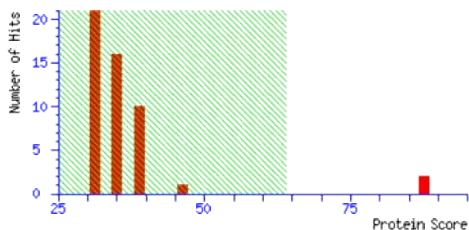


Mascot Search Results

User :
Email :
Search title : BAEDW\2020_3_5\2020_3_5\MSMS 14\N3
Database : Uniprot_bovine_bovine_20200316 (134392 sequences; 76244912 residues)
Timestamp : 31 Mar 2020 at 01:08:22 GMT
Warning : A Peptide summary report will usually give a much clearer picture of MS/MS search results.
Top Score : 88 for A0A4W2BU20, Transthyretin OS=Bos indicus x Bos taurus OX=30522 GN=TTR PE=3 SV=1

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event.
Protein scores greater than 64 are significant ($p < 0.05$).
Protein scores are derived from ion 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

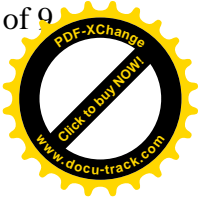
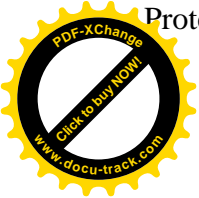
[Re-Search All](#) [Search Unmatched](#)

Index

Accession	Mass	Score	Description
1. A0A4W2BU20	15831	88	Transthyretin OS=Bos indicus x Bos taurus OX=30522 GN=TTR PE=3 SV=1
2. O46375	15831	88	Transthyretin OS=Bos taurus OX=9913 GN=TTR PE=1 SV=1
3. A0A4W2HSZ8	42719	47	Family with sequence similarity 50 member A OS=Bos indicus x Bos taurus OX=30522 GN=FAM50A PE=4 SV=1
4. A0A4W2DZA0	147145	40	SRC kinase signaling inhibitor 1 OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1
5. A0A3Q1ME33	130395	40	SRC kinase signaling inhibitor 1 OS=Bos taurus OX=9913 GN=SRCIN1 PE=4 SV=1
6. A0A4W2F662	130890	38	SRC kinase signaling inhibitor 1 OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1
7. A0A4W2FSP5	32222	38	TATA-box binding protein associated factor, RNA polymerase I subunit D OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1
8. Q32LB6	32222	38	TATA box-binding protein-associated factor RNA polymerase I subunit D OS=Bos taurus OX=9913 GN=TAF1D PE=4 SV=1
9. A0A3Q1LZS3	135577	38	SRC kinase signaling inhibitor 1 OS=Bos taurus OX=9913 GN=SRCIN1 PE=4 SV=1
10. A0A4W2EDE8	135577	38	SRC kinase signaling inhibitor 1 OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1
11. A0A3Q1MIM5	16207	37	Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1
12. A0A452DJF3	13845	37	Phosphatidylinositol transfer protein beta isoform OS=Bos taurus OX=9913 GN=PITPNB PE=4 SV=1
13. A0A3Q1N5E1	133286	37	SRC kinase signaling inhibitor 1 OS=Bos taurus OX=9913 GN=SRCIN1 PE=4 SV=1
14. A0A4W2E9X7	28070	37	Family with sequence similarity 166 member B OS=Bos indicus x Bos taurus OX=30522 GN=FAM166B PE=4 SV=1
15. A0A4W2FA54	140160	36	Calmodulin regulated spectrin associated protein 1 OS=Bos indicus x Bos taurus OX=30522 GN=CAMSAP1 PE=3 SV=1
16. A0A4W2GH39	119304	36	MCF.2 cell line derived transforming sequence-like 2 OS=Bos indicus x Bos taurus OX=30522 GN=MCF2L2 PE=4 SV=1
17. A0A4W2P647	127627	36	SRC kinase signaling inhibitor 1 OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1
18. A0A4W2DZ95	132512	35	SRC kinase signaling inhibitor 1 OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1
19. A0A4W2CC31	172499	35	Calmodulin regulated spectrin associated protein 1 OS=Bos indicus x Bos taurus OX=30522 GN=CAMSAP1 PE=3 SV=1
20. A0A3Q1N0Q9	136628	35	SRC kinase signaling inhibitor 1 OS=Bos taurus OX=9913 GN=SRCIN1 PE=4 SV=1
21. A0A4W2GMF0	148991	35	Coiled-coil domain containing 171 OS=Bos indicus x Bos taurus OX=30522 GN=CCDC171 PE=4 SV=1
22. A0A3Q1LVB1	134506	34	SRC kinase signaling inhibitor 1 OS=Bos taurus OX=9913 GN=SRCIN1 PE=4 SV=1
23. Q80RC9	50101	34	Bo17 (Fragment) OS=Bovine herpesvirus 4 OX=10385 GN=Bo17 PE=4 SV=1
24. Q80RD0	49973	34	Bo17 (Fragment) OS=Bovine herpesvirus 4 OX=10385 GN=Bo17 PE=4 SV=1
25. A0A4W2IBB1	60650	34	RIC8 guanine nucleotide exchange factor B OS=Bos indicus x Bos taurus OX=30522 GN=RIC8B PE=4 SV=1
26. A0A4W2GM11	61548	33	RIC8 guanine nucleotide exchange factor B OS=Bos indicus x Bos taurus OX=30522 GN=RIC8B PE=4 SV=1
27. E1BP35	61548	33	RIC8 guanine nucleotide exchange factor B OS=Bos taurus OX=9913 GN=RIC8B PE=4 SV=1
28. A0A3Q1M3W0	173871	33	Calmodulin regulated spectrin associated protein 1 OS=Bos taurus OX=9913 GN=CAMSAP1 PE=3 SV=1
29. A0A4W2DJY5	62224	33	RIC8 guanine nucleotide exchange factor B OS=Bos indicus x Bos taurus OX=30522 GN=RIC8B PE=4 SV=1
30. A0A4W2F4T9	128155	33	SRC kinase signaling inhibitor 1 OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1

Results List

1.	A0A4W2BU20	Mass: 15831	Score: 88	Expect: 0.00024	Matches: 5
Transthyretin OS=Bos indicus x Bos taurus OX=30522 GN=TTR PE=3 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
1408.5692	1407.5619	1407.6306	-48.82	56 - 68	0 --- K.AAETWEPFASGK.T
1408.5692	1407.5619	1407.6306	-48.81	56 - 68	0 --- K.AAETWEPFASGK.T
2470.2014	2469.1941	2469.2791	-34.42	124 - 146	0 --- R.HYTIAALLSPYSYSTTALVSSPK.A
2477.1138	2476.1065	2476.2023	-38.69	101 - 123	0 66 K.SLGISPFHEFAEVVFTANDSGPR.H
2477.1138	2476.1065	2476.2023	-38.68	101 - 123	0 --- K.SLGISPFHEFAEVVFTANDSGPR.H
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 853.4834, 856.4824, 864.4868, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1300.7965, 1302.7620, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1775.7623, 1901.1764, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2305.0723, 2321.0693, 2459.1550, 2492.1714, 2499.1167, 3337.7234					
2.	O46375	Mass: 15831	Score: 88	Expect: 0.00024	Matches: 5
Transthyretin OS=Bos taurus OX=9913 GN=TTR PE=1 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
1408.5692	1407.5619	1407.6306	-48.82	56 - 68	0 --- K.AAETWEPFASGK.T



1408.5692	1407.5619	1407.6306	-48.81	56	-	68	0	---	K.AAETWEFFASGK.T
2470.2014	2469.1941	2469.2791	-34.42	124	-	146	0	---	R.HYTIAALLSPYSYSTALTALVSSPK.A
2477.1138	2476.1065	2476.2023	-38.69	101	-	123	0	66	K.SLGISPFHEFAEVVFTANDSGPR.H
2477.1138	2476.1065	2476.2023	-38.68	101	-	123	0	---	K.SLGISPFHEFAEVVFTANDSGPR.H
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 853.4834, 856.4824, 864.4868, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1131.6659, 1131.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1300.7965, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1775.7623, 1901.1764, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2305.0723, 2321.0693, 2459.1550, 2492.1714, 2499.1167, 3337.7234									

3. [A0A4W2HSZ8](#) Mass: 42719 Score: 47 Expect: 2.9 Matches: 9
Family with sequence similarity 50 member A OS=Bos indicus x Bos taurus OX=30522 GN=FAM50A PE=4 SV=1

observed	Mr(expt)	Mr(calc)	pppm	Start	End	Miss	Ions	Peptide
842.4688	841.4615	841.5385	-91.47	258	-	264	1 ---	K.ALEILRK.D
848.4903	847.4830	847.4651	21.2	175	-	181	1 ---	R.EEITTKK.K
1179.5537	1178.5464	1178.6448	-83.44	334	-	342	1 ---	K.VVLRSWYEK.N
1775.7623	1774.7550	1774.8308	-42.71	34	-	50	0 ---	K.EYSCNAGDLGLIPGGR.S
2211.0134	2210.0061	2210.1160	-49.73	282	-	299	0 ---	K.EDLIIPHHHSFYDFIVTK.A
2321.0693	2320.0620	2320.1158	-23.16	58	-	78	0 ---	R.YPLQYSGLDNSMDNIVHGVAK.N
2477.1138	2476.1065	2476.3301	-90.29	2	-	24	0 ---	M.PPPSLYPCPLDHAVIGPHLVKLVK.G
2477.1138	2476.1065	2476.2169	-44.56	57	-	78	1 ---	K.RYPLQYSGLDNSMDNIVHGVAK.N
2499.1167	2498.1094	2498.2516	-56.90	83	-	104	1 ---	R.LSDFDFTHTVGLVTNLDMKAK.Q
No match to: 811.4696, 850.0149, 850.5021, 853.4834, 856.4824, 864.4868, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1236.6508, 1300.7965, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2305.0723, 2459.1550, 2470.2014, 2492.1714, 3337.7234								

4. [A0A4W2DZA0](#) Mass: 147145 Score: 40 Expect: 13 Matches: 19
SRC kinase signaling inhibitor 1 OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1

observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.4834	852.4761	852.4705	6.59	436	-	443	0	--- R.LPPSSSPQK.L
864.4868	863.4795	863.3998	92.3	712	-	718	0	--- R.DVSHNHR.L
953.5057	952.4984	952.4548	45.8	1320	-	1326	1	--- K.QRAEYMR.I
1033.6548	1032.6475	1032.5465	97.9	468	-	476	1	--- R.GSPVRQSFR.K
1033.6548	1032.6475	1032.5465	97.9	468	-	476	1	--- R.GSPVRQSFR.K
1131.6659	1130.6586	1130.6183	35.7	734	-	743	0	--- K.QLGETLTTELK.A
1300.7965	1299.7892	1299.6783	85.4	1302	-	1314	1	--- R.LKTAQQGAGSPDK.G
1408.5692	1407.5619	1407.6664	-74.20	867	-	879	1	--- R.SMDKAVSVEAAER.D + Oxidation (M)
1408.5692	1407.5619	1407.6664	-74.19	867	-	879	1	--- R.SMDKAVSVEAAER.D + Oxidation (M)
1427.7416	1426.7343	1426.7780	-30.58	196	-	208	1	--- K.SPNTAILIKDEAR.N
1448.8605	1447.8532	1447.7208	91.4	1192	-	1206	0	--- R.GGAGIPSPWGPAPER.T
1448.8605	1447.8532	1447.7208	91.5	1192	-	1206	0	--- R.GGAGIPSPWGPAPER.T
1457.6237	1456.6164	1456.6735	-39.21	421	-	435	0	--- K.AAGGGPLYGDGYGFR.L
1617.9929	1616.9856	1616.8900	59.2	11	-	25	1	--- R.VPPQLGWQGPAGVRV.L
1617.9929	1616.9856	1616.8900	59.2	11	-	25	1	--- R.VPPQLGWQGPAGVRV.L
1775.7623	1774.7550	1774.7904	-19.94	567	-	585	0	--- K.IEGSNGAATPSAPCGSGSR.S
1993.8938	1992.8865	1993.0051	-59.48	1322	-	1338	1	--- R.AEYMRQAQQQATKPSK.E + Oxidation (M)
2305.0723	2304.0650	2304.2181	-66.43	536	-	556	1	--- R.MEAMEKQIASLTGLVQSALLR.G + Oxidation (M)
2321.0693	2320.0620	2320.2130	-65.08	536	-	556	1	--- R.MEAMEKQIASLTGLVQSALLR.G + 2 Oxidation (M)
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 856.4824, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 996.5507, 1017.6264, 1017.6264, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1430.5653, 1475.6832, 1732.0273, 1901.1764, 1940.8547, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2459.1550, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234								

5. [A0A3Q1ME33](#) Mass: 130395 Score: 40 Expect: 14 Matches: 16
SRC kinase signaling inhibitor 1 OS=Bos taurus OX=9913 GN=SRCIN1 PE=4 SV=1

observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.4834	852.4761	852.4705	6.59	497	-	504	0 ---	R.LPPSSPQK.L
864.4868	863.4795	863.3998	92.3	773	-	779	0 ---	R.DVSHNHR.L
953.5057	952.4984	952.4548	45.8	1154	-	1160	1 ---	K.QRAEYMR.I
1033.6548	1032.6475	1032.5465	97.9	529	-	537	1 ---	R.GSPVRQSFR.K
1033.6548	1032.6475	1032.5465	97.9	529	-	537	1 ---	R.GSPVRQSFR.K
1131.6659	1130.6586	1130.6183	35.7	795	-	804	0 ---	K.QLGETLTTELK.A
1300.7965	1299.7892	1299.6783	85.4	1136	-	1148	1 ---	R.LKTAQQGAGSPDK.G
1408.5692	1407.5619	1407.6664	-74.20	928	-	940	1 ---	R.SMDKAVSVEAAER.D + Oxidation (M)
1408.5692	1407.5619	1407.6664	-74.19	928	-	940	1 ---	R.SMDKAVSVEAAER.D + Oxidation (M)
1427.7416	1426.7343	1426.7780	-30.58	257	-	269	1 ---	K.SPNTAILIKDEAR.N
1457.6237	1456.6164	1456.6735	-39.21	482	-	496	0 ---	K.AAGGGLPLYGDGYGFR.L
1775.7623	1774.7550	1774.7904	-19.94	628	-	646	0 ---	K.IEGSNGAATPSAPCGSGSR.S
1993.8938	1992.8865	1993.0051	-59.48	1156	-	1172	1 ---	R.AEYMRQAQQQATKPSK.E + Oxidation (M)
2305.0723	2304.0650	2304.2181	-66.43	597	-	617	1 ---	R.MEAMEKQIASLTGLVQSALLR.G + Oxidation (M)
2321.0693	2320.0620	2320.2130	-65.08	597	-	617	1 ---	R.MEAMEKQIASLTGLVQSALLR.G + 2 Oxidation (M)
2459.1550	2458.1477	2458.1169	12.5	1105	-	1127	1 ---	K.DEDDEDRIIALEESGGGSVPPMK.V
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 856.4824, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 996.5507, 1017.6264, 1017.6264, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1430.5653, 1448.8605, 1448.8605, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234								

6. [A0A4W2F6E2](#) Mass: 130890 Score: 38 Expect: 20 Matches: 16
SRC kinase signaling inhibitor 1 OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.4834	852.4761	852.4705	6.59	504	-	511	0	--- R.LPPSSPQK.L
864.4868	863.4795	863.3998	92.3	780	-	786	0	--- R.DVSHNHR.L
953.5057	952.4984	952.4548	45.8	1161	-	1167	1	--- K.QRAEYMR.I
1033.6548	1032.6475	1032.5465	97.9	536	-	544	1	--- R.GSPVRQSFR.K
1033.6548	1032.6475	1032.5465	97.9	536	-	544	1	--- R.GSPVRQSFR.K
1131.6659	1130.6586	1130.6183	35.7	802	-	811	0	--- K.QLGETLTTELK.A



1300.7965	1299.7892	1299.6783	85.4	1143	-	1155	1	---	R.LKTAQGQAGSPDK.G
1408.5692	1407.5619	1407.6664	-74.20	935	-	947	1	---	R.SMDKAVSVEAAER.D + Oxidation (M)
1408.5692	1407.5619	1407.6664	-74.19	935	-	947	1	---	R.SMDKAVSVEAAER.D + Oxidation (M)
1427.7416	1426.7343	1426.7780	-30.58	264	-	276	1	---	K.SPNTAILIKDEAR.N
1457.6237	1456.6164	1456.6735	-39.21	489	-	503	0	---	K.AAGGGPLYGDBGYGF.R.L
1775.7623	1774.7550	1774.7904	-19.94	635	-	653	0	---	K.IEGSNGAATPSAPCGSGSR.S
1993.8938	1992.8865	1993.0051	-59.48	1163	-	1179	1	---	R.AEYMRQAQQQATKPSK.E + Oxidation (M)
2305.0723	2304.0650	2304.2181	-66.43	604	-	624	1	---	R.MEAMEKQIASLTGLVQSALLR.G + Oxidation (M)
2321.0693	2320.0620	2320.2130	-65.08	604	-	624	1	---	R.MEAMEKQIASLTGLVQSALLR.G + 2 Oxidation (M)
2459.1550	2458.1477	2458.1169	12.5	1112	-	1134	1	---	K.DEDDEDRIIAELESGGGSGVPPMK.V
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 856.4824, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 996.5507, 1017.6264, 1017.6264, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1430.5653, 1448.8605, 1448.8605, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234									

7.	A0A4W2FSP5	Mass: 32222	Score: 38	Expect: 20	Matches: 8
TATA-box binding protein associated factor, RNA polymerase I subunit D OS=Bos indicus x Bos taurus OX=30522 GN=TAF1D PE=4 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
856.4824	855.4751	855.5039	-33.61	100	- 107 1 --- R.SVGRPKGR.R
868.5110	867.5037	867.5331	-33.81	49	- 55 1 --- R.KFVHIPK.N
1045.5144	1044.5071	1044.4698	35.7	267	- 274 1 --- K.HWIEDKMA.- + Oxidation (M)
1045.5144	1044.5071	1044.4698	35.7	267	- 274 1 --- K.HWIEDKMA.- + Oxidation (M)
1147.6840	1146.6767	1146.6397	32.3	144	- 153 0 --- K.ILTFEQAVAR.G
1901.1764	1900.1691	1899.9982	90.0	225	- 240 1 --- K.LVENSFYIISSEFPKK.K
2261.0361	2260.0288	2260.1183	-39.57	56	- 76 0 --- K.NTQATESSSDSIEPRPLTLK.A
2283.0833	2282.0760	2282.2072	-57.49	124	- 142 1 --- K.RPGFPFLESENGRKPLPWR.K
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 853.4834, 864.4868, 865.9890, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1300.7965, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1775.7623, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2265.0583, 2305.0723, 2321.0693, 2459.1550, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234					

8.	Q32LB6	Mass: 32222	Score: 38	Expect: 20	Matches: 8
TATA box-binding protein-associated factor RNA polymerase I subunit D OS=Bos taurus OX=9913 GN=TAF1D PE=2 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
856.4824	855.4751	855.5039	-33.61	100	- 107 1 --- R.SVGRPKGR.R
868.5110	867.5037	867.5331	-33.81	49	- 55 1 --- R.KFVHIPK.N
1045.5144	1044.5071	1044.4698	35.7	267	- 274 1 --- K.HWIEDKMA.- + Oxidation (M)
1045.5144	1044.5071	1044.4698	35.7	267	- 274 1 --- K.HWIEDKMA.- + Oxidation (M)
1147.6840	1146.6767	1146.6397	32.3	144	- 153 0 --- K.ILTFEQAVAR.G
1901.1764	1900.1691	1899.9982	90.0	225	- 240 1 --- K.LVENSFYIISSEFPKK.K
2261.0361	2260.0288	2260.1183	-39.57	56	- 76 0 --- K.NTQATESSSDSIEPRPLTLK.A
2283.0833	2282.0760	2282.2072	-57.49	124	- 142 1 --- K.RPGFPFLESENGRKPLPWR.K
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 853.4834, 864.4868, 865.9890, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1300.7965, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1775.7623, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2265.0583, 2305.0723, 2321.0693, 2459.1550, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234					

9.	A0A3Q1LZS3	Mass: 135577	Score: 38	Expect: 21	Matches: 16
SRC kinase signaling inhibitor 1 OS=Bos taurus OX=9913 GN=SRCIN1 PE=4 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
853.4834	852.4761	852.4705	6.59	546	- 553 0 --- R.LPPSSPQK.L
864.4868	863.4795	863.3998	92.3	822	- 828 0 --- R.DVSHNHR.L
953.5057	952.4984	952.4548	45.8	1203	- 1209 1 --- K.QRAEYMR.I
1033.6548	1032.6475	1032.5465	97.9	578	- 586 1 --- R.GSPVRQSF.R.K
1033.6548	1032.6475	1032.5465	97.9	578	- 586 1 --- R.GSPVRQSF.R.K
1131.6659	1130.6586	1130.6183	35.7	844	- 853 0 --- K.QLGETLTELK.A
1300.7965	1299.7892	1299.6783	85.4	1185	- 1197 1 --- R.LKTAQGQAGSPDK.G
1408.5692	1407.5619	1407.6664	-74.20	977	- 989 1 --- R.SMDKAVSVEAAER.D + Oxidation (M)
1408.5692	1407.5619	1407.6664	-74.19	977	- 989 1 --- R.SMDKAVSVEAAER.D + Oxidation (M)
1427.7416	1426.7343	1426.7780	-30.58	306	- 318 1 --- K.SPNTAILIKDEAR.N
1457.6237	1456.6164	1456.6735	-39.21	531	- 545 0 --- K.AAGGGPLYGDBGYGF.R.L
1775.7623	1774.7550	1774.7904	-19.94	677	- 695 0 --- K.IEGSNGAATPSAPCGSGSR.S
1993.8938	1992.8865	1993.0051	-59.48	1205	- 1221 1 --- R.AEYMRQAQQQATKPSK.E + Oxidation (M)
2305.0723	2304.0650	2304.2181	-66.43	646	- 666 1 --- R.MEAMEKQIASLTGLVQSALLR.G + Oxidation (M)
2321.0693	2320.0620	2320.2130	-65.08	646	- 666 1 --- R.MEAMEKQIASLTGLVQSALLR.G + 2 Oxidation (M)
2459.1550	2458.1477	2458.1169	12.5	1154	- 1176 1 --- K.DEDDEDRIIAELESGGGSGVPPMK.V
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 856.4824, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 996.5507, 1017.6264, 1017.6264, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1430.5653, 1448.8605, 1448.8605, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234					

10.	A0A4W2EDE8	Mass: 135577	Score: 38	Expect: 21	Matches: 16
SRC kinase signaling inhibitor 1 OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1					
Observed	Mr(expt)	Mr(calc)	ppm	Start	End Miss Ions Peptide
853.4834	852.4761	852.4705	6.59	546	- 553 0 --- R.LPPSSPQK.L
864.4868	863.4795	863.3998	92.3	822	- 828 0 --- R.DVSHNHR.L
953.5057	952.4984	952.4548	45.8	1203	- 1209 1 --- K.QRAEYMR.I
1033.6548	1032.6475	1032.5465	97.9	578	- 586 1 --- R.GSPVRQSF.R.K
1033.6548	1032.6475	1032.5465	97.9	578	- 586 1 --- R.GSPVRQSF.R.K
1131.6659	1130.6586	1130.6183	35.7	844	- 853 0 --- K.QLGETLTELK.A
1300.7965	1299.7892	1299.6783	85.4	1185	- 1197 1 --- R.LKTAQGQAGSPDK.G
1408.5692	1407.5619	1407.6664	-74.20	977	- 989 1 --- R.SMDKAVSVEAAER.D + Oxidation (M)
1408.5692	1407.5619	1407.6664	-74.19	977	- 989 1 --- R.SMDKAVSVEAAER.D + Oxidation (M)
1427.7416	1426.7343	1426.7780	-30.58	306	- 318 1 --- K.SPNTAILIKDEAR.N
1457.6237	1456.6164	1456.6735	-39.21	531	- 545 0 --- K.AAGGGPLYGDBGYGF.R.L

1775.7623	1774.7550	1774.7904	-19.94	677	-	695	0	---	K.IEGSNGAATPSAPCGSGSR.S
1993.8938	1992.8865	1993.0051	-59.48	1205	-	1221	1	---	R.AEYMRQAQQQATKPSK.E + Oxidation (M)
2305.0723	2304.0650	2304.2181	-66.43	646	-	666	1	---	R.MEAMEKQIASLTGLVQSALLR.G + Oxidation (M)
2321.0693	2320.0620	2320.2130	-65.08	646	-	666	1	---	R.MEAMEKQIASLTGLVQSALLR.G + 2 Oxidation (M)
2459.1550	2458.1477	2458.1169	12.5	1154	-	1176	1	---	K.DEDDEDRIIAELESGGGSVPPMK.V
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 856.4824, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 996.5507, 1017.6264, 1017.6264, 1045.5144, 1051.6622, 1051.6622, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1430.5653, 1448.8605, 1448.8605, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234									

11. [A0A3Q1MIM5](#) Mass: 16207 Score: 37 Expect: 24 Matches: 5

Uncharacterized protein OS=Bos taurus OX=9913 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
870.5007	869.4934	869.4130	92.5	40	-	47	0	---	K.AEEEEAPPK.E
951.5844	950.5771	950.5081	72.6	134	-	140	1	---	K.MVKMLWK.I + Oxidation (M)
1940.8547	1939.8474	1940.0190	-88.42	55	-	73	1	---	K.TPAGHAIPPKTGSMVGIIYK.G + Oxidation (M)
2056.9478	2055.9405	2055.9901	-24.13	114	-	130	0	---	K.LFYQSGSEEIESVVHYLR.E
3337.7234	3336.7161	3336.6105	31.7	76	-	104	1	---	K.TFTQSPQPGQHDSGSGFIPFKWPAWPK.T
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 853.4834, 856.4824, 864.4868, 865.9890, 868.5110, 876.9973, 882.5262, 882.5263, 892.9677, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1179.5537, 1236.6508, 1300.7965, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1775.7623, 1901.1764, 1993.8938, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2305.0723, 2321.0693, 2459.1550, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167									

12. [A0A452DJF3](#) Mass: 31845 Score: 37 Expect: 24 Matches: 9

Phosphatidylinositol transfer protein beta isoform OS=Bos taurus OX=9913 GN=PITPNB PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
848.4903	847.4830	847.5531	-82.70	195	-	201	1	---	K.LVTIKFK.W
868.5110	867.5037	867.4603	50.1	171	-	178	0	---	R.GPLGNWKK.K
996.5507	995.5434	995.5552	-11.87	171	-	179	1	---	R.GPLGNWKK.K.E
1051.6622	1050.6549	1050.5896	62.2	1	-	8	1	---	-MVLKEFR.V + Oxidation (M)
1051.6622	1050.6550	1050.5896	62.2	1	-	8	1	---	-MVLKEFR.V + Oxidation (M)
1179.5537	1178.5464	1178.6237	-65.53	200	-	208	1	---	K.PKWWGLQSK.V
1307.6320	1306.6247	1306.6227	1.53	235	-	244	0	---	K.WIDLTMEDIR.R + Oxidation (M)
1457.6237	1456.6164	1456.7384	-83.75	74	-	86	0	---	R.MIAPEGSLVFHEK.A
2321.0693	2320.0620	2320.0768	-6.39	87	-	104	1	---	K.AWNAYPYCRTILQNEYMK.D
No match to: 811.4696, 842.4688, 850.0149, 850.5021, 853.4834, 856.4824, 864.4868, 865.9890, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1045.5144, 1045.5144, 1131.6659, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1236.6508, 1300.7965, 1302.8025, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1775.7623, 1901.1764, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2305.0723, 2459.1550, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234									

13. [A0A3Q1N5E1](#) Mass: 133286 Score: 37 Expect: 27 Matches: 16

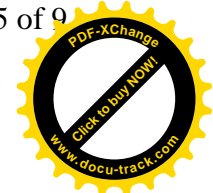
SRC kinase signaling inhibitor 1 OS=Bos taurus OX=9913 GN=SRCIN1 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
853.4834	852.4761	852.4705	6.59	521	-	528	0	---	R.LPPSSPQK.L
864.4868	863.4795	863.3998	92.3	797	-	803	0	---	R.DVSHNHR.L
953.5057	952.4984	952.4548	45.8	1178	-	1184	1	---	K.QRAEYMR.I
1033.6548	1032.6475	1032.5465	97.9	553	-	561	1	---	R.GSPVRQSF.R
1033.6548	1032.6475	1032.5465	97.9	553	-	561	1	---	R.GSPVRQSF.R
1131.6659	1130.6586	1130.6183	35.7	819	-	828	0	---	K.QLGETLTCLK.A
1300.7965	1299.7892	1299.6783	85.4	1160	-	1172	1	---	R.LKTAQQGAGSPDK.G
1408.5692	1407.5619	1407.6664	-74.20	952	-	964	1	---	R.SMDKAVSVEAAER.D + Oxidation (M)
1408.5692	1407.5619	1407.6664	-74.19	952	-	964	1	---	R.SMDKAVSVEAAER.D + Oxidation (M)
1427.7416	1426.7343	1426.7780	-30.58	281	-	293	1	---	K.SPNTAILIKDEAR.N
1457.6237	1456.6164	1456.6735	-39.21	506	-	520	0	---	K.AAGGGPLYGDBGYFR.L
1775.7623	1774.7550	1774.7904	-19.94	652	-	670	0	---	K.IEGSNGAATPSAPCGSGSR.S
1993.8938	1992.8865	1993.0051	-59.48	1180	-	1196	1	---	R.AEYMRQAQQQATKPSK.E + Oxidation (M)
2305.0723	2304.0650	2304.2181	-66.43	621	-	641	1	---	R.MEAMEKQIASLTGLVQSALLR.G + Oxidation (M)
2321.0693	2320.0620	2320.2130	-65.08	621	-	641	1	---	R.MEAMEKQIASLTGLVQSALLR.G + 2 Oxidation (M)
2459.1550	2458.1477	2458.1169	12.5	1129	-	1151	1	---	K.DEDDEDRIIAELESGGGSVPPMK.V
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 856.4824, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 996.5507, 1017.6264, 1017.6264, 1045.5144, 1051.6622, 1051.6622, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1430.5653, 1448.8605, 1448.8605, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234									

14. [A0A4W2E9X7](#) Mass: 28070 Score: 37 Expect: 28 Matches: 8

Family with sequence similarity 166 member B OS=Bos indicus x Bos taurus OX=30522 GN=FAM166B PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1131.6659	1130.6586	1130.6812	-19.94	59	-	68	0	---	R.TLLPPIQPPR.S
1133.6655	1132.6582	1132.6353	20.3	208	-	217	1	---	K.DPKHLPALSR.T
1147.6840	1146.6767	1146.6258	44.4	76	-	85	0	---	R.SLPVRPGRH.R
1408.5692	1407.5619	1407.6646	-72.92	165	-	176	0	---	K.FFMSGFTGYVPR.A
1408.5692	1407.5619	1407.6646	-72.91	165	-	176	0	---	K.FFMSGFTGYVPR.A
2233.0085	2232.0012	2231.9753	11.6	145	-	163	1	---	K.DQEPKPEASPSYMDDRDRP.K
2248.9812	2247.9739	2247.9702	1.65	145	-	163	1	---	K.DQEPKPEASPSYMDDRDRP.K + Oxidation (M)
2492.1714	2491.1641	2491.2094	-18.15	179	-	200	0	---	R.FLFGSSFPVLNSQALQEFGEK.M + Oxidation (M)
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 853.4834, 856.4824, 864.4868, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 996.5507, 1017.6264, 1017.6264, 1045.5144, 1051.6622, 1051.6622, 1133.6655, 1045.5144, 1051.6622, 1051.6622, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1300.7965, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1775.7623, 1901.1764, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2261.0361, 2265.0583, 2283.0833, 2305.0723, 2321.0693, 2459.1550, 2470.2014, 2477.1138, 2477.1138, 2499.1167, 3337.7234									

15. [A0A4W2FA54](#) Mass: 140160 Score: 36 Expect: 30 Matches: 16

Calmodulin regulated spectrin associated protein 1 OS=Bos indicus x Bos taurus OX=30522 GN=CAMSAP1 PE=3 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	



842.4688	841.4615	841.5134	-61.61	598	-	604	1	---	R.QRLQLGK.A
864.4868	863.4795	863.4613	21.1	1018	-	1023	1	---	K.QEYLRR.K
870.5007	869.4934	869.4243	79.5	471	-	477	1	---	K.VKEHDDK.D
951.5844	950.5771	950.4821	100.0	2	-	9	0	---	M.ADSLYNIR.L
1045.5144	1044.5071	1044.5451	-36.38	64	-	72	1	---	R.DVQELKDAK.S
1045.5144	1044.5071	1044.5451	-36.38	64	-	72	1	---	R.DVQELKDAK.S
1151.6809	1150.6736	1150.5843	77.6	318	-	328	1	---	R.SGDGHQPLGR.K
1165.6895	1164.6822	1164.5775	89.9	895	-	904	0	---	K.ENVPLEPPR.S
1165.6895	1164.6822	1164.5775	89.9	895	-	904	0	---	K.ENVPLEPPR.S
1179.5537	1178.5464	1178.5905	-37.37	317	-	327	1	---	R.RSGDGHQPLGR.K
1302.8025	1301.7952	1301.7078	67.1	907	-	918	0	---	K.ASLIEVDLSLK.A
2193.0378	2192.0305	2192.1048	-33.90	1248	-	1266	0	---	K.TMSVSVDAITIHNLWQPK.R + Oxidation (M)
2305.0723	2304.0650	2304.2188	-66.72	277	-	296	1	---	K.TDSFFLEPLMPAVLRPAKEK.Q + Oxidation (M)
2459.1550	2458.1477	2458.1711	-9.50	907	-	929	1	---	K.ASLIEVDLSLKAPDEDETEGR.D
2477.1138	2476.1065	2476.2420	-54.72	1174	-	1193	1	---	K.NSILEELEKCDANHYIILFR.D
2477.1138	2476.1065	2476.2420	-54.71	1174	-	1193	1	---	K.NSILEELEKCDANHYIILFR.D

No match to: 811.4696, 848.4903, 850.0149, 850.5021, 853.4834, 856.4824, 865.9890, 868.5110, 876.9973, 882.5262, 882.5263, 892.9677, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1236.6508, 1300.7965, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1775.7623, 1901.1764, 1940.8547, 1993.8938, 2056.9478, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2321.0693, 2470.2014, 2492.1714, 2499.1167, 3337.7234

16. [A0A4W2GH39](#) Mass: 119304 Score: 36 Expect: 34 Matches: 18

MCF.2 cell line derived transforming sequence-like 2 OS=Bos indicus x Bos taurus OX=30522 GN=MCF2L2 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
811.4696	810.4623	810.4309	38.7	759	-	764	0	---	K.YQMLLK.G + Oxidation (M)
853.4834	852.4761	852.4568	22.7	1	-	6	0	---	-MLFWLK.E + Oxidation (M)
882.5262	881.5189	881.4970	24.8	419	-	425	1	---	K.KHDILEK.S
882.5263	881.5190	881.4970	24.9	419	-	425	1	---	K.KHDILEK.S
1045.5144	1044.5071	1044.5134	-6.05	748	-	755	1	---	K.CLREPSQR.L
1045.5144	1044.5071	1044.5134	-6.05	748	-	755	1	---	K.CLREPSQR.L
1133.6655	1132.6582	1132.6353	20.3	48	-	58	1	---	R.QFALLSGGRGK.D
1165.6895	1164.6822	1164.6940	-10.17	756	-	764	1	---	R.LIKYQMLLK.G + Oxidation (M)
1165.6895	1164.6822	1164.6940	-10.12	756	-	764	1	---	R.LIKYQMLLK.G + Oxidation (M)
1179.5537	1178.5464	1178.5303	13.7	580	-	589	1	---	K.EDDETKSEVK.N
1307.6320	1306.6247	1306.7245	-76.33	1007	-	1017	1	---	K.KETSVIYKPSR.I
1334.8311	1333.8238	1333.7354	66.3	552	-	563	0	---	K.ISQPSTLVPHQK.T
1334.8311	1333.8238	1333.7354	66.3	552	-	563	0	---	K.ISQPSTLVPHQK.T
1940.8547	1939.8474	1939.9502	-52.98	2	-	16	1	---	M.LFWLKEEMAPQEFTR.R + Oxidation (M)
2056.9478	2055.9405	2056.0166	-37.02	664	-	679	1	---	K.EFLFGNIRELYEFHSR.T
2221.0344	2220.0271	2219.9187	48.8	721	-	737	0	---	R.AIWQECQDCTYFGVCQR.Q
2248.9812	2247.9739	2248.1865	-94.54	193	-	211	1	---	R.HSQWINHRTAIENFALALK.T
2321.0693	2320.0620	2320.2541	-82.77	634	-	652	1	---	K.EKNIIDGYIIPMDFIWLK.H

No match to: 842.4688, 848.4903, 850.0149, 850.5021, 856.4824, 864.4868, 865.9890, 868.5110, 870.5007, 876.9973, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1051.6622, 1051.6622, 1131.6659, 1147.6840, 1151.6809, 1236.6508, 1300.7965, 1302.8025, 1316.8201, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1775.7623, 1901.1764, 1993.8938, 2193.0378, 2211.0134, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2261.0361, 2265.0583, 2283.0833, 2305.0723, 2459.1550, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234

17. [A0A4W2F647](#) Mass: 127627 Score: 36 Expect: 36 Matches: 16

SRC kinase signaling inhibitor 1 OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1

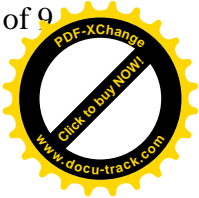
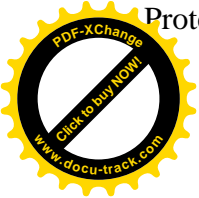
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
848.4903	847.4830	847.4586	28.9	10	-	16	0	---	R.LLSTVCR.K
853.4834	852.4761	852.4705	6.59	501	-	508	0	---	R.LPPSSPQK.L
864.4868	863.4795	863.3998	92.3	777	-	783	0	---	R.DVSHNHR.L
953.5057	952.4984	952.4548	45.8	1158	-	1164	1	---	K.QRAEYMR.I
1033.6548	1032.6475	1032.5465	97.9	533	-	541	1	---	R.GSPVRQSF.R
1033.6548	1032.6475	1032.5465	97.9	533	-	541	1	---	R.GSPVRQSF.R
1131.6659	1130.6586	1130.6183	35.7	799	-	808	0	---	K.QLGETLTCLK.A
1300.7965	1299.7892	1299.6783	85.4	1140	-	1152	1	---	R.LKTAQGQAGSPDK.G
1408.5692	1407.5619	1407.6664	-74.20	932	-	944	1	---	R.SMDKAVSVEAAER.D + Oxidation (M)
1408.5692	1407.5619	1407.6664	-74.19	932	-	944	1	---	R.SMDKAVSVEAAER.D + Oxidation (M)
1427.7416	1426.7343	1426.7780	-30.58	261	-	273	1	---	K.SPNTAILIKDEAR.N
1457.6237	1456.6164	1456.6735	-39.21	486	-	500	0	---	K.AAGGGPLYGDYGF.R
1775.7623	1774.7550	1774.7904	-19.94	632	-	650	0	---	K.IEGSNGAATPSAPCGSGSR.S
2305.0723	2304.0650	2304.2181	-66.43	601	-	621	1	---	R.MEAMEKQIASLTGLVQSALLR.G + Oxidation (M)
2321.0693	2320.0620	2320.2130	-65.08	601	-	621	1	---	R.MEAMEKQIASLTGLVQSALLR.G + 2 Oxidation (M)
2459.1550	2458.1477	2458.1169	12.5	1109	-	1131	1	---	K.DEDDEDRIAELES GGSGVPPMK.V

No match to: 811.4696, 842.4688, 850.0149, 850.5021, 856.4824, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 996.5507, 1017.6264, 1017.6264, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1430.5653, 1448.8605, 1448.8605, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234

18. [A0A4W2D295](#) Mass: 132512 Score: 35 Expect: 39 Matches: 16

SRC kinase signaling inhibitor 1 OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
853.4834	852.4761	852.4705	6.59	520	-	527	0	---	R.LPPSSPQK.L
864.4868	863.4795	863.3998	92.3	796	-	802	0	---	R.DVSHNHR.L
953.5057	952.4984	952.4548	45.8	1177	-	1183	1	---	K.QRAEYMR.I
1033.6548	1032.6475	1032.5465	97.9	552	-	560	1	---	R.GSPVRQSF.R
1033.6548	1032.6475	1032.5465	97.9	552	-	560	1	---	R.GSPVRQSF.R
1131.6659	1130.6586	1130.6183	35.7	818	-	827	0	---	K.QLGETLTCLK.A
1300.7965	1299.7892	1299.6783	85.4	1159	-	1171	1	---	R.LKTAQGQAGSPDK.G
1408.5692	1407.5619	1407.6664	-74.20	951	-	963	1	---	R.SMDKAVSVEAAER.D + Oxidation (M)
1408.5692	1407.5619	1407.6664	-74.19	951	-	963	1	---	R.SMDKAVSVEAAER.D + Oxidation (M)
1427.7416	1426.7343	1426.7780	-30.58	280	-	292	1	---	K.SPNTAILIKDEAR.N
1457.6237	1456.6164	1456.6735	-39.21	505	-	519	0	---	K.AAGGGPLYGDYGF.R
1775.7623	1774.7550	1774.7904	-19.94	651	-	669	0	---	K.IEGSNGAATPSAPCGSGSR.S
1993.8938	1992.8865	1993.0051	-59.48	1179	-	1195	1	---	R.AEYMRIQAQQATKPSK.E + Oxidation (M)
2305.0723	2304.0650	2304.2181	-66.43	620	-	640	1	---	R.MEAMEKQIASLTGLVQSALLR.G + Oxidation (M)



2321.0693 2320.0620 2320.2130 -65.08 620 - 640 1 --- R.MEAMEKQIASLTGLVQSALLR.G + 2 Oxidation (M)
2459.1550 2458.1477 2458.1169 12.5 1128 - 1150 1 --- K.DEDDEDRIIAELESGGGSVPPMK.V
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 856.4824, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 996.5507, 1017.6264, 1017.6264, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1430.5653, 1448.8605, 1448.8605, 1475.6832, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234

19. [A0A4W2CC31](#) Mass: 172499 Score: 35 Expect: 40 Matches: 17
Calmodulin regulated spectrin associated protein 1 OS=Bos indicus x Bos taurus OX=30522 GN=CAMSAP1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4688	841.4615	841.5134	-61.61	882	-	888	1 ---	R.QRLQLGK.A
864.4868	863.4795	863.4613	21.1	1302	-	1307	1 ---	K.QEYLRR.K
870.5007	869.4934	869.4243	79.5	755	-	761	1 ---	K.VKEHDDK.D
1045.5144	1044.5071	1044.5451	-36.38	342	-	350	1 ---	R.DVQELKDAK.S
1045.5144	1044.5071	1044.5451	-36.38	342	-	350	1 ---	R.DVQELKDAK.S
1151.6809	1150.6736	1150.5843	77.6	602	-	612	1 ---	R.SGDGHQPLGRK.K
1165.6895	1164.6822	1164.5775	89.9	1179	-	1188	0 ---	K.ENVPLEPPR.S
1165.6895	1164.6822	1164.5775	89.9	1179	-	1188	0 ---	K.ENVPLEPPR.S
1179.5537	1178.5464	1178.5905	-37.37	601	-	611	1 ---	R.RSGDGHQPLGR.K
1302.8025	1301.7952	1301.7078	67.1	1191	-	1202	0 ---	K.ASLIEVDLSDLK.A
1993.8938	1992.8865	1993.0341	-74.05	98	-	116	0 ---	K.GDQVASLQGHQSVIQLSR.K
2193.0378	2192.0305	2192.1048	-33.90	1532	-	1550	0 ---	K.TMSVSVDALTIHNLWQPK.R + Oxidation (M)
2305.0723	2304.0650	2304.2188	-66.72	561	-	580	1 ---	K.TDSFFLEPLMPVLRPAKEK.Q + Oxidation (M)
2459.1550	2458.1477	2458.1711	-9.50	1191	-	1213	1 ---	K.ASLIEVDLSDLKAPDEGTEGR.D
2477.1138	2476.1065	2476.2420	-54.72	1458	-	1477	1 ---	K.NSILEELEKCDANHYIILFR.D
2477.1138	2476.1065	2476.2420	-54.71	1458	-	1477	1 ---	K.NSILEELEKCDANHYIILFR.D
2492.1714	2491.1641	2491.2707	-42.77	370	-	394	1 ---	K.RSFLGSPAAASPADLQLGEPEPPGK.G
No match to: 811.4696, 848.4903, 850.0149, 850.5021, 853.4834, 856.4824, 865.9890, 868.5110, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1236.6508, 1300.7965, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1775.7623, 1901.1764, 1940.8547, 2056.9478, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2321.0693, 2470.2014, 2499.1167, 3337.7234								

20. [A0A3Q1NQ99](#) Mass: 136628 Score: 35 Expect: 43 Matches: 16
SRC kinase signaling inhibitor 1 OS=Bos taurus OX=9913 GN=SRCIN1 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.4834	852.4761	852.4705	6.59	554	-	561	0 ---	R.LPPSSPQK.L
864.4868	863.4795	863.3998	92.3	830	-	836	0 ---	R.DVSHNHR.L
953.5057	952.4984	952.4548	45.8	1211	-	1217	1 ---	K.QRAEYMR.I
1033.6548	1032.6475	1032.5465	97.9	586	-	594	1 ---	R.GSPVRQSF.R
1033.6548	1032.6475	1032.5465	97.9	586	-	594	1 ---	R.GSPVRQSF.R
1131.6659	1130.6586	1130.6183	35.7	852	-	861	0 ---	K.QLGETLTTELK.A
1300.7965	1299.7892	1299.6783	85.4	1193	-	1205	1 ---	R.LKTAQQGAGSPDK.G
1408.5692	1407.5619	1407.6664	-74.20	985	-	997	1 ---	R.SMDKAVSVEAER.D + Oxidation (M)
1408.5692	1407.5619	1407.6664	-74.19	985	-	997	1 ---	R.SMDKAVSVEAER.D + Oxidation (M)
1427.7416	1426.7343	1426.7780	-30.58	314	-	326	1 ---	K.SPNTAILIKDEAR.N
1457.6237	1456.6164	1456.6735	-39.21	539	-	553	0 ---	K.AAGGGPLYGDGYGFR.L
1775.7623	1774.7550	1774.7904	-19.94	685	-	703	0 ---	K.IEGSNGAATPSAPCGSGR.S
1993.8938	1992.8865	1993.0051	-59.48	1213	-	1229	1 ---	R.AEYMRIQAQQQATKPSK.E + Oxidation (M)
2305.0723	2304.0650	2304.2181	-66.43	654	-	674	1 ---	R.MEAMEKQIASLTGLVQSALLR.G + Oxidation (M)
2321.0693	2320.0620	2320.2130	-65.08	654	-	674	1 ---	R.MEAMEKQIASLTGLVQSALLR.G + 2 Oxidation (M)
2459.1550	2458.1477	2458.1169	12.5	1162	-	1184	1 ---	K.DEDDEDRIIAELESGGGSVPPMK.V
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 856.4824, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 996.5507, 1017.6264, 1017.6264, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234								

21. [A0A4W2GMF0](#) Mass: 148991 Score: 35 Expect: 47 Matches: 16
Coiled-coil domain containing 171 OS=Bos indicus x Bos taurus OX=30522 GN=CCDC171 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
864.4868	863.4795	863.4389	47.1	650	-	656	0 ---	K.FQEIAEK.N
996.5507	995.5434	995.5189	24.7	940	-	947	0 ---	K.QIFGFTQR.L
1045.5144	1044.5071	1044.4447	59.8	620	-	627	0 ---	K.AQESCWHK.Q
1045.5144	1044.5071	1044.4447	59.8	620	-	627	0 ---	K.AQESCWHK.Q
1179.5537	1178.5464	1178.5965	-42.47	1055	-	1064	1 ---	K.SLSEAKMELR.R + Oxidation (M)
1236.6508	1235.6435	1235.6180	20.7	18	-	28	1 ---	K.NASSDIKQMVK.S + Oxidation (M)
1475.6832	1474.6759	1474.7337	-39.18	277	-	290	0 ---	K.ASQAEAVADLEMIK.N
1617.9929	1616.9856	1616.8444	87.4	798	-	812	1 ---	R.EGIGVLVCTGELKDK.H
1617.9929	1616.9856	1616.8444	87.4	798	-	812	1 ---	R.EGIGVLVCTGELKDK.H
1732.0273	1731.0200	1730.8547	95.5	2	-	17	1 ---	M.NSNTSSNTPGDIQRLK.N
1993.8938	1992.8865	1992.9826	-48.20	277	-	294	1 ---	K.ASQAEAVADLEMIKNEFK.E
2221.0344	2220.0271	2220.1790	-68.41	718	-	735	1 ---	R.DFLQEQQVNTPELLKLEVR.T
2261.0361	2260.0288	2260.0794	-22.36	157	-	174	1 ---	R.DNIIQNCHQEYDLLTKK.S
2477.1138	2476.1065	2476.2494	-57.71	688	-	709	1 ---	R.EKTSLLVACALMAGAFYPLYSR.S + Oxidation (M)
2477.1138	2476.1065	2476.2494	-57.70	688	-	709	1 ---	R.EKTSLLVACALMAGAFYPLYSR.S + Oxidation (M)
2492.1714	2491.1641	2491.2476	-33.49	1259	-	1283	0 ---	K.ETLINSVPLASSNSSPVMTSATAK.R
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 853.4834, 856.4824, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1300.7965, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1775.7623, 1901.1764, 1940.8547, 2056.9478, 2193.0378, 2211.0134, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2265.0583, 2283.0833, 2305.0723, 2321.0693, 2459.1550, 2470.2014, 2499.1167, 3337.7234								

22. [A0A3Q1LVB1](#) Mass: 134506 Score: 34 Expect: 49 Matches: 16
SRC kinase signaling inhibitor 1 OS=Bos taurus OX=9913 GN=SRCIN1 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.4834	852.4761	852.4705	6.59	533	-	540	0 ---	R.LPPSSPQK.L
864.4868	863.4795	863.3998	92.3	809	-	815	0 ---	R.DVSHNHR.L
953.5057	952.4984	952.4548	45.8	1190	-	1196	1 ---	K.QRAEYMR.I
1033.6548	1032.6475	1032.5465	97.9	565	-	573	1 ---	R.GSPVRQSF.R



1033.6548	1032.6475	1032.5465	97.9	565	-	573	1	---	R.GSPVRQSF.R.K
1131.6659	1130.6586	1130.6183	35.7	831	-	840	0	---	K.QLGETLTELK.A
1300.7965	1299.7892	1299.6783	85.4	1172	-	1184	1	---	R.LKTAQQAGSPDK.G
1408.5692	1407.5619	1407.6664	-74.20	964	-	976	1	---	R.SMDKAVSVEAAER.D + Oxidation (M)
1408.5692	1407.5619	1407.6664	-74.19	964	-	976	1	---	R.SMDKAVSVEAAER.D + Oxidation (M)
1427.7416	1426.7343	1426.7780	-30.58	293	-	305	1	---	K.SPNTAILIKDEAR.N
1457.6237	1456.6164	1456.6735	-39.21	518	-	532	0	---	K.AAGGGPLYGDYGF.R.L
1775.7623	1774.7550	1774.7904	-19.94	664	-	682	0	---	K.IEGSNGAATPAPCGSGSR.S
1993.8938	1992.8865	1993.0051	-59.48	1192	-	1208	1	---	R.AEYMRQAQQATKPSK.E + Oxidation (M)
2305.0723	2304.0650	2304.2181	-66.43	633	-	653	1	---	R.MEAMEKQIASLTGLVQSALLR.G + Oxidation (M)
2321.0693	2320.0620	2320.2130	-65.08	633	-	653	1	---	R.MEAMEKQIASLTGLVQSALLR.G + 2 Oxidation (M)
2459.1550	2458.1477	2458.1169	12.5	1141	-	1163	1	---	K.DEDDEDRIAELESGGSVPPMK.V
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 856.4824, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 996.5507, 1017.6264, 1017.6264, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1430.5653, 1448.8605, 1448.8605, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234									

23. [Q80RC9](#) Mass: 50101 Score: 34 Expect: 50 Matches: 9

Bo17 (Fragment) OS=Bovine herpesvirus 4 OX=10385 GN=Bo17 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1475.6832	1474.6759	1474.6973	-14.50	247	-	259	1	---	K.NSMESIEPPESKK.N
1617.9929	1616.9856	1616.8708	71.0	348	-	361	1	---	K.YHISDMTAIARLVK.W
1617.9929	1616.9856	1616.8708	71.0	348	-	361	1	---	K.YHISDMTAIARLVK.W
1940.8547	1939.8474	1940.0214	-89.70	73	-	90	1	---	R.GDQEAQAQALLDNLEVKK.K
1993.8938	1992.8865	1993.0376	-75.82	171	-	188	1	---	K.EAVKAIISCLPNVFMASK.L + Oxidation (M)
2225.0469	2224.0396	2224.0259	6.17	280	-	299	0	---	K.DPPPDNLPMFTGNAYFVASR.A + Oxidation (M)
2233.0085	2232.0012	2232.0555	-24.31	200	-	218	0	---	R.VQADLNCMEDLLQSSVPWK.Y
2248.9812	2247.9739	2248.0504	-34.02	200	-	218	0	---	R.VQADLNCMEDLLQSSVPWK.Y + Oxidation (M)
2283.0833	2282.0760	2282.1113	-15.48	92	-	109	1	---	K.RPPLTDITYLINITRD.CER.F
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 853.4834, 856.4824, 864.4868, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1300.7965, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1732.0273, 1775.7623, 1901.1764, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2230.1272, 2239.0554, 2261.0361, 2265.0583, 2305.0723, 2321.0693, 2459.1550, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234									

24. [Q80RDO](#) Mass: 49973 Score: 34 Expect: 56 Matches: 9

Bo17 (Fragment) OS=Bovine herpesvirus 4 OX=10385 GN=Bo17 PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
1475.6832	1474.6759	1474.6973	-14.50	246	-	258	1	---	K.NSMESIEPPESKK.N
1617.9929	1616.9856	1616.8708	71.0	347	-	360	1	---	K.YHISDMTAIARLVK.W
1617.9929	1616.9856	1616.8708	71.0	347	-	360	1	---	K.YHISDMTAIARLVK.W
1940.8547	1939.8474	1940.0214	-89.70	72	-	89	1	---	R.GDQEAQAQALLDNLEVKK.K
1993.8938	1992.8865	1993.0376	-75.82	170	-	187	1	---	K.EAVKAIISCLPNVFMASK.L + Oxidation (M)
2225.0469	2224.0396	2224.0259	6.17	279	-	298	0	---	K.DPPPDNLPMFTGNAYFVASR.A + Oxidation (M)
2233.0085	2232.0012	2232.0555	-24.31	199	-	217	0	---	R.VQADLNCMEDLLQSSVPWK.Y
2248.9812	2247.9739	2248.0504	-34.02	199	-	217	0	---	R.VQADLNCMEDLLQSSVPWK.Y + Oxidation (M)
2283.0833	2282.0760	2282.1113	-15.48	91	-	108	1	---	K.RPPLTDITYLINITRD.CER.F
No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 853.4834, 856.4824, 864.4868, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1300.7965, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1732.0273, 1775.7623, 1901.1764, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2230.1272, 2239.0554, 2261.0361, 2265.0583, 2305.0723, 2321.0693, 2459.1550, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234									

25. [A0A4W2IBE1](#) Mass: 60650 Score: 34 Expect: 57 Matches: 6

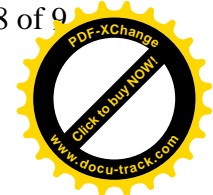
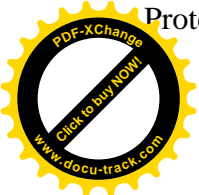
RIC8 guanine nucleotide exchange factor B OS=Bos indicus x Bos taurus OX=30522 GN=RIC8B PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
848.4903	847.4830	847.4473	42.1	515	-	521	0	---	K.LVNMLDK.L + Oxidation (M)
856.4824	855.4751	855.5430	-79.30	79	-	86	0	---	K.VLVPVITK.E
1775.7623	1774.7550	1774.8784	-69.53	247	-	261	1	---	K.ESESHQFRVMAAVLR.H + Oxidation (M)
2225.0469	2224.0396	2224.1158	-34.24	356	-	375	1	---	K.GSSYREGLTPLVSLLT.ECSR.A
2477.1138	2476.1065	2476.2584	-61.36	98	-	119	1	17	K.LNESDSDSLEKVSFPVIVESLK.C
2477.1138	2476.1065	2476.2584	-61.35	98	-	119	1	---	K.LNESDSDSLEKVSFPVIVESLK.C
No match to: 811.4696, 842.4688, 850.0149, 850.5021, 853.4834, 864.4868, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1300.7965, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2305.0723, 2321.0693, 2459.1550, 2470.2014, 2492.1714, 2499.1167, 3337.7234									

26. [A0A4W2GMI1](#) Mass: 61548 Score: 33 Expect: 61 Matches: 6

RIC8 guanine nucleotide exchange factor B OS=Bos indicus x Bos taurus OX=30522 GN=RIC8B PE=4 SV=1									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
848.4903	847.4830	847.4473	42.1	515	-	521	0	---	K.LVNMLDK.L + Oxidation (M)
856.4824	855.4751	855.5430	-79.30	79	-	86	0	---	K.VLVPVITK.E
1775.7623	1774.7550	1774.8784	-69.53	247	-	261	1	---	K.ESESHQFRVMAAVLR.H + Oxidation (M)
2225.0469	2224.0396	2224.1158	-34.24	356	-	375	1	---	K.GSSYREGLTPLVSLLT.ECSR.A
2477.1138	2476.1065	2476.2584	-61.36	98	-	119	1	17	K.LNESDSDSLEKVSFPVIVESLK.C
2477.1138	2476.1065	2476.2584	-61.35	98	-	119	1	---	K.LNESDSDSLEKVSFPVIVESLK.C
No match to: 811.4696, 842.4688, 850.0149, 850.5021, 853.4834, 864.4868, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1300.7965, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2305.0723, 2321.0693, 2459.1550, 2470.2014, 2492.1714, 2499.1167, 3337.7234									

27. [E1BD35](#) Mass: 61548 Score: 33 Expect: 61 Matches: 6

RIC8 guanine nucleotide exchange factor B OS=Bos taurus OX=9913 GN=RIC8B PE=4 SV=3									
Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide	
848.4903	847.4830	847.4473	42.1	515	-	521	0	---	K.LVNMLDK.L + Oxidation (M)
856.4824	855.4751	855.5430	-79.30	79	-	86	0	---	K.VLVPVITK.E



1775.7623 1774.7550 1774.8784 -69.53 247 - 261 1 --- K.ESESHQFRVMAAVLR.H + Oxidation (M)
 2225.0469 2224.0396 2224.1158 -34.24 356 - 375 1 --- K.GSSYREGLTPVLSLLTECSR.A
 2477.1138 2476.1065 2476.2584 -61.36 98 - 119 1 17 K.LNESDDSLSEKVSFPVIVESLK.C
 2477.1138 2476.1065 2476.2584 -61.35 98 - 119 1 --- K.LNESDDSLSEKVSFPVIVESLK.C
No match to: 811.4696, 842.4688, 850.0149, 850.5021, 853.4834, 864.4868, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1300.7965, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2305.0723, 2321.0693, 2459.1550, 2470.2014, 2492.1714, 2499.1167, 3337.7234

28. [A0A3Q1M3W0](#) Mass: 173871 Score: 33 Expect: 63 Matches: 17

Calmodulin regulated spectrin associated protein 1 OS=Bos taurus OX=9913 GN=CAMSAP1 PE=3 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
842.4688	841.4615	841.5134	-61.61	893	-	899	1 ---	R.QRLQLGK.A
864.4868	863.4795	863.4613	21.1	1313	-	1318	1 ---	K.QEYLR.R.K
870.5007	869.4934	869.4243	79.5	766	-	772	1 ---	K.VKEHDDK.D
1045.5144	1044.5071	1044.5451	-36.38	353	-	361	1 ---	R.DVQELKDAK.S
1045.5144	1044.5071	1044.5451	-36.38	353	-	361	1 ---	R.DVQELKDAK.S
1151.6809	1150.6736	1150.5843	77.6	613	-	623	1 ---	R.SGDGHQPLGRK.K
1165.6895	1164.6822	1164.5775	89.9	1190	-	1199	0 ---	K.ENVPDLDEPPR.S
1165.6895	1164.6822	1164.5775	89.9	1190	-	1199	0 ---	K.ENVPDLDEPPR.S
1179.5537	1178.5464	1178.5905	-37.37	612	-	622	1 ---	R.RSGDGHQPLGR.K
1302.8025	1301.7952	1301.7078	67.1	1202	-	1213	0 ---	K.ASLIEVDLSDLK.A
1993.8938	1992.8865	1993.0341	-74.05	98	-	116	0 ---	K.GDQVASLQGHQSVIQALSR.K
2193.0378	2192.0305	2192.1048	-33.90	1543	-	1561	0 ---	K.TMSVSVDAITIHNLWQPK.R + Oxidation (M)
2305.0723	2304.0650	2304.2188	-66.72	572	-	591	1 ---	K.TDSFFLEPLMPAVLRPAKEK.Q + Oxidation (M)
2459.1550	2458.1477	2458.1711	-9.50	1202	-	1224	1 ---	K.ASLIEVDLSDLKAPDEDEGETEGR.D
2477.1138	2476.1065	2476.2420	-54.72	1469	-	1488	1 ---	K.NSILEELEKCDANHYIILFR.D
2477.1138	2476.1065	2476.2420	-54.71	1469	-	1488	1 ---	K.NSILEELEKCDANHYIILFR.D
2492.1714	2491.1641	2491.2707	-42.77	381	-	405	1 ---	K.RSFLGSPAAASPADLQLGEPEPPGK.G

No match to: 811.4696, 848.4903, 850.0149, 850.5021, 853.4834, 856.4824, 865.9890, 868.5110, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1236.6508, 1300.7965, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1775.7623, 1901.1764, 1940.8547, 2056.9478, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2321.0693, 2470.2014, 2499.1167, 3337.7234

29. [A0A4W2IDJ5](#) Mass: 62224 Score: 33 Expect: 64 Matches: 6

RIC8 guanine nucleotide exchange factor B OS=Bos indicus x Bos taurus OX=30522 GN=RIC8B PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
848.4903	847.4830	847.4473	42.1	499	-	505	0 ---	K.LVNMLDK.L + Oxidation (M)
856.4824	855.4751	855.5430	-79.30	63	-	70	0 ---	K.VLPVPVITK.E
1775.7623	1774.7550	1774.8784	-69.53	231	-	245	1 ---	K.ESESHQFRVMAAVLR.H + Oxidation (M)
2225.0469	2224.0396	2224.1158	-34.24	340	-	359	1 ---	K.GSSYREGLTPVLSLLTECSR.A
2477.1138	2476.1065	2476.2584	-61.36	82	-	103	1 17	K.LNESDDSLSEKVSFPVIVESLK.C
2477.1138	2476.1065	2476.2584	-61.35	82	-	103	1 ---	K.LNESDDSLSEKVSFPVIVESLK.C

No match to: 811.4696, 842.4688, 850.0149, 850.5021, 853.4834, 864.4868, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 953.5057, 996.5507, 1017.6264, 1017.6264, 1033.6548, 1033.6548, 1051.6622, 1051.6622, 1131.6659, 1133.6655, 1147.6840, 1236.6508, 1300.7965, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1408.5692, 1408.5692, 1427.7416, 1430.5653, 1448.8605, 1448.8605, 1457.6237, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2305.0723, 2321.0693, 2459.1550, 2470.2014, 2492.1714, 2499.1167, 3337.7234

30. [A0A4W2F4T9](#) Mass: 128155 Score: 33 Expect: 66 Matches: 15

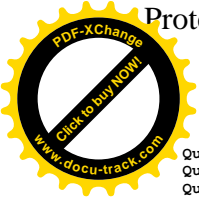
SRC kinase signaling inhibitor 1 OS=Bos indicus x Bos taurus OX=30522 GN=SRCIN1 PE=4 SV=1

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Ions	Peptide
853.4834	852.4761	852.4705	6.59	512	-	519	0 ---	R.LPPSSPQK.L
864.4868	863.4795	863.3998	92.3	788	-	794	0 ---	R.DVSHNHR.L
953.5057	952.4984	952.4548	45.8	1169	-	1175	1 ---	K.QRAEYMR.I
1033.6548	1032.6475	1032.5465	97.9	544	-	552	1 ---	R.GSPVRQSF.R.K
1033.6548	1032.6475	1032.5465	97.9	544	-	552	1 ---	R.GSPVRQSF.R.K
1131.6659	1130.6586	1130.6183	35.7	810	-	819	0 ---	K.QLGETLTTELK.A
1300.7965	1299.7892	1299.6783	85.4	1151	-	1163	1 ---	R.LKTAQQGAGSPDK.G
1408.5692	1407.5619	1407.6664	-74.20	943	-	955	1 ---	R.SMDKAVSVEAAER.D + Oxidation (M)
1408.5692	1407.5619	1407.6664	-74.19	943	-	955	1 ---	R.SMDKAVSVEAAER.D + Oxidation (M)
1427.7416	1426.7343	1426.7780	-30.58	272	-	284	1 ---	K.SPNTAILIKDEAR.N
1457.6237	1456.6164	1456.6735	-39.21	497	-	511	0 ---	K.AAGGGPLYGDGYGFR.L
1775.7623	1774.7550	1774.7904	-19.94	643	-	661	0 ---	K.IEGSNGAATPSAPCGSGSR.S
2305.0723	2304.0650	2304.2181	-66.43	612	-	632	1 ---	R.MEAMEKQIASLTGLVQSALLR.G + Oxidation (M)
2321.0693	2320.0620	2320.2130	-65.08	612	-	632	1 ---	R.MEAMEKQIASLTGLVQSALLR.G + 2 Oxidation (M)
2459.1550	2458.1477	2458.1169	12.5	1120	-	1142	1 ---	K.DEDDEDRIIAELESGGGSGVPPMK.V

No match to: 811.4696, 842.4688, 848.4903, 850.0149, 850.5021, 856.4824, 865.9890, 868.5110, 870.5007, 876.9973, 882.5262, 882.5263, 892.9677, 951.5844, 996.5507, 1017.6264, 1017.6264, 1045.5144, 1045.5144, 1051.6622, 1051.6622, 1133.6655, 1147.6840, 1151.6809, 1165.6895, 1165.6895, 1179.5537, 1236.6508, 1302.8025, 1307.6320, 1316.8201, 1334.8311, 1334.8311, 1430.5653, 1448.8605, 1448.8605, 1475.6832, 1617.9929, 1617.9929, 1732.0273, 1901.1764, 1940.8547, 1993.8938, 2056.9478, 2193.0378, 2211.0134, 2221.0344, 2225.0469, 2230.1272, 2233.0085, 2239.0554, 2248.9812, 2261.0361, 2265.0583, 2283.0833, 2470.2014, 2477.1138, 2477.1138, 2492.1714, 2499.1167, 3337.7234

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 (811.4696,+): <no title>
 Query2 (842.4688,+): <no title>
 Query3 (848.4903,+): <no title>



Query4 (850.0149,1+): <no title>
Query5 (850.5021,1+): <no title>
Query6 (853.4834,1+): <no title>
Query7 (856.4824,1+): <no title>
Query8 (864.4868,1+): <no title>
Query9 (865.9890,1+): <no title>
Query10 (868.5110,1+): <no title>
Query11 (870.5007,1+): <no title>
Query12 (876.9973,1+): <no title>
Query13 (882.5262,1+): <no title>
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Query15 (892.9677,1+): <no title>
Query16 (951.5844,1+): <no title>
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Query76 (3337.7234,1+): <no title>

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