

1. P67870 Score: 81 Expect: 0.00017 Casein kinase II subunit beta OS=Homo sapiens GN=CSNK2B PE=1 SV=1

Nominal mass (M_r): 25268; Calculated pI value: 5.33

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 69

Number of mass values matched: 7

Sequence Coverage: 16%

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
889.4958	888.4885	888.4738	0.0147	93	- 100	0	---	R.GIAQMLEK.Y
905.4865	904.4792	904.4688	0.0105	93	- 100	0	---	R.GIAQMLEK.Y + Oxidation (M)
1013.4557	1012.4484	1012.4358	0.0126	140	- 147	0	---	K.CMDVYTPK.S
1029.4467	1028.4394	1028.4307	0.0087	140	- 147	0	---	K.CMDVYTPK.S + Oxidation (M)
1084.6104	1083.6031	1083.5937	0.0094	178	- 186	0	---	K.RPANQFVPR.L
1390.5920	1389.5847	1389.5771	0.0076	101	- 111	0	58	K.YQQGDFGYCPR.V
1390.5962	1389.5889	1389.5771	0.0118	101	- 111	0	---	K.YQQGDFGYCPR.V

2. P78371 Score: 119 Expect: 2.8e-07 Chaperonin containing TCP1, subunit 2 (beta), isoform CRA_c [Homo sapiens]

Nominal mass (Mr): 53027; Calculated pI value: 6.00

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 20

Number of mass values matched: 11

Sequence Coverage: 30%

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
1130.5544	1129.5471	1129.5451	1.81	238	- 246	0	K.HGINCFINR.Q
1251.6726	1250.6653	1250.6983	-26.33	145	- 156	0	K.GSGNLEAIHIK.K
1291.6986	1290.6913	1290.7197	-21.96	74	- 84	0	K.IHPQTIIAGWR.E
1330.6541	1329.6468	1329.6524	-4.21	330	- 341	0	R.GATQQILDEAER.S
1530.6963	1529.6890	1529.6892	-0.16	420	- 434	0	R.AAHSEGNTTAGLDMR.E
1546.6851	1545.6778	1545.6842	-4.11	420	- 434	0	R.AAHSEGNTTAGLDMR.E + Oxidation (M)
1548.7639	1547.7566	1547.7865	-19.33	11	- 25	0	R.DASLMVTNDGATILK.N
1656.7777	1655.7705	1655.8002	-17.98	92	- 107	0	R.EALLSSAVDHGSDEVK.F
2041.0169	2040.0096	2040.0415	-15.63	158	- 176	1	K.LGGSLADSYLDEGFLLDKK.I
2097.1093	2096.1020	2096.1154	-6.36	276	- 295	0	R.LALVTGGEIASTFDHPELVK.L
2288.1597	2287.1524	2287.1544	-0.86	43	- 64	0	R.VQDDEVDGTTSVTVLAAELLR.E

3. P31146 Score: 118 Expect: 3.6e-07 coronin-like protein

Nominal mass (Mr): 51722; Calculated pI value: 6.12

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 10

Number of mass values matched: 8

Sequence Coverage: 19%

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
883.4526	882.4453	882.4712	-29.31	13	- 20	0	R.HVFGQPAK.A
894.5072	893.5000	893.4971	3.24	234	- 241	0	K.ILTTGFSR.M
1026.5682	1025.5609	1025.6121	-49.87	384	- 393	0	R.DAGPLLISLK.D
1138.4818	1137.4746	1137.4907	-14.18	187	- 196	0	R.DGGLICTSCR.D
1155.4611	1154.4538	1154.4662	-10.77	21	- 29	0	K.ADQCYEDVR.V
1319.6659	1318.6586	1318.6854	-20.33	215	- 225	0	K.DRPHEGTRPVR.A
1502.6999	1501.6926	1501.7009	-5.50	417	- 432	0	R.AAPEASGTPSSDAVSR.L
1796.7666	1795.7593	1795.8200	-33.79	30	- 45	0	R.VSQTTWDSGFCVNP.K.F

4. P05198 Score: 109 Expect: 2.6e-007 Eukaryotic translation initiation factor 2 subunit 1 OS=Homo sapiens GN=EIF2S1 PE=1 SV=3

Nominal mass (M_r): 36374; Calculated pI value: 5.02

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 41

Number of mass values matched: 13

Sequence Coverage: 40%

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
851.4998	850.4925	850.4912	0.0013	107	- 113	0	K.TVYSILR.H
893.5442	892.5369	892.5494	-0.0125	227	- 234	0	K.INLIAPPR.Y
1214.6241	1213.6168	1213.6013	0.0156	235	- 244	0	R.YVMTTTTLER.T
1230.6190	1229.6117	1229.5962	0.0155	235	- 244	0	R.YVMTTTTLER.T + Oxidation (M)
1240.7024	1239.6951	1239.7047	-0.0096	174	- 183	1	R.EVLINNINRR.L
1244.6217	1243.6144	1243.5985	0.0159	144	- 154	0	K.RPGYGAYDAFK.H
1264.6146	1263.6073	1263.6095	-0.0022	124	- 133	0	K.DEQLESLEFQR.T
1272.6345	1271.6272	1271.6186	0.0086	134	- 143	1	R.TAWVFDDKYK.R
1314.7419	1313.7346	1313.7237	0.0109	65	- 75	1	R.IGRNECVVIR.V
1320.6627	1319.6554	1319.6655	-0.0101	266	- 276	1	K.RGVFNVQMEPK.V + Oxidation (M)
1392.6992	1391.6919	1391.6768	0.0151	2	- 12	1	M.PGLSCRFYQHK.F
1450.6831	1449.6758	1449.6592	0.0167	214	- 226	0	R.AGLNCSTENMPIK.I + Oxidation (M)
1872.8926	1871.8853	1871.8611	0.0243	193	- 209	0	R.ADIEVACYGYEGIDAVK.E

5. P00883 Score: 190 Expect: 2.3e-14 Chain A, Human Muscle Fructose 1,6-Bisphosphate Aldolase Complexed With Fructose 1,6-Bisphosphate

Nominal mass (Mr): 39720; Calculated pI value: 8.39

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 27

Number of mass values matched: 14

Sequence Coverage: 46%

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
1434.6873	1433.6800	1433.7191	-27	1	12	0	-.PYQYPALTPEQK.K
940.4631	939.4558	939.4774	-23	14	21	0	K.ELSDIAHR.I
1332.6630	1331.6557	1331.6932	-28	28	41	0	K.GILAADESTGSIK.R
1646.7950	1645.7877	1645.8019	-9	43	56	1	R.LQSIGTENTEENRR.F
1044.5622	1043.5549	1043.5611	-6	60	68	0	R.QLLLTADDR.
2088.0665	2087.0592	2087.0874	-13	69	86	0	R.VNPCIGGVILFHETLYQK.A
1342.7024	1341.6951	1341.7041	-7	87	98	0	K.ADDGRPFQVIK.S
2272.1360	2271.1287	2271.1343	-2	111	133	0	K.GVVPLAGTNGETTTQGLDGLSER.C
2123.0775	2122.0703	2122.0840	-6	153	172	0	K.IGEHTPSALAIMENANVLAR.Y Oxidation (M)
1675.8306	1674.8233	1674.8399	-10	243	257	0	K.FSHEEIAMATVTALR.R
1691.8138	1690.8065	1690.8348	-17	243	257	0	K.FSHEEIAMATVTALR.R Oxidation (M)
1847.9185	1846.9113	1846.9359	-13	243	258	1	K.FSHEEIAMATVTALRR.T Oxidation (M)
1808.9189	1807.9117	1807.9443	-18	289	303	0	K.CPLLKPWALTFSYGR.A
1093.5652	1092.5579	1092.5563	1	322	330	1	K.AAQEEYVKR.A

6. P62081 Score: 107 Expect: 4.1e-007 40S ribosomal protein S7 OS=Homo sapiens GN=RPS7 PE=1 SV=1

Nominal mass (M_r): 22113; Calculated pI value: 10.09

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 12

Number of mass values matched: 4

Sequence Coverage: 12%

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
944.5199	943.5126	943.5086	0.0040	50	- 58	1	8	K.EIEVGGGRK.A
969.5694	968.5621	968.5555	0.0066	91	- 98	0	---	K.HVVFIAQR.R
969.5717	968.5644	968.5555	0.0089	91	- 98	0	35	K.HVVFIAQR.R
1656.8793	1655.8720	1655.8842	-0.0121	42	- 57	1	29	R.ELNITAAKEIEVGGGR.K

7. P07437 Score: 74 Expect: 0.00091 Tubulin beta chain OS=Homo sapiens GN=TUBB PE=1 SV=2

Nominal mass (M_r): 50095; Calculated pI value: 4.78

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 65

Number of mass values matched: 13

Sequence Coverage: 26%

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
1028.5284	1027.5211	1027.5121	0.0091	351	- 359	0	K.TAVCDIPPR.G
1077.5402	1076.5329	1076.5250	0.0079	155	- 162	1	K.IREEYPDR.I
1130.5961	1129.5888	1129.5880	0.0009	242	- 251	0	R.FPGQLNADLR.K
1159.6273	1158.6200	1158.6219	-0.0019	253	- 262	0	K.LAVNMVPPFR.L + Oxidation (M)
1229.5757	1228.5684	1228.5910	-0.0226	381	- 390	0	R.ISEQFTAMFR.R
1245.6050	1244.5977	1244.5859	0.0118	381	- 390	0	R.ISEQFTAMFR.R + Oxidation (M)
1301.6370	1300.6297	1300.6299	-0.0001	47	- 58	0	R.ISVYYNEATGGK.Y
1326.7136	1325.7063	1325.7125	-0.0062	351	- 362	1	K.TAVCDIPPRGLK.M
1335.6945	1334.6872	1334.6904	-0.0032	163	- 174	0	R.IMNTFSVVPSPK.V + Oxidation (M)
1615.8684	1614.8611	1614.8287	0.0325	63	- 77	0	R.AILVDLEPGTMDSVR.S
1631.8376	1630.8303	1630.8236	0.0067	63	- 77	0	R.AILVDLEPGTMDSVR.S + Oxidation (M)
1659.8854	1658.8781	1658.8879	-0.0098	283	- 297	0	R.ALTVPILTQQVFDK.N
1696.8754	1695.8681	1695.8256	0.0425	337	- 350	0	K.NSSYFVEWIPNNVK.T

8. P14625 Score: 127 Expect: 4.1e-009 Tumor rejection antigen 1 OS=Homo sapiens GN=HSP90B1 PE=1 SV=1

Nominal mass (M_r): 92696; Calculated pI value: 4.76

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 42

Number of mass values matched: 19

Sequence Coverage: 19%

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
876.4645	875.4572	875.4501	0.0071	684	- 690	0	K.TFEINPR.H
919.5422	918.5349	918.5287	0.0063	96	- 102	1	K.NKEIFLR.E
979.5009	978.4936	978.4883	0.0054	734	- 741	1	K.AYGDRIER.M
1004.5504	1003.5431	1003.5450	-0.0019	683	- 690	1	K.KTFEINPR.H
1015.4598	1014.4525	1014.4658	-0.0133	396	- 404	0	R.GLFDEYGSK.K
1081.5607	1080.5534	1080.5352	0.0182	76	- 84	0	K.FAFQAEVNR.M
1139.5865	1138.5792	1138.5730	0.0062	494	- 503	0	K.LGVIEDHSNR.T
1150.5499	1149.5426	1149.5302	0.0125	548	- 557	0	K.EAESSPFVER.L
1187.6870	1186.6797	1186.6710	0.0087	385	- 395	0	K.SILFVPTSAPR.G
1278.6436	1277.6363	1277.6251	0.0112	547	- 557	1	R.KEAESSPFVER.L
1396.7245	1395.7172	1395.7218	-0.0046	494	- 505	1	K.LGVIEDHSNRTR.L
1417.7162	1416.7089	1416.6885	0.0204	672	- 683	1	K.DISTNYASQKK.T
1418.6913	1417.6840	1417.6660	0.0181	535	- 546	1	K.QDKIYFMAGSSR.K + Oxidation (M)
1425.7090	1424.7017	1424.7048	-0.0030	73	- 84	1	K.SEKFAFQAEVNR.M
1485.7811	1484.7738	1484.7470	0.0268	435	- 448	0	K.GVVSDDDLPLNVS.R.E
1529.7734	1528.7661	1528.7667	-0.0006	143	- 156	0	K.NLLHVTDGTGVMTR.E + Oxidation (M)
1544.8385	1543.8312	1543.8205	0.0107	103	- 116	1	R.ELISNASDALDKIR.L
1627.7271	1626.7198	1626.7058	0.0140	416	- 428	0	R.VFITDDFHDMPK.Y + 2 Oxidation (M)
1783.8442	1782.8369	1782.8069	0.0300	415	- 428	1	R.RVFITDDFHDMPK.Y + 2 Oxidation (M)

9. P62258 Score: 111 Expect: 1.6e-007 14-3-3 protein epsilon OS=Homo sapiens GN=YWHAE PE=1 SV=1

Nominal mass (M_r): 29326; Calculated pI value: 4.63

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 43

Number of mass values matched: 15

Sequence Coverage: 44%

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
917.5410	916.5337	916.5229	0.0108	62	- 69	0	R.IISSIEQK.E
922.4335	921.4262	921.4127	0.0136	124	- 130	1	K.MKGDYHR.Y + Oxidation (M)
1194.5953	1193.5880	1193.5928	-0.0047	143	- 153	0	K.EAAENSLVAYK.A
1237.6423	1236.6350	1236.6462	-0.0112	107	- 118	0	K.HLIPAANTGESK.V
1256.5961	1255.5888	1255.5833	0.0056	131	- 141	0	R.YLAEFATGNDR.K
1291.5752	1290.5679	1290.5472	0.0208	20	- 29	1	R.YDEMVESMKK.V + 2 Oxidation (M)
1384.6934	1383.6861	1383.6782	0.0079	131	- 142	1	R.YLAEFATGNDRK.E
1441.7052	1440.6979	1440.6918	0.0061	84	- 94	1	R.EYRQMVETELK.L + Oxidation (M)
1447.7321	1446.7248	1446.7024	0.0224	30	- 42	0	K.VAGMDVELTVEER.N
1463.7198	1462.7125	1462.6973	0.0152	30	- 42	0	K.VAGMDVELTVEER.N + Oxidation (M)
1476.7738	1475.7665	1475.7364	0.0302	95	- 106	0	K.LICCDILDVLDK.H
1575.8325	1574.8252	1574.7973	0.0279	29	- 42	1	K.KVAGMDVELTVEER.N
1591.8267	1590.8194	1590.7923	0.0272	29	- 42	1	K.KVAGMDVELTVEER.N + Oxidation (M)
1819.9930	1818.9857	1818.9298	0.0559	154	- 170	0	K.AASDIAMTELPPTHPIR.L
1835.9967	1834.9894	1834.9247	0.0647	154	- 170	0	K.AASDIAMTELPPTHPIR.L + Oxidation (M)

10. P07910 Score: 146 Expect: 5.1e-011 Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4

Nominal mass (M_r): 33707; Calculated pI value: 4.95

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 13

Number of mass values matched: 8

Sequence Coverage: 10%

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Ions	Peptide
943.5801	942.5728	942.5651	0.0078	143	- 151	0	49	R.VPPPPPIAR.A
943.5998	942.5925	942.5651	0.0275	143	- 151	0	(49)	R.VPPPPPIAR.A
943.6174	942.6101	942.5651	0.0451	143	- 151	0	---	R.VPPPPPIAR.A
1329.6591	1328.6518	1328.6513	0.0006	51	- 61	0	34	K.GFAFVQYVNER.N
1329.6652	1328.6579	1328.6513	0.0067	51	- 61	0	(32)	K.GFAFVQYVNER.N
1329.7025	1328.6952	1328.6513	0.0440	51	- 61	0	---	K.GFAFVQYVNER.N
1343.6757	1342.6684	1342.6768	-0.0084	31	- 42	1	31	K.SDVEAIFSKYGK.I
1343.7273	1342.7200	1342.6768	0.0432	31	- 42	1	---	K.SDVEAIFSKYGK.I

11. Q16576 Score: 139 Expect: 2.6e-010 Histone-binding protein RBBP7 OS=Homo sapiens GN=RBBP7 PE=1 SV=1

Nominal mass (M_r): 48132; Calculated pI value: 4.89

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 24

Number of mass values matched: 7

Sequence Coverage: 10%

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Ions	Peptide
934.4075	933.4002	933.4742	-0.0740	251	- 257	0	---	K.LMIWDTR.S
934.4961	933.4888	933.4742	0.0146	251	- 257	0	17	K.LMIWDTR.S
973.5508	972.5435	972.5392	0.0043	296	- 303	0	16	K.TVALWDLR.N
1067.5367	1066.5294	1066.5155	0.0139	120	- 128	0	42	K.INHEGEVNR.A
1321.6486	1320.6413	1320.7077	-0.0664	15	- 24	1	---	R.VINEEYKIWK.K
1428.6493	1427.6420	1427.7231	-0.0811	131	- 142	0	---	R.YMPQNPHEIATK.T + Oxidation (M)
1428.7227	1427.7154	1427.7231	-0.0077	131	- 142	0	24	R.YMPQNPHEIATK.T + Oxidation (M)

12. Q14566 Score: 95 Expect: 0.0031 Minichromosome maintenance complex 6

Nominal mass (Mr): 94002; Calculated pI value: 5.32

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 22

Number of mass values matched: 10

Sequence Coverage: 13%

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
970.4852	969.4779	969.4742	3.81	86	- 92	0	K.LMIWDTR.S
1031.4950	1030.4877	1030.4542	32.5	715	- 722	0	K.LMIWDTR.S
1136.5860	1135.5788	1135.5986	-17.44	566	- 574	0	K.TVALWDLR.N
1282.7025	1281.6952	1281.6903	3.83	86	- 95	0	K.INHEGEVNR.A
1359.7176	1358.7103	1358.6976	9.37	518	- 529	1	R.VINEEYKIWK.K
1471.7279	1470.7206	1470.7143	4.28	109	- 120	1	R.VINEEYKIWK.K
1617.8218	1616.8146	1616.8167	-1.32	296	- 309	1	R.VINEEYKIWK.K
1629.8884	1628.8811	1628.8885	-4.57	46	- 58	1	R.VINEEYKIWK.K
1685.8642	1684.8569	1684.8533	2.17	497	- 512	0	R.YMPQNPHIATK.T + Oxidation (M)
2104.0626	2103.0553	2103.0266	13.6	383	- 402	0	R.YMPQNPHIATK.T + Oxidation (M)

13. P33993 Score: 119 Expect: 2.8e-07 Minichromosome maintenance complex 7

Nominal mass (Mr): 81856; Calculated pI value: 5.98

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 18

Number of mass values matched: 11

Sequence Coverage: 15%

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
849.4602	848.4529	848.4504	2.91	33	- 39	0	K.YGNQLVR.L
1029.5913	1028.5840	1028.5978	-13.40	472	- 481	0	K.AGILTTLNAR.C
1094.5750	1093.5678	1093.5768	-8.22	388	- 396	0	K.SQLLSYIDR.L
1187.6596	1186.6523	1186.6670	-12.40	408	- 420	0	R.GSSGVGLTAAVLR.D
1258.6384	1257.6311	1257.6353	-3.35	97	- 106	0	K.DVLDVYIEHR.L
1317.6729	1316.6657	1316.6936	-21.21	252	- 263	0	R.SITVLVEGENTR.I
1363.6683	1362.6610	1362.6714	-7.64	482	- 494	0	R.CSILAAANPAYGR.Y
1449.6691	1448.6618	1448.6718	-6.89	121	- 132	0	R.SPQNQYPAELMR.R + Oxidation (M)
1473.7885	1472.7812	1472.8100	-19.52	654	- 666	0	R.TQRPADVIFATVR.E
1589.7974	1588.7901	1588.7780	7.64	121	- 133	1	R.SPQNQYPAELMRR.F
1825.8821	1824.8748	1824.9271	-28.67	133	- 147	1	R.RFELYFQGPSSNKPR.V

14. Q01105 Score: 82 Expect: 0.00012 Protein SET

Nominal mass (Mr): 33469; Calculated pI value: 4.23

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 28

Number of mass values matched: 8

Sequence Coverage: 22%

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
908.4929	907.4856	907.4763	0.0093	69	- 75	1	K.VEQKYNK.L
1063.5929	1062.5856	1062.5974	-0.0118	76	- 83	1	K.LRQPFFQK.R
950.5245	949.5172	949.5134	0.0039	78	- 84	1	R.QPFFQKR.S
1208.6066	1207.5993	1207.5972	0.0021	123	- 132	0	R.VEVTEFEDIK.S
1671.8676	1670.8603	1670.8151	0.0452	123	- 136	1	R.VEVTEFEDIKSGYR.I
1840.8586	1839.8513	1839.7991	0.0522	137	- 150	0	R.IDFYFDENPYFENK.V
1446.6627	1445.6554	1445.6422	0.0132	155	- 167	0	K.EFHLNESGDPSSK.S
891.4749	890.4676	890.4861	-0.0185	168	- 174	1	K.STEIKWK.S

15. Q92688 Score: 103 Expect: 1e-006 Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens
GN=ANP32B PE=1 SV=1

Nominal mass (M_r): 28941; Calculated pI value: 3.94

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 65

Number of mass values matched: 13

Sequence Coverage: 40%

Observed	Mr (expt)	Mr (calc)	Delta	Start	End	Miss	Peptide
860.4653	859.4580	859.4399	0.0181	69	- 75	0	K.LELSEN.R.I
884.5167	883.5094	883.4988	0.0107	13	- 20	1	R.NRTPAAVR.E
936.5888	935.5815	935.5665	0.0151	6	- 12	1	R.RIHLELR.N
988.5496	987.5423	987.5349	0.0075	68	- 75	1	K.KLELSEN.R.I
990.5106	989.5033	989.4852	0.0182	21	- 28	0	R.ELVLDNCK.S
1015.5599	1014.5526	1014.5597	-0.0071	102	- 110	0	K.DISTLEPLK.K
1143.6549	1142.6476	1142.6547	-0.0070	102	- 111	1	K.DISTLEPLKK.L
1209.6169	1208.6096	1208.6111	-0.0014	76	- 86	0	R.IFGGLDMLAEK.L + Oxidation (M)
1256.7369	1255.7296	1255.7387	-0.0091	100	- 110	1	K.LKDISTLEPLK.K
1420.7927	1419.7854	1419.7834	0.0021	87	- 99	0	K.LPNLTHLNLSGK.L
1491.7391	1490.7318	1490.7035	0.0284	21	- 33	1	R.ELVLDNCKSNDGK.I
1566.8392	1565.8319	1565.8089	0.0230	138	- 150	0	K.LLPQLTYLDGYDR.E
1972.9976	1971.9903	1971.8996	0.0907	117	- 132	0	K.SLDLFNCEVTNLNDYR.E

16. P14866 Score: 72 Expect: 0.013 Heterogeneous nuclear ribonucleoprotein L, isoform CRA_a [Homo sapiens]

Nominal mass (Mr): 60693; Calculated pI value: 6.81

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 10

Number of mass values matched: 5

Sequence Coverage: 9%

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
923.4484	922.4411	922.4443	-3.50	313	- 321	0	R.MGPPVGGHR.R + Oxidation (M)
977.5262	976.5189	976.5341	-15.59	233	- 240	0	K.IEYAKPTR.L
1076.5939	1075.5866	1075.6138	-25.27	66	- 75	0	K.TPASPVVHIR.G
1263.5970	1262.5898	1262.6295	-31.48	537	- 547	0	K.NPNGPYPYTLK.L
1881.9111	1880.9039	1880.8687	18.7	198	- 214	0	K.NGVQAMVEFDSVQSAQR.A + Oxidation (M)

17. P19338 Score: 82 Expect: 0.0015 Nucleolin, isoform CRA_c [Homo sapiens]

Nominal mass (Mr): 58576; Calculated pI value: 4.57

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 16

Number of mass values matched: 8

Sequence Coverage: 15%

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
812.4602	811.4530	811.4552	-2.73	381	- 387	0	R.LELQGPR.G
880.4012	879.3939	879.3835	11.9	294	- 300	0	K.GQNQDYR.G
940.5023	939.4950	939.5065	-12.31	256	- 263	0	K.GIAYIEFK.T
1000.5338	999.5265	999.5349	-8.38	160	- 168	0	K.NDLAVVDVR.I
1160.5628	1159.5555	1159.5761	-17.75	284	- 293	0	R.SISLYYTGEK.G
1178.5694	1177.5621	1177.5615	0.53	237	- 246	1	K.EVFEDAAEIR.L
1192.6042	1191.5969	1191.6095	-10.62	426	- 436	0	R.IVTDRETGSSK.G
2200.0845	2199.0772	2199.0179	27.0	404	- 423	1	K.GLSEDTTEETLKESFDGSR.A

18. Q99733 Score: 73 Expect: 0.012 Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1

Nominal mass (M_r): 42968; Calculated pI value: 4.60

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 12

Number of mass values matched: 6

Sequence Coverage: 18%

Observed	Mr(expt)	Mr(calc)	ppm	Start	End	Miss	Peptide
899.5310	898.5237	898.5236	0.16	37	- 44	0	R.VLAALQER.L
1217.5430	1216.5357	1216.5870	-42.16	27	- 36	0	K.LTDQVMQNPR.V + Oxidation (M)
1328.6332	1327.6259	1327.6812	-41.64	95	- 105	0	K.YAALYQPLFDK.R
1336.6024	1335.5952	1335.6095	-10.75	84	- 93	0	K.FYEEVHDLER.K
1484.7619	1483.7546	1483.7823	-18.66	95	- 106	1	K.YAALYQPLFDKR.K
1910.9463	1909.9390	1909.9785	-20.70	45	- 61	0	R.LDNVPHTPSSYIETLPK.A

19. Q9Y3F4 Score: 90 Expect: 2.2e-005 Serine-threonine kinase receptor-associated protein OS=Homo sapiens GN=STRAP PE=1 SV=1

Nominal mass (M_r): 38756; Calculated pI value: 4.98

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 13

Number of mass values matched: 2

Sequence Coverage: 5%

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1900.8192	1899.8119	1899.8486	-0.0367	273	- 290	0	81	R.FSPDGELYASGSEDGTLR.L
1900.8564	1899.8491	1899.8486	0.0005	273	- 290	0	(80)	R.FSPDGELYASGSEDGTLR.L

20. P06576 Score: 108 Expect: 3.2e-007 ATP synthase subunit beta, mitochondrial OS=Homo sapiens GN=ATP5B PE=1 SV=3

Nominal mass (M_r): 56525; Calculated pI value: 5.26

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 17

Number of mass values matched: 3

Sequence Coverage: 6%

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Ions	Peptide
1617.8093	1616.8020	1616.7980	0.0040	265	- 279	0	16	K.VALVYQMNEPPGAR.A + Oxidation (M)
1988.0143	1987.0070	1987.0262	-0.0191	388	- 406	0	---	R.AIAELGIYPAVDPLDSTSR.I
1988.0284	1987.0211	1987.0262	-0.0050	388	- 406	0	78	R.AIAELGIYPAVDPLDSTSR.I

21. P11021 Score: 164 Expect: 9e-12 Heat shock 70 kDa protein

Nominal mass (Mr): 72185; Calculated pI value: 5.03

Fixed modifications: Carbamidomethyl (C)

Variable modifications: Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P

Number of mass values searched: 27

Number of mass values matched: 15

Sequence Coverage: 29%

Observed	Mr (expt)	Mr (calc)	ppm	Start	End	Miss	Peptide
997.5235	996.5162	996.5101	6.19	297	- 305	0	K.ALSSQHQR.I
1074.5627	1073.5554	1073.5465	8.25	523	- 531	0	K.ITITNDQNR.L
1191.6326	1190.6254	1190.6295	-3.49	464	- 473	0	K.VYEGERPLTK.D
1210.5730	1209.5657	1209.5778	-10.03	376	- 385	1	K.EFFNGKEPSR.G
1233.6096	1232.6023	1232.6183	-12.97	186	- 197	0	K.DAGTIAGLNVMR.I + Oxidation (M)
1460.7510	1459.7438	1459.7518	-5.54	353	- 366	0	K.SDIDEIVLVGGSTR.I
1528.7387	1527.7314	1527.7391	-5.07	324	- 335	1	R.AKFEELNMDLFR.S + Oxidation (M)
1555.7690	1554.7617	1527.7391	-15.79	47	- 60	1	K.NGRVEIANDQGNI.I
1566.7781	1565.7708	1565.7726	-1.11	61	- 74	0	R.ITPSYVAFTPEGER.L
1588.8400	1587.8327	1587.8468	-8.85	352	- 366	1	K.KSDIDEIVLVGGSTR.I
1604.8328	1603.8255	1603.8570	-19.61	124	- 138	0	K.TKPVIQVDIGGGQTK.T
1815.9849	1814.9776	1814.9890	-6.26	198	- 214	1	R.IINEPTAAAIAYGLDKR.E
1887.9672	1886.9599	1886.9639	-2.14	165	- 181	0	K.VTHAVVTVPAYFNDAQR.Q
1934.0055	1932.9982	1933.0058	-3.91	474	- 491	0	K.DNHLGTFDLTGIPPAPR.G
2164.9837	2163.9764	2163.9848	-3.87	306	- 323	0	R.IEIESFYEGEDFSETLTR.A