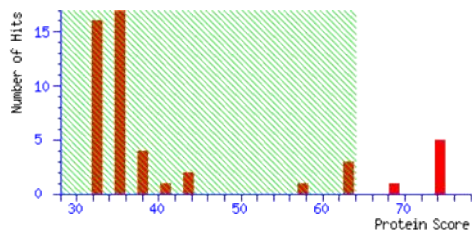


MASCOT Search Results

User :
Email :
Search title : BAEDW\2020_3_5\2020_3_5\MSMS 14\N12
Database : Uniprot_bovine_bovine_20200316 (134392 sequences; 76244912 residues)
Timestamp : 31 Mar 2020 at 01:08:42 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 74 for F1MMD7, Inter-alpha-trypsin inhibitor heavy chain H4 OS=Bos taurus OX=9913 GN=ITIH4 PE=4 SV=3

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 ion scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

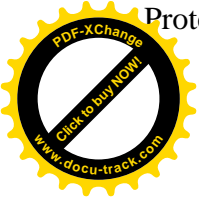
Format As [Help](#)
Significance threshold $p < 0.05$ Max. number of hits
Preferred taxonomy

Index

Accession	Mass	Score	Description
1. F1MMD7	101620	74	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Bos taurus OX=9913 GN=ITIH4 PE=4 SV=3
2. A0A4W2C1E9	101620	74	Inter-alpha-trypsin inhibitor heavy chain 4 OS=Bos indicus x Bos taurus OX=30522 GN=ITIH4 PE=4 SV=1
3. Q5EA67	101617	74	Inter-alpha (Globulin) inhibitor H4 (Plasma Kallikrein-sensitive glycoprotein) OS=Bos taurus OX=9913 GN=
4. Q3T052	101620	74	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Bos taurus OX=9913 GN=ITIH4 PE=1 SV=1
5. A0A3Q1MGQ6	103466	74	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Bos taurus OX=9913 GN=ITIH4 PE=4 SV=1
6. A0A4W2HB77	101584	68	Inter-alpha-trypsin inhibitor heavy chain 4 OS=Bos indicus x Bos taurus OX=30522 GN=ITIH4 PE=4 SV=1
7. A0A3Q1MA31	99755	64	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Bos taurus OX=9913 GN=ITIH4 PE=4 SV=1
8. A0A4W2DPE8	99755	64	Inter-alpha-trypsin inhibitor heavy chain 4 OS=Bos indicus x Bos taurus OX=30522 GN=ITIH4 PE=4 SV=1
9. A0A3Q1LZ09	100847	63	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Bos taurus OX=9913 GN=ITIH4 PE=4 SV=1
10. A0A4W2F8Z8	99718	59	Inter-alpha-trypsin inhibitor heavy chain 4 OS=Bos indicus x Bos taurus OX=30522 GN=ITIH4 PE=4 SV=1
11. A0A4W2DTX3	38736	42	Glutathione S-transferase omega 1 OS=Bos indicus x Bos taurus OX=30522 GN=GSTO1 PE=3 SV=1
12. A0A4W2FV73	38767	42	Glutathione S-transferase omega 1 OS=Bos indicus x Bos taurus OX=30522 GN=GSTO1 PE=3 SV=1
13. A0A3Q1LRF3	39309	41	Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1
14. A0A4W2F6I5	532453	39	Plectin OS=Bos indicus x Bos taurus OX=30522 GN=PLEC PE=4 SV=1
15. A0A4W2FGN9	123016	39	Coiled-coil domain containing 150 OS=Bos indicus x Bos taurus OX=30522 GN=CCDC150 PE=4 SV=1
16. A0A4W2DYM0	53619	38	NAD-dependent protein lipoamidase sirtuin-4, mitochondrial OS=Bos indicus x Bos taurus OX=30522 GN=SIRT
17. A0A4W2GWY7	132560	38	Euchromatic histone lysine methyltransferase 1 OS=Bos indicus x Bos taurus OX=30522 GN=EHMT1 PE=4 SV=1
18. A0A4W2E8Y3	132257	36	Euchromatic histone lysine methyltransferase 1 OS=Bos indicus x Bos taurus OX=30522 GN=EHMT1 PE=4 SV=1
19. A0A3Q1LPD0	132257	36	Euchromatic histone lysine methyltransferase 1 OS=Bos taurus OX=9913 GN=EHMT1 PE=4 SV=1
20. A0A4W2C1C0	67085	7	Heparanase 2 (inactive) OS=Bos indicus x Bos taurus OX=30522 GN=HPSE2 PE=4 SV=1
21. O46770	19686	35	MHC class I heavy chain (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1
22. USTGS8	86845	34	CPXV068 protein OS=Cowpox virus OX=10243 GN=CPXV068 PE=4 SV=1
23. A0A4W2CHB4	38688	34	Glutathione S-transferase omega 1 OS=Bos indicus x Bos taurus OX=30522 GN=GSTO1 PE=3 SV=1
24. A0A4W2FWN4	38719	34	Glutathione S-transferase omega 1 OS=Bos indicus x Bos taurus OX=30522 GN=GSTO1 PE=3 SV=1
25. A0A0K2TTL5	9022	34	Uncharacterized protein OS=Cowpox virus OX=10243 GN=gCPXV0248 PE=4 SV=1
26. O46724	19602	34	MHC class I heavy chain (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1
27. O46765	19602	34	MHC class I heavy chain (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1
28. A0A4W2BML3	25099	34	HESX homeobox 1 OS=Bos indicus x Bos taurus OX=30522 GN=HESX1 PE=4 SV=1
29. A0A4W2E8V9	138235	34	Euchromatic histone lysine methyltransferase 1 OS=Bos indicus x Bos taurus OX=30522 GN=EHMT1 PE=4 SV=1
30. A0A3Q1MVR5	138235	34	Euchromatic histone lysine methyltransferase 1 OS=Bos taurus OX=9913 GN=EHMT1 PE=4 SV=1

Results List

1.	F1MMD7	Mass: 101620	Score: 74	Expect: 0.005	Matches: 14
Inter-alpha-trypsin inhibitor heavy chain H4 OS=Bos taurus OX=9913 GN=ITIH4 PE=4 SV=3					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Tons Peptide
835.4214	834.4141	834.4422	-33.63	619 - 625	0 --- R.VYLGPMR.F
853.4803	852.4730	852.3946	92.0	283 - 290	1 --- K.SGSMGRK.I
853.4804	852.4731	852.3946	92.1	283 - 290	1 --- K.SGSMGRK.I
972.5108	971.5035	971.5400	-37.52	845 - 852	0 --- R.LLLQNTDR.F
1031.5133	1030.5060	1030.5229	-16.41	430 - 439	0 --- K.MALENGGLAR.R
1151.6821	1150.6748	1150.5917	72.2	616 - 625	1 --- R.GSRVYLGPMR.F + Oxidation (M)
1211.5695	1210.5622	1210.6135	-42.34	539 - 547	0 --- K.YIFHSPIER.L
1349.6478	1348.6405	1348.6987	-43.13	230 - 241	0 --- K.QDTVLDGSFIVR.Y
1368.6882	1367.6809	1367.7409	-43.82	500 - 511	0 --- R.EQSPDVLQAQIR.G
1402.7100	1401.7027	1401.7657	-44.89	829 - 841	0 --- R.VTIGLLFWDGPGK.G
1567.6902	1566.6829	1566.8116	-82.12	800 - 812	1 --- K.WKETLYSVMPGLK.V + Oxidation (M)
1581.7833	1580.7760	1580.8450	-43.62	141 - 153	0 --- K.VTFELVYEELLAR.H
1581.7833	1580.7761	1580.8450	-43.60	141 - 153	0 35 K.VTFELVYEELLAR.H
1637.8650	1636.8577	1636.9260	-41.73	498 - 511	1 --- K.LREQSPDVLQAQIR.G
No match to: 842.4716, 848.4913, 850.5007, 864.5184, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 982.5417, 996.5513, 1007.6395, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587,					



1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1383.6498, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1617.9998, 1617.9998, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440

2. [A0A4W2C1E9](#) Mass: 101620 Score: 74 Expect: 0.005 Matches: 14

Inter-alpha-trypsin inhibitor heavy chain 4 OS=Bos indicus x Bos taurus OX=30522 GN=ITIH4 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
835.4214	834.4141	834.4422	-33.63	619	625	0	---	R.VYLGPMR.F
853.4803	852.4730	852.3946	92.0	283	290	1	---	K.SGSMGGRK.I
853.4804	852.4731	852.3946	92.1	283	290	1	---	K.SGSMGGRK.I
972.5108	971.5035	971.5400	-37.52	845	852	0	---	R.LLLQNTDR.F
1031.5133	1030.5060	1030.5229	-16.41	430	439	0	---	K.MALENGGLAR.R
1151.6821	1150.6748	1150.5917	72.2	616	625	1	---	R.GSRVYLGPMR.F + Oxidation (M)
1211.5695	1210.5622	1210.6135	-42.34	539	547	0	---	K.YIFHSPIER.L
1349.6478	1348.6405	1348.6987	-43.13	230	241	0	---	K.QDTVLGDSFIVR.Y
1368.6882	1367.6809	1367.7409	-43.82	500	511	0	---	R.EQSPDVLLAQIR.G
1402.7100	1401.7027	1401.7657	-44.89	829	841	0	---	R.VTIGLLFWDGPGK.G
1567.6902	1566.6829	1566.8116	-82.12	800	812	1	---	K.WKETLYSVMPGLK.V + Oxidation (M)
1581.7833	1580.7760	1580.8450	-43.62	141	153	0	---	K.VTFELVYEELLAR.H
1581.7833	1580.7761	1580.8450	-43.60	141	153	0	35	K.VTFELVYEELLAR.H
1637.8650	1636.8577	1636.9260	-41.73	498	511	1	---	K.LREQSPDVLLAQIR.G
No match to: 842.4716, 848.4913, 850.5007, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1383.6498, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1617.9998, 1617.9998, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440								

3. [Q5EA67](#) Mass: 101617 Score: 74 Expect: 0.005 Matches: 14

Inter-alpha (Globulin) inhibitor H4 (Plasma Kallikrein-sensitive glycoprotein) OS=Bos taurus OX=9913 GN=ITIH4 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
835.4214	834.4141	834.4422	-33.63	619	625	0	---	R.VYLGPMR.F
853.4803	852.4730	852.3946	92.0	283	290	1	---	K.SGSMGGRK.I
853.4804	852.4731	852.3946	92.1	283	290	1	---	K.SGSMGGRK.I
972.5108	971.5035	971.5400	-37.52	845	852	0	---	R.LLLQNTDR.F
1031.5133	1030.5060	1030.5229	-16.41	430	439	0	---	K.MALENGGLAR.R
1151.6821	1150.6748	1150.5917	72.2	616	625	1	---	R.GSRVYLGPMR.F + Oxidation (M)
1211.5695	1210.5622	1210.6135	-42.34	539	547	0	---	K.YIFHSPIER.L
1349.6478	1348.6405	1348.6987	-43.13	230	241	0	---	K.QDTVLGDSFIVR.Y
1368.6882	1367.6809	1367.7409	-43.82	500	511	0	---	R.EQSPDVLLAQIR.G
1402.7100	1401.7027	1401.7657	-44.89	829	841	0	---	R.VTIGLLFWDGPGK.G
1567.6902	1566.6829	1566.8116	-82.12	800	812	1	---	K.WKETLYSVMPGLK.V + Oxidation (M)
1581.7833	1580.7760	1580.8450	-43.62	141	153	0	---	K.VTFELVYEELLAR.H
1581.7833	1580.7761	1580.8450	-43.60	141	153	0	35	K.VTFELVYEELLAR.H
1637.8650	1636.8577	1636.9260	-41.73	498	511	1	---	K.LREQSPDVLLAQIR.G
No match to: 842.4716, 848.4913, 850.5007, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1383.6498, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1617.9998, 1617.9998, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440								

4. [Q3T052](#) Mass: 101620 Score: 74 Expect: 0.005 Matches: 14

Inter-alpha-trypsin inhibitor heavy chain H4 OS=Bos taurus OX=9913 GN=ITIH4 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
835.4214	834.4141	834.4422	-33.63	619	625	0	---	R.VYLGPMR.F
853.4803	852.4730	852.3946	92.0	283	290	1	---	K.SGSMGGRK.I
853.4804	852.4731	852.3946	92.1	283	290	1	---	K.SGSMGGRK.I
972.5108	971.5035	971.5400	-37.52	845	852	0	---	R.LLLQNTDR.F
1031.5133	1030.5060	1030.5229	-16.41	430	439	0	---	K.MALENGGLAR.R
1151.6821	1150.6748	1150.5917	72.2	616	625	1	---	R.GSRVYLGPMR.F + Oxidation (M)
1211.5695	1210.5622	1210.6135	-42.34	539	547	0	---	K.YIFHSPIER.L
1349.6478	1348.6405	1348.6987	-43.13	230	241	0	---	K.QDTVLGDSFIVR.Y
1368.6882	1367.6809	1367.7409	-43.82	500	511	0	---	R.EQSPDVLLAQIR.G
1402.7100	1401.7027	1401.7657	-44.89	829	841	0	---	R.VTIGLLFWDGPGK.G
1567.6902	1566.6829	1566.8116	-82.12	800	812	1	---	K.WKETLYSVMPGLK.V + Oxidation (M)
1581.7833	1580.7760	1580.8450	-43.62	141	153	0	---	K.VTFELVYEELLAR.H
1581.7833	1580.7761	1580.8450	-43.60	141	153	0	35	K.VTFELVYEELLAR.H
1637.8650	1636.8577	1636.9260	-41.73	498	511	1	---	K.LREQSPDVLLAQIR.G
No match to: 842.4716, 848.4913, 850.5007, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1383.6498, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1617.9998, 1617.9998, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440								

5. [A0A3Q1MGQ6](#) Mass: 103466 Score: 74 Expect: 0.006 Matches: 14

Inter-alpha-trypsin inhibitor heavy chain H4 OS=Bos taurus OX=9913 GN=ITIH4 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
835.4214	834.4141	834.4422	-33.63	619	625	0	---	R.VYLGPMR.F
853.4803	852.4730	852.3946	92.0	283	290	1	---	K.SGSMGGRK.I
853.4804	852.4731	852.3946	92.1	283	290	1	---	K.SGSMGGRK.I
972.5108	971.5035	971.5400	-37.52	845	852	0	---	R.LLLQNTDR.F
1031.5133	1030.5060	1030.5229	-16.41	430	439	0	---	K.MALENGGLAR.R
1151.6821	1150.6748	1150.5917	72.2	616	625	1	---	R.GSRVYLGPMR.F + Oxidation (M)
1211.5695	1210.5622	1210.6135	-42.34	539	547	0	---	K.YIFHSPIER.L
1349.6478	1348.6405	1348.6987	-43.13	230	241	0	---	K.QDTVLGDSFIVR.Y
1368.6882	1367.6809	1367.7409	-43.82	500	511	0	---	R.EQSPDVLLAQIR.G
1402.7100	1401.7027	1401.7657	-44.89	829	841	0	---	R.VTIGLLFWDGPGK.G
1567.6902	1566.6829	1566.8116	-82.12	800	812	1	---	K.WKETLYSVMPGLK.V + Oxidation (M)
1581.7833	1580.7760	1580.8450	-43.62	141	153	0	---	K.VTFELVYEELLAR.H
1581.7833	1580.7761	1580.8450	-43.60	141	153	0	35	K.VTFELVYEELLAR.H
1637.8650	1636.8577	1636.9260	-41.73	498	511	1	---	K.LREQSPDVLLAQIR.G
No match to: 842.4716, 848.4913, 850.5007, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1383.6498, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1617.9998, 1617.9998, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440								

1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1383.6498, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1617.9998, 1617.9998, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440

6.

[A0A4W2HBJ7](#)

Mass: 101584

Score: 68

Expect: 0.019

Matches: 13

Inter-alpha-trypsin inhibitor heavy chain 4 OS=Bos indicus x Bos taurus OX=30522 GN=ITIH4 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
835.4214	834.4141	834.4422	-33.63	619	625	0	---	R.VYLGPMR.F
853.4803	852.4730	852.3946	92.0	283	290	1	---	K.SGSMGRK.I
853.4804	852.4731	852.3946	92.1	283	290	1	---	K.SGSMGRK.I
972.5108	971.5035	971.5400	-37.52	845	852	0	---	R.LLLQNTDR.F
1031.5133	1030.5060	1030.5229	-16.41	430	439	0	---	K.MALENGGLAR.R
1151.6821	1150.6748	1150.5917	72.2	616	625	1	---	R.GSRVYLGPMR.F + Oxidation (M)
1349.6478	1348.6405	1348.6987	-43.13	230	241	0	---	K.QDTVLDSFIVR.Y
1368.6882	1367.6809	1367.7409	-43.82	500	511	0	---	R.EQSPDVLLAQIR.G
1402.7100	1401.7027	1401.7657	-44.89	829	841	0	---	R.VTIGLLFDGPGK.G
1567.6902	1566.6829	1566.8116	-82.12	800	812	1	---	K.WKETLYSVMPLK.V + Oxidation (M)
1581.7833	1580.7760	1580.8450	-43.62	141	153	0	---	K.VTFELVYEELLAR.H
1581.7833	1580.7761	1580.8450	-43.60	141	153	0	35	K.VTFELVYEELLAR.H
1637.8650	1636.8577	1636.9260	-41.73	498	511	1	---	K.LREQSPDVLLAQIR.G
No match to: 842.4716, 848.4913, 850.5007, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1383.6498, 1421.6836, 1434.8480, 1448.8584, 1475.6868, 1479.7338, 1617.9998, 1617.9998, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440								

7.

[A0A3Q1MA31](#)

Mass: 99755

Score: 64

Expect: 0.057

Matches: 12

Inter-alpha-trypsin inhibitor heavy chain H4 OS=Bos taurus OX=9913 GN=ITIH4 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.4803	852.4730	852.3946	92.0	283	290	1	---	K.SGSMGRK.I
853.4804	852.4731	852.3946	92.1	283	290	1	---	K.SGSMGRK.I
972.5108	971.5035	971.5400	-37.52	828	835	0	---	R.LLLQNTDR.F
1031.5133	1030.5060	1030.5229	-16.41	430	439	0	---	K.MALENGGLAR.R
1211.5695	1210.5622	1210.6135	-42.34	539	547	0	---	K.YIFHSFIER.L
1349.6478	1348.6405	1348.6987	-43.13	230	241	0	---	K.QDTVLDSFIVR.Y
1368.6882	1367.6809	1367.7409	-43.82	500	511	0	---	R.EQSPDVLLAQIR.G
1402.7100	1401.7027	1401.7657	-44.89	812	824	0	---	R.VTIGLLFDGPGK.G
1567.6902	1566.6829	1566.8116	-82.12	783	795	1	---	K.WKETLYSVMPLK.V + Oxidation (M)
1581.7833	1580.7760	1580.8450	-43.62	141	153	0	---	K.VTFELVYEELLAR.H
1581.7833	1580.7761	1580.8450	-43.60	141	153	0	35	K.VTFELVYEELLAR.H
1637.8650	1636.8577	1636.9260	-41.73	498	511	1	---	K.LREQSPDVLLAQIR.G
No match to: 835.4214, 842.4716, 848.4913, 850.5007, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1383.6498, 1421.6836, 1434.8480, 1448.8584, 1475.6868, 1479.7338, 1617.9998, 1617.9998, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440								

8.

[A0A4W2DPE8](#)

Mass: 99755

Score: 64

Expect: 0.057

Matches: 12

Inter-alpha-trypsin inhibitor heavy chain 4 OS=Bos indicus x Bos taurus OX=30522 GN=ITIH4 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.4803	852.4730	852.3946	92.0	283	290	1	---	K.SGSMGRK.I
853.4804	852.4731	852.3946	92.1	283	290	1	---	K.SGSMGRK.I
972.5108	971.5035	971.5400	-37.52	828	835	0	---	R.LLLQNTDR.F
1031.5133	1030.5060	1030.5229	-16.41	430	439	0	---	K.MALENGGLAR.R
1211.5695	1210.5622	1210.6135	-42.34	539	547	0	---	K.YIFHSFIER.L
1349.6478	1348.6405	1348.6987	-43.13	230	241	0	---	K.QDTVLDSFIVR.Y
1368.6882	1367.6809	1367.7409	-43.82	500	511	0	---	R.EQSPDVLLAQIR.G
1402.7100	1401.7027	1401.7657	-44.89	812	824	0	---	R.VTIGLLFDGPGK.G
1567.6902	1566.6829	1566.8116	-82.12	783	795	1	---	K.WKETLYSVMPLK.V + Oxidation (M)
1581.7833	1580.7760	1580.8450	-43.62	141	153	0	---	K.VTFELVYEELLAR.H
1581.7833	1580.7761	1580.8450	-43.60	141	153	0	35	K.VTFELVYEELLAR.H
1637.8650	1636.8577	1636.9260	-41.73	498	511	1	---	K.LREQSPDVLLAQIR.G
No match to: 835.4214, 842.4716, 848.4913, 850.5007, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1383.6498, 1421.6836, 1434.8480, 1448.8584, 1475.6868, 1479.7338, 1617.9998, 1617.9998, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440								

9.

[A0A3Q1L209](#)

Mass: 100847

Score: 63

Expect: 0.061

Matches: 12

Inter-alpha-trypsin inhibitor heavy chain H4 OS=Bos taurus OX=9913 GN=ITIH4 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.4803	852.4730	852.3946	92.0	283	290	1	---	K.SGSMGRK.I
853.4804	852.4731	852.3946	92.1	283	290	1	---	K.SGSMGRK.I
972.5108	971.5035	971.5400	-37.52	839	846	0	---	R.LLLQNTDR.F
1031.5133	1030.5060	1030.5229	-16.41	430	439	0	---	K.MALENGGLAR.R
1211.5695	1210.5622	1210.6135	-42.34	539	547	0	---	K.YIFHSFIER.L
1349.6478	1348.6405	1348.6987	-43.13	230	241	0	---	K.QDTVLDSFIVR.Y
1368.6882	1367.6809	1367.7409	-43.82	500	511	0	---	R.EQSPDVLLAQIR.G
1402.7100	1401.7027	1401.7657	-44.89	823	835	0	---	R.VTIGLLFDGPGK.G
1567.6902	1566.6829	1566.8116	-82.12	794	806	1	---	K.WKETLYSVMPLK.V + Oxidation (M)
1581.7833	1580.7760	1580.8450	-43.62	141	153	0	---	K.VTFELVYEELLAR.H
1581.7833	1580.7761	1580.8450	-43.60	141	153	0	35	K.VTFELVYEELLAR.H
1637.8650	1636.8577	1636.9260	-41.73	498	511	1	---	K.LREQSPDVLLAQIR.G
No match to: 835.4214, 842.4716, 848.4913, 850.5007, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1383.6498, 1421.6836, 1434.8480, 1448.8584, 1475.6868, 1479.7338, 1617.9998, 1617.9998, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440								

10.

[A0A4W2F8Z8](#)

Mass: 99718

Score: 59

Expect: 0.18

Matches: 11

http://203.255.41.217/mascot/cgi/master_results.pl?file=../data/20200330/F002148.da... 2020-03-31

Inter-alpha-trypsin inhibitor heavy chain 4 OS=Bos indicus x Bos taurus OX=30522 GN=ITIH4 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.4803	852.4730	852.3946	92.0	283	-	290	1	K.SGSMGGRK.I
853.4804	852.4731	852.3946	92.1	283	-	290	1	K.SGSMGGRK.I
972.5108	971.5035	971.5400	-37.52	828	-	835	0	R.LLLQNTDR.F
1031.5133	1030.5060	1030.5229	-16.41	430	-	439	0	K.MALENGGLAR.R
1349.6478	1348.6405	1348.6987	-43.13	230	-	241	0	K.QDTVLDSFIVR.Y
1368.6882	1367.6809	1367.7409	-43.82	500	-	511	0	R.EQSPDVLQAQIR.G
1402.7100	1401.7027	1401.7657	-44.89	812	-	824	0	R.VTIGLFLWDGPGK.G
1567.6902	1566.6829	1566.8116	-82.12	783	-	795	1	K.WKETLYSVMPGLK.V + Oxidation (M)
1581.7833	1580.7760	1580.8450	-43.62	141	-	153	0	K.VTFELVYEELLAR.H
1581.7833	1580.7761	1580.8450	-43.60	141	-	153	0	K.VTFELVYEELLAR.H
1637.8650	1636.8577	1636.9260	-41.73	498	-	511	1	K.LREQSPDVLQAQIR.G
No match to: 835.4214, 842.4716, 848.4913, 850.5007, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1383.6498, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1617.9998, 1617.9998, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440								

11. [A0A4W2DTX3](#) Mass: 38736 Score: 42 Expect: 7.6 Matches: 10

Glutathione S-transferase omega 1 OS=Bos indicus x Bos taurus OX=30522 GN=GSTO1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.5007	849.4934	849.4241	81.6	304	-	310	0	K.LWMAAMK.K
870.5096	869.5023	869.5811	-90.54	140	-	146	1	K.RTLLVLR.A
1031.5133	1030.5060	1030.5335	-26.66	205	-	213	0	K.LLPGDPYEK.A
1279.7057	1278.6984	1278.5874	86.8	236	-	246	1	R.TQNKEDCSGLK.E
1300.7963	1299.7890	1299.6969	70.9	68	-	79	1	R.ADGCPSLALLRK.I
1402.7100	1401.7027	1401.7715	-49.07	311	-	323	1	K.KDPTVSSLLTDVK.T
1421.6836	1420.6763	1420.6631	9.28	129	-	139	1	R.VYSMRFCPYAK.R
1732.0293	1731.0220	1730.9679	31.3	111	-	128	1	R.SLGKGSAPPGPVPEGLIR.V
1732.0293	1731.0220	1730.9679	31.3	111	-	128	1	R.SLGKGSAPPGPVPEGLIR.V
1734.8334	1733.8261	1733.9790	-88.16	218	-	232	1	K.MVFESFSKVPPLILK.I
No match to: 835.4214, 842.4716, 848.4913, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1236.6587, 1277.6544, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1368.6882, 1383.6498, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440								

12. [A0A4W2FV73](#) Mass: 38767 Score: 42 Expect: 7.6 Matches: 10

Glutathione S-transferase omega 1 OS=Bos indicus x Bos taurus OX=30522 GN=GSTO1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.5007	849.4934	849.4241	81.6	304	-	310	0	K.LWMAAMK.K
870.5096	869.5023	869.5811	-90.54	140	-	146	1	K.RTLLVLR.A
1031.5133	1030.5060	1030.5335	-26.66	205	-	213	0	K.LLPGDPYEK.A
1279.7057	1278.6984	1278.5874	86.8	236	-	246	1	R.TQNKEDCSGLK.E
1300.7963	1299.7890	1299.6969	70.9	68	-	79	1	R.ADGCPSLALLRK.I
1402.7100	1401.7027	1401.7715	-49.07	311	-	323	1	K.KDPTVSSLLTDVK.T
1421.6836	1420.6763	1420.6631	9.28	129	-	139	1	R.VYSMRFCPYAK.R
1732.0293	1731.0220	1730.9679	31.3	111	-	128	1	R.SLGKGSAPPGPVPEGLIR.V
1732.0293	1731.0220	1730.9679	31.3	111	-	128	1	R.SLGKGSAPPGPVPEGLIR.V
1734.8334	1733.8261	1733.9790	-88.16	218	-	232	1	K.MVFESFSKVPPLILK.I
No match to: 835.4214, 842.4716, 848.4913, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1236.6587, 1277.6544, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1368.6882, 1383.6498, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440								

13. [A0A3Q1LRF3](#) Mass: 39309 Score: 41 Expect: 9.7 Matches: 5

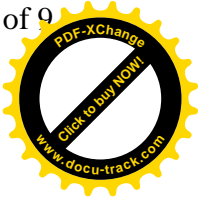
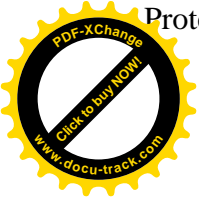
Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1236.6587	1235.6514	1235.6193	26.0	337	-	346	1	K.NVNALACRYR.-
1421.6836	1420.6763	1420.7674	-64.11	106	-	117	1	R.LFSNTLSQIRK.I
1732.0293	1731.0220	1730.8587	94.3	28	-	43	0	R.NPNNSWNSSSALLK.Y
1732.0293	1731.0220	1730.8587	94.3	28	-	43	0	R.NPNNSWNSSSALLK.Y
2872.3440	2871.3367	2871.5640	-79.16	293	-	318	0	K.SVQLNGQPLVMVDDGTLPELKPRLR.A
No match to: 835.4214, 842.4716, 848.4913, 850.5007, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1368.6882, 1383.6498, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969								

14. [A0A4W2F6I5](#) Mass: 532453 Score: 39 Expect: 15 Matches: 35

Plectin OS=Bos indicus x Bos taurus OX=30522 GN=PLEC PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
835.4214	834.4141	834.4269	-15.32	4492	-	4499	0	K.MSAAQALK.K + Oxidation (M)
850.5007	849.4934	849.4596	39.8	723	-	729	0	R.LDLQYAK.L
864.5184	863.5111	863.4501	70.7	2299	-	2305	0	K.FAEQTLR.Q
953.4929	952.4856	952.4403	47.6	3635	-	3642	0	K.GPFDPNTR.E
972.5108	971.5035	971.5148	-11.61	2205	-	2213	1	R.LRGEAEAR.R
982.5417	981.5344	981.4953	39.8	3493	-	3500	0	K.VTIYEAMR.R
996.5513	995.5440	995.5261	18.0	924	-	932	1	R.NPAQPTRGR.V
1017.6248	1016.6175	1016.5502	66.2	4587	-	4596	0	R.LLEAAQSSK.G
1017.6248	1016.6175	1016.5502	66.2	4587	-	4596	0	R.LLEAAQSSK.G
1031.5133	1030.5060	1030.5043	1.68	2266	-	2274	1	R.KEAEQEAR.R
1036.5132	1035.5059	1035.4985	7.15	130	-	139	0	R.GPPPTEDPAR.E
1045.5249	1044.5176	1044.5312	-12.99	1565	-	1573	1	R.QVEAAERSR.L
1131.6577	1130.6504	1130.6183	28.5	1976	-	1985	1	K.TEAEIALKEK.E
1133.6731	1132.6658	1132.5910	66.0	1111	-	1119	1	R.CISELKDIR.L



1165.6888	1164.6815	1164.5662	99.0	4326	-	4335	0	---	R.QYDIDEAIAK.S
1165.6888	1164.6816	1164.5662	99.0	4326	-	4335	0	---	R.QYDIDEAIAK.S
1179.5533	1178.5460	1178.5237	18.9	2501	-	2510	0	---	R.QLEMSAEAER.L + Oxidation (M)
1194.5757	1193.5684	1193.6842	-96.98	4146	-	4155	1	---	K.LISLFAQMKK.G + Oxidation (M)
1234.7560	1233.7487	1233.6618	70.4	59	-	68	1	---	R.GLVRETFAWR.H
1236.6587	1235.6514	1235.6220	23.8	4117	-	4127	1	---	R.MGIVGPEFKDK.L + Oxidation (M)
1279.7057	1278.6984	1278.7183	-15.56	3550	-	3561	1	---	K.LLSAEKAVTGYK.D
1300.7963	1299.7890	1299.7333	42.9	4468	-	4478	1	---	K.IMVDRINLAQK.A
1316.8273	1315.8200	1315.7282	69.8	4468	-	4478	1	---	K.IMVDRINLAQK.A + Oxidation (M)
1383.6498	1382.6425	1382.7630	-87.11	2161	-	2172	1	---	R.QLQAQEAQKRL
1434.8480	1433.8407	1433.7626	54.5	3643	-	3653	1	---	R.ENLTYRQLLER.C
1448.8584	1447.8511	1447.7089	98.3	2501	-	2512	1	---	R.QLEMSAEAERLR.L + Oxidation (M)
1448.8584	1447.8511	1447.7089	98.3	2501	-	2512	1	---	R.QLEMSAEAERLR.L + Oxidation (M)
1475.6868	1474.6795	1474.7263	-31.74	3290	-	3303	1	---	K.ETSTALTAPRDDAK.T
1637.8650	1636.8577	1636.8672	-5.76	1240	-	1255	0	---	K.EAQAVPAALPELEATK.A
1732.0293	1731.0220	1730.9203	58.8	3991	-	4006	1	---	R.DEASGLFLLPLSDARK.L
1732.0293	1731.0220	1730.8549	96.6	392	-	406	0	---	K.SIITYVSSLYDAMP.R + Oxidation (M)
1900.9630	1899.9557	1899.8396	61.1	951	-	966	0	---	K.GDECQMLGPAQPFHWK.V
1993.8977	1992.8904	1993.0593	-84.71	3257	-	3275	1	---	R.LLDAQSLTGGIVDPSKSHR.L
2211.0339	2210.0266	2210.1039	-34.96	2245	-	2265	1	---	K.QAAEEQAQAQAQAAAEKLR.K
2215.0857	2214.0784	2214.1168	-17.34	149	-	170	0	---	K.EPEEGAPEPPVVPATTPGTLAR.Q
No match to: 842.4716, 848.4913, 853.4803, 853.4804, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 1007.6395, 1019.6375, 1033.6567, 1033.6567, 1051.6622, 1051.6622, 1136.6519, 1147.6853, 1151.6821, 1211.5695, 1277.6544, 1302.8082, 1334.8298, 1334.8298, 1349.6478, 1368.6882, 1402.7100, 1421.6836, 1479.7338, 1567.6902, 1581.7833, 1617.9998, 1617.9998, 1707.7130, 1734.8334, 1838.8518, 1901.1735, 2015.2006, 2184.3567, 2283.0969, 2872.3440									

15. [A0A4W2FCN9](#) Mass: 123016 Score: 39 Expect: 17 Matches: 17
Coiled-coil domain containing 150 OS=Bos indicus x Bos taurus OX=30522 GN=CCDC150 PE=4 SV=1

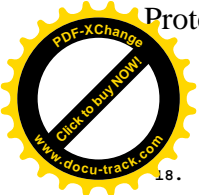
observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4913	847.4840	847.4664	20.8	642	- 648	1	---	K.KVGNFQR.Q
864.5184	863.5111	863.4422	79.8	826	- 832	1	---	R.EVTEMKK.A
868.5114	867.5041	867.4450	68.1	766	- 772	0	---	K.LDHVQEK.L
868.5114	867.5041	867.4450	68.1	766	- 772	0	---	K.LDHVQEK.L
1031.5133	1030.5060	1030.5658	-58.04	441	- 449	0	---	K.ELLESTIAR.L
1147.6853	1146.6780	1146.6067	62.2	893	- 901	1	---	R.MKQIETELR.Q
1279.7057	1278.6984	1278.6754	18.0	110	- 119	1	---	K.MNIFRLQTEK.D
1300.7963	1299.7890	1299.7510	29.2	441	- 451	1	---	K.ELLESTIARLR.G
1402.7100	1401.7027	1401.7351	-23.09	295	- 306	1	---	R.DDIISKLVENK.N
1448.8584	1447.8511	1447.7453	73.1	30	- 41	1	---	R.MRIVEEQTSSLR.D
1448.8584	1447.8511	1447.7453	73.1	30	- 41	1	---	R.MRIVEEQTSSLR.D
1475.6868	1474.6795	1474.6535	17.6	163	- 174	1	---	K.EEEDKAQDEVQR.L
1479.7338	1478.7265	1478.7551	-19.35	985	- 996	1	---	K.CRFDGLQLELTK.N
1637.8650	1636.8577	1636.7913	40.6	1	- 14	0	---	-.METTMSRPVLSPTR.I + 2 Oxidation (M)
2184.3567	2183.3494	2183.1368	97.4	747	- 765	1	---	R.KLAMSLAQQTNNHLQTK.L + Oxidation (M)
2211.0339	2210.0266	2210.0498	-10.47	964	- 981	1	---	R.QELENRCQITANLEEAHR.W
2283.0969	2282.0896	2282.1324	-18.76	359	- 377	1	---	K.MENTRIADHQAILQEEQK.M + Oxidation (M)
No match to: 835.4214, 842.4716, 850.5007, 853.4803, 853.4804, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1236.6587, 1277.6544, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1368.6882, 1383.6498, 1421.6836, 1434.8480, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2215.0857, 2872.3440								

16. [A0A4W2DYM0](#) Mass: 53619 Score: 38 Expect: 21 Matches: 8
NAD-dependent protein lipamidase sirtuin-4, mitochondrial OS=Bos indicus x Bos taurus OX=30522 GN=SIRT4 PE=3 SV=1

observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4913	847.4840	847.4287	65.3	444	- 451	0	---	R.SDDLASLK.L
864.5184	863.5111	863.5229	-13.61	202	- 208	1	---	R.FITLSKR.L
1234.7560	1233.7487	1233.7081	32.9	198	- 207	1	---	K.ELQRFITLSK.R
1383.6498	1382.6425	1382.6976	-39.86	50	- 61	1	---	R.MTTAFSLRVSDR.Q
1734.8334	1733.8261	1733.9438	-67.85	240	- 254	1	---	R.RPIQHGFVRSAPVR.Q
1900.9630	1899.9557	1899.9169	20.4	257	- 271	1	---	R.YWARNFVGWQFSSR.Q
2283.0969	2282.0896	2282.1841	-41.41	38	- 57	1	---	K.LENVSTHPLPPRMTTAFSLR.V + Oxidation (M)
2872.3440	2871.3367	2871.4225	-29.88	170	- 195	1	---	R.ANFSQQCSLRSTGLFVPPSPPLDPEK.V
No match to: 835.4214, 842.4716, 850.5007, 853.4803, 853.4804, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1031.5133, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1368.6882, 1402.7100, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1732.0293, 1732.0293, 1838.8518, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857								

17. [A0A4W2GWY7](#) Mass: 132560 Score: 38 Expect: 24 Matches: 14
Euchromatic histone lysine methyltransferase 1 OS=Bos indicus x Bos taurus OX=30522 GN=EHTM1 PE=4 SV=1

observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4716	841.4643	841.4082	66.6	1095	- 1101	0	---	R.FYGNVSR.F
848.4913	847.4840	847.4222	73.0	486	- 492	1	---	R.METPKSR.E
953.4929	952.4856	952.5342	-50.96	159	- 168	1	---	K.KAPAPGADV.K
1019.6375	1018.6302	1018.5295	98.9	866	- 874	1	---	R.DSDVTLKNK.E
1151.6821	1150.6748	1150.6169	50.4	271	- 279	1	---	K.QRTVIEMFK.S
1211.5695	1210.5622	1210.5587	2.91	1157	- 1166	1	---	K.LFSCRCGSPK.C
1368.6882	1367.6809	1367.6317	36.0	198	- 208	1	---	R.DHEEPKEELSR.G
1475.6868	1474.6795	1474.7086	-19.71	339	- 352	1	---	R.ASKDGVLPADCSQK.V
1479.7338	1478.7265	1478.8358	-73.86	393	- 405	1	---	K.GKPDSPWIKPARK.R
1567.6902	1566.6829	1566.8154	-84.56	645	- 657	1	---	K.QLYFSARQGLQK.V
1732.0293	1731.0220	1730.8675	89.3	1102	- 1115	0	---	R.FINHHCEPNLVPVR.V
1732.0293	1731.0220	1730.8675	89.3	1102	- 1115	0	---	R.FINHHCEPNLVPVR.V
1838.8518	1837.8445	1837.9244	-43.46	273	- 289	1	---	R.TVIEMFKSIHTSTGGSK.G + Oxidation (M)
2872.3440	2871.3367	2871.4185	-28.48	875	- 900	0	---	K.EGETPLQCSLNSQVWSALQVQSALR.D
No match to: 835.4214, 850.5007, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1031.5133, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1368.6882, 1383.6498, 1402.7100, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1734.8334, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969								



18. **A0A4W2E8Y3** Mass: 132257 Score: 36 Expect: 31 Matches: 14
 Euchromatic histone lysine methyltransferase 1 OS=Bos indicus x Bos taurus OX=30522 GN=EHTM1 PE=4 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------|---------------------------------------|
| 842.4716 | 841.4643 | 841.4082 | 66.6 | 1153 | - | 1159 | 0 | R.FYGNVSR.F |
| 848.4913 | 847.4840 | 847.4222 | 73.0 | 486 | - | 492 | 1 | R.METPKSR.E |
| 953.4929 | 952.4856 | 952.5342 | -50.96 | 159 | - | 168 | 1 | K.KAPAPGADV.V |
| 1019.6375 | 1018.6302 | 1018.5295 | 98.9 | 924 | - | 932 | 1 | R.DSDVTLKNN.E |
| 1151.6821 | 1150.6748 | 1150.6169 | 50.4 | 271 | - | 279 | 1 | K.QRTVIEMFK.S |
| 1211.5695 | 1210.5622 | 1210.5288 | 27.6 | 1143 | - | 1152 | 0 | K.DGELYCIDAR.F |
| 1368.6882 | 1367.6809 | 1367.6317 | 36.0 | 198 | - | 208 | 1 | R.DHEEPKEELSR.G |
| 1475.6868 | 1474.6795 | 1474.7086 | -19.71 | 339 | - | 352 | 1 | R.ASKDGVLPDCSQK.V |
| 1479.7338 | 1478.7265 | 1478.8358 | -73.86 | 393 | - | 405 | 1 | K.GKPDSPWIKPARK.R |
| 1567.6902 | 1566.6829 | 1566.8154 | -84.56 | 703 | - | 715 | 1 | K.QLYFSARQGLQK.V |
| 1732.0293 | 1731.0220 | 1730.8675 | 89.3 | 1160 | - | 1173 | 0 | R.FINHHCEPNLVPVR.V |
| 1732.0293 | 1731.0220 | 1730.8675 | 89.3 | 1160 | - | 1173 | 0 | R.FINHHCEPNLVPVR.V |
| 1838.8518 | 1837.8445 | 1837.9244 | -43.46 | 273 | - | 289 | 1 | R.TVIEMFKSITHSTGGSK.G + Oxidation (M) |
| 2872.3440 | 2871.3367 | 2871.4185 | -28.48 | 933 | - | 958 | 0 | K.EGETPLQCSALNSQVWSALQVSQALR.D |
- No match to: 835.4214, 850.5007, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1031.5133, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1383.6498, 1402.7100, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1734.8334, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969
19. **A0A3Q1LPD0** Mass: 132257 Score: 36 Expect: 31 Matches: 14
 Euchromatic histone lysine methyltransferase 1 OS=Bos taurus OX=9913 GN=EHTM1 PE=4 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------|---------------------------------------|
| 842.4716 | 841.4643 | 841.4082 | 66.6 | 1153 | - | 1159 | 0 | R.FYGNVSR.F |
| 848.4913 | 847.4840 | 847.4222 | 73.0 | 486 | - | 492 | 1 | R.METPKSR.E |
| 953.4929 | 952.4856 | 952.5342 | -50.96 | 159 | - | 168 | 1 | K.KAPAPGADV.V |
| 1019.6375 | 1018.6302 | 1018.5295 | 98.9 | 924 | - | 932 | 1 | R.DSDVTLKNN.E |
| 1151.6821 | 1150.6748 | 1150.6169 | 50.4 | 271 | - | 279 | 1 | K.QRTVIEMFK.S |
| 1211.5695 | 1210.5622 | 1210.5288 | 27.6 | 1143 | - | 1152 | 0 | K.DGELYCIDAR.F |
| 1368.6882 | 1367.6809 | 1367.6317 | 36.0 | 198 | - | 208 | 1 | R.DHEEPKEELSR.G |
| 1475.6868 | 1474.6795 | 1474.7086 | -19.71 | 339 | - | 352 | 1 | R.ASKDGVLPDCSQK.V |
| 1479.7338 | 1478.7265 | 1478.8358 | -73.86 | 393 | - | 405 | 1 | K.GKPDSPWIKPARK.R |
| 1567.6902 | 1566.6829 | 1566.8154 | -84.56 | 703 | - | 715 | 1 | K.QLYFSARQGLQK.V |
| 1732.0293 | 1731.0220 | 1730.8675 | 89.3 | 1160 | - | 1173 | 0 | R.FINHHCEPNLVPVR.V |
| 1732.0293 | 1731.0220 | 1730.8675 | 89.3 | 1160 | - | 1173 | 0 | R.FINHHCEPNLVPVR.V |
| 1838.8518 | 1837.8445 | 1837.9244 | -43.46 | 273 | - | 289 | 1 | R.TVIEMFKSITHSTGGSK.G + Oxidation (M) |
| 2872.3440 | 2871.3367 | 2871.4185 | -28.48 | 933 | - | 958 | 0 | K.EGETPLQCSALNSQVWSALQVSQALR.D |
- No match to: 835.4214, 850.5007, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1031.5133, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1383.6498, 1402.7100, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1734.8334, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969
20. **A0A4W2C1C0** Mass: 67085 Score: 36 Expect: 33 Matches: 5
 Heparanase 2 (inactive) OS=Bos indicus x Bos taurus OX=30522 GN=HPSE2 PE=4 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------|---------------------------------|
| 1236.6587 | 1235.6514 | 1235.6584 | -5.63 | 312 | - | 322 | 0 | K.NVIALLDGFMK.V + Oxidation (M) |
| 1300.7963 | 1299.7890 | 1299.7047 | 64.8 | 299 | - | 310 | 0 | R.ASLYGNIGRPR.K |
| 1732.0293 | 1731.0220 | 1730.8587 | 94.3 | 231 | - | 246 | 0 | R.NPNNSWNSSALSLLK.Y |
| 1732.0293 | 1731.0220 | 1730.8587 | 94.3 | 231 | - | 246 | 0 | R.NPNNSWNSSALSLLK.Y |
| 2872.3440 | 2871.3367 | 2871.5640 | -79.16 | 539 | - | 564 | 0 | K.SVQLNGQPLVMVDDGTLPELKPRLR.A |
- No match to: 835.4214, 842.4716, 848.4913, 850.5007, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1031.5133, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1368.6882, 1383.6498, 1402.7100, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969
21. **O46770** Mass: 19686 Score: 35 Expect: 43 Matches: 5
 MHC class I heavy chain (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------|-------------------------------|
| 1279.7057 | 1278.6984 | 1278.5993 | 77.5 | 142 | - | 152 | 0 | K.WEAAGYAEVQR.N |
| 1349.6478 | 1348.6405 | 1348.5983 | 31.3 | 106 | - | 116 | 1 | R.RGFMQYGYDGR.D |
| 1421.6836 | 1420.6763 | 1420.6834 | -4.99 | 127 | - | 139 | 0 | R.SWTAGETAQITK.R |
| 1567.6902 | 1566.6829 | 1566.7137 | -19.61 | 153 | - | 164 | 0 | R.NYLEGECVEWLR.R |
| 2872.3440 | 2871.3367 | 2871.1977 | 48.4 | 78 | - | 103 | 0 | R.GYYNQSEAGSHTLQWMSGCDVGPDR.L |
- No match to: 835.4214, 842.4716, 848.4913, 850.5007, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1031.5133, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1236.6587, 1277.6544, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1368.6882, 1383.6498, 1402.7100, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969
22. **U5TGS8** Mass: 86845 Score: 34 Expect: 48 Matches: 10
 CPXV068 protein OS=Cowpox virus OX=10243 GN=CPXV068 PE=4 SV=1
- | Observed | Mr(expt) | Mr(calc) | ppm | Start | End | Miss | Ions | Peptide |
|-----------|-----------|-----------|--------|-------|-----|------|------|-----------------------------------|
| 842.4716 | 841.4643 | 841.4909 | -31.59 | 511 | - | 518 | 0 | K.IDSIPGLK.T |
| 848.4913 | 847.4840 | 847.4803 | 4.34 | 223 | - | 229 | 0 | R.FLDIVNMK.N |
| 850.5007 | 849.4934 | 849.4266 | 78.7 | 714 | - | 720 | 0 | K.TLSLCEK.V |
| 1368.6882 | 1367.6809 | 1367.5495 | 96.1 | 417 | - | 426 | 1 | K.YGFCPPMMMKR.L + 3 Oxidation (M) |
| 1402.7100 | 1401.7027 | 1401.7292 | -18.90 | 561 | - | 572 | 0 | R.LASYGLYYIPSR.Y |
| 1421.6836 | 1420.6763 | 1420.6544 | 15.4 | 519 | - | 529 | 1 | K.TYNNMKDITYEK.S + Oxidation (M) |
| 1479.7338 | 1478.7265 | 1478.7803 | -36.35 | 511 | - | 523 | 1 | K.IDSIPGLKTYNMK.D |
| 1900.9630 | 1899.9557 | 1899.9149 | 21.5 | 491 | - | 506 | 1 | K.TNRVLCFDSLENSAFK.S |
| 2015.2006 | 2014.1933 | 2014.0292 | 81.5 | 674 | - | 691 | 0 | K.INELLSEPVSGVCIELDK.I |
| 2872.3440 | 2871.3367 | 2871.4793 | -49.66 | 265 | - | 289 | 1 | R.TEDLGIYANIFFEDAIDITKLEITK.T |
- No match to: 835.4214, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1031.5133, 1033.6567, 1033.6567, 1036.5132,

1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1383.6498, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1901.1735, 1993.8977, 2184.3567, 2211.0339, 2215.0857, 2283.0969

23. [A0A4W2CHB4](#) **Mass:** 38688 **Score:** 34 **Expect:** 50 **Matches:** 9

Glutathione S-transferase omega 1 OS=Bos indicus x Bos taurus OX=30522 GN=GSTO1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.5007	849.4934	849.4241	81.6	304	- 310	0	---	K.LWMAAMK.K
870.5096	869.5023	869.5811	-90.54	140	- 146	1	---	K.RTLLVLRL.A
1031.5133	1030.5060	1030.5335	-26.66	205	- 213	0	---	K.LLPGDPYK.A
1279.7057	1278.6984	1278.5874	86.8	236	- 246	1	---	R.TQNKEDCSGLK.E
1300.7963	1299.7890	1299.6969	70.9	68	- 79	1	---	R.ADGCPSLALLRK.I
1402.7100	1401.7027	1401.7715	-49.07	311	- 323	1	---	K.KDPTVSSLLTDVK.T
1421.6836	1420.6763	1420.6631	9.28	129	- 139	1	---	R.VYSMRFCPYAK.R
1732.0293	1731.0220	1730.9679	31.3	111	- 128	1	---	R.SLGKGSAPPGPVPEGLIR.V
1732.0293	1731.0220	1730.9679	31.3	111	- 128	1	---	R.SLGKGSAPPGPVPEGLIR.V

No match to: 835.4214, 842.4716, 848.4913, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1236.6587, 1277.6544, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1368.6882, 1383.6498, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440

24. [A0A4W2FWN4](#) **Mass:** 38719 **Score:** 34 **Expect:** 50 **Matches:** 9

Glutathione S-transferase omega 1 OS=Bos indicus x Bos taurus OX=30522 GN=GSTO1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
850.5007	849.4934	849.4241	81.6	304	- 310	0	---	K.LWMAAMK.K
870.5096	869.5023	869.5811	-90.54	140	- 146	1	---	K.RTLLVLRL.A
1031.5133	1030.5060	1030.5335	-26.66	205	- 213	0	---	K.LLPGDPYK.A
1279.7057	1278.6984	1278.5874	86.8	236	- 246	1	---	R.TQNKEDCSGLK.E
1300.7963	1299.7890	1299.6969	70.9	68	- 79	1	---	R.ADGCPSLALLRK.I
1402.7100	1401.7027	1401.7715	-49.07	311	- 323	1	---	K.KDPTVSSLLTDVK.T
1421.6836	1420.6763	1420.6631	9.28	129	- 139	1	---	R.VYSMRFCPYAK.R
1732.0293	1731.0220	1730.9679	31.3	111	- 128	1	---	R.SLGKGSAPPGPVPEGLIR.V
1732.0293	1731.0220	1730.9679	31.3	111	- 128	1	---	R.SLGKGSAPPGPVPEGLIR.V

No match to: 835.4214, 842.4716, 848.4913, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1236.6587, 1277.6544, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1368.6882, 1383.6498, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440

25. [A0A0K2YTL5](#) **Mass:** 9022 **Score:** 34 **Expect:** 51 **Matches:** 5

Uncharacterized protein OS=Cowpox virus OX=10243 GN=gCPXV0248 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1036.5132	1035.5059	1035.5501	-42.70	72	- 79	0	---	K.FNLYRPNL.-
1131.6577	1130.6504	1130.6270	20.7	31	- 39	0	---	K.YIVLMIHR.V + Oxidation (M)
1277.6544	1276.6471	1276.7292	-64.25	70	- 79	1	---	R.LKFNLYRPNL.-
1334.8298	1333.8225	1333.7275	71.2	58	- 69	0	---	R.STMELILLTASR.L
1334.8298	1333.8226	1333.7275	71.3	58	- 69	0	---	R.STMELILLTASR.L

No match to: 835.4214, 842.4716, 848.4913, 850.5007, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1031.5133, 1033.6567, 1033.6567, 1045.5249, 1051.6622, 1051.6622, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1236.6587, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1349.6478, 1368.6882, 1383.6498, 1402.7100, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969, 2872.3440

26. [O46724](#) **Mass:** 19602 **Score:** 34 **Expect:** 51 **Matches:** 5

MHC class I heavy chain (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1279.7057	1278.6984	1278.5993	77.5	142	- 152	0	---	K.WEAAGYAEVQR.N
1349.6478	1348.6405	1348.5983	31.3	106	- 116	1	---	R.RGFMQYGYDGR.D
1421.6836	1420.6763	1420.6834	-4.99	127	- 139	0	---	R.SWTAGETEAQITK.R
1567.6902	1566.6829	1566.7137	-19.61	153	- 164	0	---	R.NYLEGECVEWLR.R
2872.3440	2871.3367	2871.1977	48.4	78	- 103	0	---	R.GYYNQSEAGSHTLQWMSGCDVGPDGR.L

No match to: 835.4214, 842.4716, 848.4913, 850.5007, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1031.5133, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1236.6587, 1277.6544, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1368.6882, 1383.6498, 1402.7100, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969

27. [O46765](#) **Mass:** 19602 **Score:** 34 **Expect:** 51 **Matches:** 5

MHC class I heavy chain (Fragment) OS=Bos taurus OX=9913 PE=2 SV=1

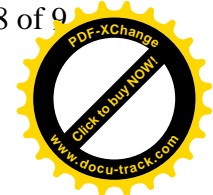
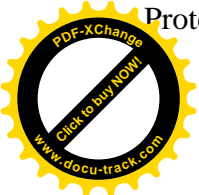
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1279.7057	1278.6984	1278.5993	77.5	142	- 152	0	---	K.WEAAGYAEVQR.N
1349.6478	1348.6405	1348.5983	31.3	106	- 116	1	---	R.RGFMQYGYDGR.D
1421.6836	1420.6763	1420.6834	-4.99	127	- 139	0	---	R.SWTAGETEAQITK.R
1567.6902	1566.6829	1566.7137	-19.61	153	- 164	0	---	R.NYLEGECVEWLR.R
2872.3440	2871.3367	2871.1977	48.4	78	- 103	0	---	R.GYYNQSEAGSHTLQWMSGCDVGPDGR.L

No match to: 835.4214, 842.4716, 848.4913, 850.5007, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 953.4929, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1031.5133, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695, 1234.7560, 1236.6587, 1277.6544, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1368.6882, 1383.6498, 1402.7100, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969

28. [A0A4W2BML3](#) **Mass:** 25099 **Score:** 34 **Expect:** 52 **Matches:** 7

HESX homeobox 1 OS=Bos indicus x Bos taurus OX=30522 GN=HESX1 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
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853.4803 852.4730 852.4130 70.4 132 - 137 0 --- R.ELSWYR.G
853.4804 852.4731 852.4130 70.5 132 - 137 0 --- R.ELSWYR.G
953.4929 952.4856 952.4688 17.7 199 - 206 0 --- R.ESQFLMAK.K
1131.6577 1130.6504 1130.5502 88.6 1 - 9 1 --- -.MQPDSELR.L
1136.6519 1135.6446 1135.6237 18.4 35 - 45 1 --- K.PSGAIGKSLEK.R
1349.6478 1348.6405 1348.6557 -11.29 196 - 206 1 --- R.SHRESQFLMAK.K + Oxidation (M)
1383.6498 1382.6425 1382.6678 -18.27 23 - 34 0 --- K.DTDLHDITTPQK.F
No match to: 835.4214, 842.4716, 848.4913, 850.5007, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828,
972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1031.5133, 1033.6567, 1033.6567, 1036.5132,
1045.5249, 1051.6622, 1051.6622, 1133.6731, 1147.6853, 1151.6821, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1211.5695,
1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1368.6882, 1402.7100,
1421.6836, 1434.8480, 1448.8584, 1448.8584, 1475.6868, 1479.7338, 1567.6902, 1581.7833, 1581.7833, 1617.9998, 1617.9998,
1637.8650, 1707.7130, 1732.0293, 1732.0293, 1734.8334, 1838.8518, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567,
2211.0339, 2215.0857, 2283.0969, 2872.3440

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29. [A0A4W2E8V9](#) Mass: 138235 Score: 34 Expect: 52 Matches: 14

Euchromatic histone lysine methyltransferase 1 OS=Bos indicus x Bos taurus OX=30522 GN=EHTM1 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4716	841.4643	841.4082	66.6	1153	1159	0	---	R.FYGNVSR.F
848.4913	847.4840	847.4222	73.0	486	492	1	---	R.METPKSR.E
953.4929	952.4856	952.5342	-50.96	159	168	1	---	K.KAPAPGADVK.V
1019.6375	1018.6302	1018.5295	98.9	924	932	1	---	R.DSDVTLKKN.E
1151.6821	1150.6748	1150.6169	50.4	271	279	1	---	K.QRTVIEMFK.S
1211.5695	1210.5622	1210.5587	2.91	1215	1224	1	---	K.LFSCRCGSPK.C
1368.6882	1367.6809	1367.6317	36.0	198	208	1	---	R.DHEEPKEELSR.G
1475.6868	1474.6795	1474.7086	-19.71	339	352	1	---	R.ASKDGVLPADCSQK.V
1479.7338	1478.7265	1478.8358	-73.86	393	405	1	---	K.GKPDSPWIKPARK.R
1567.6902	1566.6829	1566.8154	-84.56	703	715	1	---	K.QLYFSARQGLQK.V
1732.0293	1731.0220	1730.8675	89.3	1160	1173	0	---	R.FINHHCEPNLVPVR.V
1732.0293	1731.0220	1730.8675	89.3	1160	1173	0	---	R.FINHHCEPNLVPVR.V
1838.8518	1837.8445	1837.9244	-43.46	273	289	1	---	R.TVIEMFKSITHSTGGSK.G + Oxidation (M)
2872.3440	2871.3367	2871.4185	-28.48	933	958	0	---	K.EGETPLQCASLNSQVWSALQVSQALR.D

No match to: 835.4214, 850.5007, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1031.5133, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1383.6498, 1402.7100, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1734.8334, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969

30. [A0A3Q1MVR5](#) Mass: 138235 Score: 34 Expect: 52 Matches: 14

Euchromatic histone lysine methyltransferase 1 OS=Bos taurus OX=9913 GN=EHTM1 PE=4 SV=1

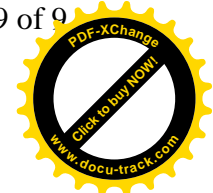
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4716	841.4643	841.4082	66.6	1153	1159	0	---	R.FYGNVSR.F
848.4913	847.4840	847.4222	73.0	486	492	1	---	R.METPKSR.E
953.4929	952.4856	952.5342	-50.96	159	168	1	---	K.KAPAPGADVK.V
1019.6375	1018.6302	1018.5295	98.9	924	932	1	---	R.DSDVTLKKN.E
1151.6821	1150.6748	1150.6169	50.4	271	279	1	---	K.QRTVIEMFK.S
1211.5695	1210.5622	1210.5587	2.91	1215	1224	1	---	K.LFSCRCGSPK.C
1368.6882	1367.6809	1367.6317	36.0	198	208	1	---	R.DHEEPKEELSR.G
1475.6868	1474.6795	1474.7086	-19.71	339	352	1	---	R.ASKDGVLPADCSQK.V
1479.7338	1478.7265	1478.8358	-73.86	393	405	1	---	K.GKPDSPWIKPARK.R
1567.6902	1566.6829	1566.8154	-84.56	703	715	1	---	K.QLYFSARQGLQK.V
1732.0293	1731.0220	1730.8675	89.3	1160	1173	0	---	R.FINHHCEPNLVPVR.V
1732.0293	1731.0220	1730.8675	89.3	1160	1173	0	---	R.FINHHCEPNLVPVR.V
1838.8518	1837.8445	1837.9244	-43.46	273	289	1	---	R.TVIEMFKSITHSTGGSK.G + Oxidation (M)
2872.3440	2871.3367	2871.4185	-28.48	933	958	0	---	K.EGETPLQCASLNSQVWSALQVSQALR.D

No match to: 835.4214, 850.5007, 853.4803, 853.4804, 864.5184, 868.5114, 868.5114, 870.5096, 882.5266, 882.5266, 951.5828, 972.5108, 982.5417, 996.5513, 1007.6395, 1017.6248, 1017.6248, 1019.6375, 1031.5133, 1033.6567, 1033.6567, 1036.5132, 1045.5249, 1051.6622, 1051.6622, 1131.6577, 1133.6731, 1136.6519, 1147.6853, 1165.6888, 1165.6888, 1179.5533, 1194.5757, 1234.7560, 1236.6587, 1277.6544, 1279.7057, 1300.7963, 1302.8082, 1316.8273, 1334.8298, 1334.8298, 1349.6478, 1383.6498, 1402.7100, 1421.6836, 1434.8480, 1448.8584, 1448.8584, 1581.7833, 1581.7833, 1617.9998, 1617.9998, 1637.8650, 1707.7130, 1734.8334, 1900.9630, 1901.1735, 1993.8977, 2015.2006, 2184.3567, 2211.0339, 2215.0857, 2283.0969

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 (835.4214,1+): <no title>
 Query2 (842.4716,1+): <no title>
 Query3 (848.4913,1+): <no title>
 Query4 (850.5007,1+): <no title>
 Query5 (853.4803,1+): <no title>
 Query6 (853.4804,1+): Locus:1..14.0.8
 Query7 (864.5184,1+): <no title>
 Query8 (868.5114,1+): <no title>
 Query9 (868.5114,1+): Locus:1..14.0.10
 Query10 (870.5096,1+): <no title>
 Query11 (882.5266,1+): <no title>
 Query12 (882.5266,1+): Locus:1..14.0.4
 Query13 (951.5828,1+): <no title>
 Query14 (953.4929,1+): <no title>
 Query15 (972.5108,1+): <no title>
 Query16 (982.5417,1+): <no title>
 Query17 (996.5513,1+): <no title>
 Query18 (1007.6395,1+): <no title>
 Query19 (1017.6248,1+): Locus:1..14.0.7
 Query20 (1017.6248,1+): <no title>
 Query21 (1019.6375,1+): <no title>
 Query22 (1031.5133,1+): <no title>
 Query23 (1033.6567,1+): <no title>



Query24 (1033.6567,1+): Locus:1..14.0.11
Query25 (1036.5132,1+): <no title>
Query26 (1045.5249,1+): <no title>
Query27 (1051.6622,1+): <no title>
Query28 (1051.6622,1+): Locus:1..14.0.1
Query29 (1131.6577,1+): <no title>
Query30 (1133.6731,1+): <no title>
Query31 (1136.6519,1+): <no title>
Query32 (1147.6853,1+): <no title>
Query33 (1151.6821,1+): <no title>
Query34 (1165.6888,1+): <no title>
Query35 (1165.6888,1+): Locus:1..14.0.6
Query36 (1179.5533,1+): <no title>
Query37 (1194.5757,1+): <no title>
Query38 (1211.5695,1+): <no title>
Query39 (1234.7560,1+): <no title>
Query40 (1236.6587,1+): <no title>
Query41 (1277.6544,1+): <no title>
Query42 (1279.7057,1+): <no title>
Query43 (1300.7963,1+): <no title>
Query44 (1302.8082,1+): <no title>
Query45 (1316.8273,1+): <no title>
Query46 (1334.8298,1+): <no title>
Query47 (1334.8298,1+): Locus:1..14.0.3
Query48 (1349.6478,1+): <no title>
Query49 (1368.6882,1+): <no title>
Query50 (1383.6498,1+): <no title>
Query51 (1402.7100,1+): <no title>
Query52 (1421.6836,1+): <no title>
Query53 (1434.8480,1+): <no title>
Query54 (1448.8584,1+): <no title>
Query55 (1448.8584,1+): Locus:1..14.0.9
Query56 (1475.6868,1+): <no title>
Query57 (1479.7338,1+): <no title>
Query58 (1567.6902,1+): <no title>
Query59 (1581.7833,1+): <no title>
Query60 (1581.7833,1+): Locus:1..14.0.2
Query61 (1617.9998,1+): Locus:1..14.0.5
Query62 (1617.9998,1+): <no title>
Query63 (1637.8650,1+): <no title>
Query64 (1707.7130,1+): <no title>
Query65 (1732.0293,1+): <no title>
Query66 (1732.0293,1+): Locus:1..14.0.12
Query67 (1734.8334,1+): <no title>
Query68 (1838.8518,1+): <no title>
Query69 (1900.9630,1+): <no title>
Query70 (1901.1735,1+): <no title>
Query71 (1993.8977,1+): <no title>
Query72 (2015.2006,1+): <no title>
Query73 (2184.3567,1+): <no title>
Query74 (2211.0339,1+): <no title>
Query75 (2215.0857,1+): <no title>
Query76 (2283.0969,1+): <no title>
Query77 (2872.3440,1+): <no title>

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