLK11 PE=3 SV=1
25. F1N4M1	37905	36	Kallikrein related peptidase 11 OS=Bos taurus OX=9913 GN=KLK11 PE=3 SV=3
26. A0A4W2H4X6	31395	35	Ketohexokinase OS=Bos indicus x Bos taurus OX=30522 GN=KHK PE=4 SV=1
27. A0A4W2C9V0	38733	35	Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=MFGE8 PE=4 SV=1
28. A0A4W2F3R1	41965	34	Reverse transcriptase domain-containing protein OS=Bos indicus x Bos taurus OX=30522 PE=4 SV=1
29. A0A4W2IP26	92361	34	Nibrin OS=Bos indicus x Bos taurus OX=30522 GN=NBIN PE=4 SV=1
30. A0A1C9HI59	67468	34	LS037 OS=Lumpy skin disease virus OX=59509 GN=LW037 PE=4 SV=1

Results List

1.	A0A1R3UGP4	Mass: 28249	Score: 66	Expect: 0.034	Matches: 10
Kallikrein G OS=Bos taurus OX=9913 GN=KLNG PE=3 SV=1					
	Observed	Mr(expt)	Mr(calcd)	ppm	Start End Miss Ions Peptide
	848.4780	847.4707	847.4473	27.6	109 - 115 0 --- R.NDIMLVK.M + Oxidation (M)
	951.5720	950.5647	950.4862	82.7	239 - 245 0 --- K.YVDWIQK.T
	1179.5499	1178.5426	1178.6482	-89.54	229 - 238 1 --- K.KPGVYTKVCK.Y
	1184.6520	1183.6447	1183.6747	-25.32	45 - 55 0 --- R.LLCGATLIAPR.W
	1211.6572	1210.6499	1210.6604	-8.69	163 - 172 1 --- R.CANVTIIKHR.E
	2015.1949	2014.1876	2013.9908	97.7	88 - 105 1 --- R.TATKSFPPHDFNNSLPNK.D
	2283.0847	2282.0774	2282.0975	-8.78	68 - 87 1 --- R.YVVLHGAHSLGRQDGCQTR.T
	2305.0740	2304.0667	2304.1793	-48.84	1 - 21 0 --- .MMTLQLIMFALVTGHVGGETR.I
	2321.0552	2320.0479	2320.1742	-54.42	1 - 21 0 --- .MMTLQLIMFALVTGHVGGETR.I + Oxidation (M)
	2528.2617	2527.2544	2527.4019	-58.33	2 - 24 1 --- M.MTLQLIMFALVTGHVGGETR.IIK.G

No match to: 813.4393, 834.4629, 838.4906, 842.4641, 846.4475, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1131.6493, 1133.6587, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1185.6776, 1185.6776, 1189.6735, 1193.6417, 1203.6858, 1207.6569, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1533.7407, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2211.0193

2. [FLN376](#) Mass: 69563 Score: 53 Expect: 0.74 Matches: 12

Tyrosine-protein phosphatase non-receptor type OS=Bos taurus OX=9913 GN=LOC526769 PE=3 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
813.4393	812.4320	812.4868	-67.44	214	220	1	---	R.QPLKATR.I
838.4906	837.4833	837.4821	1.48	538	546	0	---	R.KPVGAGPGR.G
846.4475	845.4402	845.3991	48.6	565	570	1	---	R.ERQEER.G
866.4929	865.4856	865.5134	-32.09	206	213	0	---	R.SGVVHRLR.Q
1133.6587	1132.6514	1132.6101	36.5	47	55	1	---	R.RHNEVTHIK.I
1179.5499	1178.5426	1178.5536	-9.34	547	558	0	---	R.GGACAGVTMVTR.G
1522.7052	1521.6979	1521.7762	-51.46	166	178	0	---	R.VTHIMIHFPDQK.Y
1538.7010	1537.6937	1537.7711	-50.35	166	178	0	---	R.VTHIMIHFPDQK.Y + Oxidation (M)
2015.1949	2014.1876	2014.0201	83.2	538	558	1	---	R.KPVGAGPGRGGACAGVTMVTR.G + Oxidation (M)
2211.0193	2210.0120	2210.1596	-66.79	71	90	0	---	K.FATLAEVLVQHYTGQHGGLLR.E
2321.0552	2320.0479	2320.1394	-39.41	221	242	1	---	R.ISAASIESRVQELSEATDASEK.A
2528.2617	2527.2544	2527.2819	-10.88	290	311	1	---	R.VILHDVDDRVPGADYINANYIR.Q
No match to: 834.4629, 842.4641, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1193.6417, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1533.7407, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2283.0847, 2305.0740								

3. [A0A4W2FSQ5](#) Mass: 66334 Score: 52 Expect: 0.76 Matches: 12

Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=LOC113906723 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
813.4393	812.4320	812.4868	-67.44	194	200	1	---	R.QPLKATR.I
838.4906	837.4833	837.4821	1.48	510	518	0	---	R.KPVGAGPGR.G
846.4475	845.4402	845.3991	48.6	537	542	1	---	R.ERQEER.G
866.4929	865.4856	865.5134	-32.09	186	193	0	---	R.SGVVHRLR.Q
1133.6587	1132.6514	1132.6101	36.5	27	35	1	---	R.RHNEVTHIK.I
1179.5499	1178.5426	1178.5536	-9.34	519	530	0	---	R.GGACAGVTMVTR.G
1522.7052	1521.6979	1521.7762	-51.46	146	158	0	---	R.VTHIMIHFPDQK.Y
1538.7010	1537.6937	1537.7711	-50.35	146	158	0	---	R.VTHIMIHFPDQK.Y + Oxidation (M)
2015.1949	2014.1876	2014.0201	83.2	510	530	1	---	R.KPVGAGPGRGGACAGVTMVTR.G + Oxidation (M)
2211.0193	2210.0120	2210.1596	-66.79	51	70	0	---	K.FATLAEVLVQHYTGQHGGLLR.E
2321.0552	2320.0479	2320.1394	-39.41	201	222	1	---	R.ISAASIESRVQELSEATDASEK.A
2528.2617	2527.2544	2527.2819	-10.88	270	291	1	---	R.VILHDVDDRVPGADYINANYIR.S
No match to: 834.4629, 842.4641, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1193.6417, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1533.7407, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2283.0847, 2305.0740								

4. [A0A4W2CKS5](#) Mass: 66352 Score: 52 Expect: 0.89 Matches: 12

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
813.4393	812.4320	812.4868	-67.44	194	200	1	---	R.QPLKATR.I
838.4906	837.4833	837.4821	1.48	510	518	0	---	R.KPVGAGPGR.G
846.4475	845.4402	845.3991	48.6	537	542	1	---	R.ERQEER.G
866.4929	865.4856	865.5134	-32.09	186	193	0	---	R.SGVVHRLR.Q
1133.6587	1132.6514	1132.6101	36.5	27	35	1	---	R.RHNEVTHIK.I
1179.5499	1178.5426	1178.5536	-9.34	519	530	0	---	R.GGACAGVTMVTR.G
1522.7052	1521.6979	1521.7762	-51.46	146	158	0	---	R.VTHIMIHFPDQK.Y
1538.7010	1537.6937	1537.7711	-50.35	146	158	0	---	R.VTHIMIHFPDQK.Y + Oxidation (M)
2015.1949	2014.1876	2014.0201	83.2	510	530	1	---	R.KPVGAGPGRGGACAGVTMVTR.G + Oxidation (M)
2211.0193	2210.0120	2210.1596	-66.79	51	70	0	---	K.FATLAEVLVQHYTGQHGGLLR.E
2321.0552	2320.0479	2320.1394	-39.41	201	222	1	---	R.ISAASIESRVQELSEATDASEK.A
2528.2617	2527.2544	2527.2819	-10.88	270	291	1	---	R.VILHDVDDRVPGADYINANYIR.S
No match to: 834.4629, 842.4641, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1193.6417, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1533.7407, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2283.0847, 2305.0740								

5. [A0A4W2F3Q5](#) Mass: 49802 Score: 43 Expect: 6.3 Matches: 12

Dihydrolipoamide dehydrogenase OS=Bos indicus x Bos taurus OX=30522 GN=DLD PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
868.5015	867.4942	867.4524	48.2	7	13	0	---	R.VYCSLVK.R
868.5015	867.4943	867.4524	48.2	7	13	0	---	R.VYCSLVK.R
1017.6157	1016.6084	1016.5614	46.2	393	401	1	---	K.ILGQKSTDR.V
1017.6157	1016.6084	1016.5614	46.2	393	401	1	---	K.ILGQKSTDR.V
1151.6696	1150.6623	1150.5870	65.5	363	372	1	---	K.EEGIEYKVGK.F
1165.6809	1164.6736	1164.5631	94.9	123	132	1	---	K.MMEQKSNVAVK.A
1165.6809	1164.6736	1164.5631	94.9	123	132	1	---	K.MMEQKSNVAVK.A
1193.6417	1192.6344	1192.6353	-0.72	370	380	1	---	K.VGKFPFAANSR.A
1203.6858	1202.6785	1202.6772	1.14	289	298	1	---	R.IPVNTRFQTK.I
1279.7007	1278.6934	1278.6311	48.7	118	127	1	---	R.LNLEKMMQK.S + Oxidation (M)

1533.7407 1532.7334 1532.7682 -22.69 237 - 252 1 --- K.SDGKIDVSIEAASGGK.A
 1581.7728 1580.7655 1580.7569 5.44 357 - 369 1 --- K.SEEQLKEEGIEYK.V
No match to: 813.4393, 834.4629, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1133.6587, 1147.6777, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1207.6569, 1211.6572, 1225.6708, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1538.7010, 1554.6993, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2283.0847, 2305.0740, 2321.0552, 2528.2617

6. [A0A4W2F4W9](#) Mass: 52206 Score: 42 Expect: 9.3 Matches: 12

Dihydrolipoyl dehydrogenase OS=Bos indicus x Bos taurus OX=30522 GN=DLD PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
868.5015	867.4942	867.4524	48.2	7	13	0	---	R.VYCGLVK.R
868.5015	867.4943	867.4524	48.2	7	13	0	---	R.VYCGLVK.R
1017.6157	1016.6084	1016.5614	46.2	418	426	1	---	K.ILGQKSTDR.V
1017.6157	1016.6084	1016.5614	46.2	418	426	1	---	K.ILGQKSTDR.V
1151.6696	1150.6623	1150.5870	65.5	388	397	1	---	K.EEGIEYKVGK.F
1165.6809	1164.6736	1164.5631	94.9	100	109	1	---	K.MMEQKSNVAVK.A
1165.6809	1164.6736	1164.5631	94.9	100	109	1	---	K.MMEQKSNVAVK.A
1193.6417	1192.6344	1192.6353	-0.72	395	405	1	---	K.VGKFPFAANSR.A
1203.6858	1202.6785	1202.6772	1.14	314	323	1	---	R.IPVNTRFQTK.I
1279.7007	1278.6934	1278.6311	48.7	95	104	1	---	R.LNLEKMMQK.S + Oxidation (M)
1533.7407	1532.7334	1532.7682	-22.69	262	277	1	---	K.SDGKIDVSIEAASGGK.A
1581.7728	1580.7655	1580.7569	5.44	382	394	1	---	K.SEEQLKEEGIEYK.V

No match to: 813.4393, 834.4629, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1133.6587, 1147.6777, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1207.6569, 1211.6572, 1225.6708, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1538.7010, 1554.6993, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2283.0847, 2305.0740, 2321.0552, 2528.2617

7. [A0A4W2G1C7](#) Mass: 31863 Score: 41 Expect: 11 Matches: 7

Kallikrein related peptidase 11 OS=Bos indicus x Bos taurus OX=30522 GN=KLK11 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4780	847.4707	847.4473	27.6	140	146	0	---	R.NDMLVK.M + Oxidation (M)
951.5720	950.5647	950.4862	82.7	270	276	0	---	K.YVDWIQK.T
1179.5499	1178.5426	1178.6482	-89.54	260	269	1	---	K.KPGVYTKVCK.Y
1184.6520	1183.6447	1183.6747	-25.32	76	86	0	---	R.LLCGATLIAPR.W
1211.6572	1210.6499	1210.6604	-8.69	194	203	1	---	R.CANVTIIKHR.E
2015.1949	2014.1876	2013.9908	97.7	119	136	1	---	R.TATKSPFHPDFNNSLPNK.D
2283.0847	2282.0774	2282.0975	-8.78	99	118	1	---	R.YVVLHGAHSLGRQDGEQTR.T

No match to: 813.4393, 834.4629, 838.4906, 842.4641, 846.4475, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1133.6587, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1185.6776, 1185.6776, 1189.6735, 1193.6417, 1203.6858, 1207.6569, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1533.7407, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2211.0193, 2305.0740, 2321.0552, 2528.2617

8. [A0A4W2G501](#) Mass: 23018 Score: 40 Expect: 15 Matches: 7

TMEM9 domain family member B OS=Bos indicus x Bos taurus OX=30522 GN=TMEM9B PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1131.6493	1130.6420	1130.6270	13.3	1	10	0	---	-.MATLWAGLLR.L
1147.6777	1146.6704	1146.6219	42.3	1	10	0	---	-.MATLWAGLLR.L + Oxidation (M)
1179.5499	1178.5426	1178.5390	3.07	79	88	0	---	R.GPDVEAYCLR.C
1207.6569	1206.6496	1206.6145	29.1	172	180	1	---	K.VEYQQQRWK.L
1211.6572	1210.6499	1210.6193	25.3	93	102	1	---	K.YEERSSTVIK.V
1225.6708	1224.6635	1224.5453	96.5	42	50	1	---	R.CKCICPPYK.D
2283.0847	2282.0774	2282.0606	7.37	60	78	1	---	K.NISQKDCDCLHVVDPMPVR.G

No match to: 813.4393, 834.4629, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1133.6587, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1193.6417, 1203.6858, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1533.7407, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2305.0740, 2321.0552, 2528.2617

9. [Q3ZCD6](#) Mass: 23018 Score: 40 Expect: 15 Matches: 7

TMEM9 domain family member B OS=Bos taurus OX=9913 GN=TMEM9B PE=2 SV=1

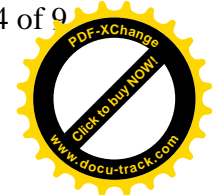
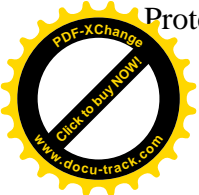
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1131.6493	1130.6420	1130.6270	13.3	1	10	0	---	-.MATLWAGLLR.L
1147.6777	1146.6704	1146.6219	42.3	1	10	0	---	-.MATLWAGLLR.L + Oxidation (M)
1179.5499	1178.5426	1178.5390	3.07	79	88	0	---	R.GPDVEAYCLR.C
1207.6569	1206.6496	1206.6145	29.1	172	180	1	---	K.VEYQQQRWK.L
1211.6572	1210.6499	1210.6193	25.3	93	102	1	---	K.YEERSSTVIK.V
1225.6708	1224.6635	1224.5453	96.5	42	50	1	---	R.CKCICPPYK.D
2283.0847	2282.0774	2282.0606	7.37	60	78	1	---	K.NISQKDCDCLHVVDPMPVR.G

No match to: 813.4393, 834.4629, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1133.6587, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1193.6417, 1203.6858, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1533.7407, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2305.0740, 2321.0552, 2528.2617

10. [A0A4W2DBF5](#) Mass: 25092 Score: 39 Expect: 16 Matches: 13

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
838.4906	837.4833	837.5072	-28.53	49	55	0	---	K.DPKPIIR.D



866.4929	865.4856	865.4215	74.1	175	-	181	1	---	R.ETTMEKEK.S
882.5173	881.5100	881.4454	73.3	5	-	13	1	---	R.STSSTKSGK.F
882.5173	881.5100	881.4454	73.3	5	-	13	1	---	R.STSSTKSGK.F
1165.6809	1164.6736	1164.6026	61.0	98	-	106	1	---	R.KLEVEYEQK.R
1165.6809	1164.6736	1164.6026	61.0	98	-	106	1	---	R.KLEVEYEQK.R
1193.6417	1192.6344	1192.6088	21.5	99	-	107	1	---	K.LEVEYEQKR.A
1207.6569	1206.6496	1206.5815	56.4	14	-	23	1	---	K.FMNPTDQARK.E
1522.7052	1521.6979	1521.7830	-55.88	162	-	174	1	---	K.VKGMNLCVTMTLR.E
1538.7010	1537.6937	1537.7779	-54.72	162	-	174	1	---	K.VKGMNLCVTMTLR.E + Oxidation (M)
1554.6993	1553.6920	1553.7728	-51.99	162	-	174	1	---	K.VKGMNLCVTMTLR.E + 2 Oxidation (M)
2211.0193	2210.0120	2210.1538	-64.16	144	-	163	1	---	R.LSMTTTLMTATVTDQVEKV.G + Oxidation (M)
2528.2617	2527.2544	2527.2662	-4.67	140	-	161	1	---	K.TWTRLSMTTTLMTATVTDQVEK.V + Oxidation (M)

No match to: 813.4393, 834.4629, 842.4641, 846.4475, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 868.5015, 868.5015, 870.4977, 876.9884, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1133.6587, 1147.6777, 1151.6696, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1203.6858, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1533.7407, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2283.0847, 2305.0740, 2321.0552

11. [FLN206](#) Mass: 54723 Score: 39 Expect: 19 Matches: 12

Dihydrolipoyl dehydrogenase OS=Bos taurus OX=9913 GN=DLD PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
868.5015	867.4942	867.4524	48.2	7	-	13	0	---	R.VYCSLVK.R
868.5015	867.4943	867.4524	48.2	7	-	13	0	---	R.VYCSLVK.R
1017.6157	1016.6084	1016.5614	46.2	441	-	449	1	---	K.ILGQKSTDR.V
1017.6157	1016.6084	1016.5614	46.2	441	-	449	1	---	K.ILGQKSTDR.V
1151.6696	1150.6623	1150.5870	65.5	411	-	420	1	---	K.EEGIEYKVGK.F
1165.6809	1164.6736	1164.5631	94.9	123	-	132	1	---	K.MMEQKSNVAVK.A
1165.6809	1164.6736	1164.5631	94.9	123	-	132	1	---	K.MMEQKSNVAVK.A
1193.6417	1192.6344	1192.6353	-0.72	418	-	428	1	---	K.VGKFPFAANSR.A
1203.6858	1202.6785	1202.6772	1.14	337	-	346	1	---	R.IPVNTRFQTK.I
1279.7007	1278.6934	1278.6311	48.7	118	-	127	1	---	R.LNLEKMMQK.S + Oxidation (M)
1533.7407	1532.7334	1532.7682	-22.69	285	-	300	1	---	K.SDGKIDVSI EAASGGK.A
1581.7728	1580.7655	1580.7569	5.44	405	-	417	1	---	K.SEEQLKEEGIEYK.V

No match to: 813.4393, 834.4629, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1133.6587, 1147.6777, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1207.6569, 1211.6572, 1225.6708, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1538.7010, 1554.6993, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2283.0847, 2305.0740, 2321.0552, 2528.2617

12. [A0A4W2H686](#) Mass: 54723 Score: 39 Expect: 19 Matches: 12

Dihydrolipoyl dehydrogenase OS=Bos indicus x Bos taurus OX=30522 GN=DLD PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
868.5015	867.4942	867.4524	48.2	7	-	13	0	---	R.VYCSLVK.R
868.5015	867.4943	867.4524	48.2	7	-	13	0	---	R.VYCSLVK.R
1017.6157	1016.6084	1016.5614	46.2	441	-	449	1	---	K.ILGQKSTDR.V
1017.6157	1016.6084	1016.5614	46.2	441	-	449	1	---	K.ILGQKSTDR.V
1151.6696	1150.6623	1150.5870	65.5	411	-	420	1	---	K.EEGIEYKVGK.F
1165.6809	1164.6736	1164.5631	94.9	123	-	132	1	---	K.MMEQKSNVAVK.A
1165.6809	1164.6736	1164.5631	94.9	123	-	132	1	---	K.MMEQKSNVAVK.A
1193.6417	1192.6344	1192.6353	-0.72	418	-	428	1	---	K.VGKFPFAANSR.A
1203.6858	1202.6785	1202.6772	1.14	337	-	346	1	---	R.IPVNTRFQTK.I
1279.7007	1278.6934	1278.6311	48.7	118	-	127	1	---	R.LNLEKMMQK.S + Oxidation (M)
1533.7407	1532.7334	1532.7682	-22.69	285	-	300	1	---	K.SDGKIDVSI EAASGGK.A
1581.7728	1580.7655	1580.7569	5.44	405	-	417	1	---	K.SEEQLKEEGIEYK.V

No match to: 813.4393, 834.4629, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1133.6587, 1147.6777, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1207.6569, 1211.6572, 1225.6708, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1538.7010, 1554.6993, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2283.0847, 2305.0740, 2321.0552, 2528.2617

13. [A0A4W2H5Z2](#) Mass: 33370 Score: 38 Expect: 19 Matches: 10

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
834.4629	833.4556	833.4065	58.9	273	-	279	0	---	K.SMQEALR.F
850.4896	849.4823	849.4821	0.25	210	-	216	1	---	R.GLYSRVR.K
850.4896	849.4823	849.4821	0.30	210	-	216	1	---	R.GLYSRVR.K
866.4929	865.4856	865.4116	85.5	280	-	287	0	---	R.FGQVAGK.K
1065.6028	1064.5955	1064.4961	93.4	289	-	298	0	---	K.CGLQGFQDGV.-
1133.6587	1132.6514	1132.5560	84.3	32	-	39	1	---	R.CLSQRWR.G
1185.6776	1184.6703	1184.6454	21.0	133	-	141	1	---	R.FKWIHIEGR.N
1185.6776	1184.6703	1184.6454	21.0	133	-	141	1	---	R.FKWIHIEGR.N
1193.6417	1192.6344	1192.5911	36.4	288	-	298	1	---	K.KCGLQGFQDGV.-
1533.7407	1532.7334	1532.7695	-23.55	153	-	165	1	---	R.IEQHNARQPPESK.I

No match to: 813.4393, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 853.4691, 856.4822, 864.4857, 865.9818, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1131.6493, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1189.6735, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2283.0847, 2305.0740, 2321.0552, 2528.2617

14. [A0A3Q1N4Y2](#) Mass: 25122 Score: 38 Expect: 20 Matches: 13

Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
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838.4906	837.4833	837.5072	-28.53	49	-	55	0	---	K.DPKPIIR.D
866.4929	865.4856	865.4215	74.1	175	-	181	1	---	R.ETTMEKEK.S
882.5173	881.5100	881.4454	73.3	5	-	13	1	---	R.STSSTKSGK.F
882.5173	881.5100	881.4454	73.3	5	-	13	1	---	R.STSSTKSGK.F
1165.6809	1164.6736	1164.6026	61.0	98	-	106	1	---	R.KLEVEYEQK.R
1165.6809	1164.6736	1164.6026	61.0	98	-	106	1	---	R.KLEVEYEQK.R
1193.6417	1192.6344	1192.6088	21.5	99	-	107	1	---	K.LEVEYEQKR.A
1207.6569	1206.6496	1206.5815	56.4	14	-	23	1	---	K.FMNPTDQARK.E
1522.7052	1521.6979	1521.7830	-55.88	162	-	174	1	---	K.VKGMNLCVTMTLR.E
1538.7010	1537.6937	1537.7779	-54.72	162	-	174	1	---	K.VKGMNLCVTMTLR.E + Oxidation (M)
1554.6993	1553.6920	1553.7728	-51.99	162	-	174	1	---	K.VKGMNLCVTMTLR.E + 2 Oxidation (M)
2211.0193	2210.0120	2210.1538	-64.16	144	-	163	1	---	R.LSMTTVLMTATVTDQVEKVK.G + Oxidation (M)
2528.2617	2527.2544	2527.2662	-4.67	140	-	161	1	---	K.TWTRLRSMTTVLMTATVTDQVEK.V + Oxidation (M)
No match to: 813.4393, 834.4629, 842.4641, 846.4475, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 868.5015, 870.4977, 876.9884, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1133.6587, 1147.6777, 1151.6696, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1203.6858, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1533.7407, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2283.0847, 2305.0740, 2321.0552									

15. [F6PSE2](#) Mass: 92262 Score: 38 Expect: 21 Matches: 13

Nibrin OS=Bos taurus OX=9913 GN=NB N PE=4 SV=2

observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
846.4475	845.4402	845.4494	-10.87	305	- 311	0	---	R.LITEENK.E
850.4896	849.4823	849.4232	69.5	684	- 690	0	---	K.ESLWSTK.E
850.4896	849.4823	849.4232	69.6	684	- 690	0	---	K.ESLWSTK.E
951.5720	950.5647	950.5073	60.4	594	- 601	0	---	K.SLFTENLK.S
1131.6493	1130.6420	1130.6118	26.8	137	- 146	0	---	K.MQNGLSQILK.S
1147.6777	1146.6704	1146.6067	55.6	137	- 146	0	---	K.MQNGLSQILK.S + Oxidation (M)
1189.6735	1188.6662	1188.5775	74.7	771	- 779	0	---	K.NTELEEWLR.Q
1207.6569	1206.6496	1206.6318	14.8	438	- 447	1	---	K.EIKIFGMEPK.C + Oxidation (M)
1316.8134	1315.8061	1315.6925	86.4	151	- 161	1	---	R.VTFGVFESKFR.V
1522.7052	1521.6979	1521.8416	-94.39	16	- 29	1	---	R.LPGLWASGLPERAR.C
1538.7010	1537.6937	1537.7386	-29.17	498	- 510	0	---	R.GWPSQHQQTNSIR.D
2211.0193	2210.0120	2210.0559	-19.84	539	- 557	0	---	R.METSCSLLEQTQPTTSLIR.K + Oxidation (M)
2528.2617	2527.2544	2527.1761	31.0	771	- 790	1	---	K.NTELEEWLRQEMEVRQNQHAKE + Oxidation (M)
No match to: 813.4393, 834.4629, 838.4906, 842.4641, 848.4780, 850.0118, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1133.6587, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1193.6417, 1203.6858, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1533.7407, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2283.0847, 2305.0740, 2321.0552								

16. [A0A4W2CAE8](#) Mass: 92262 Score: 38 Expect: 21 Matches: 13

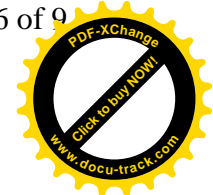
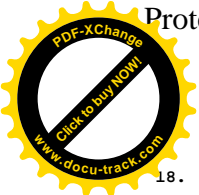
Nibrin OS=Bos indicus x Bos taurus OX=30522 GN=NB N PE=4 SV=1

observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
846.4475	845.4402	845.4494	-10.87	305	-	311	0 ---	R.LITEENK.E
850.4896	849.4823	849.4232	69.5	684	-	690	0 ---	K.ESLWSTK.E
850.4896	849.4823	849.4232	69.6	684	-	690	0 ---	K.ESLWSTK.E
951.5720	950.5647	950.5073	60.4	594	-	601	0 ---	K.SLFTENLK.S
1131.6493	1130.6420	1130.6118	26.8	137	-	146	0 ---	K.MQNGLSQILK.S
1147.6777	1146.6704	1146.6067	55.6	137	-	146	0 ---	K.MQNGLSQILK.S + Oxidation (M)
1189.6735	1188.6662	1188.5775	74.7	771	-	779	0 ---	K.NTELEEWLR.Q
1207.6569	1206.6496	1206.6318	14.8	438	-	447	1 ---	K.EIKIFGMEPK.C + Oxidation (M)
1316.8134	1315.8061	1315.6925	86.4	151	-	161	1 ---	R.VTFGVFESKFR.V
1522.7052	1521.6979	1521.8416	-94.39	16	-	29	1 ---	R.LPGLWASGLPERAR.C
1538.7010	1537.6937	1537.7386	-29.17	498	-	510	0 ---	R.GWPSQHQQTNSIR.D
2211.0193	2210.0120	2210.0559	-19.84	539	-	557	0 ---	R.METSCSLLEQTQPTSLIR.K + Oxidation (M)
2528.2617	2527.2544	2527.1761	31.0	771	-	790	1 ---	K.NTELEEWLRQEMEVRQNQHAK.E + Oxidation (M)
No match to: 813.4393, 834.4629, 838.4906, 842.4641, 848.4780, 850.0118, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1133.6587, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1193.6417, 1203.6858, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1533.7407, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2283.0847, 2305.0740, 2321.0552								

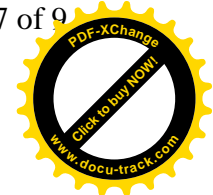
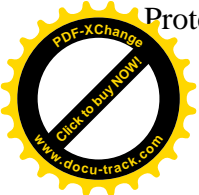
17. [A0A4W2BNU6](#) Mass: 41726 Score: 38 Expect: 21 Matches: 11

Dehydrogenase/reductase 12 OS=Bos indicus x Bos taurus OX=30522 GN=DHRS12 PE=4 SV=1

observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
834.4629	833.4556	833.4317	28.8	55	-	62	0	--- K.ATAMEIAK.R
850.4896	849.4823	849.4266	65.6	55	-	62	0	--- K.ATAMEIAK.R + Oxidation (M)
850.4896	849.4823	849.4266	65.6	55	-	62	0	--- K.ATAMEIAK.R + Oxidation (M)
866.4929	865.4856	865.4657	23.0	13	-	19	1	--- K.GLREYTK.S
1133.6587	1132.6514	1132.5989	46.4	224	-	233	1	--- R.VEVRGFSPPR.G
1189.6735	1188.6662	1188.5986	56.9	133	-	142	1	--- K.RELTEDGLEK.N
1334.8168	1333.8095	1333.7276	61.4	170	-	182	0	--- R.VITVSSGGMLVQK.L + Oxidation (M)
1334.8168	1333.8095	1333.7276	61.5	170	-	182	0	--- R.VITVSSGGMLVQK.L + Oxidation (M)
1533.7407	1532.7334	1532.6936	26.0	359	-	371	1	--- R.NRTCVSHVSTGR.Q
1901.1586	1900.1513	1900.0101	74.3	342	-	358	1	--- R.ILGWVMPSSRGSSRPR.N + Oxidation (M)
2211.0193	2210.0120	2210.1048	-41.98	115	-	133	1	--- K.QEHTLNVLINNAGCMVNRK.E
No match to: 813.4393, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 853.4691, 856.4822, 864.4857, 865.9818, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1193.6417, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 2015.1949, 2283.0847, 2305.0740, 2321.0552, 2528.2617								



18. [A0A3Q1M3R6](#) Mass: 41726 Score: 38 Expect: 21 Matches: 11
Dehydrogenase/reductase SDR family member 12 OS=Bos taurus OX=9913 GN=DHRS12 PE=4 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------|-------------------------------------|
| 834.4629 | 833.4556 | 833.4317 | 28.8 | 55 | 62 | 0 | --- | K.ATAMEIAK.R |
| 850.4896 | 849.4823 | 849.4266 | 65.6 | 55 | 62 | 0 | --- | K.ATAMEIAK.R + Oxidation (M) |
| 850.4896 | 849.4823 | 849.4266 | 65.6 | 55 | 62 | 0 | --- | K.ATAMEIAK.R + Oxidation (M) |
| 866.4929 | 865.4856 | 865.4657 | 23.0 | 13 | 19 | 1 | --- | K.GLREYTK.S |
| 1133.6587 | 1132.6514 | 1132.5989 | 46.4 | 224 | 233 | 1 | --- | R.VEVRGFSSPR.G |
| 1189.6735 | 1188.6662 | 1188.5986 | 56.9 | 133 | 142 | 1 | --- | K.RELTEDGLEK.N |
| 1334.8168 | 1333.8095 | 1333.7276 | 61.4 | 170 | 182 | 0 | --- | R.VITVSSGGMLVQK.L + Oxidation (M) |
| 1334.8168 | 1333.8095 | 1333.7276 | 61.5 | 170 | 182 | 0 | --- | R.VITVSSGGMLVQK.L + Oxidation (M) |
| 1533.7407 | 1532.7334 | 1532.6936 | 26.0 | 359 | 371 | 1 | --- | R.NRTCCHSVSTGR.Q |
| 1901.1586 | 1900.1513 | 1900.0101 | 74.3 | 342 | 358 | 1 | --- | R.ILGWVMPSSRGSSRP.N + Oxidation (M) |
| 2211.0193 | 2210.0120 | 2210.1048 | -41.98 | 115 | 133 | 1 | --- | K.QEHTLNVLINNAGCMVNKR.E |
- No match to: 813.4393, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 853.4691, 856.4822, 864.4857, 865.9818, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1193.6417, 1203.6858, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 2015.1949, 2283.0847, 2305.0740, 2321.0552, 2528.2617
19. [A0A4W2E9U7](#) Mass: 76824 Score: 38 Expect: 21 Matches: 12
Nibrin OS=Bos indicus x Bos taurus OX=30522 GN=NBIN PE=4 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------|--|
| 846.4475 | 845.4402 | 845.4494 | -10.87 | 169 | 175 | 0 | --- | R.LITEENK.E |
| 850.4896 | 849.4823 | 849.4232 | 69.5 | 547 | 553 | 0 | --- | K.ESLWSTK.E |
| 850.4896 | 849.4823 | 849.4232 | 69.6 | 547 | 553 | 0 | --- | K.ESLWSTK.E |
| 951.5720 | 950.5647 | 950.5073 | 60.4 | 457 | 464 | 0 | --- | K.SLFTEENLK.S |
| 1131.6493 | 1130.6420 | 1130.6118 | 26.8 | 1 | 10 | 0 | --- | -MQNGLSQILK.S |
| 1147.6777 | 1146.6704 | 1146.6067 | 55.6 | 1 | 10 | 0 | --- | -MQNGLSQILK.S + Oxidation (M) |
| 1189.6735 | 1188.6662 | 1188.5775 | 74.7 | 634 | 642 | 0 | --- | K.NTELEEWLR.Q |
| 1207.6569 | 1206.6496 | 1206.6318 | 14.8 | 301 | 310 | 1 | --- | K.EIKIFGMEPK.C + Oxidation (M) |
| 1316.8134 | 1315.8061 | 1315.6925 | 86.4 | 15 | 25 | 1 | --- | R.VTFGVFESKFR.V |
| 1538.7010 | 1537.6937 | 1537.7386 | -29.17 | 361 | 373 | 0 | --- | R.GWPSQHQQTNSIR.D |
| 2211.0193 | 2210.0120 | 2210.0559 | -19.84 | 402 | 420 | 0 | --- | R.METSCSLLEQTQPTTSLIR.K + Oxidation (M) |
| 2528.2617 | 2527.2544 | 2527.1761 | 31.0 | 634 | 653 | 1 | --- | K.NTELEEWLRQEMEVCNQHAK.E + Oxidation (M) |
- No match to: 813.4393, 834.4629, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1133.6587, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1193.6417, 1203.6858, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1533.7407, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2283.0847, 2305.0740, 2321.0552
20. [A0A4W2E4S5](#) Mass: 35275 Score: 38 Expect: 23 Matches: 7
Kallikrein related peptidase 11 OS=Bos indicus x Bos taurus OX=30522 GN=KLK11 PE=3 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------|-----------------------------|
| 848.4780 | 847.4707 | 847.4473 | 27.6 | 177 | 183 | 0 | --- | R.NDIMLVK.M + Oxidation (M) |
| 951.5720 | 950.5647 | 950.4862 | 82.7 | 307 | 313 | 0 | --- | K.YVDWIQK.T |
| 1179.5499 | 1178.5426 | 1178.6482 | -89.54 | 297 | 306 | 1 | --- | K.KPGVYTKVCK.Y |
| 1184.6520 | 1183.6447 | 1183.6747 | -25.32 | 113 | 123 | 0 | --- | R.LLCGATLIAPR.W |
| 1211.6572 | 1210.6499 | 1210.6604 | -8.69 | 231 | 240 | 1 | --- | R.CANVTIHKHR.E |
| 2015.1949 | 2014.1876 | 2013.9908 | 97.7 | 156 | 173 | 1 | --- | R.TATKSFPHPDFNNSLPNK.D |
| 2283.0847 | 2282.0774 | 2282.0975 | -8.78 | 136 | 155 | 1 | --- | R.YVVLHGAHSLGRQDGCQTR.T |
- No match to: 813.4393, 834.4629, 838.4906, 842.4641, 846.4475, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1133.6587, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1193.6417, 1203.6858, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1533.7407, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2283.0847, 2305.0740, 2321.0552, 2528.2617
21. [Q5EA35](#) Mass: 33326 Score: 37 Expect: 24 Matches: 10
Ketoheokinase OS=Bos taurus OX=9913 GN=KHK PE=2 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------|-------------------|
| 834.4629 | 833.4556 | 833.4065 | 58.9 | 273 | 279 | 0 | --- | K.SMQEALR.F |
| 850.4896 | 849.4823 | 849.4821 | 0.25 | 210 | 216 | 1 | --- | R.GLYSRVR.K |
| 850.4896 | 849.4823 | 849.4821 | 0.30 | 210 | 216 | 1 | --- | R.GLYSRVR.K |
| 866.4929 | 865.4856 | 865.4116 | 85.5 | 280 | 287 | 0 | --- | R.FGCQVAGK.K |
| 1065.6028 | 1064.5955 | 1064.4961 | 93.4 | 289 | 298 | 0 | --- | K.CGLQGFQDQIV.- |
| 1133.6587 | 1132.6514 | 1132.5560 | 84.3 | 32 | 39 | 1 | --- | R.CLSQRWQR.G |
| 1185.6776 | 1184.6703 | 1184.6454 | 21.0 | 133 | 141 | 1 | --- | R.FKWIHIEGR.N |
| 1185.6776 | 1184.6703 | 1184.6454 | 21.0 | 133 | 141 | 1 | --- | R.FKWIHIEGR.N |
| 1193.6417 | 1192.6344 | 1192.5911 | 36.4 | 288 | 298 | 1 | --- | K.KCGLQGFQDQIV.- |
| 1533.7407 | 1532.7334 | 1532.7695 | -23.55 | 153 | 165 | 1 | --- | R.IEQHNARQPPESK.I |
- No match to: 813.4393, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 853.4691, 856.4822, 864.4857, 865.9818, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1131.6493, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1189.6735, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2283.0847, 2305.0740, 2321.0552, 2528.2617
22. [Q0II75](#) Mass: 38414 Score: 37 Expect: 24 Matches: 10
Ketoheokinase OS=Bos taurus OX=9913 GN=KHK PE=1 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|----------|----------|----------|------|-------|-----|------|------|-------------|
| 834.4629 | 833.4556 | 833.4065 | 58.9 | 318 | 324 | 0 | --- | K.SMQEALR.F |
| 850.4896 | 849.4823 | 849.4821 | 0.25 | 255 | 261 | 1 | --- | R.GLYSRVR.K |



850.4896 849.4823 849.4821 0.30 255 - 261 1 --- R.GLYSRVR.K
 866.4929 865.4856 865.4116 85.5 325 - 332 0 --- R.FGCQVAGK.K
 1065.6028 1064.5955 1064.4961 93.4 334 - 343 0 --- K.CGLQGFDGIV.-
 1133.6587 1132.6514 1132.5560 84.3 32 - 39 1 --- R.CLSQRWQR.G
 1185.6776 1184.6703 1184.6454 21.0 178 - 186 1 --- R.FKWIHIEGR.N
 1185.6776 1184.6703 1184.6454 21.0 178 - 186 1 --- R.FKWIHIEGR.N
 1193.6417 1192.6344 1192.5911 36.4 333 - 343 1 --- K.KCGLQGFDGIV.-
 1533.7407 1532.7334 1532.7695 -23.55 198 - 210 1 --- R.IEQHNARQPPEK.I
No match to: 813.4393, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 853.4691, 856.4822, 864.4857, 865.9818, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1131.6493, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1189.6735, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2283.0847, 2305.0740, 2321.0552, 2528.2617

23. [AOA4W2EMU6](#) Mass: 31365 Score: 36 Expect: 33 Matches: 9

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
834.4629	833.4556	833.4065	58.9	257	263	0	---	K.SMQEALR.F
850.4896	849.4823	849.4821	0.25	194	200	1	---	R.GLYSRVR.K
850.4896	849.4823	849.4821	0.30	194	200	1	---	R.GLYSRVR.K
866.4929	865.4856	865.4116	85.5	264	271	0	---	R.FGCQVAGK.K
1065.6028	1064.5955	1064.4961	93.4	273	282	0	---	K.CGLQGFDGIV.-
1185.6776	1184.6703	1184.6454	21.0	117	125	1	---	R.FKWIHIEGR.N
1185.6776	1184.6703	1184.6454	21.0	117	125	1	---	R.FKWIHIEGR.N
1193.6417	1192.6344	1192.5911	36.4	272	282	1	---	K.KCGLQGFDGIV.-
1533.7407	1532.7334	1532.7695	-23.55	137	149	1	---	R.IEQHNARQPPEK.I

No match to: 813.4393, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 853.4691, 856.4822, 864.4857, 865.9818, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1131.6493, 1133.6587, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1189.6735, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2283.0847, 2305.0740, 2321.0552, 2528.2617

24. [AOA4W2G3Z2](#) Mass: 37905 Score: 36 Expect: 35 Matches: 7

Kallikrein related peptidase 11 OS=Bos indicus x Bos taurus OX=30522 GN=KLK11 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4780	847.4707	847.4473	27.6	202	208	0	---	R.NDIMLVK.M + Oxidation (M)
951.5720	950.5647	950.4862	82.7	332	338	0	---	K.YVDWIQK.T
1179.5499	1178.5426	1178.6482	-89.54	322	331	1	---	K.KPGVYTKVCK.Y
1184.6520	1183.6447	1183.6747	-25.32	138	148	0	---	R.LLCGATLIAPR.W
1211.6572	1210.6499	1210.6604	-8.69	256	265	1	---	R.CANVTIIKHR.E
2015.1949	2014.1876	2013.9908	97.7	181	198	1	---	R.TATKSPFPHDPFNNSLPNK.D
2283.0847	2282.0774	2282.0975	-8.78	161	180	1	---	R.YVVLGAHSLGRQDGCQTR.T

No match to: 813.4393, 834.4629, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1133.6587, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1185.6776, 1185.6776, 1189.6735, 1193.6417, 1203.6858, 1207.6569, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1533.7407, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2211.0193, 2305.0740, 2321.0552, 2528.2617

25. [FIN4M1](#) Mass: 37905 Score: 36 Expect: 35 Matches: 7

Kallikrein related peptidase 11 OS=Bos taurus OX=9913 GN=KLK11 PE=3 SV=3

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4780	847.4707	847.4473	27.6	202	208	0	---	R.NDIMLVK.M + Oxidation (M)
951.5720	950.5647	950.4862	82.7	332	338	0	---	K.YVDWIQK.T
1179.5499	1178.5426	1178.6482	-89.54	322	331	1	---	K.KPGVYTKVCK.Y
1184.6520	1183.6447	1183.6747	-25.32	138	148	0	---	R.LLCGATLIAPR.W
1211.6572	1210.6499	1210.6604	-8.69	256	265	1	---	R.CANVTIIKHR.E
2015.1949	2014.1876	2013.9908	97.7	181	198	1	---	R.TATKSPFPHDPFNNSLPNK.D
2283.0847	2282.0774	2282.0975	-8.78	161	180	1	---	R.YVVLGAHSLGRQDGCQTR.T

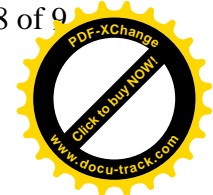
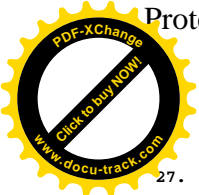
No match to: 813.4393, 834.4629, 838.4906, 842.4641, 846.4475, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1133.6587, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1185.6776, 1185.6776, 1189.6735, 1193.6417, 1203.6858, 1207.6569, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1533.7407, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2211.0193, 2305.0740, 2321.0552, 2528.2617

26. [AOA4W2H4X6](#) Mass: 31395 Score: 35 Expect: 39 Matches: 9

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
834.4629	833.4556	833.4065	58.9	257	263	0	---	K.SMQEALR.F
850.4896	849.4823	849.4821	0.25	194	200	1	---	R.GLYSRVR.K
850.4896	849.4823	849.4821	0.30	194	200	1	---	R.GLYSRVR.K
866.4929	865.4856	865.4116	85.5	264	271	0	---	R.FGCQVAGK.K
1065.6028	1064.5955	1064.4961	93.4	273	282	0	---	K.CGLQGFDGIV.-
1185.6776	1184.6703	1184.6454	21.0	117	125	1	---	R.FKWIHIEGR.N
1185.6776	1184.6703	1184.6454	21.0	117	125	1	---	R.FKWIHIEGR.N
1193.6417	1192.6344	1192.5911	36.4	272	282	1	---	K.KCGLQGFDGIV.-
1533.7407	1532.7334	1532.7695	-23.55	137	149	1	---	R.IEQHNARQPPEK.I

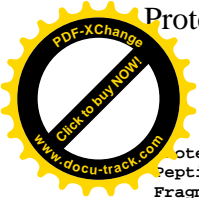
No match to: 813.4393, 838.4906, 842.4641, 846.4475, 848.4780, 850.0118, 853.4691, 856.4822, 864.4857, 865.9818, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1131.6493, 1133.6587, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1189.6735, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2283.0847, 2305.0740, 2321.0552, 2528.2617



27. [A0A4W2C9V0](#) Mass: 38733 Score: 35 Expect: 40 Matches: 8
Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=MFGE8 PE=4 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------|---------------------------|
| 838.4906 | 837.4833 | 837.4232 | 71.8 | 105 | - | 112 | 0 | R.AGSAEYLK.T |
| 842.4641 | 841.4568 | 841.4446 | 14.5 | 57 | - | 63 | 0 | R.WAPELAR.L |
| 868.5015 | 867.4942 | 867.4086 | 98.7 | 116 | - | 123 | 0 | K.VAYSTDGR.Q |
| 868.5015 | 867.4943 | 867.4086 | 98.7 | 116 | - | 123 | 0 | K.VAYSTDGR.Q |
| 1171.6676 | 1170.6603 | 1170.6833 | -19.63 | 255 | - | 265 | 1 | K.RVTGIITQGAR.D |
| 1193.6417 | 1192.6344 | 1192.6353 | -0.73 | 124 | - | 133 | 0 | R.QFQFIQVAGR.S |
| 1522.7052 | 1521.6979 | 1521.8317 | -87.90 | 323 | - | 334 | 1 | R.FVRIQPVVHNR.I |
| 2211.0193 | 2210.0120 | 2210.1154 | -46.77 | 92 | - | 112 | 1 | K.MWVTGVVTTQASRAGSAEYLK.T |
- No match to: 813.4393, 834.4629, 846.4475, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1131.6493, 1133.6587, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1533.7407, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2283.0847, 2305.0740, 2321.0552, 2528.2617
28. [A0A4W2F3R1](#) Mass: 41965 Score: 34 Expect: 51 Matches: 9
Reverse transcriptase domain-containing protein OS=Bos indicus x Bos taurus OX=30522 PE=4 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------|-----------------------------|
| 834.4629 | 833.4556 | 833.5044 | -58.57 | 173 | - | 179 | 1 | K.SLLMKVK.E + Oxidation (M) |
| 848.4780 | 847.4707 | 847.4287 | 49.6 | 178 | - | 184 | 1 | K.VKEESEK.V |
| 1131.6493 | 1130.6420 | 1130.5720 | 61.9 | 16 | - | 25 | 0 | R.ELPDVQAGFR.K |
| 1133.6587 | 1132.6514 | 1132.6162 | 31.1 | 242 | - | 251 | 0 | K.VMTNLSILK.S |
| 1179.5499 | 1178.5426 | 1178.5655 | -19.40 | 334 | - | 342 | 0 | R.QYFGHLMQR.V |
| 1193.6417 | 1192.6344 | 1192.5836 | 42.6 | 89 | - | 99 | 0 | R.NLYAGQEATAR.T |
| 1533.7407 | 1532.7334 | 1532.7578 | -15.92 | 317 | - | 330 | 0 | K.EISPGCSLEGLMLK.L |
| 1554.6993 | 1553.6920 | 1553.7694 | -49.80 | 76 | - | 88 | 0 | K.EMGIPDHLTCLLR.N |
| 1581.7728 | 1580.7655 | 1580.7697 | -2.65 | 49 | - | 60 | 1 | R.KNIYFCFIDYAK.A |
- No match to: 813.4393, 838.4906, 842.4641, 846.4475, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1184.6520, 1185.6776, 1185.6776, 1189.6735, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1538.7010, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2283.0847, 2305.0740, 2321.0552, 2528.2617
29. [A0A4W2IP26](#) Mass: 92361 Score: 34 Expect: 60 Matches: 11
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 |
|-----------|-----------|-----------|--------|-------|-----|------|------|--|
| 846.4475 | 845.4402 | 845.4494 | -10.87 | 305 | - | 311 | 0 | R.LITEENK.E |
| 951.5720 | 950.5647 | 950.5073 | 60.4 | 594 | - | 601 | 0 | K.SLPTENLK.S |
| 1131.6493 | 1130.6420 | 1130.6118 | 26.8 | 137 | - | 146 | 0 | K.MQNGLSQILK.S |
| 1147.6777 | 1146.6704 | 1146.6067 | 55.6 | 137 | - | 146 | 0 | K.MQNGLSQILK.S + Oxidation (M) |
| 1189.6735 | 1188.6662 | 1188.5775 | 74.7 | 771 | - | 779 | 0 | K.NTELEEWLR.Q |
| 1207.6569 | 1206.6496 | 1206.6318 | 14.8 | 438 | - | 447 | 1 | K.EIKIFGMEPK.C + Oxidation (M) |
| 1316.8134 | 1315.8061 | 1315.6925 | 86.4 | 151 | - | 161 | 1 | R.VTFGVFESKFR.V |
| 1522.7052 | 1521.6979 | 1521.8416 | -94.39 | 16 | - | 29 | 1 | R.LPGLWASGLPERAR.C |
| 1538.7010 | 1537.6937 | 1537.7386 | -29.17 | 498 | - | 510 | 0 | R.GWPSQHQQTNSIR.D |
| 2211.0193 | 2210.0120 | 2210.0559 | -19.84 | 539 | - | 557 | 0 | R.METSCSLLEQTQPTSLIR.K + Oxidation (M) |
| 2528.2617 | 2527.2544 | 2527.1761 | 31.0 | 771 | - | 790 | 1 | K.NTELEEWLRQEMEVDNQHAK.E + Oxidation (M) |
- No match to: 813.4393, 834.4629, 838.4906, 842.4641, 848.4780, 850.0118, 850.4896, 850.4896, 853.4691, 856.4822, 864.4857, 865.9818, 866.4929, 868.5015, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1065.6028, 1133.6587, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1184.6520, 1185.6776, 1185.6776, 1193.6417, 1203.6858, 1211.6572, 1225.6708, 1279.7007, 1300.7860, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1533.7407, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2283.0847, 2305.0740, 2321.0552
30. [A0ALC9HI59](#) Mass: 67468 Score: 34 Expect: 60 Matches: 9
LS037 OS=Lumpy skin disease virus OX=59509 GN=LW037 PE=4 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------|--|
| 846.4475 | 845.4402 | 845.4793 | -46.19 | 272 | - | 278 | 1 | R.VNKNMLK.L |
| 853.4691 | 852.4618 | 852.4276 | 40.2 | 1 | - | 6 | 1 | -MDFIRR.K + Oxidation (M) |
| 856.4822 | 855.4749 | 855.4854 | -12.28 | 449 | - | 455 | 1 | K.KFSLFSK.N |
| 1065.6028 | 1064.5955 | 1064.5695 | 24.5 | 317 | - | 324 | 1 | K.KYFIGFYK.E |
| 1184.6520 | 1183.6447 | 1183.5945 | 42.4 | 546 | - | 555 | 1 | K.TNHLTNNDKK.Y |
| 1279.7007 | 1278.6934 | 1278.6707 | 17.7 | 108 | - | 118 | 0 | K.TLVSELFDDK.F |
| 1901.1586 | 1900.1513 | 1900.0492 | 53.7 | 484 | - | 499 | 1 | K.ILSHLKCVEDVTVFIK.F |
| 2015.1949 | 2014.1876 | 2014.0081 | 89.1 | 427 | - | 443 | 1 | K.EKDPYILYNGMLTNISK.V + Oxidation (M) |
| 2283.0847 | 2282.0774 | 2282.1616 | -36.90 | 429 | - | 448 | 1 | K.DPYILYNGMLTNISKVPSNK.K + Oxidation (M) |
- No match to: 813.4393, 834.4629, 838.4906, 842.4641, 848.4780, 850.0118, 850.4896, 850.4896, 864.4857, 865.9818, 866.4929, 868.5015, 870.4977, 876.9884, 882.5173, 882.5173, 892.9574, 892.9574, 896.3969, 908.9280, 951.5720, 996.5430, 1017.6157, 1017.6157, 1019.6299, 1033.6429, 1045.5127, 1045.5127, 1051.6522, 1051.6522, 1131.6493, 1133.6587, 1147.6777, 1151.6696, 1165.6809, 1165.6809, 1169.5313, 1171.6676, 1179.5499, 1185.6776, 1185.6776, 1189.6735, 1193.6417, 1203.6858, 1207.6569, 1211.6572, 1225.6708, 1300.7860, 1316.8134, 1334.8168, 1334.8168, 1440.5756, 1448.8479, 1448.8479, 1475.6846, 1522.7052, 1533.7407, 1538.7010, 1554.6993, 1581.7728, 1617.9867, 1617.9867, 1732.0165, 1901.1586, 2015.1949, 2211.0193, 2305.0740, 2321.0552, 2528.2617

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 (813.4393,1+): <no title>
Query2 (834.4629,1+): <no title>
Query3 (838.4906,1+): <no title>
Query4 (842.4641,1+): <no title>
Query5 (846.4475,1+): <no title>
Query6 (848.4780,1+): <no title>
Query7 (850.0118,1+): <no title>
Query8 (850.4896,1+): Locus:1..14.0.6
Query9 (850.4896,1+): <no title>
Query10 (853.4691,1+): <no title>
Query11 (856.4822,1+): <no title>
Query12 (864.4857,1+): <no title>
Query13 (865.9818,1+): <no title>
Query14 (866.4929,1+): <no title>
Query15 (868.5015,1+): <no title>
Query16 (868.5015,1+): Locus:1..14.0.11
Query17 (870.4977,1+): <no title>
Query18 (876.9884,1+): <no title>
Query19 (882.5173,1+): Locus:1..14.0.1
Query20 (882.5173,1+): <no title>
Query21 (892.9574,1+): <no title>
Query22 (892.9574,1+): Locus:1..14.0.10
Query23 (896.3969,1+): <no title>
Query24 (908.9280,1+): <no title>
Query25 (951.5720,1+): <no title>
Query26 (996.5430,1+): <no title>
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Query29 (1019.6299,1+): <no title>
Query30 (1033.6429,1+): <no title>
Query31 (1045.5127,1+): <no title>
Query32 (1045.5127,1+): Locus:1..14.0.8
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Query34 (1051.6522,1+): Locus:1..14.0.2
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Query36 (1131.6493,1+): <no title>
Query37 (1133.6587,1+): <no title>
Query38 (1147.6777,1+): <no title>
Query39 (1151.6696,1+): <no title>
Query40 (1165.6809,1+): <no title>
Query41 (1165.6809,1+): Locus:1..14.0.3
Query42 (1169.5313,1+): <no title>
Query43 (1171.6676,1+): <no title>
Query44 (1179.5499,1+): <no title>
Query45 (1184.6520,1+): <no title>
Query46 (1185.6776,1+): <no title>
Query47 (1185.6776,1+): Locus:1..14.0.7
Query48 (1189.6735,1+): <no title>
Query49 (1193.6417,1+): <no title>
Query50 (1203.6858,1+): <no title>
Query51 (1207.6569,1+): <no title>
Query52 (1211.6572,1+): <no title>
Query53 (1225.6708,1+): <no title>
Query54 (1279.7007,1+): <no title>
Query55 (1300.7860,1+): <no title>
Query56 (1316.8134,1+): <no title>
Query57 (1334.8168,1+): Locus:1..14.0.4
Query58 (1334.8168,1+): <no title>
Query59 (1440.5756,1+): <no title>
Query60 (1448.8479,1+): <no title>
Query61 (1448.8479,1+): Locus:1..14.0.9
Query62 (1475.6846,1+): <no title>
Query63 (1522.7052,1+): <no title>
Query64 (1533.7407,1+): <no title>
Query65 (1538.7010,1+): <no title>
Query66 (1554.6993,1+): <no title>
Query67 (1581.7728,1+): <no title>
Query68 (1617.9867,1+): Locus:1..14.0.5
Query69 (1617.9867,1+): <no title>
Query70 (1732.0165,1+): <no title>
Query71 (1901.1586,1+): <no title>
Query72 (2015.1949,1+): <no title>
Query73 (2211.0193,1+): <no title>
Query74 (2283.0847,1+): <no title>
Query75 (2305.0740,1+): <no title>
Query76 (2321.0552,1+): <no title>
Query77 (2528.2617,1+): <no title>

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