

26S protease regulatory subunit 6B (MIP224) (MB67-interacting protein) (TAT-binding protein 7) (TBP-7)**AccessionNr:** P43686**PI:** 5,09**MW:** 47366,5**Peptide:**

1. ENAPAIIFIDEIDAIATK	Score: 14.48
2. ENAPAIIFIDEIDAIATKR	Score: 12.85
3. EFLHAQEEVKR	Score: 12.37
4. IQSIPLVIGQFLEAVDQNTAIVGSTTGSNYYVR	Score: 13.58
5. ILSTIDRELLKPNASVALHK	Score: 10.56

AA-Coverage: 19.9 %

MEEIGILVEKAQDEIPALSVSRPQTGLSFLGPEPEDLEDLYSRYKKLQQELEFLEVQEEYIKDEQKNLKK**EFLHAQEEVKRIQSIPLVIGQFLEAVDQNT**
AIVGSTTGSNYYVRILSTIDRELLKPNASVALHKHSNALVDVLPPEADSSIMMLTSDQKPDVMYADIGGMDIQKQEVREAVELPLTHFELYKQIGIDPPR
 GVLMYGPPGCGKTM LAKAVAHHTTAAFI R VVGSEFVQKYLGE GPRMVRDVFRLAK**ENAPAIIFIDEIDAIATKR**FDAQTGADREVQRILLELLNQMDGFD
 QNVNVKVI MATNRADTLDPALLRPGRLDRKIEFFLPDRRQRLIFSTITSKMNLSEVDLEDYVARPDKISGADINSICQESGMLAVRENRYIVLAKDFE
 KAYKTVIKKDEQEHEFYK

78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain-binding protein) (BiP) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78)

AccessionNr: P11021

PI: 5,07

MW: 72333,3

Peptide:

1. DNHLLGTFDLTGIPPAPR	Score: 12.06
2. ELEEIVQPIISK	Score: 17.17
3. KKELEEIVQPIISK	Score: 15.17
4. KSDIDEIVLVGGSTR	Score: 16.61
5. KVTHAVVTVPAYFNDAQR	Score: 12.99
6. LYGSAGPPPTGEEDTAEKDEL	Score: 17.92
7. NQLTSNPENTVFDAK	Score: 16.84
8. SQIFSTASDNQPTVTIK	Score: 18.17
9. TFAPEEISAMVLTK	Score: 18.04
10. TKPYIQVDIGGGQTK	Score: 15.93
11. IINEPTAAAIAAYGLDK	Score: 21.97
12. IINEPTAAAIAAYGLDKR	Score: 19.59
13. ITPSYVAFTPEGER	Score: 17.29
14. NELESYAYSLK	Score: 16.96
15. TWNDPSVQQDIK	Score: 16.12
16. VEIANDQGNR	Score: 14.04
17. NQLTSNPENTVFDAKR	Score: 9.61
18. VTHAVVTVPAYFNDAQR	Score: 13.57
19. DAGTIAGLNVMR	Score: 16.77
20. AKFEELNMDLFR	Score: 17.73
21. IEWLESHQDADIEDFK	Score: 18.15
22. MKETAEAYLGK	Score: 14.65
23. MKETAEAYLGKK	Score: 14.18
24. FEELNMDLFR	Score: 9.60
25. KTKPYIQVDIGGGQTK	Score: 15.26
26. IEIESFYEGEDFSETLTR	Score: 14.58
27. IINEPTAAAIAAYGLDK	Score: 21.97
28. AVEEKIEWLESHQDADIEDFK	Score: 15.39
29. IEWLESHQDADIEDFKAK	Score: 12.96
30. AVEEKIEWLESHQDADIEDFKAK	Score: 14.55

AA-Coverage: 44.3 %

MKLSLVAAML LLLS AARAEEDK KEDVGT VVGIDLG TTYSCVGV FKNR V E I I A N D Q N R I T P S Y V A F T P E G E R L I G D A A K N Q L T S N P E N T V F D A K R L I G R T W N D P S V Q Q D I K F L P F K V V E K K T K P Y I Q V D I G G G Q T K T F A P E E I S A M V L T K M K E T A E A Y L G K K V T H A V V T V P A Y F N D A Q R Q A T K D A G T I A G L N V M R I I N E P T A A A I A Y G L D K R E G E K N I L V F D L G G G T F D V S L L T I D N G V F E V V A T N G D T H L G G E D F D Q R V M E H F I K L Y K K K T G K D V R K D N R A V Q K L R R E V E K A K R A L S S Q H Q A R I E I E S F Y E G E D F S E T L T R A K F E E L N M D L F R S T M K P V Q K V L E D S D L K K S D I D E I V L V G G S T R I P K I Q Q L V K E F F N G K E P S R G I N P D E A V A Y G A A V Q A G V L S G D Q D T G D L V L L D V C P L T L G I E T V G G V M T K L I P R N T V V P T K K S Q I F S T A S D N Q P T V T I K V Y E G E R P L T K D N H L L G T F D L T G I P P A P R G V P Q I E V T F E I D V N G I L R V T A E D K G T G N K N K I T I T N D Q N R L T P E E I E R M V N D A E K F A E E D K K L K E R I D T R N E L E S Y A Y S L K N Q I G D K E K L G G K L S S E D K E T M E K A V E E K I E W L E S H Q D A D I E D F K A K K K E L E E I V Q P I I S K L Y G S A G P P P T G E E D T A E K D E L

Elongation factor 2 (EF-2)**AccessionNr:** P13639**PI:** 6,42**MW:** 95207,5**Peptide:**

1. ARPPFDGLAEDIDKGEVSAR	Score: 22.13
2. AYLPVNESFGFTADLR	Score: 17.74
3. EGIPALDNFLDKL	Score: 17.57
4. GPLMMYISK	Score: 10.75
5. STAISLFYELSENDLNFIK	Score: 19.02
6. TGTITTFEHAHNMR	Score: 10.74
7. ETVSEESNVLCLSK	Score: 19.31
8. KIWCFGPDGTGPNILTDITK	Score: 18.86
9. LMEPIYLVEIQCEQVVGGIYGVNLNR	Score: 16.74
10. TFCQLILDPIFK	Score: 18.00
11. VFSGLVSTGLK	Score: 12.02
12. YVEPIEDVPCGNIVGLVGVDQFLVK	Score: 11.33
13. GVQYLNEIKDSVVAGFQWATK	Score: 17.05
14. CLYASVLTAQPR	Score: 14.66
15. GHVFEESQVAGTPMFVVK	Score: 14.37
16. VFDAIMNFK	Score: 12.23
17. WLPAGDALLQMITIHLPSVTAQK	Score: 19.06
18. YLAEKYEWVVAEAR	Score: 22.19
19. NMSVIAHVDHGK	Score: 9.41
20. DGAGFLINLIDSPGHVDFSSEVTAALR	Score: 22.26
21. IWCFGPDGTGPNILTDITK	Score: 17.50
22. ALLELQLEPEELYQTFQR	Score: 18.38
23. RCLYASVLTAQPR	Score: 15.33
24. RWLPAGDALLQMITIHLPSVTAQK	Score: 19.26
25. FAAKGEGQLGPAER	Score: 15.28
26. GLKEGIPALDNFLDKL	Score: 11.58
27. LIEKLDIK	Score: 10.17
28. TFCQLILDPIFKVFDAIMNFVK	Score: 13.06

AA-Coverage: 44.5 %

MVNFVTVDQIRAIMDKKANIR**NMSVIAHVDHGK**STLTDSLVCAGIIASARAGETRFTDRKDEQERCITIK**STAISLFYELSENDLNFIK**QSKDGAGFLI
NLIDSPGHVDFSSEVTAALRVTDGALVVDCVSGVCVQTETVLRQAI AERIKPVLMMNKMDR**ALLELQLEPEELYQTFQR**IVENVNVIISTYGEGESGPM
GNIMIDPVLGTVGFGSGLHGWAFTLKQFAEMYVAK**FAAKGEGQLGPAER**AKKVEDMMKKLWGDYFDPANGKFSKSATSPGKKLPR**TFCQLILDPIFKV**
FDAIMNFVKKEETAK**LIEKLDIK**L DSEDKKEGKPLLKAVMR**RWLPAGDALLQMITIHLPSVTAQK**YRCELLYEGPPDDEAAMGIKSCDPK**GPLMMYISK**
MVPTSDKGRFYAFGR**VFSGLVSTGLK**V RIMGPNYTPGKKEDLYLKP I QRTILMMGR**YVEPIEDVPCGNIVGLVGVDQFLVK**TGTITTFEHAHNMRVMKFS
VSPVVRVAVEAKNPADLPKLV EGLKRLAKSDPMVQCIIEESGEHI IAGAGELHLEICLKDLEEDHACIPIKSDPVVSYRE**TVSEESNVLCLSK**SPNKHN
RLYMK**ARPPFDGLAEDIDKGEVSAR**QELKQRARY**LAEKYEWVVAEAR**KIWCFGPDGTGPNILTDITK**GVQYLNEIKDSVVAGFQWATK**EGALCEENMRGV
RFDVHDVTLHADAIHRGGGQIIP TAR**RCLYASVLTAQPR**LMEPIYLVEIQCEQVVGGIYGVNLNRKR**GHVFEESQVAGTPMFVVK**KAYLPVNESFGFTADL
RSNTGGQAFPQCVFDHWQIILPGDPFDNSSRPSQVVAETRKRK**GLKEGIPALDNFLDKL**

Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2)

AccessionNr: P08107**PI:** 5,48**MW:** 70052,6**Peptide:**

1. TTPSYVAFTDTER	Score: 14.20
2. VEIANDQGNR	Score: 14.04
3. IINEPTAAAIAYGLDR	Score: 19.88
4. IINEPTAAAIAYGLDR	Score: 19.88
5. AFYPEEISSMVLTK	Score: 17.64

AA-Coverage: 8.4 %

MAKAAAIGIDLGTYSVGVFQHGK**VEI IANDQGNRTTPSYVAFTDTER**LIGDAAKNQVALNPQNTVFDAKRLIGRKFQDPVVQSDMKHWPFFQVINDGDK
PKVQVSYKGD**TKAFYPEEISSMVLTK**MKEIAEAYLGYPVTNAVITVPAYFNDSQRQATKDAGVIAGLNLVLR**IINEPTAAAIAYGLDR**TGKGERNVLIFDL
GGGTFDVSILTIIDDGIFEVKATAGDTHLGGEDFDNRLVNHFVEEFKRKHKKDISQNKRAVRRRLRTACERAKRTLSSSTQASLEIDSLFEGIDFYTSITRA
RFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDLVLVGGSTRIPKVQKLLQDFNGRDLNKSINPDEAVAYGAAVQAAILMGDKSENVQDLLLLDVAPLS
LGLETAGGVMTALIKRNSTIPTKQTQIFTTYSDNQPGVLIQVYEGERAMTKDNLLGRFELSGIPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANK
ITITNDKGRLSKEEIERMVQEAKEYKAEDEVQRERVSAKNALESYAFNMKSAVEDEGLKGI SEADKKKVLDKCQEVISWLDANTLAEKDEFEHKRKELE
QVCNPIISGLYQGAGGPGGGFQAQGPKGGSGSGPTIEVD

Heat shock 70 kDa protein 4 (Heat shock 70-related protein APG-2) (HSP70RY)

AccessionNr: P34932

PI: 5,18

MW: 94300,5

Peptide:

1. GCALQCAILSPAFAK	Score: 14.89
2. ELSTTLNADEAVTR	Score: 14.11
3. VLATAFDTTLGGR	Score: 13.78
4. AGGIETIANEYSDR	Score: 16.65
5. EFSITDVVPYPISLR	Score: 11.57
6. FLEMCNDLLAR	Score: 18.26
7. NFTTEQVTAMLLSK	Score: 17.35
8. LMNETTAVALAYGIYK	Score: 14.40
9. SNLAYDIVQLPTGLTIK	Score: 11.35
10. SVM DATQIAGLNCLR	Score: 13.98
11. LMNETTAVALAYGIYKQDLPAL EEEKPR	Score: 17.61
12. LKKEDIYAVEIVGGATR	Score: 13.65

AA-Coverage: 20.5 %

MSVVGIDLGFQSCYVAVARAGGIETIANEYSDRCTPACISFGPKNRSIGAAKSQVISNAKNTVQGFKRFGRAFSDPFVEAEKSNLAYDIVQLPTGLTIK
IKVTYMEEERNFTTEQVTAMLLSKLKETAESVLKKPVVDCVVSVPFCFYTDAERRSVM DATQIAGLNCLR LMNETTAVALAYGIYKQDLPAL EEEKPRNVVF
VDMGHSAYQVSVCAFNRGKLVLATAFDTTLGGRKFDEVLVNHFC EEFGKKYKLDIKSKIRALLRLSQECEK LK LMSANASDLPLSIECFMNDVDVSGT
MNRGKFLEMCNDLLARVEPPLRSVLEQT LKKEDIYAVEIVGGATRIPAVKEKISKFFGKELSTTLNADEAVTRGCALQCAILSPAFAKVFESITDVVPY
PISLRWNSPAEEGSSDCEVF SKNHAA PFSKVLTFYRKEPFTLEAYYSSPQDL PYPDPATAQFSVQKVT PQSDGSSSKVKVVRVNVHGIFSVSSASLVEV
HKSEENEPMETDQNAKEEEKMQVDQEEPHVEEQQQQTPAENKAESEEMETSQAGSKDKKMDQPPQAKKAKVKTSTVDLPIENQLLWQIDREMLNLYIEN
EGKMIMQDKLEKERNDAKNAVREYVYEMRDKLSGEYEK FVSEDGRNSFTLKLEDTENWLYEDGEDQPKQVYVDKLAELKNLGQPIKIRFQSEERPKLFE
ELGKQIQQYMKI I SSFKNKEDQYDHLDAADMTKVEKSTNEAMEWMNNKLNQNKQSLTMDPVVKSKEIEAKIKELTSTCSPIISKPKPKVEPPKKEQKNA
EQNGPVDGQDNP GPQAAEQGTD TAVPSDSDK KLP EMDID

Heat shock protein HSP 90-beta (HSP 84) (HSP 90)

AccessionNr: P08238

PI: 4,97

MW: 83133,4

Peptide:

1. HFSVEGQLEFR	Score: 10.72
2. GVVDEDLPLNISR	Score: 18.42
3. EQVANSAFVER	Score: 10.02
4. ELISNASDALDKIR	Score: 16.56
5. YESLTDPSKLDGSK	Score: 12.91
6. IDIIPNPQER	Score: 12.95
7. YHTSQSGDEMTSLSEYVSR	Score: 15.60
8. SLTNDWEDHLAVK	Score: 17.71
9. VILHLKEDQTEYLEER	Score: 18.94
10. ELISNASDALDKIR	Score: 16.56
11. HLEINPDHPIVETLR	Score: 21.96
12. HSQFIGYPITLYLEK	Score: 21.91
13. NPDDITQEEYGEFYK	Score: 21.30
14. ELISNASDALDK	Score: 9.96
15. HSQFIGYPITLYLEKER	Score: 19.62
16. LVSSPCCIVTSTYGWTANMER	Score: 12.60
17. RAPFDLFENK	Score: 12.30
18. ELKIDIIPNPQER	Score: 13.16
19. TLTLVDTGIGMTK	Score: 20.40
20. CLELFSELAEDKENYK	Score: 13.74
21. CLELFSELAEDKENYKK	Score: 16.33
22. HNDDEQYAWESSAGGSFTVR	Score: 18.86
23. VFIMDSCELIPEYLNfir	Score: 13.93
24. IRYESLTDPSKLDGSK	Score: 9.92
25. KHLEINPDHPIVETLR	Score: 16.64
26. KHSQFIGYPITLYLEK	Score: 15.70
27. VILHLKEDQTEYLEERR	Score: 17.07
28. GFEVVYMTPEIDCYVQQLK	Score: 22.42
29. RAPFDLFENKK	Score: 12.37
30. RVFIMDSCELIPEYLNfir	Score: 18.20
31. YIDQEELNKTPIWTR	Score: 14.86
32. ADLNNLGTIAK	Score: 16.00
33. VILHLKEDQTEYLEER	Score: 21.14
34. KHSQFIGYPITLYLEKER	Score: 11.02

AA-Coverage: 44.9 %

MPEEVHHGEEVETFAFAQAEIAQLMSLIINTFYNSKEIFLRELISNASDALDKIRYESLTDPSKLDGSKELKIDIIIPNPQERTLTLVDTGIGMTKADLIN
 NLGTIAKSGTKAFMEALQAGADISMIQQFGVGFYSAYLVAEKVVVITKHNDDEQYAWESSAGGSFTVRADHGEPiGRGTKVILHLKEDQTEYLEERRVKE
 VVKKHSQFIGYPITLYLEKEREREKESDDEAEEEEKGEKEEEDKDEEKPKIEDVGSDEEDSDGDKKKKTKIKEKYIDQEELNKTPIWTRNPDDITQEE
 YGEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFIPRRAPFDLFENKKKNNIKLYVRVVFIMDSCELIPEYLNfirGVVDEDLPLNISREMLQQSKI
 LKVIKRNIVKKCLELFSELAEDKENYKKFYEAFSKNLKLGIHEDSTNRRRSELRLYHTSQSGDEMTSLSEYVSRMKETQKSIYYITGESKEQVANSAFV
 ERVRRKRGFEVVYMTPEIDCYVQQLKEFDGKSLVSVTKEGLELPEDEEEKKMEESKAKFENLCKLMKEILDKKVEKVTISNRLVSSPCCIVTSTYGWTA
 NMERIMKAQALRDNSTMGYMMAKKHLEINPDHPIVETLRQKAEADKNDKAVKDLVLLFETALLSSGFSLEDPQTHSNRIYRMIKLGIGIDEDEVAAEEP
 NAAVPDEIPPLEGDEDASRMEEVD

Heterogeneous nuclear ribonucleoprotein F (hnRNP F) (Nucleolin-like protein mcs94-1)

AccessionNr: P52597**PI:** 5,38**MW:** 45540,9**Peptide:**

1. ATENDIYNFFSPLNPVR	Score: 18.88
2. ITGEAFVQFASQELAEK	Score: 17.02
3. QSGEAFVELGSEDDVK	Score: 13.50
4. YGDSEFTVQSTTGHCVHMR	Score: 12.12
5. DLSYCLSGMYDHR	Score: 15.37

AA-Coverage: 19.8 %

MMLGPEGGEGFVVKLRGLPWSCSVEDVQNFLSDCTIHDGAAGVHFIYTRREGRQSGEAFVELGSEDDVKMALKKDRESMGHRYIEVFKSHRTEMDWVLKHS
GPNSADSANDGFVRLRGLPFGCTKEEIVQFFSGLIIVPNGITLTPVDEGKIITGEAFVQFASQELAEKALGKHKERIGHRYIEVFKSSQEEVRSYSDPPLK
FMSVQRPGPYDRPGTARRYIGIVKQAGLERMRPGAYSTGYGGYEEYSGLSDGYGFTTDLFGRDLSYCLSGMYDHRYGDEFTVQSTTGHCVHMRGLPYKA
TENDIYNFFSPLNPVRVHIEIGPDGRVTGEADVEFATHEEAVAAMSKDRANMQHRYIELFLNSTTGASNGAYSSQVMQGMGVSAQAQATYSGLESQSVSGC
YGAGYSGQNSMGGYD

Neutral alpha-glucosidase AB precursor (EC 3.2.1.84) (Glucosidase II alpha subunit)

AccessionNr: Q14697**PI:** 5,73**MW:** 106874,5**Peptide:**

1. LSFQHDPETSVLVLR	Score: 11.91
2. SLLLSVNAR	Score: 15.65
3. VVIIGAGKPAAVVLQTK	Score: 20.09
4. YRVPDVLVADPPIAR	Score: 13.32
5. VLLVLELQGLQK	Score: 15.30
6. ALLDSLQLGPDSLTVHLIHEVTK	Score: 18.72
7. FGAVWTGDNTAEWDHLK	Score: 16.96
8. KPGINVASDWSIHLR	Score: 17.87
9. VSQGSKDPAEGDGAQPEETPR	Score: 17.21
10. WYQMGAYQPFFR	Score: 9.58
11. YFTWDPSTRFPQPR	Score: 11.19
12. YSLLPFWYTLLYQAHR	Score: 12.86
13. QYASLTGTQALPPLFSLGYHQSR	Score: 16.56
14. DVHNIYGLYVHMATADGLR	Score: 17.21
15. THSDSKPYGPMVSVGLDFSLPGMEHVYGIPEHADNLR	Score: 20.09

AA-Coverage: 27.9 %

MAAVALAARRRRSWASLVLAFLGVCLGITLAVDRSNFKTCEESSFCKRQRSIRPGLSPYR**ALLDSLQLGPDSLTVHLIHEVTKVLLVLELQGLQK**NMTR
FRIDELEPRRPR**YRVPDVLVADPPIAR**LSVSGRDENSVELTMAEGPYKIILTARPFRLDLED**SLLLSVNARGLLEFEHQRAPRVSQGSKDPAEGDGAQ**
PEETPRDGDKPEETQGKAEKDEPGAWEEETFK**THSDSKPYGPMVSVGLDFSLPGMEHVYGIPEHADNLR**LKVTEGGEYRLYNLDVDFQYELYNPMALYGSVP
VLLAHNPHRDLGIFWLNAEETWVDISSNTAGKTLFGKMMDYLQGSGETPQTDVRWMSETGIIDVFLLLGPSISDVFR**QYASLTGTQALPPLFSLGYHQSR**
WNYRDEADVLEVDQGFDDHNLPCDVIWLDIEHADGKR**YFTWDPSTRFPQPR**TMLERLASKRRKLVAIVDPHIKVDSGYRVHEELRNGLYVKTRDGSYEG
WCWPGSAGYPDFTNPTMRAWANMFSYDNYEGSAPNLFVWDMNEPSVFNPEVTMLKDAQHYGGWEHR**DVHNIYGLYVHMATADGLR**QRSGMERPFVL
ARAFFAGSQR**FGAVWTGDNTAEWDHLK**ISIPMCLSLGLVGLSFCGADVGGFFKNPEPELLVR**WYQMGAYQPFFRAHAHLDTGRREPWLLPSQHNDIIRDA**
LGQR**YSLLPFWYTLLYQAHR**EGIPVMRPLWVQYPQDVTTFNIDDQYLLGDALLVHPVSDSGAHGVQVYLPQGEVWYDIQSYQKHHGPQTLYLPVTLSSI
PVFQRRGTTIVPRWVRVRSSECMKDDPITLVALSPQGTAQGELFLDDGHTFNQTRQEFLLRRFSFSGNTLVSSADPEGHFETPIWIER**VVIIGAGKPA**
AAVVLQTKGSPESRLSFQHDPETSVLVLRKPGINVASDWSIHLR

T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)

AccessionNr: P17987**PI:** 5,80**MW:** 60343,9**Peptide:**

1. FATEAAITILR	Score: 10.74
2. EQLAIAEFAR	Score: 14.79
3. ICDELILIK	Score: 14.27
4. TSASILR	Score: 9.92
5. YINENLIVNTDELGR	Score: 15.48
6. YPVNSVNILK	Score: 9.11
7. ILATGANVILTTGGIDDMCLK	Score: 15.37
8. YFVEAGAmAVR	Score: 16.95
9. SQNVmAAASIANIVK	Score: 17.69
10. LGVQVVITDPEKLDQIR	Score: 18.38
11. SLLVIPNTLAVNAAQDSTDLVAK	Score: 17.08
12. MLVDDIGDVTITNDGATILK	Score: 15.00
13. GANDFMCDEMER	Score: 16.57
14. VLCELADLQDKEVGDGTTSVVIAAELLK	Score: 16.57
15. SVVPGGAVEAALSIIYLENYATSMGSR	Score: 14.84

AA-Coverage: 43.0 %

MEGPLSVFGDRSTGETIRSQNVMAAASIANIVKSSSLGPVGLDKMLVDDIGDVTITNDGATILKLLEVEHPAAKVLCELADLQDKEVGDGTTSVVIAAELLKNADELVKQKIHPTSVISGYRLACKEAVRYINENLIVNTDELGRDCLINAAKTSMSSKIIGINGDFFANMVVDAVLAIKYTDIRGQPRYPVNSVNILKAHGRSQMESMLISGYALNCVVGSGQMPKRIVNAKIACLDFSLQKTKMKLGVQVVITDPEKLDQIRQRESDTKERIQKILATGANVILTTGGIDDMCLKYFVEAGAMAVRRVLKRDLEKRIAKASGATILSTLANLEGEETFEAAMLGQAEVQERICDELILIKNTKARTSASIIIRGANDFMCDEMERSLHDALCVVKRVLESKSVVPGGAVEAALSIIYLENYATSMGSRQLAIAEFARSLVIPNTLAVNAAQDSTDLVAKLRAFHNEAQNPERKNLKWIGLDLSNGKPRDNKQAGVFEPTIVKVKSLKFATEAAITILRIDDLIKLHPESKDDKHGSYEDAVHSGALND

T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)**AccessionNr:** P78371**PI:** 6,02**MW:** 57357,3**Peptide:**

1. LAVEAVLR	Score: 12.53
2. EALLSSAVDHGSDEVK	Score: 13.00
3. GATQQILDEAER	Score: 10.19
4. LKSGNLEAIHIK	Score: 12.39
5. LTSFIGAIAIGDLVK	Score: 13.95
6. QDLMNIAGTTLSSK	Score: 15.74
7. QVLLSAAEAAEVILR	Score: 17.27
8. SLHDALCVLAQTVK	Score: 18.31
9. VQDDEVDGTTSVTVLAAELLR	Score: 9.31
10. ILIANTGmDTDKIK	Score: 14.01
11. DASLmVTNDGATILK	Score: 21.00
12. EALLSSAVDHGSDEVKFR	Score: 15.02
13. LGGSLADSYLDEGFLLDKK	Score: 14.42
14. LIEEVMIGEDK	Score: 14.01
15. LALVTGGEIASTFDHPELVK	Score: 17.50
16. KLGSLADSYLDEGFLLDKK	Score: 18.69
17. AAHSEGNTTAGLDMR	Score: 13.04
18. MLPTIIADNAGYDSADLVAQLR	Score: 16.10
19. EGTIGDMAILGITESFQVKR	Score: 12.68
20. TVYGGGCSEMLMAHAVTQLANR	Score: 11.36
21. GATQQILDEAERSLHDALCVLAQTVK	Score: 9.34
22. GATQQILDEAERSLHDALCVLAQTVKDSR	Score: 9.12
23. LIEEVMIGEDKLIHFSGVALGEACTIVLR	Score: 18.82

AA-Coverage: 58.3 %

MASLSLAPVNIKFAGADEERAETARLTSFIGAIAIGDLVKSTLGPKGMDKILLSSGRDASLMVTNDGATILKNIGVDNPAAKVLVDMRSRVQDDEVDGTT
SVTVLAAELLREAESLIAKKIHPQTI IAGWREATKAAREALLSSAVDHGSDEVKFRQDLMNIAGTTLSSKLLTHHKDHFTKLAVEAVLRLKSGNLEAIH
I IKKLGSLADSYLDEGFLLDKKIGVNQPKRIENAKILIAN TGMDTDKIKIFGSRVRVDSTAKVAEIEHAEKEKMKKEKVERILKHGINCFINRQLIYNYP
EQLFGAAGVMAIEHADFAGVERLALVTGGEIASTFDHPELVKLGSKLIEEVMIGEDKLIHFSGVALGEACTIVLRGATQQILDEAERSLHDALCVLAQT
VKDSRTVYGGGCSEMLMAHAVTQLANRTPGKEAVAMESYAKALRMLPTIIADNAGYDSADLVAQLRAAHSEGNTTAGLDMREGTIGDMAILGITESFQVK
RQVLLSAAEAAEVILRVDNI IKAAPRKRVPDHHPC

T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon)

AccessionNr: P48643**PI:** 5,45**MW:** 59671,4**Peptide:**

1. LGFAGLVQEISFGTTK	Score: 20.25
2. DVDFELIKVEGK	Score: 19.24
3. IAILTCPFEPKPK	Score: 15.21
4. HKLDVTSVEDYK	Score: 10.94
5. QQISLATQMVR	Score: 13.02
6. WVGPEIELIAIATGGR	Score: 17.62
7. EKFEEMIQQIK	Score: 11.52
8. EMNPALGIDCLHK	Score: 17.32
9. GVIVDKDFSHQPMPK	Score: 15.09
10. SLHDALCVIR	Score: 12.27
11. YEKEKFEEMIQQIK	Score: 12.38
12. LGFAGLVQEISFGTTKDK	Score: 12.15
13. TKHKLDVTSVEDYK	Score: 9.67
14. SQDDEIGDGTGVVVLGALLEEAEQLLDR	Score: 15.84

AA-Coverage: 31.1 %

MASMGTLAFDEYGRPFLLI IKDQDRKSRMLGLEALKSHIMAAKAVANTMRTSLGPNGLDKMMVDKGDVTVTNDGATILSMMDVDHQIAKLMVELSKSQDDEIGDGTGVVVLGALLEEAEQLLDRGIHPRIADGYEQAAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGSKVVNSCHRQMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRLEDTKLIKGVIVDKDFSHQPMPKVEDAKIAILTCPFEPKPKTKHKLDVTSVEDYKALQKYEKEKFEEMIQQIKETGANLAICQWGFDDANHLLLQNNLPAVRWVGPEIELIAIATGGRIVPRFSELTAEKLGFAGLVQEISFGTTKDKMLVIEQCCKNSRAVTIFIRGGNKMIIEEAKRSLHDALCVIRNLIRDNRVYGGAAEISCALAVSQEADKCPLEQYAMRAFADALEVIMALSENSGMNPIQTMTEVRARQVKEMNPALGIDCLHKGTNDMKQQHVIEFLIGKKQQISLATQMVRMILKIDDIRKPGSESE

T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma) (hTRiC5)

AccessionNr: P49368**PI:** 6,10**MW:** 60534,3**Peptide:**

1. GISDLAQHYLMR	Score: 17.29
2. TAVETAVLLLR	Score: 17.53
3. IVLLDSSLEYK	Score: 14.55
4. IVSRPEELREDDVGTGAGLLEIK	Score: 14.11
5. NVLLDPQLVPGGGASEMAVAHALTEK	Score: 16.26
6. ALDDMISTLK	Score: 9.35
7. AMTGVEQWPYR	Score: 15.06
8. ELGIWEPLAVK	Score: 16.47
9. IPGGIIEDSCVLR	Score: 11.34
10. MLLDPMGGIVMTNDGNAILR	Score: 20.62
11. WSSLACNIALDAVK	Score: 13.84
12. KISIPVDISDSMMLNIINSITTK	Score: 11.19
13. ILQMEEYIQLCEDIIQLKPDVVITEK	Score: 20.76

AA-Coverage: 39.4 %

MMGHRPVLVLSQNTKRESGRKVQSGNINAAKTIADIIRTCLGPKSMMK**MLLDPMGGIVMTNDGNAILREIQVQHPAAKSMIEISRTQDEEVGDGTTSVII**
LAGEMLSVAEHFLEQQMHPTVVISAYRK**ALDDMISTLKKISIPVDISDSMMLNIINSITTKAISRWSSLACNIALDAVKMVQFEENGRKEIDIKKYAR**
VEK**IPGGIIEDSCVLR**GVMIKNDVTHPRMRRYIKNPRI**IVLLDSSLEYK**KGESQTDIEITREEDFTR**ILQMEEYIQLCEDIIQLKPDVVITEKGISDLA**
QHLYMRANITAIRRVKTDNNRIARACGARIVSRPEELREDDVGTGAGLLEIKKIGDEYFTFITDCKDPKACTILLRGASKEILSEVERNLDAMQVCRN
VLLDPQLVPGGGASEMAVAHALTEKSKAMTGVEQWPYRAVAQALEVIPRTLIQNCGASTIRLLTSLRAKHTQENCETWGVNGETGTLVDMKELGIWEPLA
VKLQTYKTAVETAVLLLRIDDIVSGHKKKGDDQSRQGGAPDAGQE

T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta)

AccessionNr: P50990**PI:** 5,42**MW:** 59489,7**Peptide:**

1. FAEAFEAI PR	Score: 14.14
2. LFVTNDAATIL R	Score: 18.42
3. AIADTGANVVVTGGK	Score: 21.31
4. LATNAAVTVLR	Score: 14.43
5. LIAQACVSIFPDSGHFNVDNIR	Score: 18.51
6. ILGSGISSSSVLHGMVFK	Score: 18.15
7. NVGLDIEAEVPAVK	Score: 19.45
8. LVPGGGATEIELAK	Score: 14.22
9. APGFAQMLK	Score: 9.76
10. DMLEAGILDTYLGK	Score: 21.08
11. IAVYSCPFDMITETK	Score: 17.29
12. QITSYGETCPGLEQYAIKK	Score: 13.44
13. YNIMLVR	Score: 11.10
14. DIDEVSSLLR	Score: 15.95
15. GSTDNLMDDIER	Score: 14.60
16. HFSGLEEA VYR	Score: 13.82
17. VADMALHYANKYNIMLVR	Score: 16.37
18. KFAEAFEAI PR	Score: 12.13
19. KAHEILPNLVCCSAK	Score: 15.48
20. AHEILPNLVCCSAK	Score: 13.35
21. ILGSGISSSSVLHGMVFKK	Score: 12.26

AA-Coverage: 44.0 %

MALHVPK**APGFAQMLK**EGAK**HFSGLEEA VYR**NIQACKELAQTTTRTAYGPNGMNKMVINHLEK**LFVTNDAATIL**RELEVQHPAAKMIVMASHMQEQEVGDG
 TNFVLV**FAGALLELA**EELLRIGLSVSEVIEGYE**IACRKAHEILPNLVCCSAK**NLR**DIDEVSSLLR**TSIMSKQYGNVFLAK**LIAQACVSIFPDSGHFNVD**
NIRVCKILGSGISSSSVLHGMVFKKETEGDVT**SVKDAKIAVYSCPFDMITETK**GTVLIKTAEELMNF**SKGEENLMDAQVKA**IADTGANVVVTGGK**VADM**
ALHYANKYNIMLVRLNSKWDLRRLCKTVGATALPRLTPPVLEEMGHCD**SVYLSEVGD**TQVVVFKHEKEDGAI**STIVLRGSTDNLMDDIER**AVDDGVNTFK
 VLTRDKR**LVPGGGATEIELAKQITSYGETCPGLEQYAIKKFAEAFEAI**PRALAENSGVKANEV**ISKLYAVHQEGNKNVGLDIEAEVPAVKDMLEAGILDT**
YLGKYWAIKLATNAAVTVLRVDQ**IIMAKPAGGPKPPSGK**KDWD**DDQND**

Ubiquitin carboxyl-terminal hydrolase 14 (EC 3.1.2.15) (Ubiquitin thiolesterase 14) (Ubiquitin-specific-processing protease 14) (Deubiquitinating enzyme 14)

AccessionNr: P54578**PI:** 5,20**MW:** 55938,2**Peptide:**

1. AQLFALTGVQPAR	Score: 17.66
2. LPAYLTIQMVR	Score: 12.11
3. RVEIMEESEQ	Score: 13.18
4. LEAIEDDSVKETDSSSASAATPSKK	Score: 15.92

AA-Coverage: 12.1 %

MPLYSVTVKWKKEKFEFEGVELNTDEPPMVFK**AQLFALTGVQPAR**QKVMVKGKGLKDDDWGNIKIKNGMTLLMMGSADALPEEPSAKTVFVEDMTEEQLASA
MELPCGLTNLGNTCYMNATVQCIRSVPELKDALKRYAGALRASGEMASQYITAALRDLFDSMDKTSSSIPIILLQFLHMAFPQFAEKGEQGQYLQODA
NECWIQMMRVLQQK**LEAIEDDSVKETDSSSASAATPSKK**KSLIDQFFGVFETTMKCTESEEEVTKGKENQLQLSCFINQEVKYLFTGLKLRRLQEEITK
QSPTLQRNALYIKSSKISR**LPAYLTIQMVR**FFYKEKESVNAKVLKDVKFPLMLDMYELCTPELQEKMVSFRSKFKDLEDKKVNQQPNTSDKKSSPQKEVK
YEPFSFADDIGSNCGYYDLQAVLTHQGRSSSSGHYVSWVKRKQDEWIKFDDDKVSIVTPEDILRLSGGGDWHIAYVLLYGPR**RVEIMEESEQ**