

Supplementary Table 3 – Database search report for identification of proteins from 2-D DIGE experiments.

P38646|GRP75_HUMAN Stress-70 protein, mitochondrial precursor (Spot 1294)

Protein View

Match to: GRP75_HUMAN Score: 884 Expect: 5.8e-085

(P38646) Stress-70 protein, mitochondrial precursor (75 kDa glucose-regulated protein) (GRP 75)

(Pe

Nominal mass (Mr): 73635; Calculated pI value: 5.87

NCBI BLAST search of GRP75_HUMAN against nr

Unformatted sequence string for pasting into other applications

Taxonomy: Homo sapiens

Variable modifications: Carbamidomethyl (C),Oxidation (M)

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

Sequence Coverage: 64%

Matched peptides shown in Bold Red

1 MISASRAAAA RLVGAAASRG PTAARHQDSW NGLSHEAFRL VSRRDYASEA
51 IKGAVVGIDL GTTNSCVAVM EGKQAKVLEN AEGARTPSV VAFTADGERL
101 VGMPAKRQAV TNPNTFYAT KRLIGRYYDD PEVQKDIKNV PFKIVRASNG
151 DAWVEAHGKL YSPSQIGAFV LMKMKETAEN YLGHAKNAV ITVPAYFNDS
201 QRQATKDAGQ ISGLNVLRVI NEPTAAALAY GLDKSEDKVI AVYDLGGGTF
251 DISILEIQKG VFEVKSTNGD TFLGGEDFDQ ALLRHIVKEF KRETGVDLTK
301 DNMALQVRRE AAEKAKCELS SSVQTDINLP YLTMDSSGPK HLNMKLTRAQ
351 FEGIVTDLIR RTIAPCQKAM QDAEVSKSDI GEVILVGGMT RMPKVQQTQVQ
401 DLFGRAPSKA VNPDEAVAIG AAIQGGVLAG DVTDLVLLLDV TPLSLGIETL
451 GGVFTKILNR NNTIPTKKSQ VFSTAADGQT QVEIKVCQGE REMAGDNKLL
501 GQFTLIGIPP APRGVPQIEV TFDIDANGIV HVSADKGTG REQQIVIQSS
551 GGLSKDDIEN MVKNAEKYAE EDRRKKERVE AVNMAEGIIH DTETKMEEFK
601 DQLPADECNK LKEEISKMRE LLARKDSETG ENIRQAASSL QQASLKLIFEM
651 AYKMASERE GSGSSGTGEQ KEDQKEEKQ
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
2 - 11 973.55 972.55 972.55 0.00 1 M.ISASRAAAAR.L (No match)
45 - 73 2914.51 2913.50 2913.41 0.09 1 R.DYASEAIKAVVGIDLGTTNSCVAVMEGK.Q
Oxidation (M) (No match)
53 - 73 2094.00 2092.99 2093.01 -0.02 0 K.GAVVGIDLGTTNSCVAVMEGK.Q
Carbamidomethyl (C); Oxidation (M) (No match)
77 - 85 958.53 957.52 957.49 0.03 0 K.VLENAEGAR.T (No match)
86 - 99 1450.74 1449.73 1449.71 0.02 0 R.TTPSVVAFTADGER.L (Ions score 51)
86 - 99 1450.74 1449.73 1449.71 0.02 0 R.TTPSVVAFTADGER.L (No match)
108 - 121 1568.77 1567.76 1567.76 -0.00 0 R.QAVTNPNTFYATK.R (No match)
127 - 135 1149.59 1148.58 1148.55 0.04 1 R.RYDDPEVQK.D (No match)
144 - 159 1709.82 1708.81 1708.86 -0.05 1 K.IVRASNGDAWVEAHGK.L (No match)
160 - 173 1569.80 1568.79 1568.83 -0.03 0 K.LYSPSQIGAFVLMK.M Oxidation (M) (No match)
174 - 187 1608.78 1607.77 1607.76 0.01 1 K.MKETAENYLGHAK.N Oxidation (M) (No match)
176 - 187 1333.67 1332.66 1332.63 0.03 0 K.ETAENYLGHAK.N (No match)
188 - 202 1694.87 1693.86 1693.84 0.02 0 K.NAVITVPAYFNDSQR.Q (Ions score 113)
188 - 202 1694.87 1693.86 1693.84 0.02 0 K.NAVITVPAYFNDSQR.Q (No match)
207 - 218 1242.70 1241.69 1241.67 0.02 0 K.DAGQISGLNVLR.V (Ions score 101)
207 - 218 1242.70 1241.69 1241.67 0.02 0 K.DAGQISGLNVLR.V (No match)
219 - 234 1645.88 1644.88 1644.87 0.00 0 R.VINEPTAAALAYGLDK.S (No match)
219 - 238 2105.05 2104.04 2104.07 -0.03 1 R.VINEPTAAALAYGLDKSEDK.V (No match)
235 - 259 2710.42 2709.41 2709.41 -0.00 1 K.SEDKVIAYVDLGGGTFDISILEIQK.G (No match)
239 - 259 2251.23 2250.22 2250.21 0.00 0 K.VIAYVDLGGGTFDISILEIQK.G (No match)
266 - 284 2055.98 2054.98 2054.95 0.02 0 K.STNGDTFLGGEDFDQALLR.H (Ions score 151)
266 - 284 2055.98 2054.98 2054.95 0.02 0 K.STNGDTFLGGEDFDQALLR.H (No match)
293 - 307 1706.85 1705.84 1705.83 0.01 1 R.ETGVDLTKDNMALQR.V Oxidation (M) (No match)
301 - 307 863.44 862.44 862.40 0.04 0 K.DNMALQR.V Oxidation (M) (No match)
317 - 340 2658.23 2657.23 2657.22 0.01 0 K.CELSSSVQTDINLPYLTMDSSGPK.H
Carbamidomethyl (C); Oxidation (M) (No match)
349 - 360 1361.76 1360.75 1360.74 0.02 0 R.AQFEGIVTDLIR.R (Ions score 80)
349 - 360 1361.76 1360.75 1360.74 0.02 0 R.AQFEGIVTDLIR.R (No match)
369 - 391 2438.22 2437.21 2437.18 0.03 1 K.AMQDAEVSKSDIGEVILVGGMTR.M 2
Oxidation (M) (No match)

378 - 391 1462.77 1461.76 1461.75 0.01 0 K.SDIGEVILVGGMTR.M Oxidation (M)
 (Ions score 37)
 378 - 391 1462.77 1461.76 1461.75 0.01 0 K.SDIGEVILVGGMTR.M Oxidation (M) (No
 match)
 395 - 405 1290.70 1289.69 1289.67 0.02 0 K.VQQTVDLDFGR.A (Ions score 52)
 395 - 405 1290.70 1289.69 1289.67 0.02 0 K.VQQTVDLDFGR.A (No match)
 469 - 485 1808.91 1807.90 1807.90 0.00 0 K.SQVFSTAADGQTQVEIK.V (No match)
 499 - 513 1592.98 1591.97 1591.94 0.02 0 K.LLGQFTLIGIPPAPR.G (Ions score 66)
 499 - 513 1592.98 1591.97 1591.94 0.02 0 K.LLGQFTLIGIPPAPR.G (No match)
 514 - 535 2309.20 2308.19 2308.21 -0.02 0 R.GVPQIEVTFDIDANGIVHVSAD.D (No
 match)
 542 - 555 1473.79 1472.78 1472.78 -0.00 0 R.EQQIIVIQSSGGLSK.D (No match)
 542 - 563 2434.22 2433.22 2433.21 0.01 1 R.EQQIIVIQSSGGLSKDDIENMVK.N Oxidation
 (M) (No match)
 568 - 574 938.47 937.47 937.43 0.04 1 K.YAEDRRR.K (No match)
 577 - 595 2158.04 2157.03 2157.04 -0.00 1 K.ERVEAVNMAEGIIHDTETK.M Oxidation
 (M) (No match)
 579 - 595 1872.90 1871.89 1871.89 -0.00 0 R.VEAVNMAEGIIHDTETK.M Oxidation (M)
 (No match)
 618 - 624 904.52 903.51 903.50 0.01 1 K.MRELLAR.K Oxidation (M) (No match)
 626 - 646 2233.13 2232.12 2232.10 0.02 1 K.DSETGENIRQAASSLQOASLK.L (No match)
 635 - 646 1231.67 1230.67 1230.66 0.01 0 R.QAASSLQOASLK.L (No match)
 647 - 653 917.46 916.45 916.44 0.02 0 K.LFEMAYK.K Oxidation (M) (No match)
 647 - 654 1045.58 1044.58 1044.53 0.05 1 K.LFEMAYKK.M Oxidation (M) (No
 match)

Q15056|IF4H_HUMAN Eukaryotic translation initiation factor 4H (eIF-4H) (Spot 2582)

Protein View

Match to: **IF4H_HUMAN** Score: **84** Expect: **6.5e-005**

(**Q15056**) Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Beuren syndrome
 chromosome)

Nominal mass (Mr): **27237**; Calculated pI value: **6.92**

NCBI BLAST search of **IF4H_HUMAN** against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: **Homo sapiens**

Variable modifications: Carbamidomethyl (C),Oxidation (M)

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

Sequence Coverage: **27%**

Matched peptides shown in **Bold Red**

1 ADFDTYDDRA **YSSFGGGR**GS RGSAGGHGSR SQKELPTEPP YTAYVGNLPP
 51 NTVQGDIDAI FKDLRSIRSVR LVRDKDTRDKF **KGFCYVEFDE VDSLKEALTY**
 101 **DGALLGDR**SL RVDIAEGRKQ DKGFGFRKQ GPDDRGMGSS RESRGGWDSR
 151 DDFNSGFRDD FLGGRGSRP GDRRTGPPMG SR**FRDGPPLR** GSNMDFREPT
 201 EEERAQRRL QLKPR**TVATP LNQVANPNSA IFGGARPRE** VVQKEQE
 Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
 10 - 18 901.44 900.43 900.41 0.02 0 R.AYSSFGGGR.G (No match)
 10 - 18 901.44 900.43 900.41 0.02 0 R.AYSSFGGGR.G (No match)
 82 - 95 1707.78 1706.77 1706.75 0.02 0 K.GFCYVEFDEVDSLK.E Carbamidomethyl
 (C) (No match)
 96 - 108 1393.71 1392.70 1392.69 0.01 0 K.EALTYDGALLGDR.S (Ions score 52)
 96 - 108 1393.71 1392.70 1392.69 0.01 0 K.EALTYDGALLGDR.S (No match)
 183 - 190 957.52 956.52 956.52 -0.00 1 R.FRDGPPLR.G (Ions score 13)
 183 - 190 957.52 956.52 956.52 -0.00 1 R.FRDGPPLR.G (No match)
 216 - 238 2351.27 2350.26 2350.25 0.01 0 R.TVATPLNQVANPNSAIFGGARPR.E (No
 match)

P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 precursor (Spot 1736)

Protein View

Match to: **PDIA3_HUMAN** Score: **560** Expect: **1.5e-052**

(**P30101**) Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-
 60)

(**ERp60**)

Nominal mass (Mr): **56747**; Calculated pI value: **5.98**

NCBI BLAST search of **PDIA3_HUMAN** against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: **Homo sapiens**

Variable modifications: Carbamidomethyl (C),Oxidation (M)

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **62%**

Matched peptides shown in **Bold Red**

1 MRLRRALALFP GVALLLAAAR LAAASDVLEL TDDNFESRIS DTGSAGLMLV
51 EFFAPWCGHC **KRLAPEYEAA** ATRLKGIPL AKVDCTANTN TCNKYGVSGY
101 **PTLKIFRDGE** **EAGAYDGPRT** ADGIVSHLKK **QAGPASVPLR** **TEEEFKKFFIS**
151 **DKDASIVGFF** **DDSFSEAHSE** **FLKAASNLRD** NYRFAHTNVE **SLVNEYDDNG**
201 **EGIILFRPSH** **LTNKFEDKTV** **AYTEQKMTSG** KIKKFIQENI **FGICPHMTED**
251 **NKDLIQGKDL** **LIAYYDVDE** **KNAKGSNYWR** NRVMMVAKKF **LDAGHKLNFA**
301 **VASRKTFSHE** **LSDFGLESTA** **GEIPVVAIRT** AKGEKFMVQE **EFSRDGKALE**
351 **RFLQDYFDGN** **LKRYLKSEPI** **PESNDGPVKV** **VVAENFDEIV** **NNENKDVLE**
401 **FYAPWCGHCK** **NLEPKYKELG** **EKLSKDPNIV** IAKMDATAND **VPSPYEVRGF**
451 **PTIYFSPANK** **KLNPKKYEGG** **RELSDFISYL** **QREATNPPVI** **QEEKPKKKKK**
501 AQEDL
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
62 - 73 1347.71 1346.70 1346.69 0.01 1 **K.RLAPEYEAAATR.L** (No match)
63 - 73 1191.60 1190.59 1190.59 -0.00 0 **R.LAPEYEAAATR.L** (No match)
95 - 104 1084.56 1083.55 1083.56 -0.01 0 **K.YGVSGYPTLK.I** (No match)
105 - 119 1652.78 1651.77 1651.76 0.01 1 **K.IFRDGEAGAYDGPRT** (No match)
130 - 140 1123.65 1122.65 1122.65 -0.01 1 **K.QAGPASVPLR.T** (No match)
131 - 140 995.57 994.56 994.56 0.01 0 **K.QAGPASVPLR.T** (No match)
131 - 146 1758.92 1757.91 1757.89 0.02 1 **K.QAGPASVPLRTEEEFK.K** (No match)
148 - 173 2938.42 2937.41 2937.37 0.04 1 **K.FISDKDASIVGFFDDSFSEAHSEFLK.A** (No match)
153 - 173 2348.08 2347.08 2347.06 0.01 0 **K.DASIVGFFDDSFSEAHSEFLK.A** (No match)
184 - 214 3529.72 3528.71 3528.73 -0.02 0 **R.FAHTNVELVNEYDDNGEGIILFRPSHSLTNK.F** (No match)
219 - 226 939.47 938.46 938.47 -0.01 0 **K.TVAYTEQK.M** (No match)
235 - 258 2863.40 2862.39 2862.37 0.03 1 **K.FIQENIFGICPHMTEDNKDLIQGK.D**
Carbamidomethyl (C); Oxidation (M) (No match)
259 - 271 1619.78 1618.77 1618.78 -0.01 0 **K.DLLIAYYDVDEYK.N** (Ions score 59)
259 - 271 1619.78 1618.77 1618.78 -0.01 0 **K.DLLIAYYDVDEYK.N** (No match)
275 - 280 782.37 781.37 781.35 0.02 0 **K.GSNYWR.N** (Ions score 25)
275 - 280 782.37 781.37 781.35 0.02 0 **K.GSNYWR.N** (No match)
290 - 296 787.41 786.40 786.40 -0.00 0 **K.FLDAGHK.L** (No match)
297 - 304 877.50 876.49 876.48 0.01 0 **K.LNFAVASR.K** (No match)
305 - 329 2703.43 2702.43 2702.39 0.03 1 **R.KTFSHELSDFGLESTAGEIPVVAIR.T** (No match)
306 - 329 2575.33 2574.32 2574.30 0.02 0 **K.TFSHELSDFGLESTAGEIPVVAIR.T** (No match)
336 - 344 1172.56 1171.56 1171.53 0.02 0 **K.FVMQEEFSR.D** (No match)
336 - 344 1188.53 1187.52 1187.53 -0.00 0 **K.FVMQEEFSR.D** Oxidation (M) (Ions score 8)
336 - 344 1188.53 1187.52 1187.53 -0.00 0 **K.FVMQEEFSR.D** Oxidation (M) (No match)
336 - 347 1488.68 1487.67 1487.67 0.00 1 **K.FVMQEEFSRDGK.A** Oxidation (M) (No match)
352 - 362 1359.66 1358.65 1358.65 -0.00 0 **R.FLQDYFDGNLKR.R** (No match)
352 - 363 1515.77 1514.76 1514.75 0.01 1 **R.FLQDYFDGNLKR.Y** (Ions score 62)
352 - 363 1515.77 1514.76 1514.75 0.01 1 **R.FLQDYFDGNLKR.Y** (No match)
367 - 379 1368.66 1367.66 1367.66 -0.00 0 **K.SPIPIESNDGPVK.V** (No match)
380 - 395 1832.90 1831.89 1831.90 -0.00 0 **K.VVVAENFDEIVNNENK.D** (No match)
416 - 422 866.46 865.45 865.45 0.00 1 **K.YKELGEK.L** (No match)
434 - 448 1664.76 1663.76 1663.75 0.00 0 **K.MDATANDVPSPYEVR.G** (No match)
434 - 448 1680.75 1679.74 1679.75 -0.00 0 **K.MDATANDVPSPYEVR.G** Oxidation (M) (Ions score 62)
434 - 448 1680.75 1679.74 1679.75 -0.00 0 **K.MDATANDVPSPYEVR.G** Oxidation (M) (No match)
449 - 460 1341.68 1340.67 1340.68 -0.01 0 **R.GFPTIYFSPANK.K** (Ions score 46)
449 - 460 1341.68 1340.67 1340.68 -0.01 0 **R.GFPTIYFSPANK.K** (No match)
472 - 482 1370.70 1369.70 1369.69 0.01 0 **R.ELSDFISYLR.E** (Ions score 80)
472 - 482 1370.70 1369.70 1369.69 0.01 0 **R.ELSDFISYLR.E** (No match)
483 - 496 1579.82 1578.82 1578.83 -0.01 0 **R.EATNPPVIQEEKPK.K** (No match)

P07339|CATD_HUMAN Cathepsin D precursor (Spot 2584)

Protein View

Match to: **CATD_HUMAN** Score: 337 Expect: 2.9e-030

(P07339) Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain; Cathepsin D heavy

Nominal mass (Mr): **44524**; Calculated pI value: **6.10**
NCBI BLAST search of **CATD_HUMAN** against nr
Unformatted [sequence string](#) for pasting into other applications
Taxonomy: **Homo sapiens**
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **37%**

Matched peptides shown in **Bold Red**

1 MQPSSLLPLA LCLLAAPASA LVRIPLHKFT SIRRTMSEVG GSVEDLIAKG
51 PVSKEYQAVP AVTEGPIPEV LKNYMDAQYY GEIGIGTPPQ CFTVVFDTGS
101 SNLWVPSIHC KLLDIACWIH HKYNSDKSST YVKNGTSEFDI HYGSGSLSGY
151 LSQDITVSVPC QSASSASALG GVKVERQVFG **EATKQPGITF IAAKFDGILG**
201 **MAYPRISVNN VLPVFDNLMQ QKLVQDQIFS FYLSRDPDAQ PGGELMLGGT**
251 **DSKYKGSLS YLNVTRKAYW QVHLDQVEVA SGLTLCKEGC EAIVDTGTSL**
301 **MVGPVDEVR LQKAIGAVPL IQGEYMIPCE KVSTLPAITL KLGKGYKLS**
351 **PEDYTLKVSQ AGKTLCLSGF MGMTDIPPSG PLWILGDVFI GRYTVFDRD**
401 **NNRVGFAEAA RL**
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
177 - 184 879.45 878.44 878.45 -0.01 0 R.QVFGEATK.Q (No match)
185 - 194 1045.58 1044.57 1044.60 -0.02 0 K.QPGITFIAAK.F (No match)
195 - 205 1239.62 1238.61 1238.61 -0.00 0 K.FDGILGMAYPR.I (No match)
195 - 205 1255.61 1254.60 1254.61 -0.01 0 K.FDGILGMAYPR.I Oxidation (M) (Ions score 29)
195 - 205 1255.61 1254.60 1254.61 -0.01 0 K.FDGILGMAYPR.I Oxidation (M) (No match)
206 - 222 1975.02 1974.01 1974.02 -0.01 0 R.ISVNNVLPVFDNLMQOK.L Oxidation (M) (Ions score 61)
206 - 222 1975.02 1974.01 1974.02 -0.01 0 R.ISVNNVLPVFDNLMQOK.L Oxidation (M) (No match)
223 - 235 1601.84 1600.83 1600.82 0.01 0 K.LVDQNIFSFYLSR.D (Ions score 55)
223 - 235 1601.84 1600.83 1600.82 0.01 0 K.LVDQNIFSFYLSR.D (No match)
236 - 253 1803.79 1802.78 1802.80 -0.02 0 R.DPDAQPGGELMLGGTDSK.Y Oxidation (M) (No match)
288 - 309 2350.09 2349.08 2349.08 0.00 0 K.EGCEAIVDTGTSLMVGPVDEVR.E
Carbamidomethyl (C); Oxidation (M) (No match)
314 - 331 2004.99 2003.98 2004.01 -0.02 0 K.AIGAVPLIQGEYMIPCEK.V
Carbamidomethyl (C); Oxidation (M) (No match)
332 - 341 1042.63 1041.62 1041.64 -0.02 0 K.VSTLPAITL.L (No match)
349 - 357 1065.54 1064.54 1064.54 -0.00 0 K.LSPEDYTLK.V (No match)
393 - 399 963.46 962.45 962.45 0.00 0 R.YYTVFDR.D (Ions score 38)
393 - 399 963.46 962.45 962.45 0.00 0 R.YYTVFDR.D (No match)
393 - 403 1462.67 1461.66 1461.66 -0.01 1 R.YYTVFDRDNNR.V (Ions score 38)
393 - 403 1462.67 1461.66 1461.66 -0.01 1 R.YYTVFDRDNNR.V (No match)
404 - 411 820.44 819.43 819.42 0.01 0 R.VGFAEAAR.L (Ions score 28)
404 - 411 820.44 819.43 819.42 0.01 0 R.VGFAEAAR.L (No match)

P38646|GRP75_HUMAN Stress-70 protein, mitochondrial precursor (Spot 1294)

Protein View

Match to: **GRP75_HUMAN** Score: **884** Expect: **5.8e-085**
(**P38646**) **Stress-70 protein, mitochondrial precursor (75 kDa glucose-regulated protein)**
(**GRP 75**)

(**Pe**)

Nominal mass (Mr): **73635**; Calculated pI value: **5.87**
NCBI BLAST search of **GRP75_HUMAN** against nr
Unformatted [sequence string](#) for pasting into other applications
Taxonomy: **Homo sapiens**
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **64%**

Matched peptides shown in **Bold Red**

1 **MISASRAAAA RLVGAAASRG PTAARHQDSW NGLSHEAFRL VSRRDYASEA**
51 **IKGAVVGIDL GTTNSCVAVM EGKQAKVLEN AEGARTPSV VAFTADGERL**
101 **VGMPAKRQAV TNPNTFYAT KRLIGRRYDD PEVQDKIKNV PFKIVRASNG**
151 **DAWVEAHGKL YSPSQIGAFV LMKMKETAEN YLGHTAKNAV ITVPAYFNDS**
201 **QRQATKDAGQ ISGLNVLRLVI NEPTAAALAY GLDKSEDKVI AVYDLGGGTF**
251 **DISILEIQKG VFEVKSTNGD TFLGGEDFDQ ALLRHIVKEF KRETGVDLTK**
301 **DNMALQVRRE AAEKAKCELS SSVQTDINLP YLTMDSSGPK HLNMKLTRAQ**
351 **FEQIVTDLIR RTIAPCQKAM QDAEVSKSDI GEVILVGGMT RMPKVQQTIVQ**
401 **DLFGRAPSKA VNPDEAVAIG AAIQGGVLAG DVTDVLLLDV TPLSLGIETL**
451 **GGVFTKILNR NTTIPTKKSQ VFSTAADGQT QVEIKVCQGE REMAGDNKLL**

501 GQFTLIGIPP APRGVPQIEV TFDIDANGIV HVSADKGTG REQQVIQSS
 551 GGLSKDDIEN MVKNAEKYAE EDRRKKERVE AVNMAEGIIH DTETKMEEFK
 601 DQLPADECNK LKEEISKMRE LLARKDSETG ENIRQAASSL QQASLKLKLFEM
 651 AYYKMASERE GSGSSGTGEQ KEDQKEEKQ
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
 2 - 11 973.55 972.55 972.55 0.00 1 M.ISASRAAAAR.L (No match)
 45 - 73 2914.51 2913.50 2913.41 0.09 1 R.DYASEAIKGAUVGIDLGTNNSCVAVMEGK.Q
 Oxidation (M) (No match)
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 Carbamidomethyl (C); Oxidation (M) (No match)
 77 - 85 958.53 957.52 957.49 0.03 0 K.VLENAEGAR.T (No match)
 86 - 99 1450.74 1449.73 1449.71 0.02 0 R.TTPSVVAFTADGER.L (Ions score 51)
 86 - 99 1450.74 1449.73 1449.71 0.02 0 R.TTPSVVAFTADGER.L (No match)
 108 - 121 1568.77 1567.76 1567.76 -0.00 0 R.QAVTNPNTFYATK.R (No match)
 127 - 135 1149.59 1148.58 1148.55 0.04 1 R.RYDDPEVQK.D (No match)
 144 - 159 1709.82 1708.81 1708.86 -0.05 1 K.IVRASNGDAWVEAHGK.L (No match)
 160 - 173 1569.80 1568.79 1568.83 -0.03 0 K.LYSPSQIGAFVLMK.M Oxidation (M) (No
 match)
 174 - 187 1608.78 1607.77 1607.76 0.01 1 K.MKETAENYLGHHTAK.N Oxidation (M) (No
 match)
 176 - 187 1333.67 1332.66 1332.63 0.03 0 K.ETAENYLGHHTAK.N (No match)
 188 - 202 1694.87 1693.86 1693.84 0.02 0 K.NAVITVPAYFNDSQR.Q (Ions score 113)
 188 - 202 1694.87 1693.86 1693.84 0.02 0 K.NAVITVPAYFNDSQR.Q (No match)
 207 - 218 1242.70 1241.69 1241.67 0.02 0 K.DAGQISGLNVLR.V (Ions score 101)
 207 - 218 1242.70 1241.69 1241.67 0.02 0 K.DAGQISGLNVLR.V (No match)
 219 - 234 1645.88 1644.88 1644.87 0.00 0 R.VINEPTAALAYGLDK.S (No match)
 219 - 238 2105.05 2104.04 2104.07 -0.03 1 R.VINEPTAALAYGLDKSEDK.V (No match)
 235 - 259 2710.42 2709.41 2709.41 -0.00 1 K.SEDKVIAVYDLGGTFFDISILEIQK.G (No
 match)
 239 - 259 2251.23 2250.22 2250.21 0.00 0 K.VIAVYDLGGTFFDISILEIQK.G (No match)
 266 - 284 2055.98 2054.98 2054.95 0.02 0 K.STNGDTFLGGEDFDQALLR.H (Ions score
 151)
 266 - 284 2055.98 2054.98 2054.95 0.02 0 K.STNGDTFLGGEDFDQALLR.H (No match)
 293 - 307 1706.85 1705.84 1705.83 0.01 1 R.ETGVDLTKDNMALQR.V Oxidation (M)
 (No match)
 301 - 307 863.44 862.44 862.40 0.04 0 K.DNMALQR.V Oxidation (M) (No match)
 317 - 340 2658.23 2657.23 2657.22 0.01 0 K.CELSSSVQTDINLPYLTMDSGPK.H
 Carbamidomethyl (C); Oxidation (M) (No match)
 349 - 360 1361.76 1360.75 1360.74 0.02 0 R.AQFEGIVTDLIR.R (Ions score 80)
 349 - 360 1361.76 1360.75 1360.74 0.02 0 R.AQFEGIVTDLIR.R (No match)
 369 - 391 2438.22 2437.21 2437.18 0.03 1 K.AMQDAEVSKSDIGEVLVGGMTR.M 2
 Oxidation (M) (No match)
 378 - 391 1462.77 1461.76 1461.75 0.01 0 K.SDIGEVILVGGMTR.M Oxidation (M)
 (Ions score 37)
 378 - 391 1462.77 1461.76 1461.75 0.01 0 K.SDIGEVILVGGMTR.M Oxidation (M) (No
 match)
 395 - 405 1290.70 1289.69 1289.67 0.02 0 K.VQQTVDLFR.A (Ions score 52)
 395 - 405 1290.70 1289.69 1289.67 0.02 0 K.VQQTVDLFR.A (No match)
 469 - 485 1808.91 1807.90 1807.90 0.00 0 K.SQVFSTAADGQTQVEIK.V (No match)
 499 - 513 1592.98 1591.97 1591.94 0.02 0 K.LLGQFTLIGIPPAPR.G (Ions score 66)
 499 - 513 1592.98 1591.97 1591.94 0.02 0 K.LLGQFTLIGIPPAPR.G (No match)
 514 - 535 2309.20 2308.19 2308.21 -0.02 0 R.GVPQIEVTFDIDANGIVHVSADK.D (No
 match)
 542 - 555 1473.79 1472.78 1472.78 -0.00 0 R.EQQIIVIQSSGGLSK.D (No match)
 542 - 563 2434.22 2433.22 2433.21 0.01 1 R.EQQIIVIQSSGGLSKDDIENMVK.N Oxidation
 (M) (No match)
 568 - 574 938.47 937.47 937.43 0.04 1 K.YAEEDRR.K (No match)
 577 - 595 2158.04 2157.03 2157.04 -0.00 1 K.ERVEAVNMAEGIIHDTETK.M Oxidation
 (M) (No match)
 579 - 595 1872.90 1871.89 1871.89 -0.00 0 R.VEAVNMAEGIIHDTETK.M Oxidation (M)
 (No match)
 618 - 624 904.52 903.51 903.50 0.01 1 K.MRELLAR.K Oxidation (M) (No match)
 626 - 646 2233.13 2232.12 2232.10 0.02 1 K.DSETGENIRQAASSLQQASLK.L (No match)
 635 - 646 1231.67 1230.67 1230.66 0.01 0 R.QAASSLQQASLK.L (No match)
 647 - 653 917.46 916.45 916.44 0.02 0 K.LFEMAYK.K Oxidation (M) (No match)
 647 - 654 1045.58 1044.58 1044.53 0.05 1 K.LFEMAYKK.M Oxidation (M) (No
 match)

Match to: **SPB5_HUMAN** Score: **664** Expect: **5.8e-063**
(P36952) **Serpin B5 precursor (Maspin) (Protease inhibitor 5)**
Nominal mass (Mr): **42111**; Calculated pI value: **5.72**
NCBI BLAST search of **SPB5_HUMAN** against nr
Unformatted [sequence string](#) for pasting into other applications
Taxonomy: **Homo sapiens**
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **58%**
Matched peptides shown in **Bold Red**
1 MDALQLANSA FAVDLFKQLC EKEPLGNVLF SPICLSTLS LAQVGAKGDT
51 **ANEIGQVLHF ENVK**DIPFGF QTVTSDVNKL **SSFYSLKLIK RLYVDKSLNL**
101 **STEFISSTKR** PYAKELETVD FKDKLEETKG **QINNSIKDLT DGHFENILAD**
151 **NSVNDQTKIL VVNAAYFVGK** WMKKFPESET KECPPRLNKT **DTKPVQMMNM**
201 **EATFCMGNID SINCKIIELP FQNKHLSMFI LLPK**DVEDES TGLEKIEKQL
251 **NSESLSQWTN PSTMANAKVK** LSIPKFKVEK MIDPKACLEN **LGLKHIFSED**
301 **TSDFGMSET KGVALSNIH KVCLEITEDG GDSIEVPGAR ILQHKDELNA**
351 **DHPFIYIIRH NKTRNIIFFG KFCSP**
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
48 - 64 1870.93 1869.92 1869.92 -0.00 0 **K.GDTANEIGQVLHFENVK.D** (Ions score 116)
48 - 64 1870.93 1869.92 1869.92 -0.00 0 **K.GDTANEIGQVLHFENVK.D** (No match)
80 - 87 944.52 943.51 943.50 0.01 0 **K.LSSFYSLK.L** (No match)
91 - 96 793.47 792.46 792.45 0.01 1 **K.RLYVDK.S** (No match)
97 - 109 1426.74 1425.73 1425.74 -0.00 0 **K.SLNLSTEFISSTK.R** (No match)
130 - 137 873.48 872.47 872.47 0.00 0 **K.GQINNSIK.D** (No match)
138 - 158 2346.09 2345.08 2345.08 0.01 0 **K.DLTDGHFENILADNSVNDQTK.I** (Ions score 117)
138 - 158 2346.09 2345.08 2345.08 0.01 0 **K.DLTDGHFENILADNSVNDQTK.I** (No match)
159 - 170 1293.75 1292.74 1292.75 -0.01 0 **K.ILVVNAAYFVGK.W** (No match)
190 - 215 3100.30 3099.30 3099.28 0.02 0 **K.TDTKPVQMMMEATFCMGNIDSINCK.I** 2
Carbamidomethyl (C); 4 Oxidation (M) (No match)
216 - 224 1101.63 1100.62 1100.62 -0.00 0 **K.IIELPFQNK.H** (Ions score 37)
216 - 224 1101.63 1100.62 1100.62 -0.00 0 **K.IIELPFQNK.H** (No match)
216 - 234 2297.20 2296.19 2296.30 -0.11 1 **K.IIELPFQNKHLSMFI**LLPK.D Oxidation (M) (No match)
225 - 234 1214.68 1213.68 1213.69 -0.01 0 **K.HLSMFI**LLPK.D Oxidation (M) (No match)
249 - 268 2223.03 2222.02 2222.03 -0.00 0 **K.QLNSESLSQWTNPSTMANAK.V** Oxidation (M) (No match)
286 - 294 1017.54 1016.53 1016.53 -0.00 0 **K.ACLENLGLK.H** Carbamidomethyl (C) (No match)
295 - 311 1933.81 1932.80 1932.80 -0.00 0 **K.HIFSEDTSDFGMSETK.G** Oxidation (M) (No match)
322 - 340 2016.96 2015.96 2015.95 0.01 0 **K.VCLEITEDGGDSIEVPGAR.I**
Carbamidomethyl (C) (Ions score 137)
322 - 340 2016.96 2015.96 2015.95 0.01 0 **K.VCLEITEDGGDSIEVPGAR.I**
Carbamidomethyl (C) (No match)
341 - 359 2335.28 2334.27 2334.25 0.02 1 **R.ILQHKDELNADHPFIYIIR.H** (No match)
346 - 359 1715.88 1714.88 1714.87 0.01 0 **K.DELNADHPFIYIIR.H** (Ions score 88)
346 - 359 1715.88 1714.88 1714.87 0.01 0 **K.DELNADHPFIYIIR.H** (No match)
365 - 371 838.49 837.49 837.47 0.01 0 **R.NIIFFGK.F** (Ions score 36)
365 - 371 838.49 837.49 837.47 0.01 0 **R.NIIFFGK.F** (No match)

P31930|UQCR1_HUMAN Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial precursor (Spot 1948)

Protein View

Match to: **UQCR1_HUMAN** Score: **356** Expect: **3.6e-032**
(P31930) **Ubiquinol-cytochrome-c reductase complex core protein I, mitochondrial precursor (EC 1.10.**
Nominal mass (Mr): **52612**; Calculated pI value: **5.94**
NCBI BLAST search of **UQCR1_HUMAN** against nr
Unformatted [sequence string](#) for pasting into other applications
Taxonomy: **Homo sapiens**
Variable modifications: Carbamidomethyl (C),Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **60%**
Matched peptides shown in **Bold Red**

1 MAASVVCRAA TAGAQVLLRA RRSALLRTP ALRSTATFAQ ALQFVPETQV
51 SLLDNGLRVA SEQSSQPTCT VGVWIDVGSR FETEKNNAG YFLEHLAFKG
101 TKNRPGSALE KEVESMG AHL NAYSTREHTA YYIKALSKDL PKAVELLDI
151 VQNC SLEDSQ IEKERDVILR EMQENDASMR DVVFNYLHAT AFQGTPLAQA
201 VEGPSENVRK LSRADLTEYL STHYKAPRMV LAAAGGVEHQ QLLDLAQKHL
251 GGIPTWYAE DAVPTLTPCRF TGSEIRHRDD ALPFAHVAIA VEGPGWASPD
301 NVALQVANAI IGHYDCTYGG GVHLSSPLAS GAVANKLQCS FQTF SICYAE
351 TGLLGAHFVC DRMKIDMMF VLQGGWMLC TSATESEVAR GKNILRNALV
401 SHLDGTT PVC EDIGRSLTY GRRIP LAEWE SRIA EVDASV VREIC SKYIY
451 DQCPAVAGYG PIEQLPDYNR IRSGMFWLRF

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
59 - 80 2363.16 2362.15 2362.12 0.03 0 R.VASEQSSQPTCTVGVWIDVGSR.F
Carbamidomethyl (C) (No match)
86 - 99 1580.81 1579.80 1579.78 0.02 0 K.NNGAGYFLEHLAFK.G (No match)
103 - 111 971.55 970.55 970.52 0.03 0 K.NRPGSALEK.E (Ions score 19)
103 - 111 971.55 970.55 970.52 0.03 0 K.NRPGSALEK.E (No match)
112 - 126 1664.78 1663.78 1663.76 0.01 0 K.EVESMG AHLNAYSTR.E (No match)
112 - 126 1680.78 1679.77 1679.76 0.01 0 K.EVESMG AHLNAYSTR.E Oxidation (M)
(Ions score 29)
112 - 126 1680.78 1679.77 1679.76 0.01 0 K.EVESMG AHLNAYSTR.E Oxidation (M)
(No match)
127 - 134 1024.53 1023.52 1023.50 0.02 0 R.EHTAYYIK.A (No match)
143 - 163 2360.18 2359.17 2359.16 0.02 0 K.AVELLDIVQNC SLEDSQIEK.E
Carbamidomethyl (C) (No match)
143 - 165 2588.25 2587.24 2587.28 -0.04 1 K.AVELLDIVQNC SLEDSQIEKER.D (No
match)
143 - 165 2645.33 2644.32 2644.30 0.02 1 K.AVELLDIVQNC SLEDSQIEKER.D
Carbamidomethyl (C) (No match)
164 - 170 900.54 899.54 899.52 0.02 1 K.ERDVILR.E (No match)
181 - 209 3130.58 3129.57 3129.55 0.02 0 R.DVVFNYLHATAFQGTPLAQAVEG PSENVR.K
(No match)
211 - 225 1796.86 1795.86 1795.91 -0.05 1 K.LSRADLTEYLSTHYK.A (No match)
214 - 225 1440.72 1439.71 1439.69 0.02 0 R.ADLTEYLSTHYK.A (Ions score 77)
214 - 225 1440.72 1439.71 1439.69 0.02 0 R.ADLTEYLSTHYK.A (No match)
229 - 248 2108.13 2107.12 2107.11 0.01 0 R.MVLAAGGVEHQQLLDLAQK.H Oxidation
(M) (No match)
249 - 269 2354.17 2353.17 2353.15 0.01 0 K.HLGGIPWYAE DAVPTLTPCR.F
Carbamidomethyl (C) (No match)
363 - 378 2044.97 2043.96 2043.94 0.02 1 R.MKIDMMFVLQGGWML.L Oxidation (M)
(No match)
363 - 378 2092.93 2091.92 2091.92 -0.00 1 R.MKIDMMFVLQGGWML.L 4 Oxidation (M)
(No match)
365 - 378 1817.81 1816.80 1816.79 0.01 0 K.IDMMFVLQGGWML.L 3 Oxidation (M)
(No match)
379 - 390 1323.65 1322.64 1322.61 0.03 0 R.LCTSATESEVAR.G Carbamidomethyl (C)
(No match)
397 - 415 2054.02 2053.01 2052.99 0.02 0 R.NALVSHLDGTT PVCEDIGR.S
Carbamidomethyl (C) (No match)
416 - 422 809.47 808.46 808.44 0.02 0 R.SLLTYGR.R (Ions score 21)
416 - 422 809.47 808.46 808.44 0.02 0 R.SLLTYGR.R (No match)
423 - 432 1256.70 1255.70 1255.67 0.03 1 R.RIPLAEWESR.I (Ions score 37)
423 - 432 1256.70 1255.70 1255.67 0.03 1 R.RIPLAEWESR.I (No match)
424 - 432 1100.60 1099.59 1099.57 0.03 0 R.IPLAEWESR.I (No match)
433 - 442 1058.61 1057.60 1057.58 0.03 0 R.IAEVDASVVR.E (Ions score 41)
433 - 442 1058.61 1057.60 1057.58 0.03 0 R.IAEVDASVVR.E (No match)
433 - 447 1618.90 1617.89 1617.84 0.05 1 R.IAEVDASV VREIC SK.Y (No match)
448 - 470 2702.28 2701.27 2701.25 0.02 0 K.YIYDQCPAVAGYGPIEQLPDYNR.I
Carbamidomethyl (C) (No match)
473 - 479 896.46 895.45 895.44 0.02 0 R.SGMFWLR.F (No match)
473 - 479 912.47 911.46 911.43 0.03 0 R.SGMFWLR.F Oxidation (M) (No match)

P31937|2HIDH_HUMAN 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor (Spot 2537)

Protein View

Match to: 3HIDH_HUMAN Score: 79 Expect: 0.00018

(P31937) 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor (EC 1.1.1.31) (HIBADH)

Nominal mass (Mr): 35306; Calculated pI value: 8.38

NCBI BLAST search of 3HIDH_HUMAN against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Homo sapiens](#)

Variable modifications: Carbamidomethyl (C),Oxidation (M)

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

Sequence Coverage: **39%**

Matched peptides shown in **Bold Red**

```
1 MAASLRLLGA ASGLRYWSRR LRPAAGSFAA VCSRSVASKT PVGFIGLGNM
51 GNPMAKNLMK HGYPLIIYDV FPDACKEFQD AGEQVVSSPA DVAEKADRII
101 TMLPTSINAI EAYSGANGIL KVKKGSLLI DSSTIDPAVS KELAKEVEKM
151 GAVFMDAPVS GVGGAARSGN LTFMVGVED EFAAAQELLG CMGSNVVYCG
201 AVGTGQAAKI CNMMLLAISM IGTAEMNLG IRLGLDPKLL AKILNMSSGR
251 CWSSDTYNPV PGVMDGVPSA NNYQGGFGTT LMAKDLGLAQ DSATSTKSPI
301 LLGSLAHQIY RMMCAKGYSK KDFSSVFQFL REEETF
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
40 - 56 1735.88 1734.88 1734.84 0.03 0 K.TPVGFIGLGNMGNPMAK.N 2 Oxidation
(M) (No match)
77 - 95 2005.94 2004.93 2004.93 0.00 0 K.EFQDAGEQVVSSPADVAEK.A (No match)
99 - 121 2406.29 2405.28 2405.29 -0.00 0 R.IITMLPTSINAIEAYSGANGILK.K
Oxidation (M) (No match)
125 - 141 1730.92 1729.91 1729.95 -0.03 1 K.KGSLLDSSSTIDPAVSK.E (No match)
126 - 141 1602.86 1601.85 1601.85 0.00 0 K.GSLLDSSSTIDPAVSK.E (No match)
150 - 167 1724.80 1723.80 1723.80 -0.01 0 K.MGAVFMDAPVSGVGGAAR.S 2 Oxidation
(M) (Ions score 4)
150 - 167 1724.80 1723.80 1723.80 -0.01 0 K.MGAVFMDAPVSGVGGAAR.S 2 Oxidation
(M) (No match)
243 - 250 893.47 892.46 892.44 0.02 0 K.ILNMSSGR.C Oxidation (M) (No
match)
243 - 250 893.47 892.46 892.44 0.02 0 K.ILNMSSGR.C Oxidation (M) (No
match)
298 - 311 1567.85 1566.85 1566.89 -0.04 0 K.SPILLGSLAHQIYR.M (No match)
298 - 311 1567.85 1566.85 1566.89 -0.04 0 K.SPILLGSLAHQIYR.M (No match)
321 - 331 1373.73 1372.73 1372.71 0.01 1 K.KDFSSVFQFLR.E (No match)
322 - 331 1245.65 1244.64 1244.62 0.02 0 K.DFSSVFQFLR.E (Ions score 22)
322 - 331 1245.65 1244.64 1244.62 0.02 0 K.DFSSVFQFLR.E (No match)
322 - 336 1880.88 1879.88 1879.86 0.01 1 K.DFSSVFQFLREEETF.- (No match)
```

Q15417|CNN3_HUMAN Calponin-3 (Spot 2243)

Protein View

Match to: **CNN3_HUMAN** Score: **90** Expect: **1.6e-005**

(**Q15417**) **Calponin-3 (Calponin, acidic isoform)**

Nominal mass (Mr): **36391**; Calculated pI value: **5.69**

NCBI BLAST search of [CNN3_HUMAN](#) against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Homo sapiens](#)

Variable modifications: Carbamidomethyl (C),Oxidation (M)

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

Sequence Coverage: **44%**

Matched peptides shown in **Bold Red**

```
1 MTHFNKGPSY GLSAEVKNKI ASKYDHQAE DLRNWIEEVT GMSIGPNFQL
51 GLKDGIILCE LINKLQPGSV KKVNESSLNW PLENIGNFI KAIQAYGMKP
101 HDIFEANDLF ENGNMTQVQT TLVALAGLAK TKGFHTTIDI GVKYAEKQTR
151 RFDEGKLKAG QSVIGLQMGT NKCASQAGMT AYGTRRHLVD PKMQTDKPF
201 QTTISLQMGT NKGASQAGML APGTRRDIYD QKLTLQPVDN STISLQMGTN
251 KVASQKGMSV YGLGRQVYDP KYCAAPTEPV IHNGSQGTGT NGSEISDSY
301 QAEYPDEYHG EYQDDYPRDY QYSDQGIDY
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
7 - 17 1107.58 1106.57 1106.56 0.01 0 K.GPSYGLSAEVK.N (No match)
34 - 53 2233.11 2232.11 2232.12 -0.02 0 R.NWIEEVTGMSIGPNFQLGLK.D (No match)
65 - 72 856.54 855.53 855.52 0.01 1 K.LQPGSVK.V (No match)
133 - 143 1187.64 1186.64 1186.63 0.00 0 K.GFHTTIDIGVK.Y (No match)
159 - 172 1419.72 1418.72 1418.72 -0.00 0 K.AGQSVIGLQMGTKN.C Oxidation (M)
(Ions score 27)
159 - 172 1419.72 1418.72 1418.72 -0.00 0 K.AGQSVIGLQMGTKN.C Oxidation (M) (No
match)
173 - 185 1389.59 1388.58 1388.58 -0.00 0 K.CASQAGMTAYGTR.R Carbamidomethyl
(C); Oxidation (M) (No match)
186 - 192 928.50 927.50 927.49 0.00 1 R.RHLYDPK.M (No match)
193 - 212 2316.10 2315.09 2315.08 0.02 0 K.MQTDKPFQTTISLQMGTKN.G 2 Oxidation
(M) (No match)
213 - 225 1216.62 1215.61 1215.60 0.01 0 K.GASQAGMLAPGTR.R (No match)
```


213 - 225 1232.61 1231.60 1231.60 0.01 0 K.GASQAGMLAPGTR.R Oxidation (M)
 (Ions score 17)
 213 - 225 1232.61 1231.60 1231.60 0.01 0 K.GASQAGMLAPGTR.R Oxidation (M) (No
 match)
 233 - 251 2076.06 2075.05 2075.06 -0.01 0 K.LTLQPVDNSTISLQMGTK.V Oxidation
 (M) (No match)
 257 - 265 955.48 954.47 954.46 0.01 0 K.GMSVYGLGR.Q Oxidation (M) (No
 match)
 257 - 265 955.48 954.47 954.46 0.01 0 K.GMSVYGLGR.Q Oxidation (M) (No
 match)

Q13011|ECH1_HUMAN Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (Spot 2522)

Protein View

Match to: **ECH1_HUMAN** Score: 227 Expect: 2.9e-019
 (Q13011) Delta3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial precursor (EC 5.3.3.-)

Nominal mass (Mr): 35793; Calculated pI value: 8.16

NCBI BLAST search of **ECH1_HUMAN** against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: **Homo sapiens**

Variable modifications: Carbamidomethyl (C),Oxidation (M)

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

Sequence Coverage: 32%

Matched peptides shown in **Bold Red**

1 MAAGIVASRR LRDLLTRRLT GSNYPGLSIS LRLTGSSAQE EASGVALGEA
 51 PDHSYESLRV TSAQKHVLHV QLNRPNKRNA **MNKVFWRE**EMV ECFNKISRDA
 101 DCRAVVISGA GK**MFTAGIDL** **MDMASDILQP** KGDDVARISW YLRDIITRYQ
 151 **ETFNVI**ERCP KPVIAAVHGG CIGGGVDLVT ACDIRYCAQD **AFFQVKEVDV**
 201 **GLAADVGT**LQ RLPKVIGNQS **LVNELAFTAR** **KMMADEALGS** GLVSRVFPDK
 251 EVMLDAALAL AAEISSKSPV AVQSTK**VNLL** YSRDHSVAES LNYVASWNMS
 301 MLQTQDLVKS VQATTENKEL KTVTFSKL
 Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
 79 - 87 1165.60 1164.59 1164.59 0.01 1 R.NAMNKVFWR.E (No match)
 79 - 87 1165.60 1164.59 1164.59 0.01 1 R.NAMNKVFWR.E (No match)
 113 - 131 2144.98 2143.97 2143.98 -0.01 0 K.**MFTAGIDLMDMASDILQPK.G** 3 Oxidation
 (M) (No match)
 138 - 143 837.49 836.48 836.45 0.03 0 R.ISWYLR.D (No match)
 149 - 158 1298.65 1297.64 1297.63 0.01 0 R.YQETFNVIER.C (Ions score 52)
 149 - 158 1298.65 1297.64 1297.63 0.01 0 R.YQETFNVIER.C (No match)
 186 - 196 1376.66 1375.65 1375.62 0.03 0 R.YCAQDAFFQVK.E Carbamidomethyl (C)
 (No match)
 197 - 211 1542.82 1541.81 1541.80 0.01 0 K.EVDVGLAADVGT**LQR.L** (Ions score 76)
 197 - 211 1542.82 1541.81 1541.80 0.01 0 K.EVDVGLAADVGT**LQR.L** (No match)
 215 - 230 1731.95 1730.95 1730.93 0.02 0 K.VIGNQSLV**NELAFTAR.K** (Ions score 61)
 215 - 230 1731.95 1730.95 1730.93 0.02 0 K.VIGNQSLV**NELAFTAR.K** (No match)
 231 - 245 1596.76 1595.75 1595.76 -0.01 1 R.**KMMADEALGSGLVSR.V** 2 Oxidation (M)
 (No match)
 232 - 245 1468.70 1467.69 1467.67 0.02 0 K.**MMADEALGSGLVSR.V** 2 Oxidation (M)
 (No match)
 277 - 283 864.51 863.50 863.49 0.01 0 K.VNLLYSR.D (No match)

P07339|CATD_HUMAN Cathepsin D precursor (Spot 2586)

Protein View

Match to: **CATD_HUMAN** Score: 356 Expect: 3.6e-032
 (P07339) Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain;
 Cathepsin D

heavy

Nominal mass (Mr): 44524; Calculated pI value: 6.10

NCBI BLAST search of **CATD_HUMAN** against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: **Homo sapiens**

Variable modifications: Carbamidomethyl (C),Oxidation (M)

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

Sequence Coverage: 37%

Matched peptides shown in **Bold Red**

1 MQPSSLLPLA LCLLAAPASA LVRIPLHKFT SIRRTMSEVG GSVEDLIAKG
 51 PVSKYSQAVP AVTEGPIPEV LKNYMDAQYY GEIGIGTPPQ CFTVVFDTGS

101 SNLWVPSIHC KLLDIACWIH HKYNSDKSST YVKNGTSFDI HYGSGSLSGY
151 LSQDVTVSVPK QSASSASALG GVKVERQVFG EATKQPGITF IAAKFDGILG
201 MAYPRISVNN VLPVFDNLMQ QKLVQDNIFS FYLSRDPDAQ PGGELMLGGT
251 DSKYYKGSLS YLNVTRKAYW QVHLDQVEVA SGLTLCKEGC EAIVDTGTSL
301 MVGVPVDEVR LQKAIGAVPL IQGEYMIPCE KVSTLPAITL KLGKGYKLS
351 PEDYTLKVSQ AGKTLCLSGF MGMDIPPPSG PLWILGDVFI GRYYTVFDRD
401 NNRVGFAEAA RL

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
177 - 184 879.49 878.48 878.45 0.03 0 R.QVFGAATK.Q (No match)
185 - 194 1045.60 1044.59 1044.60 -0.00 0 K.QPGITFIAAK.F (No match)
195 - 205 1239.64 1238.63 1238.61 0.02 0 K.FDGILGMAYPR.I (No match)
195 - 205 1255.63 1254.63 1254.61 0.02 0 K.FDGILGMAYPR.I Oxidation (M) (Ions score 18)
195 - 205 1255.63 1254.63 1254.61 0.02 0 K.FDGILGMAYPR.I Oxidation (M) (No match)
206 - 222 1975.03 1974.03 1974.02 0.00 0 R.ISVNNVLPVFDNLMQQK.L Oxidation (M) (Ions score 64)
206 - 222 1975.03 1974.03 1974.02 0.00 0 R.ISVNNVLPVFDNLMQQK.L Oxidation (M) (No match)
223 - 235 1601.87 1600.86 1600.82 0.04 0 K.LVDQNIFSFYLSR.D (Ions score 69)
223 - 235 1601.87 1600.86 1600.82 0.04 0 K.LVDQNIFSFYLSR.D (No match)
236 - 253 1803.80 1802.80 1802.80 -0.00 0 R.DPDAQPGGELMLGGTDSK.Y Oxidation (M) (No match)
288 - 309 2350.11 2349.11 2349.08 0.02 0 K.EGCEAIVDTGTSLMVGPVDEVR.E Carbamidomethyl (C); Oxidation (M) (No match)
314 - 331 2005.02 2004.02 2004.01 0.01 0 K.AIGAVPLIQGEYMIPCEK.V Carbamidomethyl (C); Oxidation (M) (No match)
332 - 341 1042.66 1041.65 1041.64 0.01 0 K.VSTLPAITLK.L (No match)
349 - 357 1065.56 1064.55 1064.54 0.02 0 K.LSPEDYTLK.V (No match)
393 - 399 963.49 962.48 962.45 0.03 0 R.YYTVFDR.D (Ions score 38)
393 - 399 963.49 962.48 962.45 0.03 0 R.YYTVFDR.D (No match)
393 - 403 1462.70 1461.69 1461.66 0.02 1 R.YYTVFDRDNNR.V (Ions score 56)
393 - 403 1462.70 1461.69 1461.66 0.02 1 R.YYTVFDRDNNR.V (No match)
404 - 411 820.46 819.45 819.42 0.03 0 R.VGFAEAAR.L (Ions score 41)
404 - 411 820.46 819.45 819.42 0.03 0 R.VGFAEAAR.L (No match)

Q99497|PARK7_HUMAN Protein DJ-1 (Oncogene DJ1) (Spot 2761)

Protein View

Match to: **PARK7_HUMAN** Score: 245 Expect: 4.6e-021

(**Q99497**) **Protein DJ-1 (Oncogene DJ1)**

Nominal mass (Mr): 19878; Calculated pI value: 6.33

NCBI BLAST search of **PARK7_HUMAN** against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: **Homo sapiens**

Variable modifications: Carbamidomethyl (C),Oxidation (M)

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

Sequence Coverage: 46%

Matched peptides shown in **Bold Red**

1 MASKRALVIL AK**GAEEMETV** IPVDVMRRAG IKVTVAGLAG KDPVQCSR**DV**
51 **VICPDASLED AKKEGPDVVV VLPGGNLGAQ NLSESA**AVKE ILKEQENRKG
101 LIAAICAGPT ALLAHEIGFG SKVTTHPLAK DKMMNGGHYT YSENR**VEKDG**
151 **LILTSRGPST SFEFALAIVE ALNGK**EVAAQ VKAPLVLKD

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
13 - 27 1675.78 1674.77 1674.80 -0.02 0 K.GAEEMETVIPVDVMR.R (No match)
13 - 27 1691.76 1690.75 1690.79 -0.04 0 K.GAEEMETVIPVDVMR.R Oxidation (M) (No match)
13 - 27 1707.75 1706.74 1706.79 -0.04 0 K.GAEEMETVIPVDVMR.R 2 Oxidation (M) (Ions score 76)
13 - 27 1707.75 1706.74 1706.79 -0.04 0 K.GAEEMETVIPVDVMR.R 2 Oxidation (M) (No match)
13 - 28 1863.86 1862.85 1862.89 -0.04 1 K.GAEEMETVIPVDVMRR.A 2 Oxidation (M) (No match)
49 - 63 1659.78 1658.77 1658.82 -0.05 1 R.DVVICPDASLEDAK**E** Carbamidomethyl (C) (No match)
64 - 89 2584.31 2583.30 2583.32 -0.01 0 K.EGPDVVVLPGGNLGAQ**NLSESA**AVK.E (Ions score 117)
64 - 89 2584.31 2583.30 2583.32 -0.01 0 K.EGPDVVVLPGGNLGAQ**NLSESA**AVK.E (No match)
146 - 156 1230.70 1229.69 1229.70 -0.01 1 R.VEKDGLILTSR.G (No match)

149 - 156 874.49 873.48 873.49 -0.01 0 K.DGLILTSR.G (Ions score 1)
149 - 156 874.49 873.48 873.49 -0.01 0 K.DGLILTSR.G (No match)
157 - 175 1920.97 1919.97 1920.00 -0.03 0 R.GPGTSEFEFALAIVEALNGK.E (No match)

P30101|PDIA3_HUMAN Protein disulfide-isomerase A3 precursor (Spot 1736)

Protein View

Match to: PDIA3_HUMAN Score: 560 Expect: 1.5e-052

(P30101) Protein disulfide-isomerase A3 precursor (EC 5.3.4.1) (Disulfide isomerase ER-60)

(Erp60)

Nominal mass (Mr): 56747; Calculated pI value: 5.98

NCBI BLAST search of PDIA3_HUMAN against nr

Unformatted sequence string for pasting into other applications

Taxonomy: Homo sapiens

Variable modifications: Carbamidomethyl (C),Oxidation (M)

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

Sequence Coverage: 62%

Matched peptides shown in Bold Red

1 MRLRRLALFP GVALLLAAAR LAAASDVLEL TDDNFESRIS DTGSAGLMLV
51 EFFAPWCGHC **KRLAPEYEAA ATRLK**GIVPL AKVDCTANTN TCNKYGVVSGY
101 **PTLKI**FRDGE **EAGAYD**GPRT ADGIVSHLKK **QAGPASVPLR TEEEFK**KFIS
151 **DKDASIVGFF DDSFSEAHSE FLK**AASNLRD NYRFAHTNVE **SLVNEYDDNG**
201 **EGIILLFRPSH LTNK**FEDKTV **AYTEQK**MTSG KIKK**FIQENI FGICPH**MTED
251 **NKDLIQ**GKDL **LIAYYD**VVYE **KNAGS**NYWR NRVMVAKKF **LDAGHKL**NFA
301 **VASRKTFSHE LSDF**GLESTA **GEIPV**VAIRT AKGEK**FVMQE EFSR**DGKALE
351 **RFLQDY**FDGN **LKRYL**KSEPI **PESND**GPVKV **VVAEN**FDEIV **NNENK**DVLEIE
401 **FYAPW**CGHCK **NLEPKY**KELG **EKLSK**DPNIV IAKMDATAND **VPSPYE**VRGF
451 **PTIYF**SPANK **KLNP**KYEGG **RELSDF**ISYL **QREAT**NPPVI **QEEKP**KKKKK
501 AQEDL
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
62 - 73 1347.71 1346.70 1346.69 0.01 1 K.RLAPEYEAAATR.L (No match)
63 - 73 1191.60 1190.59 1190.59 -0.00 0 R.LAPEYEAAATR.L (No match)
95 - 104 1084.56 1083.55 1083.56 -0.01 0 K.YGVSGYPTLK.I (No match)
105 - 119 1652.78 1651.77 1651.76 0.01 1 K.IFRDGEAGAYDGPR.T (No match)
130 - 140 1123.65 1122.65 1122.65 -0.01 1 K.KQAGPASVPLR.T (No match)
131 - 140 995.57 994.56 994.56 0.01 0 K.QAGPASVPLR.T (No match)
131 - 146 1758.92 1757.91 1757.89 0.02 1 K.QAGPASVPLRTEEEFK.K (No match)
148 - 173 2938.42 2937.41 2937.37 0.04 1 K.FISDKDASIVGFFDDSFSEAHSEFLK.A (No match)
153 - 173 2348.08 2347.08 2347.06 0.01 0 K.DASIVGFFDDSFSEAHSEFLK.A (No match)
184 - 214 3529.72 3528.71 3528.73 -0.02 0 R.FAHTNVESLVNEYDDNGEGIILFRPSHSLTNK.F (No match)
219 - 226 939.47 938.46 938.47 -0.01 0 K.TVAYTEQK.M (No match)
235 - 258 2863.40 2862.39 2862.37 0.03 1 K.FIQENIFGICPHMTEDNKDLIQK.D
Carbamidomethyl (C); Oxidation (M) (No match)
259 - 271 1619.78 1618.77 1618.78 -0.01 0 K.DLLIAYYDVDYK.N (Ions score 59)
259 - 271 1619.78 1618.77 1618.78 -0.01 0 K.DLLIAYYDVDYK.N (No match)
275 - 280 782.37 781.37 781.35 0.02 0 K.GSNIYWR.N (Ions score 25)
275 - 280 782.37 781.37 781.35 0.02 0 K.GSNIYWR.N (No match)
290 - 296 787.41 786.40 786.40 -0.00 0 K.FLDAGHK.L (No match)
297 - 304 877.50 876.49 876.48 0.01 0 K.LNFVAVSR.K (No match)
305 - 329 2703.43 2702.43 2702.39 0.03 1 R.KTFSHELSDFGLESTAGEIPVVAIR.T (No match)
306 - 329 2575.33 2574.32 2574.30 0.02 0 K.TFSHELSDFGLESTAGEIPVVAIR.T (No match)
336 - 344 1172.56 1171.56 1171.53 0.02 0 K.FVMQEEFSR.D (No match)
336 - 344 1188.53 1187.52 1187.53 -0.00 0 K.FVMQEEFSR.D Oxidation (M) (Ions score 8)
336 - 344 1188.53 1187.52 1187.53 -0.00 0 K.FVMQEEFSR.D Oxidation (M) (No match)
336 - 347 1488.68 1487.67 1487.67 0.00 1 K.FVMQEEFSRDGK.A Oxidation (M) (No match)
352 - 362 1359.66 1358.65 1358.65 -0.00 0 R.FLQDYFDGNLKR.R (No match)
352 - 363 1515.77 1514.76 1514.75 0.01 1 R.FLQDYFDGNLKR.Y (Ions score 62)
352 - 363 1515.77 1514.76 1514.75 0.01 1 R.FLQDYFDGNLKR.Y (No match)
367 - 379 1368.66 1367.66 1367.66 -0.00 0 K.SEPVPEPNDGPVK.V (No match)
380 - 395 1832.90 1831.89 1831.90 -0.00 0 K.VVVAENFDEIVNNENK.D (No match)
416 - 422 866.46 865.45 865.45 0.00 1 K.YKELGK.L (No match)
434 - 448 1664.76 1663.76 1663.75 0.00 0 K.MDATANDVPSPYEVR.G (No match)
434 - 448 1680.75 1679.74 1679.75 -0.00 0 K.MDATANDVPSPYEVR.G Oxidation (M) (Ions score 62)

434 - 448 1680.75 1679.74 1679.75 -0.00 0 K.MDATANDVPSPEYVR.G Oxidation (M)
 (No match)
 449 - 460 1341.68 1340.67 1340.68 -0.01 0 R.GFPITYFSPANK.K (Ions score 46)
 449 - 460 1341.68 1340.67 1340.68 -0.01 0 R.GFPITYFSPANK.K (No match)
 472 - 482 1370.70 1369.70 1369.69 0.01 0 R.ELSDFISYLQR.E (Ions score 80)
 472 - 482 1370.70 1369.70 1369.69 0.01 0 R.ELSDFISYLQR.E (No match)
 483 - 496 1579.82 1578.82 1578.83 -0.01 0 R.EATNPPVIEEKKPK.K (No match)

P04792|HSPB1_HUMAN Heat-shock protein beta-1 (HspB1) (Heat shock 27kDa protein)
 (Spot 2669)

Protein View

Match to: HSPB1_HUMAN Score: 395 Expect: 4.6e-036
 (P04792) Heat-shock protein beta-1 (HspB1) (Heat shock 27 kDa protein) (HSP 27)
 (Stressresponsive)

Nominal mass (Mr): 22768; Calculated pI value: 5.98

NCBI BLAST search of HSPB1_HUMAN against nr

Unformatted sequence string for pasting into other applications

Taxonomy: Homo sapiens

Variable modifications: Carbamidomethyl (C),Oxidation (M)

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

Sequence Coverage: 66%

Matched peptides shown in Bold Red

1 MTERVVPFSL LRGPSWDPPR DWYPHSRLEFD QAFGLPRLPE EWSQWLGSS
 51 WPGYVRPLPP AAIESPAVAA PAYSRALSRQ LSSGVSEIRH TADRWRVSLD
 101 VNHFAPELDT VKTKDGVVEI TGKHEERQDE HGYISRCFTR KYTLPPGVDP
 151 TQVSSLSPE GTLTVEAPMP KLATQSNEIT IPVTFESRAQ LGGPEAAKSD
 201 ETAAK
 Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
 5 - 12 987.60 986.59 986.60 -0.01 1 R.RVPFSLLR.G (No match)
 6 - 12 831.52 830.52 830.50 0.01 0 R.VPFSLLR.G (No match)
 6 - 20 1773.89 1772.88 1772.94 -0.06 1 R.VPFSLLRGPSWDPPR.D (No match)
 13 - 20 961.47 960.46 960.45 0.02 0 R.GPSWDPPR.D (No match)
 21 - 27 960.46 959.45 959.42 0.03 0 R.DWYPHSR.L (No match)
 21 - 37 2105.00 2103.99 2104.03 -0.03 1 R.DWYPHSRLEFDQAFGLPR.L (No match)
 28 - 37 1163.64 1162.63 1162.61 0.02 0 R.LFDQAFGLPR.L (Ions score 52)
 28 - 37 1163.64 1162.63 1162.61 0.02 0 R.LFDQAFGLPR.L (No match)
 80 - 89 1075.59 1074.58 1074.57 0.02 0 R.QLSSGVSEIR.H (Ions score 60)
 80 - 89 1075.59 1074.58 1074.57 0.02 0 R.QLSSGVSEIR.H (No match)
 97 - 112 1783.93 1782.92 1782.92 0.00 0 R.VSLDVNHFAPELDTVK.T (Ions score 69)
 97 - 112 1783.93 1782.92 1782.92 0.00 0 R.VSLDVNHFAPELDTVK.T (No match)
 113 - 123 1146.64 1145.63 1145.63 -0.00 1 K.TKDGVVEITGK.H (No match)
 128 - 136 1104.53 1103.52 1103.50 0.02 0 R.QDEHGYISR.C (No match)
 141 - 171 3242.66 3241.65 3241.64 0.01 1 R.KYTLPPGVDPQTQVSSLSPEGLTVEAPMPK.L
 Oxidation (M) (No match)
 142 - 171 3114.56 3113.55 3113.55 0.00 0 K.YTLPPGVDPQTQVSSLSPEGLTVEAPMPK.L
 Oxidation (M) (No match)
 172 - 188 1906.01 1905.00 1904.98 0.02 0 K.LATQSNEITIPVTFESR.A (Ions score 110)
 172 - 188 1906.01 1905.00 1904.98 0.02 0 K.LATQSNEITIPVTFESR.A (No match)
 189 - 198 941.52 940.51 940.50 0.01 0 R.AQLGGPEAAK.S (No match)

Q15417|CNN3_HUMAN Calponin-3 (Spot 2243)

Protein View

Match to: CNN3_HUMAN Score: 90 Expect: 1.6e-005

(Q15417) Calponin-3 (Calponin, acidic isoform)

Nominal mass (Mr): 36391; Calculated pI value: 5.69

NCBI BLAST search of CNN3_HUMAN against nr

Unformatted sequence string for pasting into other applications

Taxonomy: Homo sapiens

Variable modifications: Carbamidomethyl (C),Oxidation (M)

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

Sequence Coverage: 44%

Matched peptides shown in Bold Red

1 MTHFNKGPSY GLSAEVKMKI ASKYDHQAE E DLRNWIIEVT GMSIGPNFQL
 51 GLKDGIIICE LINKLQPGSV KKVNESSLNW PQLLENIGNFI KAIQAYGMKP
 101 HDIFEANDLF ENGNMTQVQT TLVALAGLAK TKGFHTTIDI GVKYAEKQTR
 151 RFDEGKLGAG QSVIGLQMG T NKCASQAGMT AYGTRRHLVD PKMQTDKPPD
 201 QTTISLQMG T NKGASQAGML APGTRRDIYD QKLTLLQPV DN STISLQMG TN

251 KVASQK**GMSV YGLGR**QVYDP KYCAAPTEPV IHNGSQGTGT NGSEISDSDY
301 QAEYPDEYHG EYQDDYPRDY QYSDQGIDY
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
7 - 17 1107.58 1106.57 1106.56 0.01 0 K.GPSYGLSAEVK.N (No match)
34 - 53 2233.11 2232.11 2232.12 -0.02 0 R.NWIEEVTGMSIGPNFQLGLK.D (No match)
65 - 72 856.54 855.53 855.52 0.01 1 K.LQPGSVKK.V (No match)
133 - 143 1187.64 1186.64 1186.63 0.00 0 K.GFHHTTIDIGVK.Y (No match)
159 - 172 1419.72 1418.72 1418.72 -0.00 0 K.AGQSVIGLQMG**TNK.C** Oxidation (M)
(Ions score 27)
159 - 172 1419.72 1418.72 1418.72 -0.00 0 K.AGQSVIGLQMG**TNK.C** Oxidation (M) (No
match)
173 - 185 1389.59 1388.58 1388.58 -0.00 0 K.CASQAGMTAYG**T.R** Carbamidomethyl
(C); Oxidation (M) (No match)
186 - 192 928.50 927.50 927.49 0.00 1 R.RHLYDPK.M (No match)
193 - 212 2316.10 2315.09 2315.08 0.02 0 K.MQTDKPF**DQTTISLQMG**TNK.G 2 Oxidation
(M) (No match)
213 - 225 1216.62 1215.61 1215.60 0.01 0 K.GASQAGMLAPG**T.R** (No match)
213 - 225 1232.61 1231.60 1231.60 0.01 0 K.GASQAGMLAPG**T.R** Oxidation (M)
(Ions score 17)
213 - 225 1232.61 1231.60 1231.60 0.01 0 K.GASQAGMLAPG**T.R** Oxidation (M) (No
match)
233 - 251 2076.06 2075.05 2075.06 -0.01 0 K.LTLQPV**DNSTISLQMG**TNK.V Oxidation
(M) (No match)
257 - 265 955.48 954.47 954.46 0.01 0 K.GMSVYGLGR.Q Oxidation (M) (No
match)
257 - 265 955.48 954.47 954.46 0.01 0 K.GMSVYGLGR.Q Oxidation (M) (No
match)

P40121|CAPG_HUMAN Macrophage capping protein (Actin-regulatory protein CAP-G) (Spot 2141)

Protein View

Match to: CAPG_HUMAN Score: 256 Expect: 3.6e-022

(P40121) Macrophage capping protein (Actin-regulatory protein CAP-G)

Nominal mass (Mr): 38494; Calculated pI value: 5.88

NCBI BLAST search of CAPG_HUMAN against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Homo sapiens](#)

Variable modifications: Carbamidomethyl (C),Oxidation (M)

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

Sequence Coverage: 38%

Matched peptides shown in **Bold Red**

1 MYTAIPQSGS PFPGSVQDPG LHVWRVEK**LK** PVPVAQENQG VFFSGDSYLV
51 LHNGPEEVSH LHLWIGQQSS RDEQGACAVL AVHLN**TLLGE** RPVQHR**EVQG**
101 **NESDLFMSYF PRGLKYQEGG VESAFHKTST GAPAAIK**KLY QVKGKNIRA
151 TERALNWD**SF** NTGDCFILD**L** GQNIFAWCGG KSNILERNKA RDLALAIRDS
201 ERQ**GKAQVEI** VTDG**EPAEM IQVLGPKPAL** KEGNPEEDLT ADK**ANAQAAA**
251 **LYK**VSDATGQ MNLTKVAD**SS** PFALELLISD DCFVLDNGLC **GKIYI**WKGRK
301 ANEKER**QAAL QVAEGFISRM QYAPNTQVEI** LPQGR**ESPIF** KQFFKDWK
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
97 - 112 1918.86 1917.85 1917.86 -0.00 0 R.EVQGN**ESDLFMSYFPR.G** (No match)
97 - 112 1934.86 1933.85 1933.85 -0.00 0 R.EVQGN**ESDLFMSYFPR.G** Oxidation (M)
(Ions score 12)
97 - 112 1934.86 1933.85 1933.85 -0.00 0 R.EVQGN**ESDLFMSYFPR.G** Oxidation (M)
(No match)
97 - 115 2233.13 2232.13 2232.05 0.07 1 R.EVQGN**ESDLFMSYFPRGLK.Y** Oxidation
(M) (No match)
116 - 127 1351.63 1350.62 1350.62 -0.00 0 K.YQEGGV**ESAFHK.T** (Ions score 66)
116 - 127 1351.63 1350.62 1350.62 -0.00 0 K.YQEGGV**ESAFHK.T** (No match)
128 - 137 916.53 915.52 915.50 0.02 0 K.TSTGAPAAIK.K (No match)
206 - 231 2778.46 2777.45 2777.45 -0.00 0 K.AQVEIVTDG**EPAEMIQVLGPKPALK.E**
Oxidation (M) (No match)
244 - 253 1020.55 1019.54 1019.54 -0.00 0 K.ANAQAAALYK.V (No match)
266 - 292 2955.38 2954.37 2954.40 -0.03 0 K.VADSSPFALELLISD**DCFVLDNGLCGK.I** 2
Carbamidomethyl (C) (No match)
307 - 319 1389.76 1388.75 1388.74 0.01 0 R.QAALQVAEG**FISRM** (Ions score 75)
307 - 319 1389.76 1388.75 1388.74 0.01 0 R.QAALQVAEG**FISRM** (No match)
320 - 335 1844.92 1843.92 1843.93 -0.01 0 R.MQYAPNTQVEI**LPQGR.E** (No match)
320 - 335 1860.92 1859.92 1859.92 -0.00 0 R.MQYAPNTQVEI**LPQGR.E** Oxidation (M)
(Ions score 54)

320 - 335 1860.92 1859.92 1859.92 -0.00 0 R.MQYAPNTQVEILPQGR.E Oxidation (M)
(No match)

Q03252|LMNB2_HUMAN Lamin-B2 (Spot 1442)

Protein View

Match to: **LMNB2_HUMAN** Score: 360 Expect: 1.5e-032

(Q03252) Lamin-B2

Nominal mass (Mr): 67647; Calculated pI value: 5.29

NCBI BLAST search of **LMNB2_HUMAN** against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Homo sapiens](#)

Variable modifications: Carbamidomethyl (C), Oxidation (M)

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

Sequence Coverage: 48%

Matched peptides shown in **Bold Red**

1 MATPLPGRAG **GPATPLSPTR** LSRLQEKEEL RELNDRLAHY IDRVRALLEE
51 NDRLLLKISE KEEVTTREVS **GIKALYESEL ADARRVLDET ARERARLQIE**
101 **IGKLRAELDE VNKSAKKREG ELTVAQGRVK DLESLEFHRSE VELAAALSDK**
151 **RGLSDVAEL RAQLAKAEDG HAVAKKQLEK ETLMRVDLEN RCQSLQEELD**
201 **FRKSVFEEEV RETRRRHERR LVEVDSSRQQ EYDFKMAQAL EELRSQHDEQ**
251 **VRLYKLELEQ TYQAKLDSAK LSSDQNDKAA SAAREELKEA RMRLESLSYQ**
301 **LSGLQKQASA AEDRIRELEE AMAGERDKFR KMLDAKEQEM TEMRDVMQQQ**
351 **LAEQEQLLDV KLALDMEINA YRKLLGEGEE RLKLSPPSS RVTVSRATSS**
401 **SSGSLSATGR LGRSKRKRLE VEEPLGSGPS VLGTTGGSG GFHLAQQASA**
451 **SGSVSIEEID LEGKFVQLKN NSDKDQSLGN WRIKRQVLEG EEIAYKFTPK**
501 **YILRAGQVMV VWAGAGVAH SPPSTLVWKG QSSWGTGESF RTVLVNADGE**
551 **EVAMRTVKKS SVMRENENGE EEEEEAEFGE EDLFHQQDP RTTSRGCYVM**
601

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

9 - 20 1124.63 1123.62 1123.60 0.02 0 R.AGGPATPLSPTR.L (Ions score 25)
9 - 20 1124.63 1123.62 1123.60 0.02 0 R.AGGPATPLSPTR.L (No match)
37 - 43 887.49 886.49 886.47 0.02 0 R.LAHYIDR.V (Ions score 21)
37 - 43 887.49 886.49 886.47 0.02 0 R.LAHYIDR.V (No match)
74 - 84 1237.62 1236.61 1236.60 0.02 0 K.ALYESELADAR.R (Ions score 51)
74 - 84 1237.62 1236.61 1236.60 0.02 0 K.ALYESELADAR.R (No match)
74 - 85 1393.72 1392.71 1392.70 0.01 1 K.ALYESELADARR.V (No match)
85 - 92 959.53 958.52 958.52 0.00 1 R.RVLDETAR.E (No match)
86 - 94 1088.58 1087.57 1087.56 0.01 1 R.VLDETARER.A (No match)
97 - 103 800.51 799.50 799.48 0.02 0 R.LQIEIGK.L (No match)
104 - 113 1186.66 1185.65 1185.64 0.02 1 K.LRAELDEVNK.S (No match)
119 - 128 1059.56 1058.56 1058.54 0.02 0 R.EGELTVAQGR.V (No match)
129 - 138 1243.70 1242.69 1242.67 0.02 1 R.VKDLESLEFHR.S (No match)
131 - 138 1016.53 1015.53 1015.51 0.02 0 K.DLESLEFHR.S (No match)
131 - 150 2230.18 2229.17 2229.13 0.04 1 K.DLESLEFHRSEVELAAALSDK.R (No match)
139 - 151 1388.75 1387.74 1387.73 0.01 1 R.SEVELAAALSDKR.G (Ions score 51)
139 - 151 1388.75 1387.74 1387.73 0.01 1 R.SEVELAAALSDKR.G (No match)
192 - 202 1424.67 1423.66 1423.64 0.02 0 R.CQSLQEELDFR.K Carbamidomethyl (C)
(No match)
192 - 203 1552.75 1551.74 1551.74 0.01 1 R.CQSLQEELDFRK.S Carbamidomethyl (C)
(No match)
203 - 211 1122.60 1121.59 1121.57 0.02 1 R.KSVFEEEV.R (No match)
204 - 211 994.52 993.51 993.48 0.03 0 K.SVFEEEV.R (No match)
220 - 228 1060.58 1059.57 1059.57 0.00 1 R.RLVEVDSSR.Q (No match)
236 - 244 1076.55 1075.54 1075.53 0.01 0 K.MAQALEELR.S Oxidation (M) (No
match)
236 - 252 2055.98 2054.98 2054.98 -0.00 1 K.MAQALEELRSQHDEQVR.L Oxidation (M)
(No match)
253 - 265 1626.85 1625.84 1625.87 -0.02 1 R.LYKLELEQTYQAK.L (No match)
256 - 265 1222.64 1221.63 1221.62 0.01 0 K.LELEQTYQAK.L (No match)
279 - 288 1045.58 1044.57 1044.56 0.02 1 K.AASAAREELK.E (No match)
292 - 306 1768.93 1767.92 1767.92 0.00 1 R.MRLESLSYQLSGLQK.Q Oxidation (M)
(No match)
292 - 306 1768.93 1767.92 1767.92 0.00 1 R.MRLESLSYQLSGLQK.Q Oxidation (M)
(No match)
294 - 306 1465.78 1464.78 1464.78 -0.01 0 R.LELSYQLSGLQK.Q (No match)
315 - 326 1419.69 1418.69 1418.68 0.01 1 R.IRELEEAMAGER.D Oxidation (M) (No
match)
345 - 361 2066.00 2064.99 2065.00 -0.01 0 R.DVMQQQLAEYQELLDVK.L Oxidation (M)
(No match)
362 - 372 1324.66 1323.66 1323.65 0.01 0 K.LALDMEINAYR.K Oxidation (M) (Ions

score 36)
 362 - 372 1324.66 1323.66 1323.65 0.01 0 K.LALDMEINAYR.K Oxidation (M) (No match)
 362 - 373 1452.76 1451.75 1451.74 0.00 1 K.LALDMEINAYRK.L Oxidation (M) (No match)
 382 - 391 1071.63 1070.62 1070.61 0.01 1 R.LKLSPPSSR.V (No match)
 384 - 391 830.46 829.45 829.43 0.02 0 K.LSPSPSSR.V (No match)
 397 - 410 1268.64 1267.63 1267.60 0.03 0 R.ATSSSSGSLSATGR.L (No match)
 470 - 482 1533.72 1532.71 1532.70 0.01 1 K.NNSDKDQSLGNWR.I (No match)
 485 - 496 1434.76 1433.75 1433.75 0.00 1 K.RQVLEGEETIAYK.F (No match)
 486 - 496 1278.67 1277.66 1277.65 0.01 0 R.QVLEGEETIAYK.F (No match)
 530 - 541 1298.61 1297.60 1297.57 0.03 0 K.GQSSWGTGESFR.T (No match)
 542 - 555 1519.75 1518.74 1518.73 0.00 0 R.TVLVNADGEEVAMR.T Oxidation (M) (No match)

P23229|ITA6_HUMAN Integrin alpha-6 precursor (VLA-6) (CD49f antigen)

(Spot 705)

Protein View

Match to: **ITA6_HUMAN** Score: 125 Expect: 4.6e-009

(P23229) Integrin alpha-6 precursor (VLA-6) (CD49f antigen) [Contains: Integrin alpha-6 heavy chain

Nominal mass (Mr): 126539; Calculated pI value: 6.39

NCBI BLAST search of **ITA6_HUMAN** against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Homo sapiens](#)

Variable modifications: Carbamidomethyl (C), Oxidation (M)

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

Sequence Coverage: 26%

Matched peptides shown in **Bold Red**

1 MAAAGQLCLL YLSAGLLSRL GAAFNLDTRE DNVIRKYGDP GSLFGFSLAM
 51 HWQLQPEDKR **LLLVGAPR**GE ALPLQRANRT GGLYSCDITA RGPCTRIEFD
 101 NDADPTSESK EDQWMGVTVQ SQPGGKVVV CAHRYEKRQH VNTKQESRDI
 151 FGR**CYVLSQN** LRLEDDMDGG DWSFCDGRLR **GHEKFGSCQQ** **GVAATFTKDF**
 201 HYIVFGAPGT YNWKGIVRVE QKNNTFFDMN IFEDGPEYEVG GETEHDESIV
 251 PVPANSYLGL LFLTSVSYTD PDQFVYKTRP PREQPDTFPD VMMSYSLGFS
 301 LDSGK**GIVSK** **DEITFVSGAP** RANHSAGVVL LKRDMKSAHL LPEHIFDGEG
 351 LASSFGYDVA VVDLNK**DGWQ** **DIVIGAPQYF** **DRDGEVGGAV** **YVYMNQQGRW**
 401 NNVKPIRLNG TKDSMFGIAV **KNIGDINQDG** **YDIAVGAPY** **DDLGLKVFYIH**
 451 GSAANGINTKP TQVLK**GISPY** **FGYSIAGNMD** **LDRNSYPDVA** **VGSLSDSVTI**
 501 **FRSRPVINI****Q** **KTITVTPNRI** DLRQKTACGA PSGICLQVKS CFEYTANPAG
 551 YNPSISIVGT LEAEKERRKS GLSSRVQFRN QGSEPK**YTQE** **LTLKRQKQKV**
 601 CMEETLWLQD NIRDKLR**PIP** **ITASVEIQEP** **SSRRRVNSLP** **EVLPIILNSDE**
 651 **PKTAHIDVHF** **LKEGCGDDNV** **CNSNLKLEYK** FCTREGNQDK FSYLPQKGV
 701 PELVLKDQK**D** **IALEITVTSN** **PSNPRNPTKD** **GDDAHEAKLI** **ATFPDILTYS**
 751 **AYRELRAPFE** **KQLSCVANQN** **GSQADCELGN** **PFKRNSNVTF** **YLVLSTTEVT**
 801 FDTPLDLINL KLETTSNQDN LAPITAKAKV VIELLLSVSG VAKPSQVYFG
 851 GTVVGEQAMK **SEDEVGSLIE** **YEFRVINL** **PLTNLGTATL** **NIQWPKEISN**
 901 GK**WLLYLK****V** ESKGLEKVTG EPQKEINSLN LTESHNSRKK REITEKQIDD
 951 NRKFSLFAER KYQTLNCSVN VNCVNIR**CPL** **RGLDSKASLI** **LRSLWNSTF**
 1001 **LEEYSK**LNLYL DILMRAFIDV TAAAENIRLP NAGTQVRVTV FPSKTVAQYS
 1051 GVPWIIILVA ILGILMLAL LVFILWKCGF FKRSRYDDSV PRYHAVRIRK
 1101 EEREIKDEKY IDNLEKKQWI TKWNRNESYS
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
 61 - 68 838.55 837.55 837.54 0.00 0 R.LLLVGAPR.G (No match)
 61 - 68 838.55 837.55 837.54 0.00 0 R.LLLVGAPR.G (No match)
 154 - 162 1152.60 1151.59 1151.58 0.01 0 R.CYVLSQNL.R.I Carbamidomethyl (C)
 (No match)
 181 - 198 1895.89 1894.89 1894.90 -0.01 1 R.GHEKFGSCQQGVAATFTK.D (No match)
 306 - 321 1675.88 1674.87 1674.89 -0.03 1 K.GIVSKDEITFVSGAPR.A (No match)
 311 - 321 1191.61 1190.60 1190.59 0.01 0 K.DEITFVSGAPR.A (No match)
 367 - 382 1879.92 1878.91 1878.89 0.02 0 K.DGWQDIVIGAPQYFDR.D (No match)
 383 - 399 1858.84 1857.83 1857.83 0.00 0 R.DGEVGGAVYVYMNQQGR.W Oxidation (M)
 (No match)
 422 - 445 2520.18 2519.17 2519.18 -0.01 0 K.NIGDINQDGYDIAVGAPYDDLGLK.V (No match)
 (No match)
 466 - 483 1991.90 1990.90 1990.91 -0.01 0 K.GISPYFGYSIAGNMDLDR.N Oxidation (M)
 (No match)
 484 - 502 2027.01 2026.00 2026.00 0.00 0 R.NSYPDVAVGSLSDSVTIIFR.S (Ions score

27)

484 - 502 2027.01 2026.00 2026.00 0.00 0 R.NSYPDVAVGSLSDSVTIFR.S (No match)

503 - 511 1054.64 1053.64 1053.63 0.01 0 R.SRPVINIQK.T (No match)

503 - 511 1054.64 1053.64 1053.63 0.01 0 R.SRPVINIQK.T (No match)

512 - 519 901.52 900.51 900.50 0.01 0 K.TITVTPNR.I (No match)

587 - 594 995.54 994.54 994.53 0.00 0 K.YTQELTLK.R (No match)

616 - 633 1993.11 1992.10 1992.10 0.00 0 K.LRPIPIITASVEIQEPSSR.R (No match)

636 - 652 1864.00 1862.99 1863.00 -0.00 0 R.VNSLPEVLPILNSDEPK.T (No match)

663 - 680 2057.98 2056.98 2056.88 0.09 1 K.EGCGDDNVCNSNLKLEYK.F

Carbamidomethyl (C) (No match)

710 - 725 1726.90 1725.89 1725.89 0.00 0 K.DIALEITVTNSPSNPR.N (No match)

739 - 753 1731.90 1730.89 1730.89 0.01 0 K.LIATFPDRTLTY SAYR.E (Ions score 30)

739 - 753 1731.90 1730.89 1730.89 0.01 0 K.LIATFPDRTLTY SAYR.E (No match)

861 - 874 1672.78 1671.77 1671.76 0.00 0 K.SEDEVGSLIEYEFR.V (No match)

903 - 909 934.55 933.54 933.57 -0.03 0 K.WLLYLVK.V (No match)

978 - 986 1045.58 1044.57 1044.54 0.03 1 R.CPLRGLDSK.A Carbamidomethyl (C) (No match)

P38646|GRP75_HUMAN (Spot 1294)

Protein View

Match to: GRP75_HUMAN Score: 884 Expect: 5.8e-085

(P38646) Stress-70 protein, mitochondrial precursor (75 kDa glucose-regulated protein) (GRP 75)

(Pe

Nominal mass (Mr): 73635; Calculated pI value: 5.87

NCBI BLAST search of GRP75_HUMAN against nr

Unformatted sequence string for pasting into other applications

Taxonomy: Homo sapiens

Variable modifications: Carbamidomethyl (C), Oxidation (M)

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

Sequence Coverage: 64%

Matched peptides shown in Bold Red

1 **MISASRAAAA** RLVGAAASRG PTAARHQDSW NGLSHEAFRL VSRRDYASEA

51 **IKGAVVGIDL** GTTNSCVAVM EGKQAKVLEN AEGARTPSV VAFTADGERL

101 VGMPAKRQAV **TNPNTFYAT** KRLIGRYYDD PEVQDKIKNV PFKIVRASNG

151 **DAWVEAHGKL** YSPSQIGAFV LMKMKETAEN YLGHAKNAV ITVPAYFNDS

201 **QRQATKDAQQ** ISGLNVLRVI NEPTAALAY GLDKSEDKVI AVYDLGGGTF

251 **DISILEIQKG** VFEVKSTNGD TFLGGEDFDQ ALLRHIVKEF KRETGVDLTK

301 **DNMALQRVRE** AAEKAKCELS SSVQTDINLP YLTMDSSGPK HLNMKLTRAQ

351 **FEGIVTDLIR** RTIAPCQKAM QDAEVSKSDI GEVILVGGMT RMPKVQQTQVQ

401 **DLFGRAPSKA** VNPDEAVAIG AAIQGGVLAG DVTDVLLLDV TPLSLGIETL

451 GGVFTKILNR NNTIPTKKSQ **VFSTAADGQT** QVEIKVCQGE REMAGDNKLL

501 **GQFTLIGIIP** APRGVPQIEV TFDIDANGIV HVSADKGTG REQQIIVIQSS

551 **GGLSKDDIEN** MVKNAEKYAE EDRRKKERVE AVNMAEGIIH DTETKMEEFK

601 DQLPADECNK LKEEISKMRE **LLARKDSETG** ENIRQAASSL QQASLKLIFEM

651 **AYKMASERE** GSGSSGTGEQ KEDQKEEKQ

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

2 - 11 973.55 972.55 972.55 0.00 1 M.ISASRAAAAR.L (No match)

45 - 73 2914.51 2913.50 2913.41 0.09 1 R.DYASEAIKGA VVGIDLGTNNSCVAVMEGK.Q

Oxidation (M) (No match)

53 - 73 2094.00 2092.99 2093.01 -0.02 0 K.GAVVGIDLGTNNSCVAVMEGK.Q

Carbamidomethyl (C); Oxidation (M) (No match)

77 - 85 958.53 957.52 957.49 0.03 0 K.VLENAEGAR.T (No match)

86 - 99 1450.74 1449.73 1449.71 0.02 0 R.TTPSVVAFTADGER.L (Ions score 51)

86 - 99 1450.74 1449.73 1449.71 0.02 0 R.TTPSVVAFTADGER.L (No match)

108 - 121 1568.77 1567.76 1567.76 -0.00 0 R.QAVTNPNTFYATK.R (No match)

127 - 135 1149.59 1148.58 1148.55 0.04 1 R.RYDDPEVQK.D (No match)

144 - 159 1709.82 1708.81 1708.86 -0.05 1 K.IVRASNGDAWVEAHGK.L (No match)

160 - 173 1569.80 1568.79 1568.83 -0.03 0 K.LYSPSQIGAFVLMK.M Oxidation (M) (No match)

174 - 187 1608.78 1607.77 1607.76 0.01 1 K.MKETAENYLGH TAK.N Oxidation (M) (No match)

176 - 187 1333.67 1332.66 1332.63 0.03 0 K.ETAENYLGH TAK.N (No match)

188 - 202 1694.87 1693.86 1693.84 0.02 0 K.NAVITVPAYFNDSQR.Q (Ions score 113)

188 - 202 1694.87 1693.86 1693.84 0.02 0 K.NAVITVPAYFNDSQR.Q (No match)

207 - 218 1242.70 1241.69 1241.67 0.02 0 K.DAGQISGLNVLR.V (Ions score 101)

207 - 218 1242.70 1241.69 1241.67 0.02 0 K.DAGQISGLNVLR.V (No match)

219 - 234 1645.88 1644.88 1644.87 0.00 0 R.VINEPTAALAYGLDK.S (No match)

219 - 238 2105.05 2104.04 2104.07 -0.03 1 R.VINEPTAALAYGLDKSEDK.V (No match)

235 - 259 2710.42 2709.41 2709.41 -0.00 1 K.SEDKVIAYVDLGGGTFDISILEIQK.G (No

match)

239 - 259 2251.23 2250.22 2250.21 0.00 0 K.VIAVYDLGGGTFDISILEIQK.G (No match)

266 - 284 2055.98 2054.98 2054.95 0.02 0 K.STNGDTFLGGEDFDQALLR.H (Ions score 151)

266 - 284 2055.98 2054.98 2054.95 0.02 0 K.STNGDTFLGGEDFDQALLR.H (No match)

293 - 307 1706.85 1705.84 1705.83 0.01 1 R.ETGVDLTKDNMALQR.V Oxidation (M) (No match)

301 - 307 863.44 862.44 862.40 0.04 0 K.DNMALQR.V Oxidation (M) (No match)

317 - 340 2658.23 2657.23 2657.22 0.01 0 K.CELSSSVQTDINLPYLTMDSGPK.H Carbamidomethyl (C); Oxidation (M) (No match)

349 - 360 1361.76 1360.75 1360.74 0.02 0 R.AQFEGIVTDLIR.R (Ions score 80)

349 - 360 1361.76 1360.75 1360.74 0.02 0 R.AQFEGIVTDLIR.R (No match)

369 - 391 2438.22 2437.21 2437.18 0.03 1 K.AMQDAEVSKSDIGEVILVGGMTR.M 2 Oxidation (M) (No match)

378 - 391 1462.77 1461.76 1461.75 0.01 0 K.SDIGEVILVGGMTR.M Oxidation (M) (Ions score 37)

378 - 391 1462.77 1461.76 1461.75 0.01 0 K.SDIGEVILVGGMTR.M Oxidation (M) (No match)

395 - 405 1290.70 1289.69 1289.67 0.02 0 K.VQQTVDLFR.A (Ions score 52)

395 - 405 1290.70 1289.69 1289.67 0.02 0 K.VQQTVDLFR.A (No match)

469 - 485 1808.91 1807.90 1807.90 0.00 0 K.SQVFSTAADGQTQVEIK.V (No match)

499 - 513 1592.98 1591.97 1591.94 0.02 0 K.LLGQFTLIGIPPAPR.G (Ions score 66)

499 - 513 1592.98 1591.97 1591.94 0.02 0 K.LLGQFTLIGIPPAPR.G (No match)

514 - 535 2309.20 2308.19 2308.21 -0.02 0 R.GVPQIEVTFDIDANGIVHVSAD.D (No match)

542 - 555 1473.79 1472.78 1472.78 -0.00 0 R.EQQIVIQSSGGLSK.D (No match)

542 - 563 2434.22 2433.22 2433.21 0.01 1 R.EQQIVIQSSGGLSKDDIENMVK.N Oxidation (M) (No match)

568 - 574 938.47 937.47 937.43 0.04 1 K.YAEEDRR.K (No match)

577 - 595 2158.04 2157.03 2157.04 -0.00 1 K.ERVEAVNMAEGIIHDTETK.M Oxidation (M) (No match)

579 - 595 1872.90 1871.89 1871.89 -0.00 0 R.VEAVNMAEGIIHDTETK.M Oxidation (M) (No match)

618 - 624 904.52 903.51 903.50 0.01 1 K.MRELLAR.K Oxidation (M) (No match)

626 - 646 2233.13 2232.12 2232.10 0.02 1 K.DSETGENIRQAASSLQASLK.L (No match)

635 - 646 1231.67 1230.67 1230.66 0.01 0 R.QAASSLQASLK.L (No match)

647 - 653 917.46 916.45 916.44 0.02 0 K.LFEMAYK.K Oxidation (M) (No match)

647 - 654 1045.58 1044.58 1044.53 0.05 1 K.LFEMAYKK.M Oxidation (M) (No match)

P31947|1433S_HUMAN 14-3-3 protein sigma (Stratifin) (Epithelial cell marker protein 1) (Spot 2602)

Protein View

Match to: 1433S_HUMAN Score: 245 Expect: 4.6e-021

(P31947) 14-3-3 protein sigma (Stratifin) (Epithelial cell marker protein 1)

Nominal mass (Mr): 27757; Calculated pI value: 4.68

NCBI BLAST search of 1433S_HUMAN against nr

Unformatted sequence string for pasting into other applications

Taxonomy: Homo sapiens

Variable modifications: Carbamidomethyl (C),Oxidation (M)

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

Sequence Coverage: 66%

Matched peptides shown in Bold Red

1 MERASLIQKA **KLAEQAERYE DMAAFMK**GAV EKGEELSCEE **RNLLSVAYKN**

51 VVGQRAAWR **VLSSIEQKSN EEGSEEGPE VREYREK**VET **ELQGVC**DTVL

101 **GLLD**SHLIKE AGDAESRVFY LKMKGDYRY **LAEVATGDDK** KRIIDSARSA

151 **YQEAMDISK EMPPTNPIRL GLALNFSVFH YEIANSPEEA ISLAKTTFDE**

201 **AMADLHTLSE DSYKDSTLIM QLLRD**NLTLW TADNAGEEGG EAPQEPQS

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

12 - 18 816.43 815.43 815.41 0.01 0 K.LAEQAER.Y (No match)

19 - 27 1137.44 1136.44 1136.45 -0.02 0 R.YEDMAAFMK.G 2 Oxidation (M) (No match)

42 - 49 907.52 906.52 906.52 -0.00 0 R.NLLSVAYK.N (No match)

61 - 68 903.52 902.51 902.51 0.00 0 R.VLSSIEQK.S (No match)

69 - 82 1546.70 1545.69 1545.69 0.00 1 K.SNEEGSEKGPV.R.E (No match)

86 - 109 2696.41 2695.40 2695.41 -0.01 1 R.EKVETELQGVCDTVLGLLD**SHLIK.E**

Carbamidomethyl (C) (No match)

88 - 109 2439.26 2438.25 2438.27 -0.02 0 K.VETELQGVCDTVLGLLD**SHLIK.E**

Carbamidomethyl (C) (No match)

123 - 129 932.47 931.46 931.42 0.04 1 K.MKGDYYR.Y (No match)

123 - 129 948.42 947.42 947.42 0.00 1 K.MKGDYYR.Y Oxidation (M) (Ions score 22)

123 - 129 948.42 947.42 947.42 0.00 1 K.MKGDYYR.Y Oxidation (M) (No match)

130 - 140 1181.56 1180.55 1180.56 -0.01 0 R.YLAEVATGDDK.K (No match)

149 - 159 1258.55 1257.54 1257.55 -0.01 0 R.SAYQEAMDISK.K Oxidation (M) (No match)

149 - 160 1386.64 1385.64 1385.65 -0.01 1 R.SAYQEAMDISK.K.E Oxidation (M) (No match)

160 - 169 1182.59 1181.58 1181.62 -0.04 1 K.KEMPPTNPIR.L (No match)

160 - 169 1198.62 1197.61 1197.62 -0.01 1 K.KEMPPTNPIR.L Oxidation (M) (Ions score 19)

160 - 169 1198.62 1197.61 1197.62 -0.01 1 K.KEMPPTNPIR.L Oxidation (M) (No match)

161 - 169 1054.54 1053.53 1053.53 0.00 0 K.EMPPTNPIR.L (No match)

161 - 169 1070.52 1069.52 1069.52 -0.00 0 K.EMPPTNPIR.L Oxidation (M) (Ions score 10)

161 - 169 1070.52 1069.52 1069.52 -0.00 0 K.EMPPTNPIR.L Oxidation (M) (No match)

170 - 195 2833.45 2832.44 2832.47 -0.03 0 R.LGLALNFSVFHYEIANSPPEAISLAK.T (No match)

196 - 214 2189.93 2188.93 2188.95 -0.02 0 K.TTFDEAMADLHTLSEDSYK.D Oxidation (M) (Ions score 70)

196 - 214 2189.93 2188.93 2188.95 -0.02 0 K.TTFDEAMADLHTLSEDSYK.D Oxidation (M) (No match)

215 - 224 1189.66 1188.65 1188.65 -0.00 0 K.DSTLIMQLLR.D (No match)

215 - 224 1205.65 1204.64 1204.65 -0.01 0 K.DSTLIMQLLR.D Oxidation (M) (Ions score 22)

215 - 224 1205.65 1204.64 1204.65 -0.01 0 K.DSTLIMQLLR.D Oxidation (M) (No match)

Q15417|CNN3_HUMAN Calponin-3 (Spot 2243)

Protein View

Match to: **CNN3_HUMAN** Score: **90** Expect: **1.6e-005**

(**Q15417**) **Calponin-3 (Calponin, acidic isoform)**

Nominal mass (Mr): **36391**; Calculated pI value: **5.69**

NCBI BLAST search of **CNN3_HUMAN** against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: **Homo sapiens**

Variable modifications: Carbamidomethyl (C), Oxidation (M)

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

Sequence Coverage: **44%**

Matched peptides shown in **Bold Red**

1 MTHFNK**GPSY GLSAEVK**NKI ASKYDHAEE DLR**NWIEEVT GMSIGPNFQL**

51 **GLK**DGIILCE LINK**LQPGSV K**VNESSLNW PLENIGNFI KAIQAYGMKP

101 HDIFEANDLF ENGNMTQVQT TLVALAGLAK TK**GFHTTIDI G**VKYAEKQTR

151 RFDEGK**LKAG Q**SVIGL**MGMT N**KCASQAGMT AYGT**RRHLYD PKM**QTDK**PF**D

201 **QTTISLQMG**T **NKGASQAGML AP**GTRRDIYD QK**LTLQ**PVDN **STISLQMG**TN

251 **KVASQKGM**SV **YGLGR**QVYDP KYCAAPTEPV IHNGSQGTGT NGSEISDSYD

301 QAEYPDEYHG EYQDDYPRDY QYSDQGIDY

Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence

7 - 17 1107.58 1106.57 1106.56 0.01 0 K.GPSYGLSAEVK.N (No match)

34 - 53 2233.11 2232.11 2232.12 -0.02 0 R.NWIEEVTGMSIGPNFQLGLK.D (No match)

65 - 72 856.54 855.53 855.52 0.01 1 K.LQPGSVKK.V (No match)

133 - 143 1187.64 1186.64 1186.63 0.00 0 K.GFHTTIDIGVK.Y (No match)

159 - 172 1419.72 1418.72 1418.72 -0.00 0 K.AGQSVIGLQMG**TNK.C** Oxidation (M) (Ions score 27)

159 - 172 1419.72 1418.72 1418.72 -0.00 0 K.AGQSVIGLQMG**TNK.C** Oxidation (M) (No match)

173 - 185 1389.59 1388.58 1388.58 -0.00 0 K.CASQAGMTAYGTR.R Carbamidomethyl (C); Oxidation (M) (No match)

186 - 192 928.50 927.50 927.49 0.00 1 R.RHLYDPK.M (No match)

193 - 212 2316.10 2315.09 2315.08 0.02 0 K.MQTDK**PF**D**QTTISLQMG**T**NK.G** 2 Oxidation (M) (No match)

213 - 225 1216.62 1215.61 1215.60 0.01 0 K.GASQAGMLAPGTR.R (No match)

213 - 225 1232.61 1231.60 1231.60 0.01 0 K.GASQAGMLAPGTR.R Oxidation (M) (Ions score 17)

213 - 225 1232.61 1231.60 1231.60 0.01 0 K.GASQAGMLAPGTR.R Oxidation (M) (No match)

233 - 251 2076.06 2075.05 2075.06 -0.01 0 K.LTLQPVDNSTISLQMGTK.V Oxidation (M) (No match)
257 - 265 955.48 954.47 954.46 0.01 0 K.GMSVYGLGR.Q Oxidation (M) (No match)
257 - 265 955.48 954.47 954.46 0.01 0 K.GMSVYGLGR.Q Oxidation (M) (No match)

P07339|CATD_HUMAN Cathepsin D precursor (Spot 2586)

Protein View

Match to: **CATD_HUMAN** Score: 356 Expect: 3.6e-032

(P07339) Cathepsin D precursor (EC 3.4.23.5) [Contains: Cathepsin D light chain; Cathepsin D

heavy

Nominal mass (Mr): 44524; Calculated pI value: 6.10

NCBI BLAST search of **CATD_HUMAN** against nr

Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Homo sapiens](#)

Variable modifications: Carbamidomethyl (C), Oxidation (M)

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

Sequence Coverage: 37%

Matched peptides shown in **Bold Red**

1 MQPSSLLPLA LCLLAAPASA LVRIPLHKFT SIRRTMSEVG GSVEDLIAKG
51 PVSKYSQAVP AVTEGPIPEV LKNYMDAQYY GEIGIGTPPQ CFTVVVFDTGS
101 SNLWVPSIHC KLLDIACWIH HKYNSDKSST YVKNGTSFDI HYGSGSLSGY
151 LSQDTSVPC QSASSASALG GVKVERQVFG **EATKQPGITF IAAKFDGILG**
201 **MAYPRISVNN VLPVFDNLMQ QKLVDQNIFS FYLSRDPDAQ PGGELMLGGT**
251 **DSKYKGSLS YLNVTRKAYW QVHLDQVEVA SGLTLCKEGC EAIVDTGTSL**
301 **MVGPVDEVRE LQKAIGAVPL IQGEYMIPCE KVSTLPAITL KLGKGYKLS**
351 **PEDYTLKVSQ AGKTLCLSGF MGDIPPPSG PLWILGDVFI GRYYTVFDRD**
401 **NNRVGFAEAA RL**
Start - End Observed Mr(expt) Mr(calc) Delta Miss Sequence
177 - 184 879.49 878.48 878.45 0.03 0 R.QVFG**EATK.Q** (No match)
185 - 194 1045.60 1044.59 1044.60 -0.00 0 K.QPGIT**FIAAK.F** (No match)
195 - 205 1239.64 1238.63 1238.61 0.02 0 K.FDGIL**GMA YPR.I** (No match)
195 - 205 1255.63 1254.63 1254.61 0.02 0 K.FDGIL**GMA YPR.I** Oxidation (M) (Ions score 18)
195 - 205 1255.63 1254.63 1254.61 0.02 0 K.FDGIL**GMA YPR.I** Oxidation (M) (No match)
206 - 222 1975.03 1974.03 1974.02 0.00 0 R.ISVNNVLPVFDN**LMQ QK.L** Oxidation (M) (Ions score 64)
206 - 222 1975.03 1974.03 1974.02 0.00 0 R.ISVNNVLPVFDN**LMQ QK.L** Oxidation (M) (No match)
223 - 235 1601.87 1600.86 1600.82 0.04 0 K.LVDQ**NIFS FYLSR.D** (Ions score 69)
223 - 235 1601.87 1600.86 1600.82 0.04 0 K.LVDQ**NIFS FYLSR.D** (No match)
236 - 253 1803.80 1802.80 1802.80 -0.00 0 R.DPDAQ**PGGELMLGGTDSK.Y** Oxidation (M) (No match)
288 - 309 2350.11 2349.11 2349.08 0.02 0 K.EGCEA**IVDTGTSLMVGPVDEVRE.E**
Carbamidomethyl (C); Oxidation (M) (No match)
314 - 331 2005.02 2004.02 2004.01 0.01 0 K.AIGAV**PLIQGEYMIPCEK.V**
Carbamidomethyl (C); Oxidation (M) (No match)
332 - 341 1042.66 1041.65 1041.64 0.01 0 K.VSTL**PAITLK.L** (No match)
349 - 357 1065.56 1064.55 1064.54 0.02 0 K.LSPED**YTLK.V** (No match)
393 - 399 963.49 962.48 962.45 0.03 0 R.YY**TVFDR.D** (Ions score 38)
393 - 399 963.49 962.48 962.45 0.03 0 R.YY**TVFDR.D** (No match)
393 - 403 1462.70 1461.69 1461.66 0.02 1 R.YY**TVFDRDNNR.V** (Ions score 56)
393 - 403 1462.70 1461.69 1461.66 0.02 1 R.YY**TVFDRDNNR.V** (No match)
404 - 411 820.46 819.45 819.42 0.03 0 R.VG**FAEAAR.L** (Ions score 41)
404 - 411 820.46 819.45 819.42 0.03 0 R.VG**FAEAAR.L** (No match)

