

ID	Protein name	UniProt Accession	MW [kDa]	pI	Score	Queries matched	Sequence coverage (%)	MS/MS analysis
6355	Spectrin alpha chain, brain	Q13813	284	5.2	60	5	2	Start-End Observed M(xcpt) M(cale) Delta Miss Sequence 1335-1343 520,7646 1039,5146 1039,5047 0.0100 0 K.LIGDSDHLDLQRF 1360-1369 509,7782 1017,5418 1017,5342 0.0076 0 R.GLVSDELAKD 1620-1630 532,7423 1063,4700 1063,4604 0.0096 0 R.GACAGSEDAVKA Carbamidomethyl (C) 1689-1698 543,8162 1085,6178 1085,6080 0.0098 0 K.DLAASVNNLLK 2007-2017 602,8475 1203,6804 1203,6711 -0.0094 0 R.DLSSVQNLTKQ Miss Sequence K.LIGDSDHLDLQRF R.GLVSDELAKD R.GACAGSEDAVKA K.DLAASVNNLLK R.DLSSVQNLTKQ
6488	Gelsolin	P06396	85.6	5.9	143	4	4	Start-End Observed M(xcpt) M(cale) Delta Miss Sequence 584-588 441,7265 883,4594 883,4494 0.0088 0 K.HASDPTIKM 584-584 537,7705 1073,5264 1073,5101 0.0163 0 R.EGGGTAPASTRL 616-623 444,2583 886,5020 886,4872 0.0148 0 K.TGAQELLRV 730-738 539,7720 1077,5294 1077,5091 0.0204 0 R.YHETDPANRD Miss Sequence K.HASDPTIKM R.EGGGTAPASTRL K.TGAQELLRV YHETDPANRD
6491	Gelsolin	P06396	85.6	5.9	178	4	4	Start-End Observed M(xcpt) M(cale) Delta Miss Sequence 169-177 425,7389 849,4632 849,4709 -0.0076 1 K.KGGVANGFK.H 354-364 537,7607 1073,5248 1073,5101 0.0147 0 R.EGGGTAPASTRL 416-423 444,2583 886,5020 886,4872 0.0148 0 K.TGAQELLRV 460-467 539,7720 1077,5294 1077,5091 0.0204 0 R.YHETDPANRD Miss Sequence K.KGGVANGFK.H R.EGGGTAPASTRL K.TGAQELLRV YHETDPANRD
6499	Mitochondrial inner membrane protein (Mitofilin)	Q16891	83.6	6.1	153	7	8	Start-End Observed M(xcpt) M(cale) Delta Miss Sequence 33-45 623,2793 1244,5440 1244,5885 -0.0444 0 R.YSTSGSGLTIGKI 258-270 460,5325 1378,5757 1378,6398 -0.0641 1 K.AAMDNSEIAGEKKS Oxidation (M) 287-297 558,2816 1114,5886 1114,5870 -0.0383 0 K.AYDEADALLKA 443-451 482,7455 963,4764 963,5138 -0.0373 1 K.RAFDSAFAKA 444-451 404,6966 807,3786 807,4127 -0.0340 0 R.AFDSAFAKA 517-525 575,2766 1148,5386 1148,5826 -0.0439 0 K.LSQEQLQPR.R 618-623 444,2583 886,5020 886,4872 0.0148 0 K.TGAQELLRV Miss Sequence R.YSTSGSGLTIGKI K.AAMDNSEIAGEKKS Oxidation (M) K.AYDEADALLKA K.RAFDSAFAKA R.AFDSAFAKA K.LSQEQLQPR.R K.TGAQELLRV
6532	Vesicle-tuning ATPase	P46459	82.5	6.5	120	6	7	Start-End Observed M(xcpt) M(cale) Delta Miss Sequence 28-38 643,3224 1284,6302 1284,6575 -0.0273 0 K.IPFGSQHVIVR.T 151-161 624,2993 1246,5840 1246,6115 -0.0274 0 K.DIEADMPISLK.G Oxidation (M) 470-477 452,2353 902,4560 902,4821 -0.0261 0 K.AESLQVTR.G 573-581 500,2309 998,4472 998,4743 -0.0270 0 K.MIGFSETAK.C Oxidation (M) 640-648 487,2864 972,5582 972,5968 -0.0385 0 K.LLIGTTSR.K 692-699 444,7489 887,4832 887,5076 -0.0244 0 R.ITLMAQQVK.G Miss Sequence K.IPFGSQHVIVR.T K.DIEADMPISLK.G Oxidation (M) K.AESLQVTR.G K.MIGFSETAK.C Oxidation (M) K.LLIGTTSR.K R.ITLMAQQVK.G
6542	78 kDa glucose-regulated protein	P11021	72.3	5.1	75	3	4	Start-End Observed M(xcpt) M(cale) Delta Miss Sequence 64-74 618,8248 1237,6277 1237,6277 0.0000 0 K.DAGTHAGLVNMR.I Oxidation (M) 186-197 617,3221 1232,6296 1232,6183 0.0113 0 K.DAGTHAGLVNMR.I Oxidation (M) 533-540 493,7645 985,5144 985,5080 0.0065 0 R.LTPEEER.M Miss Sequence K.DAGTHAGLVNMR.I Oxidation (M) R.LTPEEER.M
6543	NADH-nucleonine oxidoreductase 75 kDa subunit, mitochondrial	P28331	79.4	5.9	291	5	9	Start-End Observed M(xcpt) M(cale) Delta Miss Sequence 185-200 804,9145 1607,8144 1607,7791 0.0353 0 R.FASEIAGVDLITGTR.G 326-336 591,3159 1180,6172 1180,5910 0.0262 0 R.VAGMLQSQFGK.D Oxidation (M) 484-499 764,9375 1527,8604 1527,8256 0.0348 0 R.NDGAALAAVSSIAQK.I 502-511 449,2585 1096,5024 1096,4889 0.0165 0 R.MFSGYVGDWIK.V Oxidation (M) 518-527 575,2766 1148,5386 1148,5826 -0.0439 0 K.LSQEQLQPR.R Miss Sequence R.FASEIAGVDLITGTR.G R.VAGMLQSQFGK.D Oxidation (M) R.NDGAALAAVSSIAQK.I R.MFSGYVGDWIK.V Oxidation (M) K.LSQEQLQPR.R
6625	Syntaxin-binding protein 1	P61764	67.5	6.5	154	10	14	Start-End Observed M(xcpt) M(cale) Delta Miss Sequence 14-20 436,2430 870,4714 870,4633 0.0081 0 K.IMHDIKK.Oxidation (M) 14-21 500,2895 998,5644 998,5583 0.0062 1 K.IMHDIKK.V Oxidation (M) 30-39 588,3324 1174,6502 1174,6380 0.0122 0 K.VLVVQLSMRM Oxidation (M) 197-208 671,3821 1340,7496 1340,7299 0.0197 0 K.DNALLAQIQDK.L 214-225 624,7628 1247,5310 1247,4976 0.0334 0 K.ADDPTMIGEGPDK.A Oxidation (M) 228-235 479,2864 956,5582 956,5655 -0.0072 0 R.SQLLILDR.G Miss Sequence K.IMHDIKK.Oxidation (M) K.VLVVQLSMRM Oxidation (M) K.DNALLAQIQDK.L K.ADDPTMIGEGPDK.A Oxidation (M) R.SQLLILDR.G

6777	ATP synthase subunit alpha, mitochondrial	P25705	59.7	9.2	793	10	15	205-305 326-333 468-477 498-505	634.8405 489.7718 612.8185 518.7656	1267.6664 977.5290 1223.6224 1035.5138	0.0144 0.0075 0.0079 0.0029	0 K.HIAEYSOEYTR.S 1 R.DLSQLMK.M Oxidation (M) 0 R.ISEQYQLSR.W 0 K.HYPIYTR.S
6805	GliA fibrillary acidic protein	P14136	50	5.4	398	8	17	74-83 84-93 183-194 195-204 219-230 254-261 254-262 262-270 323-329 331-339	500.9254 486.7448 458.9163 513.8802 658.8820 423.2578 501.3111 518.2578 438.7563 453.7448	999.5702 992.5713 1373.7271 1025.5938 1315.7494 844.5010 1000.6076 1035.5019 875.4899 923.4730	-0.0010 -0.0006 -0.0066 0.0069 0.0147 -0.0008 0.0047 -0.0008 0.0082 0.0041	0 K.VLSIGDGLAR.Y 0 K.VLQKDKG 1 R.SVRFHQIQGKA Oxidation (M) 0 K.AVDSLVPGR.G 0 K.TSHADITHNQK.R 0 R.STVAQLVK.R 1 R.STVAQLVK.R.L 1 K.RLTDADAMKY Oxidation (M) 0 R.CONSLLIRK Oxidation (M) 0 K.IELVQYR.E
6810	GliA fibrillary acidic protein	P14136	50	5.4	177	4	8	42-49 80-86 96-105 112-121 127-136 142-152 152-161 331-339	462.7495 429.2213 549.8221 589.3173 544.7901 608.3271 515.2654	923.4844 856.4280 1097.6296 1176.6139 1087.5856 1214.6255 1031.5162	-0.0054 -0.0050 0.0104 0.0114 0.0035 0.0141 0.0038	0 R.MPPPLPTR.V Oxidation (M) 0 R.FASYIEK.V 0 K.ALAELNQLR.A 0 K.LADYQAELE 0 R.LDQLTANSAR.L 0 R.DNLAQDLATVR.Q 0 R.DPDKLAL.L 0 R.DIEFGQLER.D
6811	GliA fibrillary acidic protein	P14136	50	5.4	302	6	12	42-49 80-86 96-105 112-121 210-217	462.7313 429.2211 549.8201 589.3158 493.7654	923.4880 856.4276 1097.6256 1176.6139 985.5192	-0.0018 -0.0084 0.0064 0.0032 -0.0030	0 K.MPPPLPTR.V Oxidation (M) 0 R.FASYIEK.V 0 K.ALAELNQLR.A 0 K.LADYQAELE 0 R.ELQELAR.Q
6986	Tubulin beta chain	Q13885	50	4.8	174	3	6	242-251 252-262 310-318	565.8047 580.3204 572.3101	1129.5948 1158.6262 1052.6019	0.0069 0.0043 0.0082	0 R.FPGQLNADLR.K 0 K.LAVNNVPPRL Oxidation (M) 0 R.KLYTVAIRK.G
6923	Fructose-bisphosphate aldolase A	P04075	39.4	8.3	86	5	17	29-42 44-57 244-259 323-331 332-342	666.8514 549.5922 616.6468 547.2745 566.7822	1331.6882 1645.7548 1846.9359 1092.5344 1131.5706	-0.0050 -0.0472 -0.0174 -0.0219 -0.0208	0 K.GILAADESTGSIAR.R 1 R.LQSIGTENTENR.R F 1 K.FSHEEAMATVTLRR.T Oxidation (M) 1 K.AAQEYVRR.A 0 R.ALANSLACQGY Carbamidomethyl (C)
6929	Aspartate aminotransferase, mitochondrial	P00505	47.5	9.1	665	10	27	60-68 69-78 95-107 126-139	498.7282 548.7441 748.8846 725.3704	995.4624 1158.6219 1495.7346 1448.7262	-0.0234 0.0043 0.0166 -0.0725	0 K.MNIGVGYR.D Oxidation (M) 0 R.FVYVQIISGIGALR.I 0 K.EYDPLGALAECK.A Carbamidomethyl (C) 0 R.FVYVQIISGIGALR.I

7025	N(G),N(G)- dimethylarginine dimethylaminohydrolase 1	O94760	31	5.3	314	7	18				<p>146-147 446-2320 890-4104 890-4074 -0.0470 0 R.LGASITLOR.F</p> <p>186-200 823-8751 1645-7356 1645-7294 -0.0062 0 K.TCGFDTGAIVEDISK.I Carbamidomethyl (C)</p> <p>280-287 478-2166 954-4186 954-4229 -0.0042 0 K.NMGLGHERY.V Oxidation (M)</p> <p>310-325 609-9976 1826-9710 1826-9825 -0.0115 0 K.ILRPMYSNPNLNGAR.I Oxidation (M)</p> <p>326-337 634-3727 1266-7308 1266-7296 0.0013 0 R.IAAALNTPDLR.K</p> <p>356-364 515-8088 1029-6030 1029-6182 -0.0152 1 R.TOLVSNLKK.E</p> <p>Start-End Observed M(pep) M(calc) Delta Miss Sequence</p> <p>35-42 4377133 873-4120 873-4192 -0.0072 0 K.GFVDVAR.A</p> <p>112-120 424-7422 1025-7025 1025-7056 -0.0028 0 K.GFVDPK.D Oxidation (M)</p> <p>137-145 541-7591 1254-6896 1254-6909 -0.0013 1 R.FHFGLSK.R</p> <p>137-145 541-8013 1081-5880 1081-5920 -0.0040 1 R.FEYVGLSKR.T</p> <p>150-159 532-7863 1063-5580 1063-5550 0.0031 0 R.GAEILADTFKD</p> <p>231-237 416-2475 830-4804 830-4875 -0.0071 0 K.GHVLHLR.T</p> <p>238-247 575-7648 1149-5150 1149-5190 -0.0039 0 R.TPEYVESAK.V</p> <p>Start-End Observed M(pep) M(calc) Delta Miss Sequence</p> <p>92-104 609-8918 1337-7690 1337-7126 0.0565 0 K.GGDVVVVPAGVPR.K Carbamidomethyl (C)</p> <p>177-185 406-7946 991-5746 991-5338 0.0408 0 R.ANTPVLEL.G (Ions.score.L3)</p> <p>202-209 675-8506 1469-6796 1469-6769 0.0287 0 K.GVVECFVKS.V Oxidation (M)</p> <p>242-257 727-8922 1453-7698 1453-6983 0.0715 0 K.AGAGSATLSMAYAGAR.F (Ions.score.I05)</p> <p>242-257 735-8912 1469-7678 1469-6933 0.0746 0 K.AGAGSATLSMAYAGAR.F Oxidation (M)</p> <p>270-279 577-3153 1152-6160 1152-5485 0.0675 0 K.EGVVCECFVKS.V Carbamidomethyl (C)</p> <p>315-324 566-8248 1131-6350 1131-5845 0.0505 0 K.MBSDAIPELK.A Oxidation (M)</p> <p>Start-End Observed M(pep) M(calc) Delta Miss Sequence</p> <p>177-185 496-7901 991-5656 991-5338 0.0318 0 R.ANTPVAELK.G</p> <p>192-203 574-3519 1146-6892 1146-6510 0.0383 0 R.VNVPVGGHAGK.T</p> <p>202-209 675-8506 1469-6796 1469-6769 0.0287 0 K.GVVECFVKS.V Oxidation (M)</p> <p>230-239 537-3137 1073-6128 1072-5764 0.0364 0 R.IQEAETEVK.A</p> <p>242-257 727-8895 1453-7644 1453-6983 0.0661 0 K.AGAGSATLSMAYAGAR.F</p> <p>270-279 577-3031 1152-5916 1152-5485 0.0431 0 K.EGVVCECFVKS.V Carbamidomethyl (C)</p> <p>315-324 566-8194 1131-6242 1131-5845 0.0397 0 K.MBSDAIPELK.A Oxidation (M)</p> <p>Start-End Observed M(pep) M(calc) Delta Miss Sequence</p> <p>79-91 745-3664 1488-7182 1488-7283 -0.0100 0 K.GYLGPQLDCLK.G Carbamidomethyl (C)</p> <p>92-104 609-8882 1337-7018 1337-7126 -0.0107 0 K.GGDVVVVPAGVPR.K Carbamidomethyl (C)</p> <p>177-185 406-7946 991-5746 991-5338 0.0408 0 R.ANTPVLEL.K</p> <p>177-185 406-7465 991-4784 991-5338 -0.0553 0 R.ANTPVAELK.A</p> <p>204-215 685-8841 1369-7536 1369-7639 -0.0103 0 K.TIPLISQCTPK.V Carbamidomethyl (C)</p> <p>216-229 780-8992 1559-7838 1559-7944 -0.0105 0 K.VDPQDQTLALIGR.I</p> <p>230-239 537-2898 1072-5650 1072-5764 -0.0114 0 R.IQEAETEVK.A</p> <p>242-257 727-8528 1453-6910 1453-6983 -0.0073 0 K.AGAGSATLSMAYAGAR.F</p> <p>238-269 672-3311 1342-6476 1342-6591 -0.0115 0 R.FVSLVDAMNGK.E Oxidation (M)</p> <p>315-324 566-7940 1131-5736 1131-5845 -0.0109 0 K.MBSDAIPELK.A Carbamidomethyl (C)</p> <p>Start-End Observed M(pep) M(calc) Delta Miss Sequence</p> <p>124-149 875-4641 2623-3705 2623-3705 -0.0000 0 R.IPADVPLTITSSLSDDGLVTVNGPR.K</p>
7065	Malate dehydrogenase, mitochondrial	P40926	35.5	8.9	326	7	20				
7081					313	7	23				
7086					682	12	38				
7216	Alpha-crystallin B chain	P02511	20	6.8	88	1	14				

7301	14-3-3 protein epsilon	P62258	29	4.6	215	8	22	 <p>Mass spectrometry plot for 14-3-3 protein epsilon (P62258). The plot shows observed peaks (red) and theoretical peaks (black) with Delta Miss Sequence values. The x-axis is labeled 'm/z' and the y-axis is labeled 'Relative Abundance'.</p> <table border="1"> <thead> <tr> <th>Start-End</th> <th>Observed</th> <th>Mf(calc)</th> <th>Delta</th> <th>Miss Sequence</th> </tr> </thead> <tbody> <tr><td>43-50</td><td>454.2573</td><td>906.5000</td><td>906.5174</td><td>-0.0174</td></tr> <tr><td>62-69</td><td>459.2584</td><td>916.5022</td><td>916.5229</td><td>-0.0207</td></tr> <tr><td>87-94</td><td>489.2439</td><td>976.4732</td><td>976.4899</td><td>-0.0167</td></tr> <tr><td>95-106</td><td>738.8693</td><td>1475.7240</td><td>1475.7364</td><td>-0.0123</td></tr> <tr><td>131-141</td><td>628.7911</td><td>1255.5876</td><td>1255.5833</td><td>-0.0157</td></tr> <tr><td>175-185</td><td>606.2566</td><td>1186.6588</td><td>1186.6536</td><td>-0.0190</td></tr> <tr><td>217-225</td><td>603.2260</td><td>1188.6594</td><td>1188.6505</td><td>-0.0210</td></tr> </tbody> </table>	Start-End	Observed	Mf(calc)	Delta	Miss Sequence	43-50	454.2573	906.5000	906.5174	-0.0174	62-69	459.2584	916.5022	916.5229	-0.0207	87-94	489.2439	976.4732	976.4899	-0.0167	95-106	738.8693	1475.7240	1475.7364	-0.0123	131-141	628.7911	1255.5876	1255.5833	-0.0157	175-185	606.2566	1186.6588	1186.6536	-0.0190	217-225	603.2260	1188.6594	1188.6505	-0.0210
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217-225	603.2260	1188.6594	1188.6505	-0.0210																																												
7339	14-3-3 protein gamma	P61981	29	4.8	211	4	10	 <p>Mass spectrometry plot for 14-3-3 protein gamma (P61981). The plot shows observed peaks (red) and theoretical peaks (black) with Delta Miss Sequence values. The x-axis is labeled 'm/z' and the y-axis is labeled 'Relative Abundance'.</p> <table border="1"> <thead> <tr> <th>Start-End</th> <th>Observed</th> <th>Mf(calc)</th> <th>Delta</th> <th>Miss Sequence</th> </tr> </thead> <tbody> <tr><td>43-50</td><td>454.2809</td><td>906.5472</td><td>906.5174</td><td>0.0298</td></tr> <tr><td>62-69</td><td>452.2772</td><td>902.5398</td><td>902.5073</td><td>0.0326</td></tr> <tr><td>133-143</td><td>540.8051</td><td>1079.5956</td><td>1079.5499</td><td>0.0458</td></tr> <tr><td></td><td>618.8468</td><td>1235.6790</td><td>1235.6510</td><td>0.0281</td></tr> </tbody> </table>	Start-End	Observed	Mf(calc)	Delta	Miss Sequence	43-50	454.2809	906.5472	906.5174	0.0298	62-69	452.2772	902.5398	902.5073	0.0326	133-143	540.8051	1079.5956	1079.5499	0.0458		618.8468	1235.6790	1235.6510	0.0281															
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7387	Enoyl-CoA hydratase, mitochondrial	P90084	31	8.3	120	2	7	 <p>Mass spectrometry plot for Enoyl-CoA hydratase, mitochondrial (P90084). The plot shows observed peaks (red) and theoretical peaks (black) with Delta Miss Sequence values. The x-axis is labeled 'm/z' and the y-axis is labeled 'Relative Abundance'.</p> <table border="1"> <thead> <tr> <th>Start-End</th> <th>Observed</th> <th>Mf(calc)</th> <th>Delta</th> <th>Miss Sequence</th> </tr> </thead> <tbody> <tr><td>44-56</td><td>489.6080</td><td>1465.8022</td><td>1463.5365</td><td>-0.0343</td></tr> <tr><td>274-283</td><td>592.2639</td><td>1182.5372</td><td>1182.5703</td><td>-0.0130</td></tr> </tbody> </table>	Start-End	Observed	Mf(calc)	Delta	Miss Sequence	44-56	489.6080	1465.8022	1463.5365	-0.0343	274-283	592.2639	1182.5372	1182.5703	-0.0130																									
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44-56	489.6080	1465.8022	1463.5365	-0.0343																																												
274-283	592.2639	1182.5372	1182.5703	-0.0130																																												
7553	Peroxiredoxin-2	P32119	22	5.7	471	7	29	 <p>Mass spectrometry plot for Peroxiredoxin-2 (P32119). The plot shows observed peaks (red) and theoretical peaks (black) with Delta Miss Sequence values. The x-axis is labeled 'm/z' and the y-axis is labeled 'Relative Abundance'.</p> <table border="1"> <thead> <tr> <th>Start-End</th> <th>Observed</th> <th>Mf(calc)</th> <th>Delta</th> <th>Miss Sequence</th> </tr> </thead> <tbody> <tr><td>8-16</td><td>486.7679</td><td>971.5212</td><td>971.5440</td><td>-0.0228</td></tr> <tr><td>17-26</td><td>489.7389</td><td>977.5032</td><td>977.5382</td><td>-0.0130</td></tr> <tr><td>17-29</td><td>443.5722</td><td>1333.6948</td><td>1333.7242</td><td>-0.0294</td></tr> </tbody> </table>	Start-End	Observed	Mf(calc)	Delta	Miss Sequence	8-16	486.7679	971.5212	971.5440	-0.0228	17-26	489.7389	977.5032	977.5382	-0.0130	17-29	443.5722	1333.6948	1333.7242	-0.0294																				
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17-29	443.5722	1333.6948	1333.7242	-0.0294																																												

7566	Phosphatidylethanolamine binding protein 1	P30086	21	7.0	301	5	34	Start-End Observed M(ncxp) M(ncalc) Delta Miss Sequence 148-87 577.2968 1152.5790 1152.5887 -0.0087 0 R.KLGGHNTNLR.K 149-88 577.2968 1152.5790 1152.5887 -0.0087 0 R.KLGGHNTNLR.K 159-173 814.3902 1026.7658 1026.7599 0.0059 0 K.MGGAPSGIAEYFDKH 174-183 537.7133 1073.4120 1073.4261 -0.0141 0 K.HTLGDSNDES-
7569	Ferritin heavy chain	P02794	21	5.3	95	4	22	Start-End Observed M(ncxp) M(ncalc) Delta Miss Sequence 181-187 469.2567 936.4988 936.4916 0.0072 0 K.LYEQISGK- 182-187 469.2567 936.4988 936.4916 0.0072 0 K.LYEQISGK- 183-187 469.2567 936.4988 936.4916 0.0072 0 K.LYEQISGK- 184-187 469.2567 936.4988 936.4916 0.0072 0 K.LYEQISGK- 185-187 469.2567 936.4988 936.4916 0.0072 0 K.LYEQISGK- 186-187 469.2567 936.4988 936.4916 0.0072 0 K.LYEQISGK- 187-187 469.2567 936.4988 936.4916 0.0072 0 K.LYEQISGK-
7593	Alpha-crystallin B chain	P02511	20	6.8	374	7	41	Start-End Observed M(ncxp) M(ncalc) Delta Miss Sequence 12-22 458.8979 1373.6719 1373.6993 -0.0274 0 R.RPFPFHPSR.L 57-69 756.8438 1511.6730 1511.6715 0.0016 0 R.APQWEDTGLSEMRL Oxidation (M) 75-82 461.2354 920.4562 920.4967 -0.0405 0 R.FSNVLDVK.H 83-90 659.7742 985.4738 985.4869 -0.0130 0 K.HFSFLKLR.K 83-103 553.7342 1066.6666 1066.6666 0.0000 0 R.FEEDVHGHGKH 108-116 544.7391 1087.4636 1087.5047 -0.0410 0 R.ODEHGFISR.E 164-175 423.5680 1267.6822 1267.7136 -0.0314 1.R.EERPAVTAAPKK-
9528	Annexin-A6	P08133	76	5.4	353	13	16	Start-End Observed M(ncxp) M(ncalc) Delta Miss Sequence 103-113 553.2690 1104.5234 1104.5299 -0.0064 0 K.DAISGGTDEK.C 114-122 537.7961 1073.5776 1073.5903 -0.0126 0 K.CLEIASR.T Carbamidomethyl (C) 157-166 573.3334 1144.6522 1144.6638 -0.0116 0 K.MLVVLIQTR.E Oxidation (M) 213-220 513.7692 1025.5238 1025.5433 -0.0195 0 R.LVDFEYLR.T 221-229 496.8666 1007.6666 1007.6666 0.0000 0 R.LVDFEYLR.T 300-316 429.2165 856.4264 856.4364 -0.0100 0 K.SIYSAHK.N Oxidation (M) 412-418 426.2077 850.4008 850.4106 -0.0098 0 R.DIAMTDLK.S Oxidation (M) 419-427 474.2369 946.4392 946.4720 -0.0127 0 K.SERSGDLAR.L 457-465 500.3055 998.5964 998.6124 -0.0159 0 K.ALEILATR.T 547-554 529.2560 1056.4974 1056.5096 -0.0122 0 R.FMTILCTR.S Carbamidomethyl (C); Oxidation (M) 582-588 455.7473 989.4800 989.4960 -0.0160 0 R.VFQEFHK.M 582-588 455.7473 989.4800 989.4960 -0.0160 0 R.VFQEFHK.M 589-607 540.2918 1078.5690 1078.5811 -0.0121 0 K.NRPLFFADK.L
10783	Spectrin alpha chain, brain	Q13813	284	5.2	164	6	2	Start-End Observed M(ncxp) M(ncalc) Delta Miss Sequence 1360-1369 509.7826 1017.5506 1017.5342 0.0164 0 R.GLVSSDELAK. 1608-1619 660.3327 1318.6908 1318.6551 0.0358 0 R.GVIDMGNLSLIER.G Oxidation (M) 2007-2017 662.8557 1203.6968 1203.6711 0.0258 0 R.DLSSVQTLTK.Q 2079-2087 550.8065 1099.5994 1099.5774 0.0210 0 K.LLEAOSHF.R.K 2088-2098 655.8846 1309.7546 1309.7282 0.0265 1.EKVEDLFLIFAK.K 2097-2114 572.7830 1135.5314 1135.5251 0.0063 0 K.SSEIEENFRA
40267	Heat shock protein HSP 90	P07900	83	5	82	5	6	Start-End Observed M(ncxp) M(ncalc) Delta Miss Sequence 56-64 520.2590 1038.5034 1038.4869 0.0165 0 R.YEFLTDPSK.L 73-82 597.8373 1193.6600 1193.6404 0.0196 0 K.DHFNPOERT 276-284 576.2880 1150.5614 1150.5506 0.0109 0 K.YIDQELNKT 331-337 415.2710 828.5274 828.5221 0.0053 0 R.ALLFRR.R 482-491 580.8096 1159.6046 1159.5761 0.0286 0 K.SIYYITGESK.E