

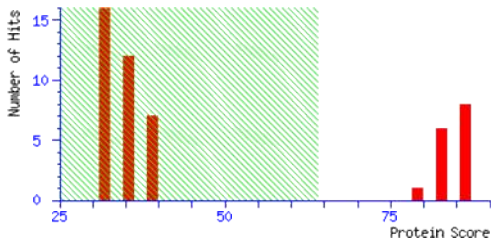
MATRIX SCIENCE

Mascot Search Results

User :  
Email :  
Search title : BAEDW\2020\_3\_5\2020\_3\_5\MSMS 14\M17  
Database : Uniprot\_bovine\_bovine\_20200316 (134392 sequences; 76244912 residues)  
Timestamp : 31 Mar 2020 at 01:07:59 GMT  
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.  
Top Score : 86 for A0A4W2D411, Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1

Mascot Score Histogram

Protein score is -10\*Log(P), where P is the probability that the observed match is a random event.  
Protein scores greater than 64 are significant (p<0.05).  
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Protein Summary Report

Format As Protein Summary (deprecated) Help

Significance threshold p< 0.05 Max. number of hits 30

Preferred taxonomy All entries

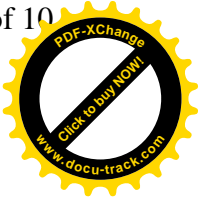
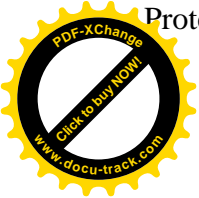
Re-Search All Search Unmatched

Index

Accession	Mass	Score	Description
1. <a href="#">A0A4W2D411</a>	190190	86	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
2. <a href="#">A0A4W2CZQ8</a>	170639	86	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
3. <a href="#">A0A4W2D441</a>	186349	85	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
4. <a href="#">A0A4W2CZN6</a>	192486	85	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
5. <a href="#">A0A4W2EPV7</a>	179159	85	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
6. <a href="#">A0A4W2D408</a>	180682	85	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
7. <a href="#">A0A4W2HFJ5</a>	188690	85	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
8. <a href="#">Q2UVX4</a>	188675	85	Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=2
9. <a href="#">A0A4W2D406</a>	186684	84	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
10. <a href="#">A0A3Q1MGT0</a>	183008	84	Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=1
11. <a href="#">A0A4W2D3Y9</a>	185555	84	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
12. <a href="#">A0A3Q1M2B2</a>	185169	83	Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=1
13. <a href="#">A0A0F6QNP7</a>	188604	83	Complement component 3 OS=Bos taurus OX=9913 GN=C3 PE=2 SV=1
14. <a href="#">A0A4W2EPI5</a>	182918	82	Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1
15. <a href="#">A0A3Q1MHV6</a>	181738	81	Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=1
16. <a href="#">A0A4W2FTD2</a>	57549	40	Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=LOC113883749 PE=3 SV=1
17. <a href="#">A0A4W2BNQ3</a>	57413	40	Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=LOC113883746 PE=3 SV=1
18. <a href="#">A0A4W2HPR9</a>	57408	40	Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=LOC113883749 PE=3 SV=1
19. <a href="#">A0A4W2BMU5</a>	57554	40	Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=LOC113883746 PE=3 SV=1
20. <a href="#">Q3T047</a>	57540	40	Cytochrome P450, family 3, subfamily A, polypeptide 5 OS=Bos taurus OX=9913 GN=CYP3A5 PE=1 SV=1
21. <a href="#">A0A3Q1MUB2</a>	54957	39	Glucosaminyl (N-acetyl) transferase 4 OS=Bos taurus OX=9913 GN=GCNT4 PE=4 SV=1
22. <a href="#">F1MDR5</a>	92495	38	Uncharacterized protein OS=Bos taurus OX=9913 GN=MIA2 PE=4 SV=1
23. <a href="#">Q08DU7</a>	51251	37	mTERF protein (Fragment) OS=Bos taurus OX=9913 GN=MTERF PE=2 SV=1
24. <a href="#">A0A4W2FV66</a>	129413	37	Replication factor C subunit 1 OS=Bos indicus x Bos taurus OX=30522 GN=RFC1 PE=3 SV=1
25. <a href="#">A0A4W2EXE5</a>	129354	36	Replication factor C subunit 1 OS=Bos indicus x Bos taurus OX=30522 GN=RFC1 PE=3 SV=1
26. <a href="#">A0A4W2BTQ2</a>	97692	36	Kinesin-like protein OS=Bos indicus x Bos taurus OX=30522 GN=KIF9 PE=3 SV=1
27. <a href="#">A0A0K2YTL5</a>	9022	36	Uncharacterized protein OS=Cowpox virus OX=10243 GN=gCPXV0248 PE=4 SV=1
28. <a href="#">A0A3Q1N5S1</a>	128941	36	Replication factor C subunit 1 OS=Bos taurus OX=9913 GN=RFC1 PE=3 SV=1
29. <a href="#">A0A4W2H4H4</a>	50468	35	Interferon induced protein 44 like OS=Bos indicus x Bos taurus OX=30522 GN=IFI44L PE=4 SV=1
30. <a href="#">A0A4W2BTP7</a>	104127	35	Kinesin-like protein OS=Bos indicus x Bos taurus OX=30522 GN=KIF9 PE=3 SV=1

Results List

1.	<a href="#">A0A4W2D411</a>	Mass: 190190	Score: 86	Expect: 0.00032	Matches: 18
Complement C3 OS=Bos indicus x Bos taurus OX=30522 GN=C3 PE=4 SV=1					
	Observed	Mr(expt)	Mr(calc)	ppm	Start End Miss Ions Peptide
	833.4543	832.4470	832.4807	-40.43	868 - 874 0 --- R.LPYSVVVR.N
	833.4543	832.4471	832.4807	-40.37	868 - 874 0 29 R.LPYSVVVR.N
	848.4947	847.4874	847.4400	56.0	1453 - 1460 0 --- K.TLSTGVDR.Y
	850.5049	849.4976	849.4266	83.6	704 - 710 0 --- R.SVQLMEK.R + Oxidation (M)
	864.5046	863.4973	863.4939	3.99	823 - 829 0 --- K.LMNVFLK.D
	887.4306	886.4233	886.4508	-31.02	875 - 881 0 --- R.NEQVEIR.A
	912.4536	911.4463	911.4865	-44.04	882 - 888 0 --- R.AILYNYR.E
	912.4536	911.4463	911.4865	-44.03	882 - 888 0 28 R.AILYNYR.E
	996.5558	995.5485	995.4672	81.7	715 - 723 0 --- K.AGQYSSDLR.K
	1090.4866	1089.4793	1089.4873	-7.34	655 - 665 0 --- K.ADICTPGSGR.N
	1164.6057	1163.5984	1163.6411	-36.67	915 - 924 0 --- R.HQQTITIPAR.S
	1349.6270	1348.6197	1348.6809	-45.38	743 - 754 0 --- R.AQPILQGDACVK.A



1420.6680	1419.6607	1419.7147	-37.99	947	-	959	0	---	K.AAVYNHFISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	521	-	531	1	---	R.YYTYMIMNKGK.L + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	897	-	912	0	---	R.VELLYNPAFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	797	-	812	0	---	R.SQFPESWLWTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	895	-	912	1	---	K.VRVELLYNPAFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	847	-	867	0	---	K.GICVADPYEVTVMQDFFIDLR.L
No match to: 842.4758, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456									

2. [A0A4W2CZQ8](#) Mass: 170639 Score: 86 Expect: 0.00033 Matches: 18

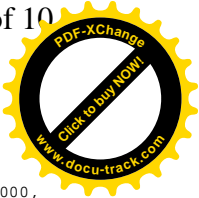
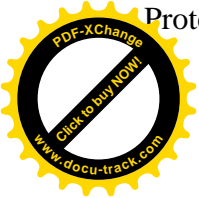
Complement	C3	OS=Bos	indicus x Bos taurus	OX=30522	GN=C3	PE=4	SV=1		
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
833.4543	832.4470	832.4807	-40.43	803	-	809	0	---	R.LPYSVVR.N
833.4543	832.4471	832.4807	-40.37	803	-	809	0	29	R.LPYSVVR.N
848.4947	847.4874	847.4400	56.0	1281	-	1288	0	---	K.TLSTGVDR.Y
850.5049	849.4976	849.4266	83.6	639	-	645	0	---	R.SVQLMEK.R + Oxidation (M)
864.5046	863.4973	863.4939	3.99	758	-	764	0	---	K.LMNVFLK.D
887.4306	886.4233	886.4508	-31.02	810	-	816	0	---	R.NEQVEIR.A
912.4536	911.4463	911.4865	-44.04	817	-	823	0	---	R.AILYNYR.E
912.4536	911.4463	911.4865	-44.03	817	-	823	0	28	R.AILYNYR.E
996.5558	995.5485	995.4672	81.7	650	-	658	0	---	K.AGQYSSDLR.K
1090.4866	1089.4793	1089.4873	-7.34	590	-	600	0	---	K.ADIGCTPGSGR.N
1164.6057	1163.5984	1163.6411	-36.67	850	-	859	0	---	R.HQQTITIPAR.S
1349.6270	1348.6197	1348.6809	-45.38	678	-	689	0	---	R.AQFILQGDACVK.A
1420.6680	1419.6607	1419.7147	-37.99	882	-	894	0	---	K.AAVYNHFISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	487	-	497	1	---	R.YYTYMIMNKGK.L + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	832	-	847	0	---	R.VELLYNPAFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	732	-	747	0	---	R.SQFPESWLWTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	830	-	847	1	---	K.VRVELLYNPAFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	782	-	802	0	---	K.GICVADPYEVTVMQDFFIDLR.L
No match to: 842.4758, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456									

3. [A0A4W2D441](#) Mass: 186349 Score: 85 Expect: 0.00039 Matches: 18

Complement	C3	OS=Bos	indicus x Bos taurus	OX=30522	GN=C3	PE=4	SV=1		
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
833.4543	832.4470	832.4807	-40.43	834	-	840	0	---	R.LPYSVVR.N
833.4543	832.4471	832.4807	-40.37	834	-	840	0	29	R.LPYSVVR.N
848.4947	847.4874	847.4400	56.0	1419	-	1426	0	---	K.TLSTGVDR.Y
850.5049	849.4976	849.4266	83.6	670	-	676	0	---	R.SVQLMEK.R + Oxidation (M)
864.5046	863.4973	863.4939	3.99	789	-	795	0	---	K.LMNVFLK.D
887.4306	886.4233	886.4508	-31.02	841	-	847	0	---	R.NEQVEIR.A
912.4536	911.4463	911.4865	-44.04	848	-	854	0	---	R.AILYNYR.E
912.4536	911.4463	911.4865	-44.03	848	-	854	0	28	R.AILYNYR.E
996.5558	995.5485	995.4672	81.7	681	-	689	0	---	K.AGQYSSDLR.K
1090.4866	1089.4793	1089.4873	-7.34	621	-	631	0	---	K.ADIGCTPGSGR.N
1164.6057	1163.5984	1163.6411	-36.67	881	-	890	0	---	R.HQQTITIPAR.S
1349.6270	1348.6197	1348.6809	-45.38	709	-	720	0	---	R.AQFILQGDACVK.A
1420.6680	1419.6607	1419.7147	-37.99	913	-	925	0	---	K.AAVYNHFISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	487	-	497	1	---	R.YYTYMIMNKGK.L + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	863	-	878	0	---	R.VELLYNPAFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	763	-	778	0	---	R.SQFPESWLWTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	861	-	878	1	---	K.VRVELLYNPAFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	813	-	833	0	---	K.GICVADPYEVTVMQDFFIDLR.L
No match to: 842.4758, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456									

4. [A0A4W2CZN6](#) Mass: 192486 Score: 85 Expect: 0.00039 Matches: 18

Complement	C3	OS=Bos	indicus x Bos taurus	OX=30522	GN=C3	PE=4	SV=1		
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
833.4543	832.4470	832.4807	-40.43	868	-	874	0	---	R.LPYSVVR.N
833.4543	832.4471	832.4807	-40.37	868	-	874	0	29	R.LPYSVVR.N
848.4947	847.4874	847.4400	56.0	1453	-	1460	0	---	K.TLSTGVDR.Y
850.5049	849.4976	849.4266	83.6	704	-	710	0	---	R.SVQLMEK.R + Oxidation (M)
864.5046	863.4973	863.4939	3.99	823	-	829	0	---	K.LMNVFLK.D
887.4306	886.4233	886.4508	-31.02	875	-	881	0	---	R.NEQVEIR.A
912.4536	911.4463	911.4865	-44.04	882	-	888	0	---	R.AILYNYR.E
912.4536	911.4463	911.4865	-44.03	882	-	888	0	28	R.AILYNYR.E
996.5558	995.5485	995.4672	81.7	715	-	723	0	---	K.AGQYSSDLR.K
1090.4866	1089.4793	1089.4873	-7.34	655	-	665	0	---	K.ADIGCTPGSGR.N
1164.6057	1163.5984	1163.6411	-36.67	915	-	924	0	---	R.HQQTITIPAR.S
1349.6270	1348.6197	1348.6809	-45.38	743	-	754	0	---	R.AQFILQGDACVK.A
1420.6680	1419.6607	1419.7147	-37.99	947	-	959	0	---	K.AAVYNHFISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	521	-	531	1	---	R.YYTYMIMNKGK.L + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	897	-	912	0	---	R.VELLYNPAFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	797	-	812	0	---	R.SQFPESWLWTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	895	-	912	1	---	K.VRVELLYNPAFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	847	-	867	0	---	K.GICVADPYEVTVMQDFFIDLR.L



No match to: 842.4758, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456

5. [A0A4W2EPV7](#) Mass: 179159 Score: 85 Expect: 0.00041 Matches: 18

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4807	-40.43	803	-	809	0	R.LPYSVVR.N
833.4543	832.4471	832.4807	-40.37	803	-	809	0	R.LPYSVVR.N
848.4947	847.4874	847.4400	56.0	1355	-	1362	0	K.TLSTGVDR.Y
850.5049	849.4976	849.4266	83.6	639	-	645	0	R.SVQLMEK.R + Oxidation (M)
864.5046	863.4973	863.4939	3.99	758	-	764	0	K.LMNVFLK.D
887.4306	886.4233	886.4508	-31.02	810	-	816	0	R.NEQVEIR.A
912.4536	911.4463	911.4865	-44.04	817	-	823	0	R.AILYNYR.E
912.4536	911.4463	911.4865	-44.03	817	-	823	0	R.AILYNYR.E
996.5558	995.5485	995.4672	81.7	650	-	658	0	K.AGQYSSDLR.K
1090.4866	1089.4793	1089.4873	-7.34	590	-	600	0	K.ADIGCTPGSGR.N
1164.6057	1163.5984	1163.6411	-36.67	850	-	859	0	R.HQQTITIPAR.S
1349.6270	1348.6197	1348.6809	-45.38	678	-	689	0	R.AQFILQGDACVK.A
1420.6680	1419.6607	1419.7147	-37.99	882	-	894	0	K.AAVYNHFISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	487	-	497	1	R.YITYMIMNKGL + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	832	-	847	0	R.VELLYNPAPFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	732	-	747	0	R.SQFPESLWLTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	830	-	847	1	K.VRVVELLYNPAPFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	782	-	802	0	K.GICVADPYEVTVMQDFFIDLR.L

No match to: 842.4758, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456

6. [A0A4W2D408](#) Mass: 180682 Score: 85 Expect: 0.00046 Matches: 18

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4807	-40.43	803	-	809	0	R.LPYSVVR.N
833.4543	832.4471	832.4807	-40.37	803	-	809	0	R.LPYSVVR.N
848.4947	847.4874	847.4400	56.0	1368	-	1375	0	K.TLSTGVDR.Y
850.5049	849.4976	849.4266	83.6	639	-	645	0	R.SVQLMEK.R + Oxidation (M)
864.5046	863.4973	863.4939	3.99	758	-	764	0	K.LMNVFLK.D
887.4306	886.4233	886.4508	-31.02	810	-	816	0	R.NEQVEIR.A
912.4536	911.4463	911.4865	-44.04	817	-	823	0	R.AILYNYR.E
912.4536	911.4463	911.4865	-44.03	817	-	823	0	R.AILYNYR.E
996.5558	995.5485	995.4672	81.7	650	-	658	0	K.AGQYSSDLR.K
1090.4866	1089.4793	1089.4873	-7.34	590	-	600	0	K.ADIGCTPGSGR.N
1164.6057	1163.5984	1163.6411	-36.67	850	-	859	0	R.HQQTITIPAR.S
1349.6270	1348.6197	1348.6809	-45.38	678	-	689	0	R.AQFILQGDACVK.A
1420.6680	1419.6607	1419.7147	-37.99	882	-	894	0	K.AAVYNHFISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	487	-	497	1	R.YITYMIMNKGL + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	832	-	847	0	R.VELLYNPAPFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	732	-	747	0	R.SQFPESLWLTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	830	-	847	1	K.VRVVELLYNPAPFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	782	-	802	0	K.GICVADPYEVTVMQDFFIDLR.L

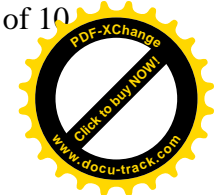
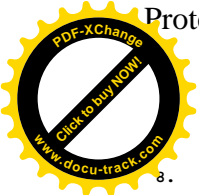
No match to: 842.4758, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456

7. [A0A4W2HFJ5](#) Mass: 188690 Score: 85 Expect: 0.00047 Matches: 18

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4807	-40.43	834	-	840	0	R.LPYSVVR.N
833.4543	832.4471	832.4807	-40.37	834	-	840	0	R.LPYSVVR.N
848.4947	847.4874	847.4400	56.0	1419	-	1426	0	K.TLSTGVDR.Y
850.5049	849.4976	849.4266	83.6	670	-	676	0	R.SVQLMEK.R + Oxidation (M)
864.5046	863.4973	863.4939	3.99	789	-	795	0	K.LMNVFLK.D
887.4306	886.4233	886.4508	-31.02	841	-	847	0	R.NEQVEIR.A
912.4536	911.4463	911.4865	-44.04	848	-	854	0	R.AILYNYR.E
912.4536	911.4463	911.4865	-44.03	848	-	854	0	R.AILYNYR.E
996.5558	995.5485	995.4672	81.7	681	-	689	0	K.AGQYSSDLR.K
1090.4866	1089.4793	1089.4873	-7.34	621	-	631	0	K.ADIGCTPGSGR.N
1164.6057	1163.5984	1163.6411	-36.67	881	-	890	0	R.HQQTITIPAR.S
1349.6270	1348.6197	1348.6809	-45.38	709	-	720	0	R.AQFILQGDACVK.A
1420.6680	1419.6607	1419.7147	-37.99	913	-	925	0	K.AAVYNHFISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	487	-	497	1	R.YITYMIMNKGL + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	863	-	878	0	R.VELLYNPAPFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	763	-	778	0	R.SQFPESLWLTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	861	-	878	1	K.VRVVELLYNPAPFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	813	-	833	0	K.GICVADPYEVTVMQDFFIDLR.L

No match to: 842.4758, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456



8.

**Q2UVX4** Mass: 188675 Score: 85 Expect: 0.00047 Matches: 18

Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=2

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4807	-40.43	834	-	840	0	R.LPYSVVR.N
833.4543	832.4471	832.4807	-40.37	834	-	840	0	29 R.LPYSVVR.N
848.4947	847.4874	847.4400	56.0	1419	-	1426	0	K.TLSTGVDR.Y
850.5049	849.4976	849.4266	83.6	670	-	676	0	R.SVQLMEK.R + Oxidation (M)
864.5046	863.4973	863.4939	3.99	789	-	795	0	K.LMNVFLK.D
887.4306	886.4233	886.4508	-31.02	841	-	847	0	R.NEQVEIR.A
912.4536	911.4463	911.4865	-44.04	848	-	854	0	R.AILYNYR.E
912.4536	911.4463	911.4865	-44.03	848	-	854	0	28 R.AILYNYR.E
996.5558	995.5485	995.4672	81.7	681	-	689	0	K.AGQYSSDLR.K
1090.4866	1089.4793	1089.4873	-7.34	621	-	631	0	K.ADIGCTPGSGR.N
1164.6057	1163.5984	1163.6411	-36.67	881	-	890	0	R.HQQTITIPAR.S
1349.6270	1348.6197	1348.6809	-45.38	709	-	720	0	R.AQFILQGDACVK.A
1420.6680	1419.6607	1419.7147	-37.99	913	-	925	0	K.AAVYNHFISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	487	-	497	1	R.YITYMIMNKGK.L + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	863	-	878	0	R.VELLYNPAFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	763	-	778	0	R.SQFPESWLWTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	861	-	878	1	K.VRVELLYNPAFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	813	-	833	0	K.GICVADPYEVTVMQDFFIDLR.L

No match to: 842.4758, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456

9.

**AOA4W2D406** Mass: 186684 Score: 84 Expect: 0.00056 Matches: 18

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4807	-40.43	837	-	843	0	R.LPYSVVR.N
833.4543	832.4471	832.4807	-40.37	837	-	843	0	29 R.LPYSVVR.N
848.4947	847.4874	847.4400	56.0	1422	-	1429	0	K.TLSTGVDR.Y
850.5049	849.4976	849.4266	83.6	673	-	679	0	R.SVQLMEK.R + Oxidation (M)
864.5046	863.4973	863.4939	3.99	792	-	798	0	K.LMNVFLK.D
887.4306	886.4233	886.4508	-31.02	844	-	850	0	R.NEQVEIR.A
912.4536	911.4463	911.4865	-44.04	851	-	857	0	R.AILYNYR.E
912.4536	911.4463	911.4865	-44.03	851	-	857	0	28 R.AILYNYR.E
996.5558	995.5485	995.4672	81.7	684	-	692	0	K.AGQYSSDLR.K
1090.4866	1089.4793	1089.4873	-7.34	624	-	634	0	K.ADIGCTPGSGR.N
1164.6057	1163.5984	1163.6411	-36.67	884	-	893	0	R.HQQTITIPAR.S
1349.6270	1348.6197	1348.6809	-45.38	712	-	723	0	R.AQFILQGDACVK.A
1420.6680	1419.6607	1419.7147	-37.99	916	-	928	0	K.AAVYNHFISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	521	-	531	1	R.YITYMIMNKGK.L + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	866	-	881	0	R.VELLYNPAFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	766	-	781	0	R.SQFPESWLWTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	864	-	881	1	K.VRVELLYNPAFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	816	-	836	0	K.GICVADPYEVTVMQDFFIDLR.L

No match to: 842.4758, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456

10.

**AOA3Q1MGTO** Mass: 183008 Score: 84 Expect: 0.00056 Matches: 18

Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4807	-40.43	803	-	809	0	R.LPYSVVR.N
833.4543	832.4471	832.4807	-40.37	803	-	809	0	29 R.LPYSVVR.N
848.4947	847.4874	847.4400	56.0	1368	-	1375	0	K.TLSTGVDR.Y
850.5049	849.4976	849.4266	83.6	639	-	645	0	R.SVQLMEK.R + Oxidation (M)
864.5046	863.4973	863.4939	3.99	758	-	764	0	K.LMNVFLK.D
887.4306	886.4233	886.4508	-31.02	810	-	816	0	R.NEQVEIR.A
912.4536	911.4463	911.4865	-44.04	817	-	823	0	R.AILYNYR.E
912.4536	911.4463	911.4865	-44.03	817	-	823	0	28 R.AILYNYR.E
996.5558	995.5485	995.4672	81.7	650	-	658	0	K.AGQYSSDLR.K
1090.4866	1089.4793	1089.4873	-7.34	590	-	600	0	K.ADIGCTPGSGR.N
1164.6057	1163.5984	1163.6411	-36.67	850	-	859	0	R.HQQTITIPAR.S
1349.6270	1348.6197	1348.6809	-45.38	678	-	689	0	R.AQFILQGDACVK.A
1420.6680	1419.6607	1419.7147	-37.99	882	-	894	0	K.AAVYNHFISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	487	-	497	1	R.YITYMIMNKGK.L + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	832	-	847	0	R.VELLYNPAFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	732	-	747	0	R.SQFPESWLWTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	830	-	847	1	K.VRVELLYNPAFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	782	-	802	0	K.GICVADPYEVTVMQDFFIDLR.L

No match to: 842.4758, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456

11.

**AOA4W2D3Y9** Mass: 185555 Score: 84 Expect: 0.0006 Matches: 18

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

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4807	-40.43	837	-	843	0	R.LPYSVVR.N
833.4543	832.4471	832.4807	-40.37	837	-	843	0	29 R.LPYSVVR.N

848.4947	847.4874	847.4400	56.0	1422	-	1429	0	---	K.TLSTGVDR.Y
850.5049	849.4976	849.4266	83.6	673	-	679	0	---	R.SVQLMEK.R + Oxidation (M)
864.5046	863.4973	863.4939	3.99	792	-	798	0	---	K.LMNVFLK.D
887.4306	886.4233	886.4508	-31.02	844	-	850	0	---	R.NEQVEIR.A
912.4536	911.4463	911.4865	-44.04	851	-	857	0	---	R.AILYNYR.E
912.4536	911.4463	911.4865	-44.03	851	-	857	0	28	R.AILYNYR.E
996.5558	995.5485	995.4672	81.7	684	-	692	0	---	K.AGQYSSDLR.K
1090.4866	1089.4793	1089.4873	-7.34	624	-	634	0	---	K.ADIGCTPGSGR.N
1164.6057	1163.5984	1163.6411	-36.67	884	-	893	0	---	R.HQQTITIPAR.S
1349.6270	1348.6197	1348.6809	-45.38	712	-	723	0	---	R.AQFILQGDACVK.A
1420.6680	1419.6607	1419.7147	-37.99	916	-	928	0	---	K.AAVYNHFISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	521	-	531	1	---	R.YITYMIMNKGK.L + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	866	-	881	0	---	R.VELLYNPAFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	766	-	781	0	---	R.SQFPESWLWTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	864	-	881	1	---	K.VRVELLYNPAFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	816	-	836	0	---	K.GICVADPYEVTVMQDFFIDLR.L
No match to: 842.4758, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456									

12. AOA3Q1M2B2 Mass: 185169 Score: 83 Expect: 0.00072 Matches: 18

Complement	C3	OS=Bos	taurus	OX=9913	GN=C3	PE=1	SV=1		
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
833.4543	832.4470	832.4807	-40.43	803	-	809	0	---	R.LPYSVVR.N
833.4543	832.4471	832.4807	-40.37	803	-	809	0	29	R.LPYSVVR.N
848.4947	847.4874	847.4400	56.0	1388	-	1395	0	---	K.TLSTGVDR.Y
850.5049	849.4976	849.4266	83.6	639	-	645	0	---	R.SVQLMEK.R + Oxidation (M)
864.5046	863.4973	863.4939	3.99	758	-	764	0	---	K.LMNVFLK.D
887.4306	886.4233	886.4508	-31.02	810	-	816	0	---	R.NEQVEIR.A
912.4536	911.4463	911.4865	-44.04	817	-	823	0	---	R.AILYNYR.E
912.4536	911.4463	911.4865	-44.03	817	-	823	0	28	R.AILYNYR.E
996.5558	995.5485	995.4672	81.7	650	-	658	0	---	K.AGQYSSDLR.K
1090.4866	1089.4793	1089.4873	-7.34	590	-	600	0	---	K.ADIGCTPGSGR.N
1164.6057	1163.5984	1163.6411	-36.67	850	-	859	0	---	R.HQQTITIPAR.S
1349.6270	1348.6197	1348.6809	-45.38	678	-	689	0	---	R.AQFILQGDACVK.A
1420.6680	1419.6607	1419.7147	-37.99	882	-	894	0	---	K.AAVYNHFISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	487	-	497	1	---	R.YITYMIMNKGK.L + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	832	-	847	0	---	R.VELLYNPAFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	732	-	747	0	---	R.SQFPESWLWTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	830	-	847	1	---	K.VRVELLYNPAFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	782	-	802	0	---	K.GICVADPYEVTVMQDFFIDLR.L
No match to: 842.4758, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456									

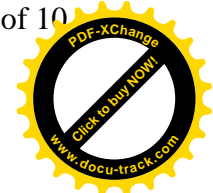
13. AOA0F6QNP7 Mass: 188604 Score: 83 Expect: 0.00074 Matches: 18

Complement	component	3	OS=Bos	taurus	OX=9913	GN=C3	PE=2	SV=1		
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide		
833.4543	832.4470	832.4807	-40.43	834	-	840	0	---	R.LPYSVVR.N	
833.4543	832.4471	832.4807	-40.37	834	-	840	0	29	R.LPYSVVR.N	
848.4947	847.4874	847.4400	56.0	1419	-	1426	0	---	K.TLSTGVDR.Y	
850.5049	849.4976	849.4266	83.6	670	-	676	0	---	R.SVQLMEK.R + Oxidation (M)	
853.4832	852.4759	852.4779	-2.32	789	-	795	0	---	K.LMSVFLK.D + Oxidation (M)	
887.4306	886.4233	886.4508	-31.02	841	-	847	0	---	R.NEQVEIR.A	
912.4536	911.4463	911.4865	-44.04	848	-	854	0	---	R.AILYNYR.E	
912.4536	911.4463	911.4865	-44.03	848	-	854	0	28	R.AILYNYR.E	
996.5558	995.5485	995.4672	81.7	681	-	689	0	---	K.AGQYSSDLR.K	
1090.4866	1089.4793	1089.4873	-7.34	621	-	631	0	---	K.ADIGCTPGSGR.N	
1164.6057	1163.5984	1163.6411	-36.67	881	-	890	0	---	R.HQQTITIPAR.S	
1349.6270	1348.6197	1348.6809	-45.38	709	-	720	0	---	R.AQFILQGDACVK.A	
1420.6680	1419.6607	1419.7147	-37.99	913	-	925	0	---	K.AAVYNHFISDGVK.K	
1427.7352	1426.7279	1426.6625	45.9	487	-	497	1	---	R.YITYMIMNKGK.L + Oxidation (M)	
1796.8849	1795.8776	1795.9178	-22.39	863	-	878	0	---	R.VELLYNPAFCSLATAK.K	
1977.9272	1976.9199	1976.9884	-34.62	763	-	778	0	---	R.SQFPESWLWTVIDLK.Q	
2052.0193	2051.0120	2051.0874	-36.73	861	-	878	1	---	K.VRVELLYNPAFCSLATAK.K	
2488.1152	2487.1079	2487.1814	-29.56	813	-	833	0	---	K.GICVADPYEVTVMQDFFIDLR.L	
No match to: 842.4758, 853.4832, 855.4396, 864.5046, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456										

14. AOA4W2EP15 Mass: 182918 Score: 82 Expect: 0.00077 Matches: 17

Complement	C3	OS=Bos	indicus x Bos	taurus	OX=30522	GN=C3	PE=4	SV=1		
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide		
833.4543	832.4470	832.4807	-40.43	834	-	840	0	---	R.LPYSVVR.N	
833.4543	832.4471	832.4807	-40.37	834	-	840	0	29	R.LPYSVVR.N	
850.5049	849.4976	849.4266	83.6	670	-	676	0	---	R.SVQLMEK.R + Oxidation (M)	
864.5046	863.4973	863.4939	3.99	789	-	795	0	---	K.LMNVFLK.D	
887.4306	886.4233	886.4508	-31.02	841	-	847	0	---	R.NEQVEIR.A	
912.4536	911.4463	911.4865	-44.04	848	-	854	0	---	R.AILYNYR.E	
912.4536	911.4463	911.4865	-44.03	848	-	854	0	28	R.AILYNYR.E	
996.5558	995.5485	995.4672	81.7	681	-	689	0	---	K.AGQYSSDLR.K	





1090.4866 1089.4793 1089.4873 -7.34 621 - 631 0 --- K.ADIGCTPGSGR.N  
 1164.6057 1163.5984 1163.6411 -36.67 881 - 890 0 --- R.HQQTITIPAR.S  
 1349.6270 1348.6197 1348.6809 -45.38 709 - 720 0 --- R.AQFILQGDACVK.A  
 1420.6680 1419.6607 1419.7147 -37.99 913 - 925 0 --- K.AAVYNHFIISDGVK.K  
 1427.7352 1426.7279 1426.6625 45.9 487 - 497 1 --- R.YYTYMIMNKGK.L + Oxidation (M)  
 1796.8849 1795.8776 1795.9178 -22.39 863 - 878 0 --- R.VELLYNPAFCSLATAK.K  
 1977.9272 1976.9199 1976.9884 -34.62 763 - 778 0 --- R.SQFPESWLWTVIDLK.Q  
 2052.0193 2051.0120 2051.0874 -36.73 861 - 878 1 --- K.VRVELLYNPAFCSLATAK.K  
 2488.1152 2487.1079 2487.1814 -29.56 813 - 833 0 --- K.GICVADPYEVTVMQDFFIDL.R

**No match to:** 842.4758, 848.4947, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456

15. [A0A3Q1MHV6](#) Mass: 181738 Score: 81 Expect: 0.0011 Matches: 17

Complement C3 OS=Bos taurus OX=9913 GN=C3 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4807	-40.43	803	-	809	0	R.LPYSVVR.N
833.4543	832.4471	832.4807	-40.37	803	-	809	0	R.LPYSVVR.N
850.5049	849.4976	849.4266	83.6	639	-	645	0	R.SVQLMEK.R + Oxidation (M)
864.5046	863.4973	863.4939	3.99	758	-	764	0	K.LMNVFLK.D
887.4306	886.4233	886.4508	-31.02	810	-	816	0	R.NEQVEIR.A
912.4536	911.4463	911.4865	-44.04	817	-	823	0	R.AILYNYR.E
912.4536	911.4463	911.4865	-44.03	817	-	823	0	R.AILYNYR.E
996.5558	995.5485	995.4672	81.7	650	-	658	0	K.AGQYSSDLR.K
1090.4866	1089.4793	1089.4873	-7.34	590	-	600	0	K.ADIGCTPGSGR.N
1164.6057	1163.5984	1163.6411	-36.67	850	-	859	0	R.HQQTITIPAR.S
1349.6270	1348.6197	1348.6809	-45.38	678	-	689	0	R.AQFILQGDACVK.A
1420.6680	1419.6607	1419.7147	-37.99	882	-	894	0	K.AAVYNHFIISDGVK.K
1427.7352	1426.7279	1426.6625	45.9	487	-	497	1	R.YYTYMIMNKGK.L + Oxidation (M)
1796.8849	1795.8776	1795.9178	-22.39	832	-	847	0	R.VELLYNPAFCSLATAK.K
1977.9272	1976.9199	1976.9884	-34.62	732	-	747	0	R.SQFPESWLWTVIDLK.Q
2052.0193	2051.0120	2051.0874	-36.73	830	-	847	1	K.VRVELLYNPAFCSLATAK.K
2488.1152	2487.1079	2487.1814	-29.56	782	-	802	0	K.GICVADPYEVTVMQDFFIDL.R

**No match to:** 842.4758, 848.4947, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1383.6307, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1796.8849, 1838.8502, 1901.1791, 1993.9021, 2211.0298, 2283.1060, 2398.9456

16. [A0A4W2FTD2](#) Mass: 57549 Score: 40 Expect: 13 Matches: 5

Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=LOC113883749 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4629	-19.10	366	-	372	0	R.MFPIAVR.L
833.4543	832.4471	832.4629	-19.04	366	-	372	0	R.MFPIAVR.L
1151.6833	1150.6760	1150.6234	45.7	131	-	141	0	R.TLLSPTFTSGK.L
1193.5681	1192.5608	1192.6452	-70.74	380	-	390	0	K.DVEIHGVSIPIK.G
2052.0193	2051.0120	2051.1680	-76.05	36	-	54	0	K.LGVPGPRPLPLFGNVLSYR.K

**No match to:** 842.4758, 848.4947, 850.5049, 853.4832, 855.4396, 864.5046, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 887.4306, 892.9702, 912.4536, 912.4536, 951.5852, 969.4808, 973.4983, 996.5558, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1090.4866, 1131.6697, 1157.5516, 1164.6057, 1165.6611, 1165.6611, 1179.5520, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1349.6270, 1351.6090, 1365.5970, 1383.6307, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1796.8849, 1838.8502, 1901.1791, 1977.9272, 1993.9021, 2211.0298, 2283.1060, 2398.9456, 2488.1152

17. [A0A4W2BNQ3](#) Mass: 57413 Score: 40 Expect: 13 Matches: 5

Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=LOC113883746 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4629	-19.10	366	-	372	0	R.MFPIAVR.L
833.4543	832.4471	832.4629	-19.04	366	-	372	0	R.MFPIAVR.L
1151.6833	1150.6760	1150.6234	45.7	131	-	141	0	R.TLLSPTFTSGK.L
1193.5681	1192.5608	1192.6452	-70.74	380	-	390	0	K.DVEIHGVSIPIK.G
2052.0193	2051.0120	2051.1680	-76.05	36	-	54	0	K.LGVPGPRPLPLFGNVLSYR.K

**No match to:** 842.4758, 848.4947, 850.5049, 853.4832, 855.4396, 864.5046, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 887.4306, 892.9702, 912.4536, 912.4536, 951.5852, 969.4808, 973.4983, 996.5558, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1090.4866, 1131.6697, 1157.5516, 1164.6057, 1165.6611, 1165.6611, 1179.5520, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1349.6270, 1351.6090, 1365.5970, 1383.6307, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1796.8849, 1838.8502, 1901.1791, 1977.9272, 1993.9021, 2211.0298, 2283.1060, 2398.9456, 2488.1152

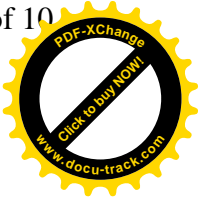
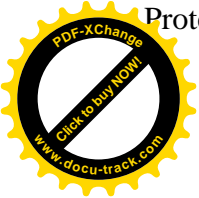
18. [A0A4W2HPR9](#) Mass: 57408 Score: 40 Expect: 13 Matches: 5

Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=LOC113883749 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4629	-19.10	366	-	372	0	R.MFPIAVR.L
833.4543	832.4471	832.4629	-19.04	366	-	372	0	R.MFPIAVR.L
1151.6833	1150.6760	1150.6234	45.7	131	-	141	0	R.TLLSPTFTSGK.L
1193.5681	1192.5608	1192.6452	-70.74	380	-	390	0	K.DVEIHGVSIPIK.G
2052.0193	2051.0120	2051.1680	-76.05	36	-	54	0	K.LGVPGPRPLPLFGNVLSYR.K

**No match to:** 842.4758, 848.4947, 850.5049, 853.4832, 855.4396, 864.5046, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 887.4306, 892.9702, 912.4536, 912.4536, 951.5852, 969.4808, 973.4983, 996.5558, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1090.4866, 1131.6697, 1157.5516, 1164.6057, 1165.6611, 1165.6611, 1179.5520, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1349.6270, 1351.6090, 1365.5970, 1383.6307, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1796.8849, 1838.8502, 1901.1791, 1977.9272, 1993.9021, 2211.0298, 2283.1060, 2398.9456, 2488.1152

19. [A0A4W2BMU5](#) Mass: 57554 Score: 40 Expect: 13 Matches: 5



Uncharacterized protein OS=Bos indicus x Bos taurus OX=30522 GN=LOC113883746 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4629	-19.10	366	- 372	0	---	R.MFPIAVR.L
833.4543	832.4471	832.4629	-19.04	366	- 372	0	29	R.MFPIAVR.L
1151.6833	1150.6760	1150.6234	45.7	131	- 141	0	---	R.TLLSPTFTSGK.L
1193.5681	1192.5608	1192.6452	-70.74	380	- 390	0	---	K.DVEIHGVSIPIK.G
2052.0193	2051.0120	2051.1680	-76.05	36	- 54	0	---	K.LGVPGPRPLPLFGNVLSYR.K
<b>No match to:</b> 842.4758, 848.4947, 850.5049, 853.4832, 855.4396, 864.5046, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 887.4306, 892.9702, 912.4536, 912.4536, 951.5852, 969.4808, 973.4983, 996.5558, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1090.4866, 1131.6697, 1157.5516, 1164.6057, 1165.6611, 1165.6611, 1179.5520, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1349.6270, 1351.6090, 1365.5970, 1383.6307, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1796.8849, 1838.8502, 1901.1791, 1977.9272, 1993.9021, 2211.0298, 2283.1060, 2398.9456, 2488.1152								

20. [Q3T047](#) Mass: 57540 Score: 40 Expect: 13 Matches: 5

Cytochrome P450, family 3, subfamily A, polypeptide 5 OS=Bos taurus OX=9913 GN=CYP3A5 PE=1 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4629	-19.10	366	- 372	0	---	R.MFPIAVR.L
833.4543	832.4471	832.4629	-19.04	366	- 372	0	29	R.MFPIAVR.L
1151.6833	1150.6760	1150.6234	45.7	131	- 141	0	---	R.TLLSPTFTSGK.L
1193.5681	1192.5608	1192.6452	-70.74	380	- 390	0	---	K.DVEIHGVSIPIK.G
2052.0193	2051.0120	2051.1680	-76.05	36	- 54	0	---	K.LGVPGPRPLPLFGNVLSYR.K
<b>No match to:</b> 842.4758, 848.4947, 850.5049, 853.4832, 855.4396, 864.5046, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 887.4306, 892.9702, 912.4536, 912.4536, 951.5852, 969.4808, 973.4983, 996.5558, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1090.4866, 1131.6697, 1157.5516, 1164.6057, 1165.6611, 1165.6611, 1179.5520, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1349.6270, 1351.6090, 1365.5970, 1383.6307, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1796.8849, 1838.8502, 1901.1791, 1977.9272, 1993.9021, 2211.0298, 2283.1060, 2398.9456, 2488.1152								

21. [A0A3Q1MUB2](#) Mass: 54957 Score: 39 Expect: 18 Matches: 12

Glucosaminyl (N-acetyl) transferase 4 OS=Bos taurus OX=9913 GN=GCNT4 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4178	35.1	137	- 143	0	---	K.LVSEEEK.S
833.4543	832.4471	832.4178	35.2	137	- 143	0	---	K.LVSEEEK.S
996.5558	995.5485	995.5651	-16.69	359	- 368	0	---	R.VPGIPGEISK.T
1033.6599	1032.6526	1032.5968	54.1	448	- 456	1	---	R.KWITLSSAK.L
1131.6697	1130.6624	1130.5760	76.4	328	- 336	0	---	K.YIFNNSFVK.D
1165.6611	1164.6538	1164.6026	44.0	249	- 258	0	---	K.SNFELVSELK.K
1165.6611	1164.6539	1164.6026	44.0	249	- 258	0	---	K.SNFELVSELK.K
1448.8667	1447.8594	1447.7267	91.7	369	- 381	1	---	K.TAQDVS DLQSKTR.L
1697.8160	1696.8087	1696.8939	-50.19	2	- 15	0	---	M.CLLCHRPLIISGMK.T
1697.8160	1696.8088	1696.8939	-50.17	2	- 15	0	---	M.CLLCHRPLIISGMK.T
1732.0361	1731.0288	1730.8873	81.8	260	- 275	0	---	K.LNGSNMLETVPKPPSTK.T + Oxidation (M)
1796.8849	1795.8776	1795.9113	-18.75	403	- 417	1	---	R.SVCIYGAELRLMK.Y
<b>No match to:</b> 842.4758, 848.4947, 850.5049, 853.4832, 855.4396, 864.5046, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 887.4306, 892.9702, 912.4536, 912.4536, 951.5852, 969.4808, 973.4983, 996.5558, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1090.4866, 1131.6697, 1157.5516, 1164.6057, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1349.6270, 1351.6090, 1365.5970, 1383.6307, 1420.6680, 1427.7352, 1434.7792, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1707.7140, 1716.7928, 1838.8502, 1901.1791, 1977.9272, 1993.9021, 2052.0193, 2211.0298, 2283.1060, 2398.9456, 2488.1152								

22. [F1MDR5](#) Mass: 92495 Score: 38 Expect: 21 Matches: 16

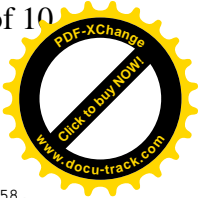
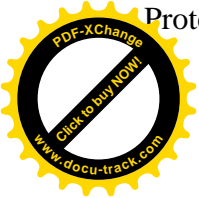
Uncharacterized protein OS=Bos taurus OX=9913 GN=MIA2 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4758	841.4685	841.4657	3.30	640	- 647	0	---	R.LSGPAELR.S
850.5049	849.4976	849.4821	18.3	67	- 73	1	---	R.SRLYVGR.E
864.5046	863.4973	863.4865	12.6	69	- 75	1	---	R.LYVGREK.K
868.5154	867.5081	867.4311	88.8	485	- 491	1	---	R.KENAHNR.Q
868.5154	867.5082	867.4311	88.9	485	- 491	1	---	R.KENAHNR.Q
973.4983	972.4910	972.4876	3.53	240	- 247	0	---	R.EQVNELNK.Q
996.5558	995.5485	995.4897	59.1	486	- 493	1	---	K.ENAHNRQK.L
1066.4620	1065.4547	1065.4913	-34.33	202	- 209	0	---	K.IFQMNEER.L
1157.5516	1156.5443	1156.5183	22.5	248	- 256	1	---	K.QRMTFEDSK.V + Oxidation (M)
1179.5520	1178.5447	1178.5489	-3.52	168	- 177	0	---	K.QDELMSEISK.R
1307.6257	1306.6184	1306.6703	-39.72	202	- 211	1	---	K.IFQMNEERLK.I
1307.6257	1306.6185	1306.6703	-39.69	202	- 211	1	---	K.IFQMNEERLK.I
1351.6090	1350.6017	1350.6449	-31.96	168	- 178	1	---	K.QDELMSEISK.R + Oxidation (M)
1707.7140	1706.7067	1706.8239	-68.66	722	- 738	0	---	R.GPFPFPPPPGSMYGGPR.D
1838.8502	1837.8429	1837.9356	-50.44	257	- 271	1	---	K.VHVEQVLC DKENQIK.S
1993.9021	1992.8948	1992.9476	-26.47	521	- 538	0	---	R.EHSPYGPSPLGRPSPEMR.A
<b>No match to:</b> 833.4543, 833.4543, 848.4947, 853.4832, 855.4396, 865.9906, 870.5118, 877.0043, 882.5307, 882.5307, 887.4306, 892.9702, 912.4536, 912.4536, 951.5852, 969.4808, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1090.4866, 1131.6697, 1151.6833, 1164.6057, 1165.6611, 1165.6611, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1320.5388, 1334.8374, 1334.8374, 1349.6270, 1383.6307, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1716.7928, 1732.0361, 1796.8849, 1901.1791, 1977.9272, 2052.0193, 2211.0298, 2283.1060, 2398.9456, 2488.1152								

23. [Q08DU7](#) Mass: 51251 Score: 37 Expect: 27 Matches: 10

mTERF protein (Fragment) OS=Bos taurus OX=9913 GN=MTERF PE=2 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
973.4983	972.4910	972.5253	-35.29	128	- 135	1	---	K.RQPGVFNR.T
1164.6057	1163.5984	1163.6339	-30.48	218	- 227	0	---	K.FLYSVGLTHK.D
1179.5520	1178.5447	1178.5965	-43.94	334	- 344	1	---	K.DKLSLGLCTAK.E
1193.5681	1192.5608	1192.6750	-95.77	50	- 60	0	---	K.GLGHLLTIMVPR.K
1334.8374	1333.8301	1333.7024	95.8	336	- 347	1	---	K.LSSLGLCTAKEIR.K
1334.8374	1333.8301	1333.7024	95.8	336	- 347	1	---	K.LSSLGLCTAKEIR.K
1365.5970	1364.5897	1364.6540	-47.13	317	- 327	1	---	K.ILDLSSDCMRR.S
1475.6919	1474.6846	1474.8031	-80.33	430	- 441	1	---	K.KLYIEQNIIVLEN.-
1732.0361	1731.0288	1730.9679	35.2	151	- 166	1	---	K.GASIEVIASIIISRYPR.A



2211.0298 2210.0225 2210.0603 -17.11 199 - 217 1 --- R.SPESFFRSSDNLNLENNIK.F  
**No match to:** 833.4543, 833.4543, 842.4758, 848.4947, 850.5049, 853.4832, 855.4396, 864.5046, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 887.4306, 892.9702, 912.4536, 912.4536, 951.5852, 969.4808, 996.5558, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1090.4866, 1131.6697, 1151.6833, 1157.5516, 1165.6611, 1165.6611, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1349.6270, 1351.6090, 1383.6307, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1458.6595, 1487.6974, 1612.7894, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1796.8849, 1838.8502, 1901.1791, 1977.9272, 1993.9021, 2052.0193, 2283.1060, 2398.9456, 2488.1152

24. [AOA4W2FV66](#) Mass: 129413 Score: 37 Expect: 29 Matches: 15

Replication factor C subunit 1 OS=Bos indicus x Bos taurus OX=30522 GN=RFC1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
951.5852	950.5779	950.5226	58.2	6	14	0	---	K.FFGVIPSGK.K
969.4808	968.4735	968.4749	-1.47	443	450	0	---	K.TNYLVMGR.D + Oxidation (M)
1090.4866	1089.4793	1089.4826	-2.98	363	372	0	---	K.ESVSPDEAEK.R
1151.6833	1150.6760	1150.5982	67.6	824	833	1	---	R.NKALTYDQAK.A
1300.8000	1299.7927	1299.7411	39.7	771	780	1	---	R.FQRPRVEQIK.G
1307.6257	1306.6184	1306.5832	27.0	745	754	0	---	K.IPIICMCNDR.N + Oxidation (M)
1307.6257	1306.6185	1306.5832	27.0	745	754	0	---	K.IPIICMCNDR.N + Oxidation (M)
1349.6270	1348.6197	1348.6623	-31.54	51	61	1	---	K.EDEFKPKQSNK.K
1383.6307	1382.6234	1382.7340	-79.98	974	985	0	---	R.TVQDLALHMSLR.T
1458.6595	1457.6522	1457.6998	-32.62	206	217	0	---	K.QLQLDEDAELER.Q
1475.6919	1474.6846	1474.7164	-21.57	826	838	1	---	K.ALTYDQAKADSHR.A
1796.8849	1795.8776	1795.8121	36.5	854	869	0	---	K.VFVSGEETAHMSLMDK.S + Oxidation (M)
1977.9272	1976.9199	1977.0353	-58.36	794	811	0	---	K.IPPPPAMNEIILGANQDIR.Q + Oxidation (M)
1993.9021	1992.8948	1993.0105	-58.02	761	775	1	---	R.SLVHYCFDLRFQRP.R.V
2398.9456	2397.9383	2398.0900	-63.23	1032	1052	0	---	K.DDFENIMEISSWGRSPFSK.L
<b>No match to:</b> 833.4543, 833.4543, 842.4758, 848.4947, 850.5049, 853.4832, 855.4396, 864.5046, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 887.4306, 892.9702, 912.4536, 912.4536, 973.4983, 996.5558, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1157.5516, 1164.6057, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 2052.0193, 2211.0298, 2283.1060, 2488.1152								

25. [AOA4W2EXE5](#) Mass: 129354 Score: 36 Expect: 32 Matches: 15

Replication factor C subunit 1 OS=Bos indicus x Bos taurus OX=30522 GN=RFC1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
951.5852	950.5779	950.5226	58.2	6	14	0	---	K.FFGVIPSGK.K
969.4808	968.4735	968.4749	-1.47	443	450	0	---	K.TNYLVMGR.D + Oxidation (M)
1090.4866	1089.4793	1089.4826	-2.98	363	372	0	---	K.ESVSPDEAEK.R
1151.6833	1150.6760	1150.5982	67.6	823	832	1	---	R.NKALTYDQAK.A
1300.8000	1299.7927	1299.7411	39.7	770	779	1	---	R.FQRPRVEQIK.G
1307.6257	1306.6184	1306.5832	27.0	744	753	0	---	K.IPIICMCNDR.N + Oxidation (M)
1307.6257	1306.6185	1306.5832	27.0	744	753	0	---	K.IPIICMCNDR.N + Oxidation (M)
1349.6270	1348.6197	1348.6623	-31.54	51	61	1	---	K.EDEFKPKQSNK.K
1383.6307	1382.6234	1382.7340	-79.98	973	984	0	---	R.TVQDLALHMSLR.T
1458.6595	1457.6522	1457.6998	-32.62	206	217	0	---	K.QLQLDEDAELER.Q
1475.6919	1474.6846	1474.7164	-21.57	825	837	1	---	K.ALTYDQAKADSHR.A
1796.8849	1795.8776	1795.8121	36.5	853	868	0	---	K.VFVSGEETAHMSLMDK.S + Oxidation (M)
1977.9272	1976.9199	1977.0353	-58.36	793	810	0	---	K.IPPPPAMNEIILGANQDIR.Q + Oxidation (M)
1993.9021	1992.8948	1993.0105	-58.02	760	774	1	---	R.SLVHYCFDLRFQRP.R.V
2398.9456	2397.9383	2398.0900	-63.23	1031	1051	0	---	K.DDFENIMEISSWGRSPFSK.L
<b>No match to:</b> 833.4543, 833.4543, 842.4758, 848.4947, 850.5049, 853.4832, 855.4396, 864.5046, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 887.4306, 892.9702, 912.4536, 912.4536, 973.4983, 996.5558, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1157.5516, 1164.6057, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 2052.0193, 2211.0298, 2283.1060, 2488.1152								

26. [AOA4W2BTQ2](#) Mass: 97692 Score: 36 Expect: 32 Matches: 12

Kinesin-like protein OS=Bos indicus x Bos taurus OX=30522 GN=KIF9 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4807	-40.43	184	190	0	---	R.ALQQVFK.M
833.4543	832.4471	832.4807	-40.37	184	190	0	---	R.ALQQVFK.M
848.4947	847.4874	847.5140	-31.40	177	183	1	---	K.HRGILPR.A
864.5046	863.4973	863.4236	85.4	586	593	0	---	K.DLDVSTSK.T
887.4306	886.4233	886.4984	-84.72	665	671	1	---	K.SILNERR.K
996.5558	995.5485	995.4892	59.6	49	56	1	---	K.LSQMMRSK.N + Oxidation (M)
1179.5520	1178.5447	1178.5931	-41.07	515	525	0	---	K.NDYAASAVQK.A
1458.6595	1457.6522	1457.7409	-60.80	268	280	1	---	R.IIASHTMNKNSSR.S
1475.6919	1474.6846	1474.6787	4.01	614	627	0	---	R.ETSNTPEPLASDPK.E
1901.1791	1900.1718	1900.0014	89.7	492	507	1	---	R.VVLSSQEQEVESTLRR.K
1977.9272	1976.9199	1977.0294	-55.40	33	48	0	---	R.HHPVLQAACYLIWELK.L
2488.1152	2487.1079	2487.1523	-17.83	141	164	0	---	K.DVVSQALNGFNGTMCYGTGAGK.T
<b>No match to:</b> 842.4758, 850.5049, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 912.4536, 912.4536, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1090.4866, 1131.6697, 1151.6697, 1151.6697, 1157.5516, 1164.6057, 1165.6611, 1165.6611, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1349.6270, 1351.6090, 1365.5970, 1383.6307, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1487.6974, 1612.7894, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1796.8849, 1838.8502, 1993.9021, 2052.0193, 2211.0298, 2283.1060, 2398.9456								

27. [AOAOK2YTL5](#) Mass: 9022 Score: 36 Expect: 33 Matches: 6

Uncharacterized protein OS=Cowpox virus OX=10243 GN=GCPXV0248 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
1131.6697	1130.6624	1130.6270	31.3	31	39	0	---	K.YIVLMIAHR.V + Oxidation (M)
1277.6617	1276.6544	1276.7292	-58.53	70	79	1	---	R.LKFNLYRPNL.-
1277.6617	1276.6545	1276.7292	-58.50	70	79	1	---	R.LKFNLYRPNL.-
1334.8374	1333.8301	1333.7275	76.9	58	69	0	---	R.STMELILLTASR.L
1334.8374	1333.8301	1333.7275	76.9	58	69	0	---	R.STMELILLTASR.L
2052.0193	2051.0120	2051.1714	-77.69	13	30	1	---	K.LALRVLVISNGYCHVPLK.Y



No match to: 833.4543, 833.4543, 842.4758, 848.4947, 850.5049, 853.4832, 855.4396, 864.5046, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 887.4306, 892.9702, 912.4536, 912.4536, 951.5852, 969.4808, 973.4983, 996.5558, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1090.4866, 1151.6833, 1157.5516, 1164.6057, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1349.6270, 1351.6090, 1365.5970, 1383.6307, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1796.8849, 1838.8502, 1901.1791, 1977.9272, 1993.9021, 2211.0298, 2283.1060, 2398.9456, 2488.1152

28. AOA3Q1N5S1      Mass: 128941      Score: 36      Expect: 38      Matches: 14

Replication factor C subunit 1 OS=Bos taurus OX=9913 GN=RFC1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
969.4808	968.4735	968.4749	-1.47	437	444	0	---	K.TNYLVMGR.D + Oxidation (M)
1090.4866	1089.4793	1089.4826	-2.98	357	366	0	---	K.ESVSPDEAEK.R
1151.6833	1150.6760	1150.5982	67.6	818	827	1	---	R.NKALTYDQAK.A
1300.8000	1299.7927	1299.7411	39.7	765	774	1	---	R.FQRPVVEIK.G
1307.6257	1306.6184	1306.5832	27.0	739	748	0	---	K.IPIICMCNDR.N + Oxidation (M)
1307.6257	1306.6185	1306.5832	27.0	739	748	0	---	K.IPIICMCNDR.N + Oxidation (M)
1349.6270	1348.6197	1348.6623	-31.54	34	44	1	---	K.EDEFKPKQSNK.K
1383.6307	1382.6234	1382.7340	-79.98	968	979	0	---	R.TVQDLALHMSLR.T
1458.6595	1457.6522	1457.6998	-32.62	203	214	0	---	K.QLQLDEDAELER.Q
1475.6919	1474.6846	1474.7164	-21.57	820	832	1	---	K.ALTYDQAKADSHR.A
1796.8849	1795.8776	1795.8121	36.5	848	863	0	---	K.VFVSGEETAHMSLMDK.S + Oxidation (M)
1977.9272	1976.9199	1977.0353	-58.36	788	805	0	---	K.IPPPAMNEIILGANQDIR.Q + Oxidation (M)
1993.9021	1992.8948	1993.0105	-58.02	755	769	1	---	R.SLVHYCFDLRFQRP.V
2398.9456	2397.9383	2398.0900	-63.23	1026	1046	0	---	K.DDFENIMEISSWGRSPFSK.L

No match to: 833.4543, 833.4543, 842.4758, 848.4947, 850.5049, 853.4832, 855.4396, 864.5046, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 887.4306, 892.9702, 912.4536, 912.4536, 951.5852, 973.4983, 996.5558, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1131.6697, 1151.6833, 1157.5516, 1164.6057, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1320.5388, 1334.8374, 1334.8374, 1351.6090, 1365.5970, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1838.8502, 1901.1791, 2052.0193, 2211.0298, 2283.1060, 2488.1152

29. AOA4W2H4H4      Mass: 50468      Score: 35      Expect: 39      Matches: 11

Interferon induced protein 44 like OS=Bos indicus x Bos taurus OX=30522 GN=IFI44L PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
868.5154	867.5081	867.5542	-53.07	392	399	0	---	K.ILGIPLSR.I
868.5154	867.5082	867.5542	-53.03	392	399	0	---	K.ILGIPLSR.I
887.4306	886.4233	886.4872	-72.07	181	188	0	---	R.NSLPADVR.A
1307.6257	1306.6184	1306.6629	-34.06	165	175	1	---	K.DEAGYINRITR.A
1307.6257	1306.6185	1306.6629	-34.04	165	175	1	---	K.DEAGYINRITR.A
1420.6680	1419.6607	1419.6994	-27.24	2	13	0	---	M.AVTITLTWNEER.S
1434.7792	1433.7719	1433.7554	11.5	293	304	0	---	R.YEFSQKPKITPK.H
1838.8502	1837.8429	1837.9026	-32.46	376	391	1	---	K.MNKAMISQSQIQNVSK.I + 2 Oxidation (M)
1977.9272	1976.9199	1976.9877	-34.28	400	416	1	---	R.ILVVDNYASEREMDPVK.D
1993.9021	1992.8948	1992.9826	-44.05	400	416	1	---	R.ILVVDNYASEREMDPVK.D + Oxidation (M)
2283.1060	2282.0987	2282.2780	-78.55	379	399	1	---	K.AMISQSQIQNVSKILGIPLSR.I

No match to: 833.4543, 833.4543, 842.4758, 848.4947, 850.5049, 853.4832, 855.4396, 864.5046, 865.9906, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 912.4536, 912.4536, 951.5852, 969.4808, 973.4983, 996.5558, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1090.4866, 1131.6697, 1151.6833, 1157.5516, 1164.6057, 1164.6057, 1165.6611, 1165.6611, 1179.5520, 1193.5681, 1277.6617, 1277.6617, 1320.5388, 1334.8374, 1334.8374, 1349.6270, 1351.6090, 1365.5970, 1383.6307, 1427.7352, 1448.8667, 1458.6595, 1475.6919, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1796.8849, 1901.1791, 2052.0193, 2211.0298, 2398.9456, 2488.1152

30. AOA4W2BTP7      Mass: 104127      Score: 35      Expect: 40      Matches: 12

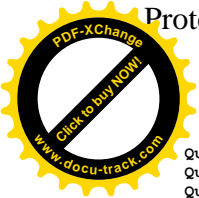
Kinesin-like protein OS=Bos indicus x Bos taurus OX=30522 GN=KIF9 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
833.4543	832.4470	832.4807	-40.43	184	190	0	---	R.ALQQVFK.M
833.4543	832.4471	832.4807	-40.37	184	190	0	---	R.ALQQVFK.M
848.4947	847.4874	847.5140	-31.40	177	183	1	---	K.HRGILLPR.A
864.5046	863.4973	863.4236	85.4	586	593	0	---	K.DLDVSTSK.T
887.4306	886.4233	886.4984	-84.72	665	671	1	---	K.SILNERR.K
996.5558	995.5485	995.4892	59.6	49	56	1	---	K.LSQMMRSK.N + Oxidation (M)
1179.5520	1178.5447	1178.5931	-41.07	515	525	0	---	K.NDYAASAVQK.A
1458.6595	1457.6522	1457.7409	-60.80	268	280	1	---	R.IIASHTMNKNSSR.S
1475.6919	1474.6846	1474.6787	4.01	614	627	0	---	R.ETSNTPLASDSPK.E
1901.1791	1900.1718	1900.0014	89.7	492	507	1	---	R.VVLSQQEQEVESTLRR.K
1977.9272	1976.9199	1977.0294	-55.40	33	48	0	---	R.HHPVLQAACYLIWELK.L
2488.1152	2487.1079	2487.1523	-17.83	141	164	0	---	K.DVVSQALNGFNGTIMCYGQTGAGK.T

No match to: 842.4758, 850.5049, 853.4832, 855.4396, 865.9906, 868.5154, 868.5154, 870.5118, 877.0043, 882.5307, 882.5307, 892.9702, 912.4536, 912.4536, 951.5852, 969.4808, 973.4983, 1017.6315, 1017.6315, 1019.6440, 1033.6599, 1045.5276, 1051.6682, 1051.6682, 1066.4620, 1090.4866, 1131.6697, 1151.6833, 1157.5516, 1164.6057, 1165.6611, 1165.6611, 1193.5681, 1277.6617, 1277.6617, 1300.8000, 1307.6257, 1307.6257, 1320.5388, 1334.8374, 1334.8374, 1349.6270, 1351.6090, 1365.5970, 1383.6307, 1420.6680, 1427.7352, 1434.7792, 1448.8667, 1487.6974, 1612.7894, 1618.0076, 1618.0076, 1697.8160, 1697.8160, 1707.7140, 1716.7928, 1732.0361, 1796.8849, 1838.8502, 1993.9021, 2052.0193, 2211.0298, 2283.1060, 2398.9456

Search Parameters

Type of search	: Sequence Query
Enzyme	: Trypsin
Fixed modifications	: <a href="#">Carbamidomethyl (C)</a>
Variable modifications	: <a href="#">Oxidation (M)</a>
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 (833.4543,1+):	<no title>
Query2 (833.4543,1+):	Locus:1..14.0.1
Query3 (842.4758,1+):	<no title>
Query4 (848.4947,1+):	<no title>



Query5 (850.5049,1+): <no title>  
Query6 (853.4832,1+): <no title>  
Query7 (855.4396,1+): <no title>  
Query8 (864.5046,1+): <no title>  
Query9 (865.9906,1+): <no title>  
Query10 (868.5154,1+): <no title>  
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Query12 (870.5118,1+): <no title>  
Query13 (877.0043,1+): <no title>  
Query14 (882.5307,1+): <no title>  
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Query16 (887.4306,1+): <no title>  
Query17 (892.9702,1+): <no title>  
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Query27 (1033.6599,1+): <no title>  
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Query41 (1277.6617,1+): <no title>  
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Query44 (1307.6257,1+): <no title>  
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Query76 (2398.9456,1+): <no title>  
Query77 (2488.1152,1+): <no title>

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