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Supplementary Data

Low-Abundant Cerebrospinal Fluid Proteome Alterations in Dementia with Lewy Bodies

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Accepted 6 November 2012

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<table>
<tr><th>Nr</th><th>Protein name</th><th>UniProt Accession</th><th>MW [kDa]</th><th>pI</th><th>Score</th><th>Queries matched</th><th>Sequence coverage [%]</th><th>MS/MS analysis</th></tr>
<tr><td>1</td><td>Complement C4a</td><td>P0C0L4</td><td>193</td><td>6.7</td><td>867</td><td>22</td><td>11</td><td>
<table>
<tr><th>Start – End</th><th>Observed</th><th>Mr(expt)</th><th>Mr(calc)</th><th>Delta</th><th>Miss</th><th>Sequence</th></tr>
<tr><td>54 – 63</td><td>566.8101</td><td>1131.6056</td><td>1131.6149</td><td>-0.0092</td><td>1</td><td>K.GSVFLRNPSR.N</td></tr>
<tr><td>64 – 71</td><td>458.2205</td><td>914.4264</td><td>914.4280</td><td>-0.0015</td><td>0</td><td>R.NNVPCSPK.V + Carbamidomethyl (C)</td></tr>
<tr><td>72 – 80</td><td>527.2482</td><td>1052.4818</td><td>1052.5138</td><td>-0.0320</td><td>0</td><td>K.VDFTLSSER.D</td></tr>
<tr><td>96 – 104</td><td>542.2864</td><td>1082.5582</td><td>1082.5655</td><td>-0.0072</td><td>0</td><td>K.SCGLHQLLR.G + Carbamidomethyl (C)</td></tr>
<tr><td>105 – 118</td><td>520.9521</td><td>1559.8345</td><td>1559.8460</td><td>-0.0115</td><td>0</td><td>R.GPEVQLVAHSPWLK.D</td></tr>
<tr><td>124 – 137</td><td>782.4249</td><td>1562.8352</td><td>1562.8416</td><td>-0.0064</td><td>0</td><td>R.TTNIQGINLLFSSR.R</td></tr>
<tr><td>139 – 155</td><td>661.9963</td><td>1982.9671</td><td>1982.9963</td><td>-0.0292</td><td>0</td><td>R.GHLFLQTDQPIYNPGQR.V</td></tr>
<tr><td>235 – 244</td><td>618.8412</td><td>1235.6678</td><td>1235.6914</td><td>-0.0235</td><td>1</td><td>K.KYVLPNFEVK.I</td></tr>
<tr><td>236 – 244</td><td>554.7994</td><td>1107.5842</td><td>1107.5964</td><td>-0.0122</td><td>0</td><td>K.YVLPNFEVK.I</td></tr>
<tr><td>270 – 283</td><td>538.2894</td><td>1611.8464</td><td>1611.8773</td><td>-0.0309</td><td>0</td><td>R.YIYGKPVQGVAYVR.F</td></tr>
<tr><td>284 – 292</td><td>497.2465</td><td>992.4784</td><td>992.4815</td><td>-0.0030</td><td>0</td><td>R.FGLLDEDGK.K</td></tr>
<tr><td>284 – 293</td><td>561.2926</td><td>1120.5706</td><td>1120.5764</td><td>-0.0058</td><td>1</td><td>R.FGLLDEDGKK.T</td></tr>
<tr><td>305 – 316</td><td>428.2347</td><td>1281.6823</td><td>1281.7041</td><td>-0.0218</td><td>0</td><td>K.LVNGQSHISLSK.A</td></tr>
<tr><td>317 – 325</td><td>525.7399</td><td>1049.4652</td><td>1049.5029</td><td>-0.0377</td><td>0</td><td>K.AEFQDALEK.L</td></tr>
<tr><td>326 – 337</td><td>665.8536</td><td>1329.6926</td><td>1329.7075</td><td>-0.0148</td><td>0</td><td>K.LNMGITDLQGLR.L</td></tr>
<tr><td>392 – 404</td><td>630.3144</td><td>1258.6142</td><td>1258.6227</td><td>-0.0085</td><td>0</td><td>R.EMSGSPASGIPVK.V</td></tr>
<tr><td>392 – 404</td><td>638.3172</td><td>1274.6198</td><td>1274.6176</td><td>0.0022</td><td>0</td><td>R.EMSGSPASGIPVK.V + Oxidation (M)</td></tr>
<tr><td>485 – 494</td><td>557.8029</td><td>1113.5912</td><td>1113.6142</td><td>-0.0230</td><td>0</td><td>R.VGDTLNLNLR.A</td></tr>
<tr><td>513 – 520</td><td>482.7514</td><td>963.4882</td><td>963.4960</td><td>-0.0078</td><td>0</td><td>R.GQIVFMNR.E</td></tr>
<tr><td>513 – 523</td><td>659.8469</td><td>1317.6792</td><td>1317.6863</td><td>-0.0071</td><td>1</td><td>R.GQIVFMNREPK.R</td></tr>
<tr><td>560 – 570</td><td>567.2663</td><td>1132.5180</td><td>1132.5183</td><td>-0.0002</td><td>0</td><td>R.VDVQAGACEGK.L + Carbamidomethyl (C)</td></tr>
<tr><td>571 – 579</td><td>466.2521</td><td>930.4896</td><td>930.5022</td><td>-0.0125</td><td>0</td><td>K.LELSVDGAK.Q</td></tr>
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<tr><td>2</td><td>nd</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>3</td><td>nd</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
<tr><td>4</td><td>Ganglioside GM2 activator</td><td>P17900</td><td>21</td><td>5.2</td><td>44</td><td>1</td><td>5</td><td>
<table>
<tr><th>Start – End</th><th>Observed</th><th>Mr(expt)</th><th>Mr(calc)</th><th>Delta</th><th>Miss</th><th>Sequence</th></tr>
<tr><td>170 – 179</td><td>503.7948</td><td>1005.5750</td><td>1005.5342</td><td>0.0408</td><td>0</td><td>R.IESVLSSSGK.R</td></tr>
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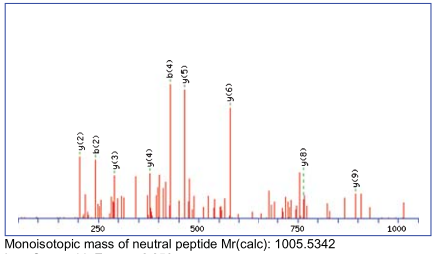

Monoisotopic mass of neutral peptide Mr(calc): 1005.5342
Ions Score: 44 Expect: 0.053
Matches : 9/84 fragment ions using 20 most intense peaks
MS/MS Fragmentation of IESVLSSSGK</td></tr>
<tr><td>5</td><td></td><td></td><td></td><td></td><td>69</td><td>2</td><td>5</td><td>
<table>
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<tr><td>170 – 179</td><td>503.7733</td><td>1005.5320</td><td>1005.5342</td><td>-0.0022</td><td>0</td><td>R.IESVLSSSGK.R</td></tr>
<tr><td>170 – 180</td><td>581.8215</td><td>1161.6284</td><td>1161.6353</td><td>-0.0069</td><td>1</td><td>R.IESVLSSSGKR.L</td></tr>
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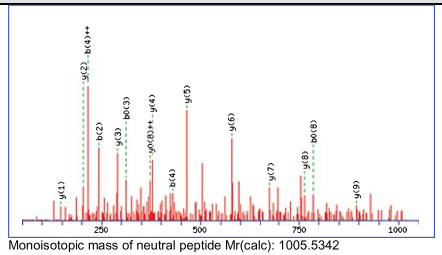
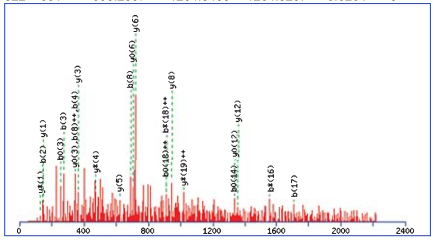
<table>
<tr><th>Nr</th><th>Protein name</th><th>UniProt Accession</th><th>MW [kDa]</th><th>pI</th><th>Score</th><th>Queries matched</th><th>Sequence coverage [%]</th><th>MS/MS analysis</th></tr>
<tr><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td> 

Monoisotopic mass of neutral peptide Mr(calc): 1005.5342
Ions Score: 63 Expect: 0.0006
Matches : 15/84 fragment ions using 30 most intense peaks
MS/MS Fragmentation of IESVLSSSGK</td></tr>
<tr><td>6
7</td><td>Chromogranin A</td><td>P10645</td><td>51</td><td>4.6</td><td>110</td><td>3</td><td>11</td><td>Start – End | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Sequence
142 – 162 | 733.6974 | 2198.0704 | 2198.0273 | 0.0430 | 0 | K.SGEATDGARPQALPEPMQESK.A
272 – 294 | 742.6888 | 2225.0446 | 2225.0448 | -0.0002 | 0 | R.SEALAVDGAGKPGAEEAQDPEGK.G
322 – 331 | 603.2807 | 1204.5468 | 1204.5207 | 0.0261 | 0 | K.SGELEQEEER.L
 

Monoisotopic mass of neutral peptide Mr(calc): 2198.0273
Ions Score: 9 Expect: 92
Matches : 23/222 fragment ions using 88 most intense peaks
MS/MS Fragmentation of SGEATDGARPQALPEPMQESK</td></tr>
<tr><td>8
9
10
11</td><td></td><td></td><td></td><td></td><td>171</td><td>6</td><td>19</td><td>Start – End | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Sequence
142 – 162 | 733.7046 | 2198.0920 | 2198.0273 | 0.0646 | 0 | K.SGEATDGARPQALPEPMQESK.A
194 – 213 | 1038.0164 | 2074.0182 | 2073.9603 | 0.0579 | 0 | K.YPGPQAEGDSEGLSQGLVDR.E
194 – 215 | 778.0621 | 2331.1645 | 2331.0979 | 0.0666 | 1 | K.YPGPQAEGDSEGLSQGLVDREK.G
216 – 226 | 572.3082 | 1142.6018 | 1142.5720 | 0.0298 | 0 | K.GLSAEPGWQAK.R
272 – 294 | 742.7106 | 2225.1100 | 2225.0448 | 0.0652 | 0 | R.SEALAVDGAGKPGAEEAQDPEGK.G
322 – 331 | 603.2872 | 1204.5598 | 1204.5207 | 0.0391 | 0 | K.SGELEQEEER.L</td></tr>
<tr><td>12</td><td>Alpha-Enolase</td><td>P06733</td><td>47</td><td>7</td><td>143</td><td>5</td><td>13</td><td>Start – End | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Sequence
16 – 28 | 703.8824 | 1405.7502 | 1405.7089 | 0.0413 | 0 | R.GNPTVEVDLFTSK.G
93 – 103 | 640.8121 | 1279.6096 | 1279.5788 | 0.0309 | 0 | K.LMIEMDGTENK.S
270 – 281 | 713.3877 | 1424.7608 | 1424.7187 | 0.0421 | 0 | R.YISPDQLADLYK.S
344 – 358 | 817.4378 | 1632.8610 | 1632.8141 | 0.0469 | 0 | K.VNQIGSVTESLQACK.L + Carbamidomethyl (C)
413 – 420 | 452.7499 | 903.4852 | 903.4549 | 0.0304 | 0 | R.IEEELGSK.A</td></tr>
<tr><td>13
14</td><td>Angiotensinogen</td><td>P01019</td><td>53</td><td>5.9</td><td>96</td><td>3</td><td>7</td><td>Start – End | Observed | Mr(expt) | Mr(calc) | Delta | Miss | Sequence
64 – 75 | 649.3776 | 1296.7406 | 1296.7078 | 0.0329 | 0 | K.DPTFIPAPIQAK.T
83 – 94 | 634.8981 | 1267.7816 | 1267.7500 | 0.0317 | 0 | K.ALQDQLVLVAAK.L
238 – 250 | 719.3801 | 1436.7456 | 1436.7035 | 0.0422 | 0 | R.SLDFTELDVAAEK.I</td></tr>
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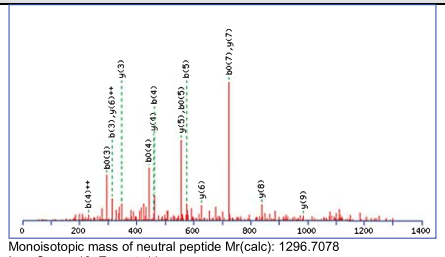
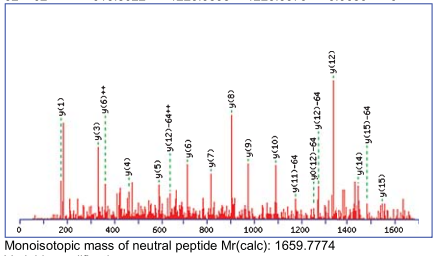
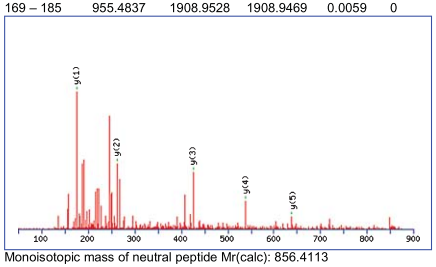
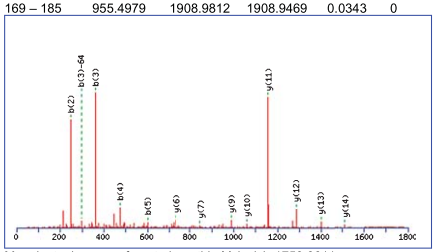
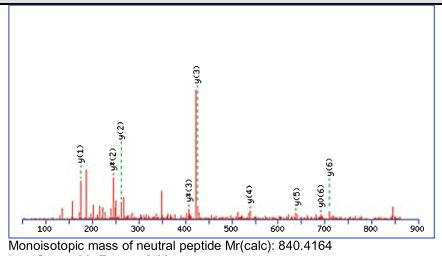
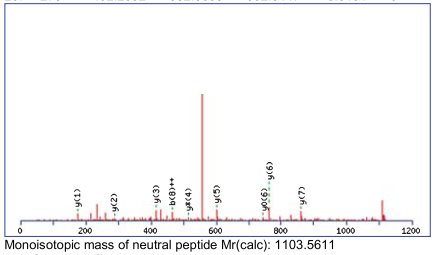
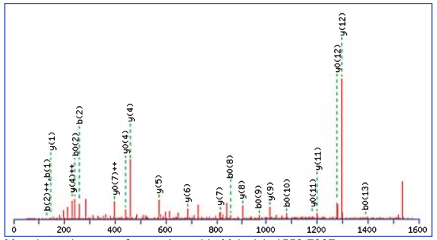
Nr	Protein name	UniProt Accession	MW [kDa]	pI	Score	Queries matched	Sequence coverage [%]	MS/MS analysis
								 Monoisotopic mass of neutral peptide Mr(calc): 1296.7078 Ions Score: 19 Expect: 11 Matches : 16/96 fragment ions using 51 most intense peaks MS/MS Fragmentation of DPTFIPAPIQAK
15	Serum albumin	P02768	69	5.9	1081	31	45	Start – End / Observed / Mr(expt) / Mr(calc) / Delta / Miss / Sequence 35 – 44 / 613.7917 / 1225.5688 / 1225.5979 / -0.0290 / 1 / R.FKDLGEENFK.A 37 – 44 / 476.2217 / 950.4288 / 950.4345 / -0.0057 / 0 / K.DLGEENFK.A 66 – 75 / 575.2657 / 1148.5168 / 1148.6077 / -0.0909 / 0 / K.LVNEVTEFAK.T 76 – 88 / 749.7616 / 1497.5086 / 1497.5712 / -0.0625 / 0 / K.TCVADESAENCDK.S + 2 Carbamidomethyl (C) 98 – 105 / 467.2490 / 932.4834 / 932.5113 / -0.0279 / 0 / K.LCTVATLR.E + Carbamidomethyl (C) 106 – 117 / 717.7554 / 1433.4962 / 1433.5261 / -0.0299 / 0 / R.ETYGEMADCCAK.Q + 2 Carbamidomethyl (C) 131 – 138 / 470.7188 / 939.4230 / 939.4410 / -0.0179 / 0 / K.DDNPNLPR.L 162 – 168 / 464.2387 / 926.4628 / 926.4861 / -0.0233 / 0 / K.YLYEIAR.R 187 – 198 / 686.2653 / 1370.5160 / 1370.5595 / -0.0434 / 0 / K.AAFTECCQAADK.A + 2 Carbamidomethyl (C) 206 – 214 / 537.7612 / 1073.5078 / 1073.5353 / -0.0274 / 1 / K.LDELRDEGK.A 250 – 257 / 440.6985 / 879.3824 / 879.4338 / -0.0513 / 0 / K.AEFAEVSK.L 299 – 310 / 516.2610 / 1545.7612 / 1545.7894 / -0.0283 / 1 / K.LKECCEKPLLEK.S + 2 Carbamidomethyl (C) 301 – 310 / 435.8785 / 1304.6137 / 1304.6104 / 0.0032 / 0 / K.ECCEKPLLEK.S + 2 Carbamidomethyl (C) 348 – 360 / 820.3826 / 1638.7506 / 1638.7752 / -0.0246 / 0 / K.DVFLGMFLYEYAR.R + Oxidation (M) 361 – 372 / 489.9483 / 1466.8231 / 1466.8358 / -0.0127 / 1 / R.RHPDYSVVLLLR.L 362 – 372 / 656.3722 / 1310.7298 / 1310.7347 / -0.0048 / 0 / R.HPDYSVVLLLR.L 376 – 383 / 492.7267 / 983.4388 / 983.4811 / -0.0423 / 0 / K.TYETTLEK.C 384 – 396 / 518.1872 / 1551.5398 / 1551.5905 / -0.0507 / 0 / K.CCAAADPHECYAK.V + 3 Carbamidomethyl (C) 397 – 413 / 682.3423 / 2044.0051 / 2044.0881 / -0.0830 / 0 / K.VFDEFKPLVEEPQNLIK.Q 414 – 426 / 829.3553 / 1656.6960 / 1656.7453 / -0.0493 / 0 / K.QNCELFEQLGEYK.F + Carbamidomethyl (C) 427 – 434 / 480.7665 / 959.5184 / 959.5552 / -0.0368 / 0 / K.FQNALLVR.Y 438 – 452 / 547.3059 / 1638.8959 / 1638.9305 / -0.0346 / 1 / K.KVPQVSTPTLVEVSR.N 439 – 452 / 756.4003 / 1510.7860 / 1510.8355 / -0.0495 / 0 / K.VPQVSTPTLVEVSR.N 491 – 499 / 501.7832 / 1001.5518 / 1001.5506 / 0.0013 / 1 / K.TPVSDRVTK.C 500 – 508 / 569.7213 / 1137.4280 / 1137.4907 / -0.0626 / 0 / K.CCTESLVNR.R + 2 Carbamidomethyl (C) 509 – 524 / 637.6440 / 1909.9102 / 1909.9244 / -0.0142 / 0 / R.RPCFSALEVDETYVPK.E + Carbamidomethyl (C) 549 – 558 / 564.8453 / 1127.6760 / 1127.6914 / -0.0153 / 1 / K.KQTALVELVK.H 550 – 558 / 500.7747 / 999.5348 / 999.5964 / -0.0616 / 0 / K.QTALVELVK.H 570 – 581 / 671.8269 / 1341.6392 / 1341.6275 / 0.0118 / 0 / K.AVMDDFAAFVEK.C 570 – 581 / 679.8027 / 1357.5908 / 1357.6224 / -0.0316 / 0 / K.AVMDDFAAFVEK.C + Oxidation (M) 599 – 609 / 507.2986 / 1012.5826 / 1012.5917 / -0.0090 / 0 / K.LVAASQAALGL.-
16					1037	25	40	Start – End / Observed / Mr(expt) / Mr(calc) / Delta / Miss / Sequence 35 – 44 / 409.5187 / 1225.5343 / 1225.5979 / -0.0636 / 1 / R.FKDLGEENFK.A 66 – 75 / 575.2461 / 1148.4776 / 1148.6077 / -0.1301 / 0 / K.LVNEVTEFAK.T 76 – 88 / 749.7745 / 1497.5344 / 1497.5712 / -0.0367 / 0 / K.TCVADESAENCDK.S + 2 Carbamidomethyl (C) 89 – 97 / 509.2563 / 1016.4980 / 1016.5291 / -0.0311 / 0 / K.SLHTLFGDK.L 98 – 105 / 467.2471 / 932.4796 / 932.5113 / -0.0317 / 0 / K.LCTVATLR.E + Carbamidomethyl (C) 106 – 117 / 717.7524 / 1433.4902 / 1433.5261 / -0.0359 / 0 / R.ETYGEMADCCAK.Q + 2 Carbamidomethyl (C) 106 – 117 / 725.7548 / 1449.4950 / 1449.5210 / -0.0260 / 0 / R.ETYGEMADCCAK.Q + 2 Carbamidomethyl (C); Oxidation (M) 131 – 138 / 470.7163 / 939.4180 / 939.4410 / -0.0229 / 0 / K.DDNPNLPR.L 162 – 168 / 464.2294 / 926.4442 / 926.4861 / -0.0419 / 0 / K.YLYEIAR.R 187 – 198 / 686.2701 / 1370.5256 / 1370.5595 / -0.0338 / 0 / K.AAFTECCQAADK.A + 2 Carbamidomethyl (C) 206 – 214 / 537.7645 / 1073.5144 / 1073.5353 / -0.0208 / 1 / K.LDELRDEGK.A 250 – 257 / 440.7136 / 879.4126 / 879.4338 / -0.0211 / 0 / K.AEFAEVSK.L 287 – 298 / 722.3010 / 1442.5874 / 1442.6347 / -0.0473 / 0 / K.YICENQDSISSK.L + Carbamidomethyl (C) 299 – 310 / 516.2537 / 1545.7393 / 1545.7894 / -0.0502 / 1 / K.LKECCEKPLLEK.S + 2 Carbamidomethyl (C) 361 – 372 / 489.9258 / 1466.7556 / 1466.8358 / -0.0802 / 1 / R.RHPDYSVVLLLR.L

Nr	Protein name	UniProt Accession	MW [kDa]	pI	Score	Queries matched	Sequence coverage [%]	MS/MS analysis
								376 – 383 492.7228 983.4310 983.4811 -0.0501 0 K.TYETTLEK.C 384 – 396 518.1920 1551.5542 1551.5905 -0.0363 0 K.CCAAADPHECYAK.V + 3 Carbamidomethyl (C) 414 – 426 829.2983 1656.5820 1656.7453 -0.1633 0 K.QNCELFEQLGEYK.F + Carbamidomethyl (C) 427 – 434 480.7268 959.4390 959.5552 -0.1162 0 K.FQNALLVR.Y 438 – 452 547.3039 1638.8899 1638.9305 -0.0406 1 K.KVPQVSTPTLVEVSR.N 439 – 452 756.3926 1510.7706 1510.8355 -0.0649 0 K.VPQVSTPTLVEVSR.N 500 – 508 569.7248 1137.4350 1137.4907 -0.0556 0 K.CCTESLVNR.R + 2 Carbamidomethyl (C) 509 – 524 955.9426 1909.8706 1909.9244 -0.0537 0 R.RPCFSALEVDETYVPK.E + Carbamidomethyl (C) 550 – 558 500.7707 999.5268 999.5964 -0.0696 0 K.QTALVELVK.H 570 – 581 679.7673 1357.5200 1357.6224 -0.1024 0 K.AVMDDFAAFVEK.C + Oxidation (M)
17					812	20	32	Start – End Observed Mr(expt) Mr(calc) Delta Miss Sequence 35 – 44 409.5058 1225.4956 1225.5979 -0.1023 1 R.FKDLGEENFK.A 66 – 75 575.2251 1148.4356 1148.6077 -0.1721 0 K.LVNEVTEFAK.T 89 – 97 509.2621 1016.5096 1016.5291 -0.0195 0 K.SLHTLFGDK.L 98 – 105 467.2278 932.4410 932.5113 -0.0703 0 K.LCTVATLR.E + Carbamidomethyl (C) 162 – 168 464.2092 926.4038 926.4861 -0.0823 0 K.YLYEIAR.R 206 – 214 537.7495 1073.4844 1073.5353 -0.0508 1 K.LDELRDEGK.A 250 – 257 440.6907 879.3668 879.4338 -0.0669 0 K.AEFAEVSK.L 265 – 281 696.2667 2085.7783 2085.8303 -0.0520 0 K.VHTECCHGDLLECADDR.A + 3 Carbamidomethyl (C) 287 – 298 722.3054 1442.5962 1442.6347 -0.0385 0 K.YICENQDSISSK.L + Carbamidomethyl (C) 361 – 372 489.9305 1466.7697 1466.8358 -0.0661 1 R.RHPDYSVVLLLR.L 362 – 372 656.3613 1310.7080 1310.7347 -0.0266 0 R.HPDYSVVLLLR.L 384 – 396 518.1898 1551.5476 1551.5905 -0.0429 0 K.CCAAADPHECYAK.V + 3 Carbamidomethyl (C) 414 – 426 829.3529 1656.6912 1656.7453 -0.0541 0 K.QNCELFEQLGEYK.F + Carbamidomethyl (C) 427 – 434 480.7242 959.4338 959.5552 -0.1214 0 K.FQNALLVR.Y 438 – 452 547.3019 1638.8839 1638.9305 -0.0466 1 K.KVPQVSTPTLVEVSR.N 500 – 508 569.7209 1137.4272 1137.4907 -0.0634 0 K.CCTESLVNR.R + 2 Carbamidomethyl (C) 509 – 524 637.6105 1909.8097 1909.9244 -0.1147 0 R.RPCFSALEVDETYVPK.E + Carbamidomethyl (C) 549 – 558 564.8293 1127.6440 1127.6914 -0.0473 1 K.KQTALVELVK.H 550 – 558 500.7481 999.4816 999.5964 -0.1148 0 K.QTALVELVK.H 570 – 581 679.7514 1357.4882 1357.6224 - 0.1342 0 K.AVMDDFAAFVEK.C + Oxidation (M)
18					429	14	20	Start – End Observed Mr(expt) Mr(calc) Delta Miss Sequence 35 – 44 409.5323 1225.5751 1225.5979 -0.0228 1 R.FKDLGEENFK.A 66 – 75 575.3024 1148.5902 1148.6077 -0.0175 0 K.LVNEVTEFAK.T 98 – 105 467.2602 932.5058 932.5113 -0.0055 0 K.LCTVATLR.E + Carbamidomethyl (C) 131 – 138 470.7205 939.4264 939.4410 -0.0145 0 K.DDNPNLPR.L 162 – 168 464.2498 926.4850 926.4861 -0.0011 0 K.YLYEIAR.R 250 – 257 440.7164 879.4182 879.4338 -0.0155 0 K.AEFAEVSK.L 376–383 492.7343 983.4540 983.4811 -0.0271 0 K.TYETTLEK.C 384 – 396 518.1988 1551.5746 1551.5905 -0.0159 0 K.CCAAADPHECYAK.V + 3 Carbamidomethyl (C) 427 – 434 480.7913 959.5680 959.5552 0.0128 0 K.FQNALLVR.Y 438 – 452 547.3143 1638.9211 1638.9305 -0.0094 1 K.KVPQVSTPTLVEVSR.N 439 – 452 756.4244 1510.8342 1510.8355 -0.0013 0 K.VPQVSTPTLVEVSR.N 500 – 508 569.7566 1137.4986 1137.4907 0.0080 0 K.CCTESLVNR.R + 2 Carbamidomethyl (C) 550 – 558 500.8086 999.6026 999.5964 0.0062 0 K.QTALVELVK.H 570 – 581 679.8020 1357.5894 1357.6224 -0.0330 0 K.AVMDDFAAFVEK.C + Oxidation (M)
19 20	Cystatin-C	P01034	16	9	227	3	19	35 – 50 830.9057 1659.7968 1659.7774 0.0194 0 R.LVGGPMDASVEEEGVR.R + Oxidation (M) 35 – 51 606.2949 1815.8629 1815.8785 -0.0156 1 R.LVGGPMDASVEEEGVRR.A + Oxidation (M) 52 – 62 613.8022 1225.5898 1225.5979 -0.0080 0 R.ALDFAVGEYNK.A  Monoisotopic mass of neutral peptide Mr(calc): 1659.7774 Variable modifications: M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983 Ions Score: 77 Expect: 1.6e-05

Nr	Protein name	UniProt Accession	MW [kDa]	pI	Score	Queries matched	Sequence coverage [%]	MS/MS analysis
								Matches : 18/200 fragment ions using 34 most intense peaks MS/MS Fragmentation of LVGGPMDASVEEEGVR
21	Prostaglandin-H2 D-isomerase	P41222	21	7.7	97	2	12	Start – End Observed Mr(expt) Mr(calc) Delta Miss Sequence 145 – 151 429.2165 856.4184 856.4113 0.0072 0 R.MATLYSR.T + Oxidation (M) 169 – 185 955.4837 1908.9528 1908.9469 0.0059 0 K.AQGFTEDTIVFLPQTDK.C  Monoisotopic mass of neutral peptide Mr(calc): 856.4113 Variable modifications: M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983 Ions Score: 34 Expect: 0.48 Matches : 5/74 fragment ions using 9 most intense peaks MS/MS Fragmentation of MATLYSR
22					166	3	21	Start – End Observed Mr(expt) Mr(calc) Delta Miss Sequence 93 – 108 880.4453 1758.8760 1758.8611 0.0150 0 R.TMLLQPAGSLGSYSYR.S + Oxidation (M) 145 – 151 429.2178 856.4210 856.4113 0.0098 0 R.MATLYSR.T + Oxidation (M) 169 – 185 955.4979 1908.9812 1908.9469 0.0343 0 K.AQGFTEDTIVFLPQTDK.C  Monoisotopic mass of neutral peptide Mr(calc): 1758.8611 Variable modifications: M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983 Ions Score: 62 Expect: 0.00054 Matches : 13/252 fragment ions using 18 most intense peaks MS/MS Fragmentation of TMLLQPAGSLGSYSYR
23					156	4	21	Start – End Observed Mr(expt) Mr(calc) Delta Miss Sequence 93 – 108 872.4959 1742.9772 1742.8661 0.1111 0 R.TMLLQPAGSLGSYSYR.S 93 – 108 880.4971 1758.9796 1758.8611 0.1186 0 R.TMLLQPAGSLGSYSYR.S + Oxidation (M) 145 – 151 421.2356 840.4566 840.4164 0.0403 0 R.MATLYSR.T 169 – 185 955.5453 1909.0760 1908.9469 0.1291 0 K.AQGFTEDTIVFLPQTDK.C
24					77	2	12	Start – End Observed Mr(expt) Mr(calc) Delta Miss Sequence 145 – 151 421.2380 840.4614 840.4164 0.0451 0 R.MATLYSR.T 169 – 185 955.5477 1909.0808 1908.9469 0.1339 0 K.AQGFTEDTIVFLPQTDK.C

Nr	Protein name	UniProt Accession	MW [kDa]	pI	Score	Queries matched	Sequence coverage [%]	MS/MS analysis
								 Monoisotopic mass of neutral peptide Mr(calc): 840.4164 Ions Score: 30 Expect: 0.99 Matches : 9/54 fragment ions using 24 most intense peaks MS/MS Fragmentation of MATLYSR
25	Transthyretin	P02766	16	5.5	498	7	63	Start – End / Observed / Mr(expt) / Mr(calc) / Delta / Miss / Sequence 42 – 54 / 683.8073 / 1365.6000 / 1365.7517 / -0.1517 / 0 / R.GSPAINVAVHVFR.K 42 – 55 / 498.9325 / 1493.7757 / 1493.8467 / -0.0710 / 1 / R.GSPAINVAVHVFRK.A 55 – 68 / 508.2154 / 1521.6244 / 1521.7100 / -0.0856 / 1 / R.KAADDTWEPFASGK.T 56 – 68 / 697.7576 / 1393.5006 / 1393.6150 / -0.1144 / 0 / K.AADDTWEPFASGK.T 69 – 90 / 819.0488 / 2454.1246 / 2454.1438 / -0.0192 / 0 / K.TSESGELHGLTTEEEFVEGIYK.V 101 – 123 / 817.7530 / 2450.2372 / 2450.1979 / 0.0393 / 0 / K.ALGISPFHEHAEVVFTANDSGPR.R 125 – 146 / 1180.5553 / 2359.0960 / 2359.2311 / -0.1351 / 0 / R.YTIAALLSPYSYSTTAVVTNPK.E
26	Apolipoprotein A-IV	P06727	45	5.3	53	2	4	Start – End / Observed / Mr(expt) / Mr(calc) / Delta / Miss / Sequence 135 – 143 / 552.7957 / 1103.5768 / 1103.5611 / 0.0158 / 0 / R.LEPYADQLR.T 267 – 275 / 492.2892 / 982.5638 / 982.5447 / 0.0191 / 0 / R.LAPLAEDVR.G  Monoisotopic mass of neutral peptide Mr(calc): 1103.5611 Ions Score: 15 Expect: 31 Matches : 9/76 fragment ions using 33 most intense peaks MS/MS Fragmentation of LEPYADQLR
27	Pigment epithelium-derived factor	P36955	46	6	464	11	27	Start – End / Observed / Mr(expt) / Mr(calc) / Delta / Miss / Sequence 54 – 67 / 780.3855 / 1558.7564 / 1558.7780 / -0.0215 / 0 / K.LAAAVSNFGYDLYR.V 100 – 106 / 428.2339 / 854.4532 / 854.4610 / -0.0078 / 0 / R.TESIIHR.A 124 – 134 / 607.8320 / 1213.6494 / 1213.6554 / -0.0060 / 0 / K.ELLDTVTAPQK.N 152 – 160 / 489.2591 / 976.5036 / 976.5229 / -0.0193 / 0 / K.SSFVAPLEK.S 226 – 237 / 758.8453 / 1515.6760 / 1515.6729 / 0.0032 / 0 / K.TSLEDFYLDEER.T 238 – 248 / 431.5524 / 1291.6354 / 1291.6264 / 0.0089 / 1 / R.TVRVPMMSDPK.A + 2 Oxidation (M) 253 – 262 / 579.2522 / 1156.4898 / 1156.5070 / -0.0172 / 0 / R.YGLDSDLSCK.I + Carbamidomethyl (C) 307 – 316 / 528.3231 / 1054.6316 / 1054.6387 / -0.0070 / 0 / K.TVQAVLTVPK.L 319 – 327 / 513.2581 / 1024.5016 / 1024.5077 / -0.0060 / 0 / K.LSYEGEVTK.S 334 – 345 / 692.3337 / 1382.6528 / 1382.6718 / -0.0190 / 0 / K.LQSLFDSPDFSK.I 400 – 411 / 625.8311 / 1249.6476 / 1249.6554 / -0.0078 / 0 / R.DTDTGALLFIGK.I
28	Insulin-like growth factor-binding protein 2	P18065	35	7.5	325	6	21	Start – End / Observed / Mr(expt) / Mr(calc) / Delta / Miss / Sequence 73 – 80 / 488.2629 / 974.5112 / 974.4677 / 0.0435 / 0 / R.MPCAELVR.E + Carbamidomethyl (C) 81 – 92 / 706.8022 / 1411.5898 / 1411.5101 / 0.0797 / 0 / R.EPGCGCCSVCAR.L + 4 Carbamidomethyl (C) 93 – 104 / 676.3547 / 1350.6948 / 1350.6238 / 0.0711 / 0 / R.LEGEACGVYTPR.C + Carbamidomethyl (C) 225 – 237 / 808.4325 / 1614.8504 / 1614.7672 / 0.0833 / 0 / R.TPCQQELDQVLER.I + Carbamidomethyl (C) 293 – 301 / 484.8208 / 967.6270 / 967.5815 / 0.0456 / 0 / K.LIQGAPTIR.G

Nr	Protein name	UniProt Accession	MW [kDa]	pI	Score	Queries matched	Sequence coverage [%]	MS/MS analysis
								302 – 317 664.9866 1991.9380 1991.8432 0.0948 0 R.GDPECHLFYNEQQEAR.G + Carbamidomethyl (C)
29	Glutathione peroxidase 3	P22352	26	8.3	112	3	16	Start – End Observed Mr(expt) Mr(calc) Delta Miss Sequence 107 – 120 777.9576 1553.9006 1553.7937 0.1070 0 K.QEPGENSEILPTLK.Y 154 – 168 817.4371 1632.8596 1632.7413 0.1183 0 K.NSCPPTSELLGTSDR.L + Carbamidomethyl (C) 209 – 216 514.7836 1027.5526 1027.4830 0.0696 0 K.MDILSYMR.R  Monoisotopic mass of neutral peptide Mr(calc): 1553.7937 Ions Score: 69 Expect: 0.00011 Matches : 22/150 fragment ions using 31 most intense peaks MS/MS Fragmentation of QEPGENSEILPTLK
30	nd							
31	nd							
32	nd							
33	nd							
34	N-acetyllactosaminide beta-1,3-N-acetylglucosaminyl-transferase	Q43505	47	6.8	182	6	12	Start – End Observed Mr(expt) Mr(calc) Delta Miss Sequence 65 – 80 776.9407 1551.8668 1551.7529 0.1139 0 R.TALASGGVLDASGDYR.V 163 – 171 509.2853 1016.5560 1016.4927 0.0634 0 R.YEAAVPDPR.E 172 – 180 516.3110 1030.6074 1030.5447 0.0627 0 R.EPGEFALLR.S 181 – 188 506.7554 1011.4962 1011.4332 0.0631 0 R.SCQEVFDK.L + Carbamidomethyl (C) 181 – 191 451.5862 1351.7368 1351.6554 0.0813 1 R.SCQEVFDKLAR.V + Carbamidomethyl (C) 335 – 341 432.2432 862.4718 862.4185 0.0534 0 K.VPTFDER.F
35	Gelsolin	P06396	86	5.9	87	4	6	Start – End Observed Mr(expt) Mr(calc) Delta Miss Sequence 178 – 188 638.4065 1274.7984 1274.7095 0.0889 0 K.HVVPNEVVVQR.L 585 – 597 660.3989 1318.7832 1318.6881 0.0952 0 K.AGALNSNDAFVLK.T 714 – 728 555.9647 1664.8723 1664.7740 0.0982 1 K.DSQEEEKTEALTSAK.R 741 – 748 457.3260 912.6374 912.5757 0.0618 1 R.RTPITVVK.Q
36	Contactin-1	Q12860	113	5.6	179	6	6	Start – End Observed Mr(expt) Mr(calc) Delta Miss Sequence 69 – 76 454.7765 907.5384 907.4803 0.0581 0 R.ASPFPVYK.W 79 – 90 668.8413 1335.6680 1335.5725 0.0956 0 R.MNNGDVDLTSDR.Y 91 – 105 810.9601 1619.9056 1619.7977 0.1079 0 R.YSMVGGNLVINNPDK.Q 226 – 235 597.9055 1193.7964 1193.7172 0.0792 0 K.FIPLIPIPER.T 432 – 439 493.8212 985.6278 985.5630 0.0648 0 R.VIIECKPK.A + Carbamidomethyl (C) 477 – 490 815.9092 1629.8038 1629.6842 0.1197 0 R.NDGGIYTCFAENNR.G + Carbamidomethyl (C)
37	Prothrombin	P00734	70	5.6	643	20	40	Start – End Observed Mr(expt) Mr(calc) Delta Miss Sequence 87 – 94 486.2465 970.4784 970.4178 0.0606 0 K.YTACETAR.T + Carbamidomethyl (C) 98 – 117 738.0562 2211.1468 2211.0048 0.1419 1 R.DKLAACLEGNCAEGLGTNYR.G + 2 Carbamidomethyl (C) 125 – 133 574.8149 1147.6152 1147.5444 0.0708 0 R.SGIECQLWR.S + Carbamidomethyl (C) 159 – 177 1078.0493 2154.0840 2153.9324 0.1516 0 R.NPDSSTTGPWCYTTDPTVR.R + Carbamidomethyl (C) 178 – 198 811.4415 2431.3027 2431.1407 0.1620 1 R.RQECSIPVCGQDQVTVAMTPR.S + 2 Carbamidomethyl (C) 178 – 198 816.7748 2447.3026 2447.1356 0.1670 1 R.RQECSIPVCGQDQVTVAMTPR.S + 2 Carbamidomethyl (C); Oxidation (M) 225 – 243 665.7294 1994.1664 1994.0408 0.1256 0 R.LAVTTHGLPCLAWASAQAK.A + Carbamidomethyl (C) 248 – 263 655.3495 1963.0267 1962.9007 0.1260 0 K.HQDFNSAVQLVENFCR.N + Carbamidomethyl (C) 315 – 327 781.4192 1560.8238 1560.7209 0.1030 0 R.TATSEYQTFFNPR.T 354 – 363 597.8409 1193.6672 1193.5928 0.0745 0 R.ELLESYIDGR.I 384 – 399 592.0125 1773.0157 1772.9091 0.1066 1 R.KSPQELLCGASLISDR.W + Carbamidomethyl (C) 385 – 399 823.4692 1644.9238 1644.8141 0.1097 0 K.SPQELLCGASLISDR.W + Carbamidomethyl (C) 453 – 461 422.5608 1264.6606 1264.5948 0.0657 1 R.YNWRENLDR.D 487 – 498 626.3713 1250.7280 1250.6506 0.0774 0 R.ETAASLLQAGYK.G 501 – 508 437.7684 873.5222 873.4709 0.0514 0 R.VTGWGNLK.E

Nr	Protein name	UniProt Accession	MW [kDa]	pI	Score	Queries matched	Sequence coverage [%]	MS/MS analysis						
								509 – 517	503.2841	1004.5536	1004.4927	0.0609	0	K.ETWTANVGK.G
								518 – 537	744.8035	2231.3887	2231.2460	0.1427	0	K.GQPSVLQVVNLPIVERPVCK.D + Carbamidomethyl (C)
								544 – 560	668.0181	2001.0325	2000.9084	0.1241	1	R.ITDNMFCAGYKPDEGKR.G + Carbamidomethyl (C)
								561 – 575	763.8714	1525.7282	1525.6178	0.1105	0	R.GDACEGDSGGPFVMK.S + Carbamidomethyl (C)
								600 – 608	595.3350	1188.6554	1188.5716	0.0838	0	K.YGFYTHVFR.L
38	Amyloid-like protein 1	P51693	72	5.5	301	14	19	Start – End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
								71 – 80	414.5616	1240.6630	1240.5949	0.0681	1	R.TGRWEPDPQR.S
								74 – 80	464.2463	926.4780	926.4246	0.0534	0	R.WEPDPQR.S
								91 – 96	420.2317	838.4488	838.4007	0.0481	0	R.VLEYCR.Q + Carbamidomethyl (C)
								97 – 106	624.8622	1247.7098	1247.6332	0.0766	0	R.QMYPELQIAR.V
								107 – 118	686.8911	1371.7676	1371.6816	0.0860	0	R.VEQATQAIPMER.W
								313 – 320	496.2785	990.5424	990.4804	0.0621	1	R.AKMDLEER.R
								324 - 330	445.2590	888.5034	888.4487	0.0547	0	R.QINEVMR.E
								380 – 388	521.3385	1040.6624	1040.5978	0.0646	0	R.VIALINDQR.R
								380 – 389	399.9278	1196.7616	1196.6989	0.0626	1	R.VIALINDQRR.A
								390 – 408	656.7171	1967.1295	1967.0112	0.1183	0	R.AALEGFLAALQADPPQAER.V
								447 – 459	545.9923	1634.9551	1634.8529	0.1022	0	R.FQVHTHLQVIEER.V
								517 – 525	509.2798	1016.5450	1016.4848	0.0602	0	K.DDTPMTLPK.G
								526 – 539	492.9282	1475.7628	1475.6740	0.0888	1	K.GSTEQDAASPEKEK.M
								540 – 548	590.3149	1178.6152	1178.5390	0.0763	0	K.MNPLEQYER.K
39	Complement C3	P01024	187	6	428	20	13	Start – End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
								749 – 764	908.9800	1815.9454	1815.8850	0.0605	0	R.SNLDEDIIAEENIVSR.S
								1835 – 841	417.2571	832.4996	832.4807	0.0190	0	R.LPYSVVR.N
								842– 848	444.2441	886.4736	886.4508	0.0228	0	R.NEQVEIR.A
								882 – 891	574.8425	1147.6704	1147.6350	0.0355	0	R.HQQTVTIPPK.S
								892 – 904	701.4422	1400.8698	1400.8279	0.0420	0	K.SSLSVPYVIVPLK.T
								905 – 913	501.7915	1001.5684	1001.5393	0.0291	0	K.TGLQEVEVK.A
								914 – 926	491.2650	1470.7732	1470.7368	0.0364	0	K.AAVYHHFISDGVR.K
								980 – 999	725.0524	2172.1354	2172.0732	0.0621	0	R.ILLQGTPVAQMTEDAVDAER.L + Oxidation (M)
								1052 – 1060	542.2993	1082.5840	1082.5509	0.0332	0	K.GYTQQLAFR.Q
								1061 – 1071	576.8247	1151.6348	1151.5975	0.0373	0	R.QPSSAFAAFVK.R
								1156 – 1171	895.4681	1788.9216	1788.8564	0.0653	0	K.DICEEQVNSLPGSITK.A + Carbamidomethyl (C)
								1172 – 1185	821.4158	1640.8170	1640.7617	0.0554	0	K.AGDFLEANYMNLQR.S
								1245 – 1254	595.8301	1189.6456	1189.6132	0.0325	0	K.DFDFVPPVVR.W
								1365 – 1375	404.9079	1211.7019	1211.6761	0.0257	0	K.VTIKPAPETEK.R
								1382 – 1391	633.8342	1265.6538	1265.6108	0.0431	0	K.NTMILEICTR.Y + Carbamidomethyl (C); Oxidation (M)
								1442 – 1450	546.8326	1091.6506	1091.6226	0.0280	0	R.NTLIIYLDK.V
								1479 – 1491	834.4008	1666.7870	1666.7297	0.0574	0	K.VYAYYNLEESCTR.F + Carbamidomethyl (C)
								1513 – 1522	649.7972	1297.5798	1297.5431	0.0368	0	R.CAEENCFIQK.S + 2 Carbamidomethyl (C)
								1536 – 1546	650.8206	1299.6266	1299.5805	0.0461	0	K.ACEPGVDYVYK.T + Carbamidomethyl (C)
								1571 – 1582	645.3288	1288.6430	1288.6008	0.0423	0	K.SGSDEVQVGQQR.T
40a	Inter-alpha-trypsin inhibitor heavy chain H4*	Q14624	103	6.5	580	18	19	Start – End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
								48 – 56	509.3000	1016.5854	1016.5403	0.0451	0	R.FAHTVVTSR.V
								61 – 75	853.9618	1705.9090	1705.8345	0.0745	0	R.ANTVQEATFQMELPK.K
								97 – 111	522.2933	1563.8581	1563.7892	0.0688	1	K.EKAEAQAQYSAAVAK.G
								99 – 111	654.3599	1306.7052	1306.6517	0.0536	0	K.AEAQAQYSAAVAK.G
								140 – 151	748.9485	1495.8824	1495.8174	0.0651	0	K.ITFELVYEELLK.R
								154 – 162	524.3472	1046.6798	1046.6376	0.0423	0	R.LGVYELLLK.V
41a								163 – 170	484.3264	966.6382	966.5974	0.0408	0	K.VRPQQLVK.H
								215 – 224	602.8656	1203.7166	1203.6612	0.0555	0	R.FKPTLSQQQK.S
								225 – 240	906.5162	1811.0178	1810.9425	0.0754	0	K.SPEQQETVLDGNLIIR.Y
								274 – 281	467.2937	932.5728	932.5331	0.0397	0	K.NVVFVIDK.S
								300 – 307	464.7769	927.5392	927.5025	0.0367	0	K.ILDDLSPR.D
								429 – 438	500.3022	998.5898	998.5509	0.0390	0	K.LALDNGGLAR.R
								497 – 512	552.9907	1655.9503	1655.8843	0.0660	1	K.LQDRGPDVLTATVSGK.L
								501 – 512	572.8363	1143.6580	1143.6136	0.0445	0	R.GPDVLTATVSGK.L
								658 – 668	421.9112	1262.7118	1262.6554	0.0564	0	R.MNFRPGVLSSR.Q
								778 – 788	642.8643	1283.7140	1283.6550	0.0590	0	K.AGFSWIEVTFK.N
								832 – 842	586.3381	1170.6616	1170.6496	0.0121	0	K.TGLLLLSDPDK.V
								843 – 853	638.8841	1275.7536	1275.6976	0.0561	0	K.VTIGLLFWDGR.G
40b	Calsyntenin-1*	P094985	110	4.8	328	8	9	Start – End	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Sequence
								89 – 103	546.6559	1636.9459	1636.8573	0.0885	0	K.IHGQNVPFDAVVVDK.S
								235 – 244	564.3027	1126.5908	1126.5329	0.0580	0	K.LTVTAYDCGK.K + Carbamidomethyl (C)
								373 – 383	549.3374	1096.6602	1096.6128	0.0474	0	R.IPDGVVSVSPK.E
41b								402 – 410	526.7722	1051.5298	1051.4856	0.0443	0	K.ETILCSSDK.T + Carbamidomethyl (C)
								537 – 545	457.7939	913.5732	913.5345	0.0387	0	R.GNLAGLTLR.S
								563 – 575	715.8916	1429.7686	1429.7049	0.0638	0	K.EGLDLQVLEDSGR.G
								666 – 683	1008.0316	2014.0486	2013.9684	0.0803	0	R.AASEFESSEGVFLFPELR.I
								792 – 800	531.2950	1060.5754	1060.5335	0.0419	0	K.LICSELNGR.Y + Carbamidomethyl (C)

<table>
<tr><th>Nr</th><th>Protein name</th><th>UniProt Accession</th><th>MW [kDa]</th><th>pI</th><th>Score</th><th>Queries matched</th><th>Sequence coverage [%]</th><th>MS/MS analysis</th></tr>
<tr><td>42</td><td>Fructose-bisphosphate aldolase C</td><td>P09972</td><td>39</td><td>6.4</td><td>60</td><td>3</td><td>8</td><td>
<table>
<tr><th>Start – End</th><th>Observed</th><th>Mr(expt)</th><th>Mr(calc)</th><th>Delta</th><th>Miss</th><th>Sequence</th></tr>
<tr><td>15 – 22</td><td>458.7667</td><td>915.5188</td><td>915.5025</td><td>0.0163</td><td>0</td><td>K.ELSDIALR.I</td></tr>
<tr><td>61 – 69</td><td>525.7691</td><td>1049.5236</td><td>1049.5142</td><td>0.0095</td><td>0</td><td>R.QVLFSADDR.V</td></tr>
<tr><td>319 – 331</td><td>711.3534</td><td>1420.6922</td><td>1420.6946</td><td>-0.0024</td><td>1</td><td>R.DNAGAATEEFIKR.A</td></tr>
</table>

Monoisotopic mass of neutral peptide Mr(calc): 915.5025
Ions Score: 4 Expect: 5.1e+02
Matches : 4/62 fragment ions using 18 most intense peaks
MS/MS Fragmentation of ELSDIALR
</td></tr>
<tr><td>43</td><td>Pyruvate kinase isozymes M1/M2</td><td>P14618</td><td>58</td><td>8</td><td>556</td><td>17</td><td>30</td><td>
<table>
<tr><th>Start – End</th><th>Observed</th><th>Mr(expt)</th><th>Mr(calc)</th><th>Delta</th><th>Miss</th><th>Sequence</th></tr>
<tr><td>44 – 56</td><td>680.3737</td><td>1358.7328</td><td>1358.6976</td><td>0.0352</td><td>0</td><td>R.NTGIICTIGPASR.S + Carbamidomethyl (C)</td></tr>
<tr><td>57 – 66</td><td>589.3376</td><td>1176.6606</td><td>1176.6424</td><td>0.0183</td><td>1</td><td>R.SVETLKEMIK.S</td></tr>
<tr><td>126 – 135</td><td>495.7728</td><td>989.5310</td><td>989.5029</td><td>0.0281</td><td>0</td><td>K.GSGTAEVELK.K</td></tr>
<tr><td>126 – 136</td><td>559.8220</td><td>1117.6294</td><td>1117.5979</td><td>0.0316</td><td>1</td><td>K.GSGTAEVELKK.G</td></tr>
<tr><td>142 – 151</td><td>599.2990</td><td>1196.5834</td><td>1196.5747</td><td>0.0088</td><td>0</td><td>K.ITLDNAYMEK.C</td></tr>
<tr><td>174 – 186</td><td>731.9200</td><td>1461.8254</td><td>1461.8079</td><td>0.0176</td><td>0</td><td>K.IYVDDGLISLQVK.Q</td></tr>
<tr><td>189 – 206</td><td>890.4500</td><td>1778.8854</td><td>1778.8687</td><td>0.0168</td><td>0</td><td>K.GADFLVTEVENGGSLGSK.K</td></tr>
<tr><td>208 – 224</td><td>818.9701</td><td>1635.9256</td><td>1635.8832</td><td>0.0425</td><td>0</td><td>K.GVNLPGAAVDLPAVSEK.D</td></tr>
<tr><td>279 – 294</td><td>613.3253</td><td>1836.9541</td><td>1836.9040</td><td>0.0501</td><td>1</td><td>R.RFDEILEASDGIMVAR.G + Oxidation (M)</td></tr>
<tr><td>280 – 294</td><td>833.4384</td><td>1664.8622</td><td>1664.8080</td><td>0.0543</td><td>0</td><td>R.FDEILEASDGIMVAR.G</td></tr>
<tr><td>295 – 305</td><td>571.3281</td><td>1140.6416</td><td>1140.6026</td><td>0.0390</td><td>0</td><td>R.GDLGIEIPAEK.V</td></tr>
<tr><td>368 – 376</td><td>510.2427</td><td>1018.4708</td><td>1018.5083</td><td>-0.0375</td><td>0</td><td>K.GDYPLEAVR.M</td></tr>
<tr><td>377 – 383</td><td>434.7600</td><td>867.5054</td><td>867.4749</td><td>0.0306</td><td>0</td><td>R.MQHLIAR.E</td></tr>
<tr><td>448 – 455</td><td>420.7550</td><td>839.4954</td><td>839.5229</td><td>-0.0274</td><td>0</td><td>R.APIIAVTR.N</td></tr>
<tr><td>468 – 475</td><td>467.2757</td><td>932.5368</td><td>932.5154</td><td>0.0215</td><td>0</td><td>R.GIFPVLCK.D + Carbamidomethyl (C)</td></tr>
<tr><td>490 – 498</td><td>490.2530</td><td>978.4914</td><td>978.4957</td><td>-0.0042</td><td>0</td><td>R.VNFAMNVGK.A</td></tr>
<tr><td>490 – 498</td><td>498.2719</td><td>994.5292</td><td>994.4906</td><td>0.0386</td><td>0</td><td>R.VNFAMNVGK.A + Oxidation (M)</td></tr>
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</td></tr>
<tr><td>44</td><td>nd</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></tr>
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