

```
25 2n8i_A Designed protein DA05;
                                                                                             9-54 (100)
                                                 42 0.0012
                                                              27.0
                                                                      6.5
                                                                            46 517-562
  26 Scqs_A Elongator complex prote 50.9
                                                 59
                                                     0.0016
                                                              36.4
                                                                     9.5
                                                                           108
                                                                                520-650
                                                                                            94-204 (435)
  27 4d0p A COP9 signalosome comple 47.5 3.5E+02
                                                     0.0096
                                                              29.4
                                                                    18.8
                                                                           155
                                                                                500-672
                                                                                            86-255 (387)
  28 5cgs A Elongator complex prote
                                       45.3 2.6E+02
                                                     0.0071
                                                               31.1
                                                                     13.6
                                                                           146
                                                                                389-568
                                                                                            50-199 (435)
  29 2rkl_A Vacuolar protein sortin
                                       42.2
                                                     0.0026
                                                                                683-737
                                                                                             2-49
                                                                                                   (53)
                                       41.1 2.6E+02
                                                                                            34-227 (537)
  30 5ft9_A Proteinaceous RNAse P 2
                                                     0.0071
                                                               31.5
                                                                     13.0
                                                                           164
                                                                                482-671
  31 2wpv_A GET4, UPF0363 protein Y
                                       39.3 2.9E+02
                                                     0.0081
                                                               29.4
                                                                     12.2
                                                                            80
                                                                                517-596
                                                                                            14-100 (312)
  32 3jck_D 26S proteasome regulato 39.1 4.9E+02
                                                      0.013
                                                               28.6
                                                                     18.6
                                                                           201
                                                                                517-743
                                                                                           111-345 (429)
                                                                                517-743
  33 4d10 A COP9 signalosome comple
                                       38.8 5.2E+02
                                                      0.014
                                                               28.9
                                                                     19.4
                                                                           202
                                                                                           132-370 (480)
  34 3mkq A Coatomer beta'-subunit;
                                                     0.0026
                                                                                           625-716 (814)
                                       36.7
                                                                      8.8
                                                                            60
                                                                                512-571
                                                               36.6
  35 4yvo_A Protein fluorescent in
                                       35.3
                                                     0.0027
                                                                                517-562
                                                                                            73-118 (165)
                                                                                            67-112 (159)
  36 4yvq_C Protein fluorescent in
                                                                                517-562
                                       34.6
                                                 89
                                                     0.0025
                                                               27.9
                                                                      6.5
  37 31pz A GET4 (YOR164C homolog);
                                       32.9 3.8E+02
                                                       0.01
                                                               28.9
                                                                     11.9
                                                                            80
                                                                                517-596
                                                                                            13-102 (336)
  38 3ro3_A PINS homolog, G-protein
39 3lpz A GET4 (YOR164C homolog);
                                       32.8 3.1E+02
                                                                                517-584
                                                     0.0084
                                                               24.5
                                                                     10.4
                                                                            68
                                                                                            70-144 (164)
                                                                                            15-194 (336)
                                       32.2 5.8E+02
                                                               27.5
                                                                                389-595
                                                      0.016
                                                                     16.0
                                                                           161
  40 3ro3_A PINS homolog, G-protein 31.8 3.2E+02
                                                     0.0088
                                                                                            30-104 (164)
                                                                     10.4
  41 3mzk_B Protein transport prote
                                       30.8 3.5E+02
                                                     0.0097
                                                               30.2
                                                                                390-564
                                                                                           154-306 (441)
                                                                                           173-281 (383)
  42 4a5p_A Protein MXIA, protein V
                                       30.1 1.6E+02
                                                     0.0045
                                                               32.5
                                                                      8.5
                                                                            82
                                                                                657-744
  43 4ui9_0 Anaphase-promoting comp
                                       28.6 3.3E+02
                                                     0.0091
                                                               31.9
                                                                    11.6
                                                                           122
                                                                                517-654
                                                                                           563-700 (756)
  44 3iko C Nucleoporin NUP84; NPC,
                                                                                336-425
                                                                                           186-295 (460)
                                       28.3
                                             1E+02
                                                     0.0028
                                                               34.7
                                                                      6.7
                                                                            90
                                                                                           347-459 (925)
  45 5a9q 4 Nuclear pore complex pr
                                                 84
                                                     0.0023
                                                               38.8
                                                                      6.3
                                                                            95
                                                                                332-426
  46 3mix_A Flagellar biosynthesis
                                                     0.0083
                                                               30.3
                                                                                606-744
                                                                                           168-277 (382)
                                                                                517-562
  47 4yvo_A Protein fluorescent in
                                       26.9
                                                     0.0027
                                                               27.8
                                                                            46
                                                                                           113-158 (165)
  48 3a5i_A Flagellar biosynthesis
                                       26.1
                                              2E+02
                                                     0.0054
                                                               31.9
                                                                      8.3
                                                                            80
                                                                                659-744
                                                                                           181-288 (389)
  49 2x49 A INVA, invasion protein
                                       26.0 1.7E+02
                                                     0.0048
                                                               31.5
                                                                      7.8
                                                                            79
                                                                                659-743
                                                                                           125-230 (333)
  50 4yvq C Protein fluorescent in
                                       23.7 1.1E+02
                                                      0.003
                                                                                517-562
                                                                                           107-152 (159)
                                                               27.4
                                                                      4.9
                                                                            46
  51 5ft9 A Proteinaceous RNAse P 2 21.8 5.3E+02
                                                      0.015
                                                                     11.2
                                                                                517-741
                                                                                            14-237 (537)
                                                               28.9
                                                                           196
52 3fxd_A Protein ICMQ; helix bun 21.0 1.8E+02
                                                      0.005
                                                               23.1
                                                                            42
                                                                                683-740
                                                                                             5-51
                                      PDB<sup>™</sup>
PROTEIN DATA BANK
  No 1
                  NCBI
                                                             Pub Med
>4xmm_D Nucleoporin NUP85; structural protein, immune system, transport protein-immune complex; 7.38A
  {Saccharomyces cerevisiae S288C} PDB: 4xmn _D
  Probab=100.00 E-value=2.9e-159 Score=1398.74 Aligned_cols=704 Identities=100% Similarity=1.477 Sum_probs=0.0
                        Q ss pred
  Q Fri Mar 04 23:
                     41 DPVSGAILVPMTVNDQPIEKNGDKMPLKFKLGPLSYQNMAFITAKDKYKLYPVRIPRLDTSKEFSAYVSGLFEIYRDLGD
                                                                                                              120 (744)
  Q Consensus
                      41
                                          120 (744)
                         T Consensus
                     12
                                                ----1-f--
                                                                                   ----s----v---f-if--1--
                                                                                                               91 (715)
                     12 DQPSGAILVPMTVNDQPIEKNGDKMPLKFKLGPLSYQNMAFITAKDKYKLYPVRIPRLDTSKEFSAYVSGLFEIYRDLGD
  T 4xmm D
                                                                                                               91 (715)
  T ss dssp
                         T ss_pred
                        Q ss_pred
  Q Fri_Mar_04_23: 121 DRVFNVPTIGVVNSNFAKEHNATVNLAMEAILNELEVFIGRVKDQDGRVNRFYELEESLTVLNCLRTMYFILDGQDVEEN
                                                                                                              200 (744)
  O Consensus
                     121
                                       ----al----L---i-----l-----l-----lw-L-e--vf--
                                                                                                              200 (744)
                         T 4xmm D
                      92 DRVFNVPTIGVVNSNFAKEHNATVNLAMEAILNELEVFIGRVKDODGRVNRFYELEESLTVLNCLRTMYFILDGODVEEN
                                                                                                              171 (715)
                        T ss dssp
  T ss pred
                        сснининининне
  Q ss pred
  Q Fri_Mar_04_23: 201 RSEFIESLLNWINRSDGEPDEEYIEQVFSVKDSTAGKKVFETQYFWKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAV
                                                                                                              280 (744)
                    Q Consensus
                                                                                                              280 (744)
  T Consensus
                     172 RSEFIESLLNWINRSDGEPDEEYIEQVFSVKDSTAGKKVFETQYFWKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAV
  T 4xmm D
                                                                                                              251 (715)
  T ss dssp
                        T ss_pred
                        ссьнинининные СССССинининный ресссСССсссьнининный ресссьный в делигийний в делигийнийн в делигийн в 
                         Q ss_pred
  Q Fri_Mar_04_23:
                    {\bf 281~SFDAVSDSIELLKQYPKDSSSTFREWKNLVLKLSQAFGSSATDISGELRDYIEDFLLVIGGNQRKILQYSRTWYESFCGF}
                                                                                                              360 (744)
                     281 ----v----LL---P------w--Wk-----l-----------L--l--IL-Gd---I---s--WyE-l-a-
                                                                                                              360 (744)
  O Consensus
                         T Consensus
                                                                                                              331 (715)
                     252 SFDAVSDSIELLKQYPKDSSSTFREWKNLVLKLSQAFGSSATDISGELRDYIEDFLLVIGGNQRKILQYSRTWYESFCGF
  T 4xmm D
                                                                                                              331 (715)
  T ss_dssp
                         T ss_pred
                        Q ss pred
  Q Fri_Mar_04_23:
                    361 LLYYIPSLELSAEYLQMSLEANVVDITNDWEQPCVDIISGKIHSILPVMESLDSCTAAFTAMICEAKGLIENIFEGEKNS
                                                                                                              440 (744)
                     440 (744)
  T Consensus
                                                                                                              411 (715)
                     332 LLYYIPSLELSAEYLQMSLEANVVDITNDWEQPCVDIISGKIHSILPVMESLDSCTAAFTAMICEAKGLIENIFEGEKNS
  T 4xmm D
                                                                                                              411 (715)
  T ss dssp
                        T ss_pred
                         hheeCCCchhннннннннhcCCCCcнннннннннннсСнннннннннhcChнннннннннhccccccccccc
  Q ss_pred
                        Q Fri Mar 04 23:
                     441 DDYSNEDNEMLEDLFSYRNGMASYMLNSFAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDDIE 520 (744)
                     441 -----dl-----lre--Ll-YA--l-l-----LW-vai-YL--c---g----r--i-elL-r-pl-t----e
  Q Consensus
                                                                                                              520 (744)
                    T Consensus
                                                                                                              491 (715)
                     412 DDYSNEDNEMLEDLFSYRNGMASYMLNSFAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDDIE 491 (715)
  T 4xmm D
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T ss_dssp
                     T ss_pred
                     ссссссеруру в состоем в него в политиру в пол
                     нининнесссинининнинниннинниннесссининниннесссининнинниннинн
 Q ss_pred
 Q Fri_Mar_04_23: 521 WMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRAGKYELVKSYSWLLFEASCMEGQKLDDPVLNAIVSKNSP
                                                                                                 600 (744)
                 600 (744)
 O Consensus
 T Consensus
                                                                                                 571 (715)
                     WMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRAGKYELVKSYSWLLFEASCMEGQKLDDPVLNAIVSKNSP
 T 4xmm D
                                                                                                 571 (715)
                     T ss_dssp
                     нинининессинининининининин
 T ss pred
                     Q ss pred
 Q Fri_Mar_04_23:
                 601\ \texttt{AEDDVIIPQDILDCVVTNSMRQTLAPYAVLSQFYELRDREDWGQALR} LLLLLLEFPYLPKHYLVLLVAKFLYPIFLLDDK
                                                                                                 680 (744)
                 601 -----p---le-----le--Ls-ya-lreF-----g-----Aa--Lv-Ll-s---Pk-f----LL-dalp--lL--
                                                                                                 680 (744)
                 T Consensus
                                                                                                 651 (715)
 T 4xmm D
                                                                                                 651 (715)
                     T ss dssp
                     T ss_pred
                     сссСнинининининин
 Q ss pred
 Q Fri Mar 04_23: 681 KLMDEDSVATVIEVIETKWDDADEKSSNLYETIIEADKSLPSSMATLLKNLRKKLNFKLCQAFM 744 (744)
                 Q Consensus
                                                                                  744 (744)
 T Consensus
                 652 ~-fs~-q~--LL~-LE~-----y~--l~----lp~-----lR~-l~-l~
                                                                                  715 (715)
                 652 KIMDEDSVATVIEVIETKWDDADEKSSNLYETIIEADKSLPSSMATLLKNLRKKLNFKLCQAFM
 T 4xmm D
                                                                                  715 (715)
                     T ss dssp
                     сссСнининининининининининин
 T ss pred
                                 PDB
 No 2
                                                             Pub Med
>3f3f_C Nucleoporin NUP85; structural protein, protein complex, nucleopori complex, nuclear pore complex,
 macromolecular assembly, MEM coat; 2.90A {Saccharomyces cerevisiae} PDB: 3f3g _C 3f3p _C 3ewe
 Probab=100.00 E-value=1.7e-129 Score=1120.70 Aligned cols=570 Identities=100% Similarity=1.478 Sum probs=0.0
 Q ss pred
                     CCcccHHhhhcccccccccccccccccccchheeecccCCCceeecCCcCCcccccCCCccceeecChHHHHhHh
 Q Fri_Mar_04_23:
                   1 MTIDDSNRLLMDVDQFDFLDDGTAQLSNNKTDEEEQLYKRDPVSGAILVPMTVNDQPIEKNGDKMPLKFKLGPLSYQNMA
                                                                                                  80 (744)
 Q Consensus
                                                                                                  80 (744)
                     T Consensus
                                                                                ~~~1~F
                                                                                                  80 (570)
                   1 \ \mathtt{MTIDDSNRLLMDVDQFDFLDDGTAQLSNNKTDEEEQLYKRDPVSGAILVPMTVNDQPIEKNGDKMPLKFKLGPLSYQNMA}
 T 3f3f C
                                                                                                  80 (570)
 T ss dssp
                      -----CEECSCSSCCSCCSSTTCCCEEEEEEETTEEEE
 T ss pred
                     Q ss_pred
                     Q Fri_Mar_04_23:
                                                                                                 160 (744)
                  81 FITAKDKYKLYPVRTPRLDTSKEFSAYVSGLFETYRDLGDDRVFNVPTTGVVNSNFAKEHNATVNLAMEATLNELEVFTG
 Q Consensus
                  81 -----t-if--l------q--
                                                                             -----al-----L---i-
                                                                                                 160 (744)
                     T Consensus
                                                                                                 160 (570)
                  81 FITAKDKYKLYPVRIPRLDTSKEFSAYVSGLFEIYRDLGDDRVFNVPTIGVVNSNFAKEHNATVNLAMEAILNELEVFIG
 T 3f3f C
                                                                                                 160 (570)
 T ss_dssp
                     T ss_pred
                     heeceeechhнинниннинниннинниннинн
 Q ss_pred
 Q Fri_Mar_04_23: 161 RVKDQDGRVNRFYELEESLTVLNCLRTMYFILDGQDVEENRSEFIESLLNWINRSDGEPDEEYIEQVFSVKDSTAGKKVF
                                                                                                 240 (744)
 O Consensus
                 161 -----p--e---p--
                                                                                                 240 (744)
                     T Consensus
                                                                                                 240 (570)
                 161 RVKDQDGRVNRFYELEESLTVLNCLRTMYFILDGQDVEENRSEFIESLLNWINRSDGEPDEEYIEQVFSVKDSTAGKKVF
 T 3f3f C
                                                                                                 240 (570)
                     T ss_dssp
 T ss_pred
                     Q ss pred
 Q Fri_Mar_04_23:
                 {\tt 241~ETQYFWKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYPKDSSSTFREWKNLVLKLSQAFGSS}
                                                                                                 320 (744)
                 241 ~hp~FW~~V~~lvLrG~~~~A~~lL~~~~~~~~v~~~~LL~~~P~~~~w~~Wk~~~~~l~~~
 Q Consensus
                                                                                                 320 (744)
                 T Consensus
                                                                                                 320 (570)
                 241 ETQYFWKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYPKDSSSTFREWKNLVLKLSQAFGSS
 T 3f3f C
                                                                                                 320 (570)
 T ss dssp
                     T ss_pred
                     сссСсНунниннинннинсССнинннинннунннынннынн
 Q ss pred
 Q Fri Mar 04 23:
                 321 ATDISGELRDYIEDFLLVIGGNQRKILQYSRTWYESFCGFLLYYIPSLELSAEYLQMSLEANVVDITNDWEQPCVDIISG
                                                                                                 400 (744)
                     -----L--l--IL-Gd---I---s--WyE-l-a--ly--Pt---l--y------d-----E-----i-eg
 Q Consensus
                                                                                                 400 (744)
                 T Consensus
                                                                                                 400 (570)
 T 3f3f C
                                                                                                 400 (570)
                     T ss dssp
                     ссСсснынниннинннынносссенинниннынынынныессссьныннинннынноссссссенинниннин
 T ss pred
 Q ss pred
```

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Q Fri_Mar_04_23: 401 KIHSILPVMESLDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNSFAFELCSLGDKE 480 (744)
 O Consensus
                           480 (744)
                          T Consensus
                                                                                                                                                  480 (570)
                           401 KIHSILPVMESLDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNSFAFELCSLGDKE
 T 3f3f C
                                                                                                                                                  480 (570)
                                T ss_dssp
                                T ss pred
                                снинининн
 Q ss pred
 Q Fri_Mar_04_23:
                           481 LWPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNOMLSAHNIIESIANFS
                                                                                                                                                  560 (744)
                          560 (570)
 T Consensus
                          481 LWPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNOMLSAHNIIESIANFS
 T 3f3f C
                                                                                                                                                  560 (570)
                                T ss dssp
 T ss_pred
                                ссьнининным оссественний посторований посторовании посторований посторований посторований посторований посторовании посторований посторований посторований посторований посторований посторований посторований посторований посторований посторо
                                НСССИННИНИ
 Q ss pred
 Q Fri Mar 04 23: 561 RAGKYELVKS 570 (744)
                          561 rA~d~~~V~~
                                                570 (744)
 Q Consensus
                                |||+.++|++
                           561 rA~~~~Vk~ 570 (570)
 T Consensus
 T 3f3f C
                          561 RAGKYELVKS 570 (570)
 T ss dssp
                                HcCChhhccC
 T ss_pred
 No 3
                                                                                           Pub Med
>5a9q 8 Nuclear pore complex protein NUP85; transport protein; 23.00A {Homo sapiens}
  Probab=100.00 E-value=5.1e-97 Score=866.61 Aligned_cols=611 Identities=17% Similarity=0.222 Sum_probs=0.0
                                eeecccCCCcceecCCcccccCCCcceeecChHHHHhhhh-ccccc------CccccccccccCCCHHHHHHHH
 Q ss_pred
                           {\tt 37~LYKRDPVSGAILVPMTVNDQPIEKNGDKMPLKFKLGPLSYQNMAF-ITAKD------KYKLYPVRIPRLDTSKEFSAYV}
 Q Fri Mar 04 23:
                                                                                                                                                  108 (744)
 Q Consensus
                                        ...|.|+|+....-+..++ +.++|.|+|..+-++|++|++|
                                                                                                                                                  108 (744)
 T Consensus
                                                                              -w--g--1-----i---
                                                                                                                                                    72 (656)
 T 5a9q_8
                             1 MEELDGEPT--VTLIPGVNSK-----KNQMYFDWGPGEMLVCETSFNKKEKSEMVPSCPFIYIIRKDVDVYSQILRKLF
                                                                                                                                                    72 (656)
 T ss_dssp
                                -----CCCEEEECCSSCCC----CSSCEEECSSTTCEEEECCCC-----CCCEEEEECCSSCCCCTTTTTHH
                                T ss pred
 Q ss_pred
                                Q Fri_Mar_04_23: 109 SGLFEIYRDLGDDRVFNVPTIGVVNSNFAKEHNATVNLAMEAILNELEVFIGRVKDQ---DGRVNRFYELEESLTVLNCL
                                                                                                                                                  185 (744)
                           109 ---f-if--l-------q------q------al------L---i-------l------lw-L-
 O Consensus
                                                                                                                                                  185 (744)
                            149 (656)
 T Consensus
                            73\ \text{NESH} \\ \text{GIFLGL} \\ \text{QR} - - \text{IDE-ELTGKSRKSQLVRVSKNYRSVIRACMEEMH} \\ \text{QVAIAAKDPANGRQFSSQVSILSAMELIWNLC}
 T 5a9q 8
                                                                                                                                                  149 (656)
 T ss_dssp
                                ННИНИНИНGG--GGS-CCC-----СТТИНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИ
                                нирнининин--инр-рссСсссринининининининининининирроссСсругинининининининини
 T ss_pred
 Q ss_pred
                                Q Fri_Mar_04_23: 186 RTMYFILDGQDVEENRSEFIESLLNWINRSDGEPDEEYIEQVFSVKDSTAGKKVFETQYFWKLLNQLVLRGLLSQAIGCI
                                                                                                                                                  265 (744)
                          Q Consensus
                                                                                                                                                  265 (744)
 T Consensus
                                                                                                                                                  216 (656)
                           150 EILFIEVAPAG-----PLLLHLLDWVRLHVCEVDS-LSADVLGS-----ENPSKHDSFWNLVTILVLQGRLDEARQML
 T 5a9g 8
                                HCCCCCCSSHH------НИНИНИНИНИНИНСССSST-ИНИНИНИS-----SSSSCSHHHHHHHHHHHHHHHHHHHHHHH
 T ss_dssp
 T ss pred
                                НННьссСССС-----сснининининьСССсhн-ннининсС-----СССссhhнинининньнын
                                0 ss pred
 Q Fri_Mar_04_23:
                           266 ERSDLLPYLSDTCAVSFDAVSDSIELLKQYPKDS-----SSTFREWKNLVLKLSQAFGSSATDISGELRDYIEDF
                                                                                                                                                  335 (744)
                          335 (744)
                                                                                                                                                  283 (656)
 T Consensus
                           217 SKEADAS-----PASAGICRIMGDLMRTMPILSPGNTQTLTELELKWQHWHEECERYLQ---DSTFATS----PHLESL
 T 5a9q 8
                                                                                                                                                  283 (656)
                                T ss dssp
                                HhCCCcc----chhнининининнhCCCCccccChнининининнннннн.---cccchн----нинин
 T ss pred
                                НННhCCCHHHHHH---hhhHHHHHHHhhheeCCCchh--ННHННHHHHCCC--СССснннннннннссснннннн
 Q ss pred
 Q Fri Mar 04 23: 336 LLVIGGNORKILQY---SRTWYESFCGFLLYYIPSLEL--SAEYLQMSLEANVV--DITNDWEQPCVDIISGKIHSILPV
                                                                                                                                                  408 (744)
                           336 ---IL-Gd---I-----i--gd----vL--
                                                                                                                                                  408 (744)
                          ++||+|++++|.+. |++||++|++|++|++|.++++|.++++|.+++|.+++||+|+|.++||+|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.+++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|.++|
 T Consensus
                                                                                                   -----i-e-d---vL--
                                                                                                                                                  363 (656)
 T 5a9q 8
                          284 LKIMLGDEAALLEOKELLSNWYHFLVTRLLYSNPTVKPIDLHYYAOSSLDLFLGGESSPEPLDNILLAAFEFDIHOVIKE
                                                                                                                                                  363 (656)
                                НИНИТСИВНИЧНИС---ССИНИНИНИСССССССС--СТИНИНИНИНЕС--СССТТ5ТИНИНИНИНИТССТТИНИН
 T ss dssp
 T ss_pred
                                ниньсссинининины
 Q ss_pred
                                Q Fri_Mar_04_23: 409 MESL--DSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNSFAFELCSLGDKELWPVAI
                                                                                                                                                  486 (744)
 Q Consensus
                           409 l--l--d-w-aAHladLl---q-L-----------dl------lre--Ll-YA--l-l-----LW-vai
                                                                                                                                                  486 (744)
                           T Consensus
                                                                                                                                                  421 (656)
 T 5a9q 8
                           364 CSIALSNWWFVAHLTDLLDHCKLLQSHN------LYFGSNMREFLLLEYASG--LFAHPSLWQLGV
 T ss dssp
```

```
T ss_pred
              НННhcCCccннннннннннн--нhcCccchнннн
              нинньссеенинининныныессиссинининнынныессининнынныннынныессининнынныессин
0 ss pred
Q Fri_Mar_04_23: 487 GLIALSATGTRSAKKMVIAELLPHYPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRAGKYE
                                                                 566 (744)
            566 (744)
                                                                 497 (656)
T Consensus
            422 DYFDYCPELGR----VSLELHIERIPLNTEQKALKVLRICEQRQMTEQVRSICKILAMKAVRNNRLGSALSWSIRAKDAA
T 5a9q 8
                                                                 497 (656)
              HHHHHSSSCHH----ННИНННGGGCCCCSSTTHHHHHHHHHHHHHHHHHHHHHHHHHH
T ss_dssp
T ss_pred
              Q ss pred
Q Fri Mar 04 23: 567 LVKSYSWLLFEASCMEGQKLDDPVLNAIVSKNSPAEDDVIIPQDILDCVVTNSMR-QTLAPYAVLSQFYELRDREDWGQA
                                                                 645 (744)
           567 ~V~~i~~l~~sl~~g~~~D~L~~iv~~~~~~p~~le~~~~l~~~Ls~ya~lreF~~~~g~
                                                                 645 (744)
O Consensus
           .+.++. ..|.++++|++||++++|
                                                             -~~~A
T Consensus
                                                                 556 (656)
            T 5a9q_8
                                                                 556 (656)
T ss_dssp
T ss pred
              Q ss_pred
              646 LRLLLLLIEFPYLPKHYLVLLVAKFLYPIFLLDDKKLMDEDSVATVIEVIETKWDDADE-----KSSNLYETIIEADKS
                                                                 719 (744)
Q Fri Mar 04 23:
            719 (744)
Q Consensus
T Consensus
                                                                 631 (656)
T 5a9q_8
            557 ASLLLSLMTSRIAPRSFWMTLLTDALP--LLEQKQVIFSAEQTYELMRCLEDL--TSRRPVHGESDTEQLQDDDIETTK-
T ss dssp
              НИНИНИНЕСССССИНИНИНИНИННЫ—-heeCCCCeeCHHHHHHHHHHHH—-HheeceCeececechHHHH—
T ss_pred
Q ss_pred
              ССсснинниннинниннинн
Q Fri_Mar_04_23: 720 LPSSMATLLKNLRKKLNFKLCQAFM 744 (744)
           720 lp~~~~lR~~la~~l~~~~
O Consensus
                               744 (744)
                 ++.||.+||+|||++|
            632 -----l~~~RlaLarnLara~~
T Consensus
                               648 (656)
            632 -----VEMLRLSLARNLARAII
T 5a9q 8
                               648 (656)
T ss_dssp
              -----
T ss_pred
                    PDB"
PROTEIN DATA BANK
No 4
                                        Pub Med
🗌 >4ycz_B NUP85; structural protein complex, nuclear pore complex, macromolec assemblies, structural protein; 4.10A
{Thielavia heterothallica}
Probab=100.00 E-value=3e-94 Score=848.54 Aligned cols=579 Identities=16% Similarity=0.228 Sum probs=0.0
Q ss_pred
              нинининининининин----нhheececcc------hhнининининининининин
Q Fri_Mar_04_23: 142 ATVNLAMEAILNELEVF----IGRVKDQDGRV------NRFYELEESLTVLNCLRTMYFILDGQDVEENRSEFIESLLN 210 (744)
           Q Consensus
T Consensus
            115 QKMDDTLATAAAQLAALWREHVDELPRPTEDHAAEIGPGPHATPFEKANYLANLALQIHHTRYEEGGLIRAEPLPQTLFR
T 4ycz_B
                                                                 194 (933)
              T ss_dssp
              ннинининининининининин
T ss pred
              Q ss pred
Q Fri_Mar_04_23: 211 WINRSDGEPDEEYIEQVFSVKDSTAGKKVFETQYFWKLLNQLVLRGLLSQAIGCIERSDLLPYLSDT------CA
O Consensus
            279 (744)
            T Consensus
                                                                 267 (933)
T 4ycz_B
            195 WLNEYH-DMYGSQVDDILRH--R---PSPACHSLFWQAVFIALLRGKVGDAARLLDQAG-WGHVRRGQRGEYAYVGQALE 267 (933)
              T ss dssp
              ННННhC-CCCHHHHHHHHhc--C---CCCCcCchнннннннннсCCннннннннhc-c-cchhhcccccccchhhhh
T ss pred
              нининининининиссиh-------hec
Q ss pred
320 (744)
            280 ~~~~v~~~~LL~~P~~~~~w~~wk~~~~l~~~~l~~~~
                                                                 320 (744)
Q Consensus
            T Consensus
T 4ycz B
              СНИНИНИНИНТЅСС-----СНИНИНИНИНИНИНИНС------
T ss dssp
T ss_pred
              нинининининин
              сссСснынинниннныннынныннынныннынныннынныннын
Q ss_pred
Q Fri_Mar_04_23: 321 ATDISGELRDYIEDFLLVIGGNQRKILQYSRTWYESFCGFLLYYIPSL-----------ELSAEYL 375 (744)
Q Consensus 321 ~~~~~~~L~1~IL~Gd~~I~~s~~WyE-1~a~~ly~~Pt~-----------------1~-y~ 375 (744)
Q Consensus
            T Consensus
T 4ycz_B
            348 ESQVPWEIYENLNIVFDIVLGQQGAILEAAQDWLEATVGLFGWWDERASRTEKPLSTSQSLSRSQALVLASAPANSESYL
                                                                 427 (933)
T ss_dssp
              ----CHHHHHHHHHHHHTCHHHHTTCCSSHHHHHHCC-------CCHHHHH
T ss pred
              Н---НИН------ hCCCCCCcнининининнессининининныныныныныныныныныны
Q ss pred
Q Fri Mar 04 23: 376 Q---MSLE----ANVVDITNDWEQPCVDIISGKIHSILPVMESLDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNED 447 (744)
```

```
Q Consensus
           T Consensus
           428 DRLARAFHTAVESDFHFNSQNAVEIGMACVFEDNIKGVIGLLRGWSLPIAAAVAEIASLGKWLPPHRPSGVYGLE---- 502 (933)
T 4vcz B
             T ss dssp
             T ss pred
             сссhhhc--ссс-----ссhнинининннhhhcc------Сссс-----hнининин
Q ss pred
Q Fri_Mar_04_23: 448 NEMLEDLF--SYR-----NGMASYMLNSFAFELCSLG-----DKEL-----WPVAIGLIALSATGTRS--AKKMV
                                                             503 (744)
Q Consensus
           448 ~~~~dl~_~~~~lre~~Ll~YA~~l~l~~~~~L_-----W~vai~YL~~c~~~q~~-
                                                             503 (744)
           T Consensus
                                                             580 (933)
           503 DLDMDDLEVLGMDPGAPDEVDGIKDSTLVQYAQA--LADYEGLSSVQDRSGTSKDGWELSISVLGRMDSPERSEEMVRDL
T 4ycz B
                                                             580 (933)
T ss_dssp
             -----CCSSSSSHHHHHHHHH-HTTCCCCCCSSCC----CCCHHHHHHHTTC--CCCCHHHHHHHH
T ss_pred
             Q ss_pred
             Q Fri_Mar_04_23: 504 IAELLPHYPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSA-HNIIESIANFSRAGKYELVKSYSWLLFEASCME
                                                             582 (744)
           Q Consensus
                                                             582 (744)
                                                             660 (933)
T Consensus
                                                             660 (933)
T 4ycz B
T ss_dssp
             нинньссссссинининниннессининниннинниннин
T ss pred
Q ss_pred
             Q Fri Mar 04 23: 583 GQKLD-----DPVLNAIVSKNSP--AEDDVIIPQDILDCVVTNSMRQTLAPYAVLSQFYELRDREDW-------GQA
                                                             645 (744)
           583 g-----D--L--iv-----p---le------la--ya-lreF-----g-----A
O Consensus
                                                             645 (744)
                   |++++++.++.. ++.++| ++ ++++|+++|++||+||+||+||+.+++++. ++|
           661 s-a-p---LD--l--Ll-sp---L---a--d----e--aa-lL--fLs-YA-Lr-Fy--rd------
T Consensus
                                                             734 (933)
           661 STAFPPANDLDDYLYKLLNDRKNTLEQCASQD----ME--AAELLGKMLSGYASLRQFYDIRDNEDALPHATPLSRRKQA
T 4ycz_B
T ss_dssp
             СССССерринининининин
T ss_pred
             Q ss_pred
Q Fri Mar 04 23:
           646 LRLLLLLIEFP------YLPKHYLVLLVAKFLYPIFLL-----DDKKLMDEDSVATVIEVIETKW
                                                             699 (744)
           Q Consensus
                                                             699 (744)
T Consensus
                                                             811 (933)
T 4ycz_B
           735 ATALISVIASSDDNIRGGLYDQTRDGIVSEDFLLALLGEALV--FVSDPDNTNVHHGQLATPVITLDQIDVLLKAIEDL-
                                                             811 (933)
             T ss dssp
             T ss pred
             0 ss pred
Q Fri_Mar_04_23:
           700 DDAD----EKSSNLYETIIE------A
           T Consensus
                                                             890 (933)
           812 -QAVGSRVYNACDEFLQLVLASAPGGLKGSTPADLLKKSAGPGPGGSGNAMLAGSSLVASQLQRSLSGTGGGLGKVAVKR
T 4ycz B
                                                             890 (933)
             -TTSCSHHHHHHHHHTTSSCSCCC-----HHHHHHHHTTSCCCCC--
T ss dssp
T ss_pred
             -С---ССССс--снинининининининин
Q ss pred
Q Fri Mar 04 23: 717 -D----KSLPS--SMATLLKNLRKKLNFKLCQAFM 744 (744)
O Consensus
           717 -~---1p~--~~1R~~la~~l~~~~
           . +.+|+ +.++++.||+.||++||+.|+
891 ~gwDWR~~~~~dilr~LRl~la~~la~~~~
T Consensus
                                   925 (933)
T 4ycz B
           891 RGWDWRSEVTAKTKGEDIMRRLRLGLAKDLAGLWL 925 (933)
             -----ннининининининин
T ss dssp
T ss_pred
             cCCchhccCccCCННННННННННННННН
                   PDB<sup>M</sup>
PROTEIN DATA BANK

NCBI
                                      Pub Med
                                 >4xmm B Nucleoporin NUP145; structural protein, immune system, transport protein-immune complex; 7.38A
{Saccharomyces cerevisiae S288C} PDB: 4xmn _B
Probab=98.38 E-value=6.7e-05 Score=88.32 Aligned cols=312 Identities=12% Similarity=0.076 Sum probs=0.0
             нинининининын hccccccccc------cchнинининин hcccccнининин hcccccccccchh
Q ss pred
Q FTI Mar 04 23: 177 ESLTVLNCLRTMYFILDGQDVEEN-----RSEFIESLLNWINRSDGEPDEEYIEQVFSVKDSTAGKKVFETQYF 245 (744)
         T Consensus
           170 SDYNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERHC---RLTSWIVSQ----IGPEIEEKIRN--S--SNEI---- 232 (652)
T 4xmm B
             ННИНИНИНИНИЯ CCCCCSCCS НИНИНИНИНИН --- НИНИНИНИ --- НИНИНИНИН --- C--CCH
T ss dssp
             T ss_pred
Q ss_pred
             Q Fri_mar_04_23: 246 WKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYPKD------SSSTFREWKNLVLKLSQAFG 318 (744)
           246 W~-V~-lvLrG~~~A~-lL~~~~~l~~~~v~~~LL~~P~~~~w~~Wk~~~~l~~~~ 318 (744)
Q Consensus
             ..|+.+++.|+++.|.++.-.++ +..+ ..||.++...
           233 -e-if--L----I-eA---Ai--g------d-rL-----A-Llsq-gs-----r----QL--W-----
T Consensus
T 4xmm B
           233 -EQIFLYLLLNDVVRASKLAIESK------NGHL------SVLISYLGSNDPRIRDLAELQLQKWS------
                                                             285 (652)
T ss dssp
```

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T ss_pred
                                -ННИННИНСССИНИНИНИНИСС------Ссси------ННИНИНИСССИНИНИНИНИНИНИНИ
                                ссссСснынниннинннсСсн-----нниннныннннннныннннннннннннннннс-сссссни
 0 ss pred
 Q Fri_Mar_04_23: 319 SSATDISGELRDYIEDFLLVIGGNQ-----RKILQYSRTWYESFCGFLLYYIPSLELSAEYLQMSLEAN-VVDITNDW
                                                                                                                                                   390 (744)
                          Q Consensus
                                                                                                                                                   390 (744)
 T Consensus
                                                                                                                                                   360 (652)
 T 4xmm B
                                                                                                                                                   360 (652)
                                T ss_dssp
 T ss_pred
                                НССС----сССНИНИНИННННСССссссссссньее нестранции и нестранции нестр
                                ННИНИНИССИНИНИНИНЫ—---cChнинининининыноссессессессессессь hhheccecchнини
 Q ss pred
 Q Fri Mar 04 23: 391 EQPCVDIISGKIHSILPVMES----LDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYML
                                                                                                                                                   466 (744)
                           391 E----i-egd---vL--l-----ld-w-aAHladLl---g-L-----
                                                                                                                  ----dl-----lre--L 466 (744)
 O Consensus
                          T Consensus
                                                                                                                                                   415 (652)
 T 4xmm B
                                                                                                                                                   415 (652)
                                T ss_dssp
 T ss pred
                                Q ss_pred
                                ннинный расСессиннинний Ссессиннинний рас-ССССиннинний и в сестиний в сестини
 Q Fri_Mar_04_23: 467 NSFAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQ
                                                                                                                                                   545 (744)
                           467 l-YA--l-l-----LW-vai-YL--c---g----r--i-elL-r--pl-t----ek-L-iC-----L---a--I-----g--
                                                                                                                                                   545 (744)
 Q Consensus
                           +.||.+|. ..+|+|+=+|.+.+ ...-+..|.+|.| ++...++++ +...-+...++|...=|++...|.+|.| 416 --fa-QLe----Glw-waifVllHl---d---R--air-lL-R----------L-e-L-IP----Wi-eAkal-
 T Consensus
                                                                                                                                                   485 (652)
 T 4xmm B
                           416 FAFAAQLE---FAQLHGHSLFVSCFLN--DDKAAEDTIKRLVMREITLLRAST-ND--HILNRLKIP--SQLIFNAQALK
                                T ss dssp
                                НИНИНИН---HCCCcнинининиhCC--Сининининининиhhcccccchи-ин--ининиhccc--ининининин
 T ss_pred
 Q ss_pred
                                нинсссининининнессининини
 Q Fri_Mar_04_23: 546 MLSAHNIIESIANFSRAGKYELVKSYS 572 (744)
                          546 ~l~~g~~g~AL~~~~rA~d~~~V~~i~ 572 (744)
 O Consensus
                           ...+|++..++.++||.+...+++.
486 a---gd---e---Ll-A----eAH-v-
 T Consensus
                                                                         512 (652)
                           486 DRYEGNYLSEVQNLLLGSSYDLAEMAI 512 (652)
 T 4xmm_B
                                ННННС---СНННННС----СННННН
 T ss_dssp
 T ss_pred
                                нньсссининниннессининнин
                                                PDB<sup>IM</sup>
PROTEIN DATA BANK
 No 6
                                                                                            Pub Med
>5a9q_5 Nuclear pore complex protein NUP96; transport protein; 23.00A {Homo sapiens}
 Probab=97.92 E-value=0.00031 Score=85.79 Aligned cols=341 Identities=15% Similarity=0.143 Sum probs=0.0
                                Q ss_pred
 Q Fri_Mar_04_23: 155 LEVFIGRVKDQDGRVNRFYELEESLTVLNCLRTMYFILDGQDVEEN------RSEFIESLLNWINRSDGEPDEEYI 224 (744)
                           224 (744)
 O Consensus
                                T Consensus
                           366 IHDYADWVKEASGDLPEAQIVKHWSLTWTLCEALWGHLKELDSQLNEPREYIQILERRR---AFSRWLSCT----ATPQI
 T 5a9q 5
                                НИНИНС------CCSSSHИНИНИНИННЯSCCCCSCCSHИНИНИНИНН---НИНИНИНН----НИНИН
 T ss_dssp
                                T ss_pred
                                Q ss pred
 Q Fri_Mar_04_23: 225 EQVFSVKDSTAGKKVFETQYFWKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYPKD----- 298 (744)
                          Q Consensus
 T Consensus
 T 5a9g 5
                                T ss dssp
                                ниниhh------ссССС----нинининhhссснинининнсс-------Сссн-------нининhссснинин
 T ss pred
                                ннининининининининининининининининин
 Q ss_pred
 Q Fri Mar 04 23: 299 SSSTFREWKNLVLKLSQAFGSSATDISGELRDYIEDFLLVIGGNQR------KILQYSR-TWYESFCGFLLYYIPSLEL 370 (744)
                          370 (744)
 Q Consensus
 T Consensus
                           495 LTMQLVDWHQ------LQADSFIQDERLRIFALLAGKPVWQLSEKKQINVCSQLDWKRSLAIHLWYLLPPTAS
 T 5a9q_5
                                                                                                                                                   561 (937)
                                T ss dssp
                                НИНИНИНИН
 T ss pred
 Q ss_pred
                                371 l-~y~~~~i~e----qd~~~vL~l~~---ld 413 (744)
 O Consensus
                           ++.++.--.+.+ ..+-..+.|+. .++..+|-...+|

562 l--av-y----a--P-P-Y-e------Dl---LLKLya----Le-vL-P-s-t--plD
 T Consensus
                           562 ISRALSMYEEAFQNTSDSDRYACSPLPSYLEGSGCVIAEEQNSQTPLRDVCFHLLKLYSDRHYDLNQLLEPRSITADPLD
 T 5a9q 5
 T ss_dssp
                                HHHHHHHHHHSCC------CCSCHHHHHHHHHHTCC-CHHHHHHHHHTTCCCSC
                                T ss_pred
                                Q ss pred
 Q Fri_Mar_04_23: 414 SCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNSFAFELCSLGDKELWPVAIGLIALSA 493 (744)
                          414 ~w~aAHladLl~~~g~L~~~~~~dl~~~~~dl~~~~~dl~~~~~ll~yA~~l~l~~~~Lw~vai~yL~~c~ 493 (744)
```

```
....+.+-+.||.+|..
                              --++=|+.-+|.+.|+-.-
                                                                                                                   .++|+-||=+|.+.+
 T Consensus
                         642 ~rLsW~L~~vL~alg~~~~~GlW~wAiFVLLHL~
                                                                                                                                         693 (937)
                         642 YRLSWHLWEVLRALNYTHL-----SAOCEGVLOASYAGOLES--EGLWEWAIFVLLHID
 T 5a9α 5
                                                                                                                                         693 (937)
                              T ss dssp
 T ss_pred
                              Q ss pred
 Q Fri_Mar_04_23: 494 TGTR--SAKKMVIAELLPHYPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRAGKYELVKSY
                                                                                                                                         571 (744)
                         494 ~-g----r--i-ell-r-pl-t---ek-L-iC----L---a--I----g---l--gg--g-AL----rA-d---V--i
... .+.|..|...++.-.+.+. .++.++.+ .=|++..|.+...+|++..+|+...+++.++.|
694 d---Re-aIrelL-R------------------fL-e-L-IP----WI-eAkAl-ar--gd---e---Ll-A----eAH-v
 Q Consensus
                                                                                                                                         571 (744)
 T Consensus
                         694 NSGTREKAVRELLTRHCOLLETPESWAKET--FLTOKLRVP--AKWIHEAKAVRAHMESDKHLEALCLFKAEHWNRCHKL
 T 5a9q 5
                                                                                                                                         769 (937)
                              T ss dssp
                              СНИНИНИНИНИННИН НИСССССОВ НИНИН НЕСССССТВИНИНИН НЕССИВЕНИЕМ НЕССИВЕНИЕМ НЕССИВЕНИЕМ НЕССИВЕНИЕМ НЕСССИВЕНИЕМ НЕСССИВ НЕСССИВЕНИЕМ НЕСССИВ НЕССОВИВЕНИЕМ НЕСССИВ НЕССОВИЕМ НЕСССИВ НЕССОВИЕМ НЕСССИВ НЕССОВИЕМ НЕСССИВ НЕССОВИЕМ НЕССОВИЕМ НЕССОВИЕМ НЕССОВИВЕНИЕМ НЕССОВИВЕНИЕМ НЕССОВИЕМ НЕССОВИВ НЕССОВИЕМ НЕССОВИЕМ НЕССОВИЕМ НЕССОВИЕМ НЕССОВИВЕНИЕМ НЕССОВИЕМ НЕССОВИВИЕМ НЕ
 T ss pred
                                            PDB* SNCBI Pub Med
 No 7
>3bg1 B Nucleoporin NUP145; NPC, transport, WD repeat, autocatalytic cleavage, mRNA transport, nuclear pore
 complex, nucleus, phosphoprotein; 3.00A {Saccharomyces cerevisiae} PDB: 3bg0 B 3iko B
 Probab=97.76 E-value=0.0019 Score=72.83 Aligned cols=295 Identities=12% Similarity=0.033 Sum probs=0.0
                              ннинининные СССССссссс------ссьининининные ССССнинининные в сссссссствинин в ссссссссствинин в сссссссссствини в сссссссствини в ссссссссствини в сссссссствини в сссссссствини в ссссссствини в ссссссствини в ссссссствини в сссссствини в ссссствини в сссссствини в ссссствини в сссссствини в ссссссствини в сссссствини в сссссствини в ссссствини в сссссствини в ссссствини в сссссствини в ссссствини в сссствини в сссствини в сссствини в сссствини в сссствини в сссствини в ссссствини в сссствини в сссствини в сссствини в сссствини в сссствини в ссствини в сствини в ссствини в сствини в сствини в сствини в сствини в ссствини в сствини в стрини в сствини в с
 Q ss pred
 Q Fri Mar 04 23: 179 LTVLNCLRTMYFILDGQDVEEN------RSEFIESLLNWINRSDGEPDEEYIEQVFSVKDSTAGKKVFETQYFWK 247 (744)
                         O Consensus
                         T Consensus
 T 3bg1_B
                        121 YNLWKLSSILFDPVSYPYKTDNDOVKMALLKKERHC---RLTSWIVSO----IGPEIEEKIRN--S---SNEI------E
                                                                                                                                        182 (442)
                              T ss dssp
 T ss pred
                              Q ss_pred
                              нинининеснининининессийнинининин
 Q Fri_Mar_04_23: 248 LLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYP---KDSSSTFREWKNLVLKLSQAFGSSATDI
                                                                                                                                         324 (744)
                         324 (744)
 Q Consensus
 T Consensus
 T 3bg1_B
                         183 QIFLYLLLNDVVRASKLAIESK------NGHLSVLISYLGSNDPRIRDLAELQLQKWS-----TGGC-
                                                                                                                                         238 (442)
                              НИНИНИТТТСИНИНИНИНИТТ------CHHHHHHHHHHHHHTSCCHHHHHHHHHHHHTT-----SSCC--
 T ss_dssp
 T ss_pred
                              сныннинниннинссси-----нинниныныннынынынынынынынынсссссыниннин
 Q ss_pred
 Q Fri_Mar_04_23: 325 SGELRDYIEDFLLVIGGNQ------RKILQYSRTWYESFCGFLLYYIPSLELSAEYLQMSLEAN-VVDITNDWEQPCVD
                                                                                                                                         396 (744)
 O Consensus
                        396 (744)
                         T Consensus
                         239 --SIDKNISKIYKLLSGSPFEGLFSLKELES-EFSWLCLLNLTLCYGQIDEYSLESLVQSHLDKFSLPYDDPIGVIFQLY
 T 3bg1_B
                                                                                                                                         315 (442)
                              T ss_dssp
 T ss_pred
                              ннссснинининнн----ссhининининин
 Q ss pred
 Q Fri_Mar_04_23: 397 IISGKIHSILPVMES----LDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNSFAFE
                                                                                                                                         472 (744)
                         397 i~egd~~vL~~l~~---ld~w~aAHladLl~~-g~L~~~~~~dl~~~~dl~~~~lre~~Ll~YA~~
 Q Consensus
                                                                                                                                         472 (744)
                         T Consensus
                                                                                                                                         370 (442)
                         316 AANENTEKLYKEVRORTNALDVOFCWYLIQTLRFNGTRVF-----SKETSDEATFAFAAQ
 T 3bg1 B
                                                                                                                                         370 (442)
 T ss dssp
                              T ss_pred
                              Q ss pred
 Q Fri Mar 04 23: 473 LCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNI
                                                                                                                                         552 (744)
                        473 l-l-----LW-vai-YL--c---g----r--i-elL-r-pl-t----ek-L-iC-----L---a--I-----g--
 O Consensus
                                                                                                                                         552 (744)
                         T Consensus
                                                                                                                                         441 (442)
                         371 LE---FAOLHGHSLFVSCFLN--DDKAAEDTIKRLVMREITLLRASTND--HILNRLKIP--SOLIFNAOALKDRYEGNY
 T 3bg1_B
                                                                                                                                         441 (442)
                              T ss dssp
                              HH---hCCCcннинининнhcc--снининининннннннн--нниннccc--инининининннн
 T ss pred
                                               PDB
                                                            NCBI
                                                                           Pub Med
 No 8
>2qx5_A Nucleoporin NIC96; mRNA transport, nuclear pore complex, nucleus, protein transport, translocation,
  transport, transport protein; 2.50A {Saccharomyces cerevisiae} PDB: 2rfo_A
 Probab=97.69 E-value=0.0058 Score=72.27 Aligned_cols=362 Identities=15% Similarity=0.133 Sum_probs=0.0
                              Q ss_pred
 Q Fri_Mar_04_23: 246 WKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQY------PKDSSSTF-REWKNLVLKLSQA 316 (744)
                         246 W~V~lvLrG~~~A~lL~~~~~l~~~v~~~~LL~~~~p~~~~wk~~~~l~~~316 (744)
 Q Consensus
                              |..|+-|+=.|..+.|.++++.++
                                                                                                      |....+. .+|+..++
                         T Consensus
                         156 WALIFYLLRAGLIKEALQVLVENK-----ANIKKVEQSFLTYFKAYASSKDHGLPVEYSTKLHTEYNQHIK----
 T 2qx5 A
                              НННННННТТТСННННННННТG------GGC-----СННННННС------
 T ss dssp
                              T ss_pred
 Q ss pred
                              hbcccccCcHhHHHHHHHHHCC-----CHHHHHHHHhhhhHHHHHHhhbbeeCCCchh-----HHHHHHHHHHCCCC
 Q Fri Mar 04 23: 317 FGSSATDISGELRDYIEDFLLVIGG-----NQRKILQYSRTWYESFCGFLLYYIPSLEL----SAEYLQMSLEANVVD 385 (744)
```

```
Q Consensus
          317 ------L--l--IL-G-----d---I--s--WyE-l-a--ly--Pt-----l--y-----d 385 (744)
          ++...| .=.+++||.| +...|+||.=+=...-... .=++|..+..+...

222 ------Dp----yK-avY-iig-cd------v--tiED-LW--L-lir----e-ytL--LQ--I----Ge-
T Consensus
                                                             294 (661)
          222 --SSLDGDP----YRLAVYKLIGRCDLSRKNIPAVTLSIEDWLWMHLMLIKEKDAENDPVYERYSLEDFONIIISYGPS
T 2qx5_A
                                                             294 (661)
             T ss_dssp
             --сСССССН-----НИНИНИННЕССССссссенНИНИННЕСНИННИНННИННЕССССссссссссснинниннниннныннын
T ss pred
             Q ss pred
Q Fri_Mar_04_23: 386 ITNDWEQPCVDIISGKIHSILPVMESLDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMA-SY
                                                              464 (744)
Q Consensus
          386 ~~~~E~~~~i~egd~~~vL~~l~~ld~w~aAHladLl~~~g~L~~
                                                              464 (744)
          T Consensus
                                                             358 (661)
          295 RFSN-YYLQTLLLSGLYGLAIDYTYTFSEMDAVHLAIGLASLKLFKIDSSTRLTKKP------KRDIRFAN
T 2qx5 A
                                                             358 (661)
T ss_dssp
             T ss_pred
             сссс-ининининининининин
Q ss_pred
             Q Fri_Mar_04_23:
          465 MLNSFAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDDIEWML-----SICVEWRL-
                                                              531 (744)
Q Consensus
          465 ~Ll~YA~~l~l~~~~~LW~vai~YL~~c~~g~~~~r~~i~elL~r~pl~t~~~ek~L------iC~~~~L-
                                                              531 (744)
          +|..|... --... +.|++|+.........+...+..|. +...++ -+..++.=

359 LI--Yt---F--d----Al-Y--li----d----l--Llg-i--dG-r--G-Ie---li
          359 ILANYTKS--FRYSDP--RVAVEYLVLITLNEGPTDVELCHEALRELVLETK-EFTVLLGKIGRDGARIPGVIEERQPLL
T 2qx5_A
                                                              433 (661)
             HHHHHHTT--TTTTCH--HHHHHHHHGGGGGSCCHHHHHHHHHHHHHHHHHC-CHHHHHCECTTSCEECCHHHHTCGGG
T ss_dssp
             НИНИНИН---HhcCCH---НИНИНИНИНИНССССонинининининининос-сининссСССССССССССининининининин
T ss pred
Q ss_pred
             Q Fri_Mar_04_23: 532 ----PEIAKEIYTTLGNQMLSAHNIIESIANFSRAGKYELVKSYSWLLFEASCMEGQKLD------DPVLNAI
                                                             594 (744)
          532 ----a~I~~q~~l~~q~qAL~~~rA~d~~V~i~~l~~sl~~q~~~-----D~L~i
O Consensus
                                                             594 (744)
          T Consensus
                                                              513 (661)
          434 HVRDEKEFLHTITEQAARRADEDGRIYDSILLYQLAEEYDIVITLVNSLLSDTLSASDLDQPLVGPDDNSETNPVLLARR
T 2qx5_A
T ss_dssp
             T ss_pred
             Q ss_pred
Q Fri Mar 04 23:
          595 VSKNSPAEDDVIIPQDILDCVVTNSMRQTLAPYAVLSQFYELRDREDWGQALRLLLLLIEFPYLP
          Q Consensus
T Consensus
                                                    568 (661)
T 2qx5_A
          514 MASIYFD----NAG--ISRQIHVKNKEICMLLLNISSIRELYFNKQWQETLSQMELL---DLLP
             T ss dssp
             НННННН----chh--hhhccСнннннннннннннннннннссснннннннннс---ссс
T ss pred
                   PDB NCBI Pub Med
No 9
     Fusion protein of SEC13 and NUP145C; structural protein complex, nuclear pore complex, macromolec
assemblies, structural protein; 4.10A {Thielavia heterothallica}
Probab=97.68 E-value=0.0003 Score=85.83 Aligned_cols=330 Identities=12% Similarity=0.133 Sum_probs=0.0
             Q ss pred
Q Fri_Mar_04_23: 149 EAILNELEVFIGRVKDQDG---RVNRFYELEESLTVLNCLRTMYFILDGQDVEENRSEFIESLLNWINRSDGEPDEEYIE 225 (744)
          T Consensus
                                                             454 (876)
          391 PENLARLORYIDSVSFKEGQPIASPEFRELAQGDPSWELAS-LLFDDNGY------GLPAFWRQLVSEATD--- 454 (876)
T 4ycz_A
             T ss_dssp
T ss pred
             0 ss pred
             Q Fri_Mar_04_23: 226 QVFSVKDSTAGKKVFETQYFWKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYPKD---SSST
                                                              302 (744)
          T Consensus
          455 -----ATLVSGIGMQDGDMKAQ
T 4ycz A
                                                             508 (876)
             -----TTSTTCC--CHHHHHHHSSSCCHHHHHHHHHSSGGGH------HHHHHHTTC-
T ss dssp
             ------ннньессининининессининининессьн------ннининесссининин
T ss pred
             Q ss pred
364 (744)
          364 (744)
          T Consensus
                                                              575 (876)
          509 LKDWRE-----SNVLAEFSQPVRAIYELLAGNAGVCAGVKNVPIENRVDSFTISQRFGLDWMRSFGLRLFYT
T 4ycz A
                                                             575 (876)
             -----CCCSCCTTHHHHHHHHC-------CCCSCCTTHHHHHHHHSS
T ss dssp
T ss_pred
             НННННh------СССсссССНннннннннhсСссссссССсссссссссссСССНннннннннhсС
Q ss_pred
             Q Fri_Mar_04_23: 365 IP-SL---ELSAEYLQMSLEANVVDITNDWEQPCVDIISGKIHSILPVMESLDSCTAAFTAMICEAKGLIENIFEGEKNS 440 (744)
          Q Consensus
                                                              440 (744)
T Consensus
T 4ycz A
          576 TGATANVAEAVRSFQADIEQDKEPEPDSALWSLLKAFANQEF-----DWSDTRLGWLLTKAIYATGKVSFG-----
                                                              641 (876)
T ss dssp
             SSSSCCSHHHHHHHHHTSSSCSCSCHHHHHHHHTTSSCSC----CSCC---CCHHHHHHHHSCC---C-----
```

```
T ss_pred
                       0 ss pred
 Q Fri_Mar_04_23: 441 DDYSNEDNEMLEDLFSYRNGMASYMLNSFAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPH----YPFVTN
                                                                                                         516 (744)
                   516 (744)
 T Consensus
                                                                                                          701 (876)
                   642 QD-----AAEKLDKASLAYASALTAQS--QWVPATFVLLQLS-DAASREAAVRDHLGRHARRIGSPRN
 T 4ycz A
                                                                                                          701 (876)
                       T ss_dssp
 T ss_pred
                       cc-----hhhHHHHHHHHHHHHHHHCC---CchhhheeeecC--ChHHHHHHHHHHHHhhhhhhccCccc
                       ннинининнессинининнининнинисссининнин
 Q ss pred
 Q Fri Mar 04 23: 517 DDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRAGKYELVKSY 571 (744)
                   517 ---ek-L-iC----L---a--I----g---l--g--g-AL----rA-d---V--i 571 (744)
...++ .++.++.| ..=|++..|++..+|++..++.++|+...+++
702 -----l-iP----wi-ea-a-------l-a----ah-- 752 (876)
 O Consensus
 T Consensus
                   702 PNSAF--SSLRKFGVP--ETWIWEAKALDFRARGDSQQEFLALVWAQNYSEANQA 752 (876)
 T 4ycz A
                       SHHHH--HHHHTTTCC--ТТННННННННННС--ССТНННННТТТССТННННТ
 T ss_dssp
                       T ss pred
                                  PDB<sup>N</sup>
 No 10
                                                          Pub Med
>3jro A Fusion protein of protein transport protein SEC13 nucleoporin NUP145; protein complex, cytoplasmic
 vesicle, endoplasmic reticulum, transport, membrane, mRNA transport; 4.00A {Saccharomyces cerevisiae}
 Probab=97.19 E-value=0.019 Score=68.49 Aligned_cols=308 Identities=10% Similarity=-0.003 Sum_probs=0.0
                       0 ss pred
 Q Fri Mar 04 23: 179 LTVLNCLRTMYFILDGQDVEENRSEFIESLLNWINRSDGEPDEEYIEQVFSVKDSTAGKKVFETQYFWKLLNQLVLRGLL 258 (744)
                   179 -- Iw-L-e--yf-----g------l---Ll-Wln-----p--e---ev------p--hp-FW--V--lvLrg--
 O Consensus
                                                                                                          258 (744)
                   T Consensus
                                                                                                          502 (753)
                   430 YNLWKLSSILFDPVSYPYKTD-NDQVKMALLKKERHCR---LTSWIVSQIGPEIE---EKIRNSSNEIEQIFLYLLLNDV
 T 3jro_A
                                                                                                          502 (753)
                       T ss_dssp
 T ss pred
                       Q ss_pred
                       нинининнессь в в составления в сос
 Q Fri_Mar_04_23: 259 SQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYPKDSSSTF-REWKNLVLKLSQAFGSSATDISGELRDYIEDFLL
                                                                                                         337 (744)
 Q Consensus
                   337 (744)
                                                     ..||.++-. = ..+|..+.+..+.+.++
                       ++|+++.-.++.+..
                                                                                            +.+..||.
                                                     -A-11a----iy
 T Consensus
                   503 VRASKLAIESKNGHL-----SVLISYLGS----NDPRIRDLAELQLQKWSTGGCSID---KNISKIYK
 T 3jro A
                                                                                                          558 (753)
 T ss dssp
                       T ss_pred
                       HhCCCH------ННИНИНЬННИННННННННННННННННННС-ССССССИННИНННННННСССИВИННННН
 Q ss_pred
 Q Fri_Mar_04_23: 338 VIGGNQ-----RKILQYSRTWYESFCGFLLYYIPSLELSAEYLQMSLEAN-VVDITNDWEQPCVDIISGKIHSILPVM
                                                                                                          409 (744)
                   Q Consensus
                                                                                                          409 (744)
                   T Consensus
                                                                                                          637 (753)
                   559 LLSGSPFEGLFSLKELES-EFSWLCLLNLTLCYGQIDEYSLESLVQSHLDKFSLPYDDPIGVIFQLYAANENTEKLYKEV
 T 3jro_A
                                                                                                          637 (753)
                       T ss_dssp
                       T ss pred
                       Q ss pred
 Q Fri_Mar_04_23: 410 ES----LDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNSFAFELCSLGDKELWPVA
 O Consensus
                   485 (744)
                      .. +|--+=|+.-+|.+.|+-.-
                                                                           ....+.+-+.||.+|+ ..++|+-|
                   638 ~~~~~d~1~w-1~~~1~~~~q~~~~a
 T Consensus
                                                                                                          689 (753)
 T 3jro_A
                   638 RORTNALDVQFCWYLIQTLRFNGTRVF-----SKETSDEATFAFAAQLE--FAQLHGHS
                                                                                                          689 (753)
                       HTTCTTSCHHHHHHHHHTTTTTCSCC-----HTTCHHHH
 T ss dssp
                       hCCCCCcchнниннинннин---нCCchни
 T ss pred
                       Q ss pred
 Q Fri Mar 04 23: 486 IGLIALSATGTRSAKKMVIAELLPHYPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNI
                                                                                            552 (744)
                   486 i~YL~c~~g~~~r~i~elL~r~pl~t~~~ek~L~iC~~~L~~a~~I~~~g~~l~~g~~
 Q Consensus
                                                                                            552 (744)
                   +=+|.+.+ ....+..|.++|.|.--...+-+. -++.+++.| ..=|++..|.+.-.+|++
690 fv~h~--~v~-l~r~-~~v~-l~r~-~l~ip-~wi~a~a~-~~v~--
 T Consensus
                                                                                            750 (753)
                   690 LFVSCFLN--DDKAAEDTIKRLVMREITLLRASTND--HILNRLKIP--SQLIFNAQALKDRYEGNY
 T 3jro A
                                                                                            750 (753)
                       ННИНТСS--СНИНИНИНИННИННЯ SCTTSSTTTT--TTTTTTCC--НИНИНИНИНИНИНИН
 T ss dssp
 T ss_pred
                       НННhhhcc--снининининининессесссhh--ининессес--инининининин
                                    PDB STOCK PROTEIN DATA BANK PUB MED
 No 11
>5a9q 4 Nuclear pore complex protein NUP107; transport protein; 23.00A (Homo sapiens)
 Probab=97.15 E-value=0.0036 Score=76.60 Aligned cols=283 Identities=14% Similarity=0.139 Sum probs=0.0
 Q ss_pred
                       Q Fri_Mar_04_23: 245 FWKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQY------PKDSSSTFREWKNLVLK 312 (744)
                   Q Consensus
                                                                                                          312 (744)
                       ||.+++.+|.+|++++|+++-+..| ..-+.++ ..-.-+
                                                                                      |....+.-||..|-+
                         ~~if~llR~G~~~eA~elC~~~g-----q~WRAas---L~G~~l~~dp~~~~~~
                                                                                       ~~~Gn~~r~LWK~~c~~
                                                                                                          413 (925)
                   346 LLKYLETLTRAGMTERAORICKRCG-----OAWRAAT--LEGWKLYHDPNVNGGTELEPVEGNPYRRIWKISCWR
 T 5a9q_4
                                                                                                         413 (925)
 T ss dssp
                       HHHHHHHHHTCHHHHHHHHHT-----CHHHHHH---HHTTSBCBCTTTCCTTCCSSCBSBSCHHHHHHHHH
```

```
T ss_pred
                              НННННННННСССНННННННННСС-----снннннн---нсCchhhcCcccCCcccccCChhнннннннн
                              ННННhhccccCcнhннннннhhcccннннннhhhнннннhh-----ee
 0 ss pred
 364 (744)
                         313 1~~~~~~~L~~l~~l~~IL~Gd~~~I~~~s~~WyE~l~a~~l------y~
                                                                                                                                             364 (744)
                         T Consensus
                                                                                                                                             484 (925)
 T 5a9q 4
                                                                                                                                            484 (925)
                              T ss_dssp
 T ss_pred
                               СС-Сећинининини СССССенининини СССНИН СССССЕНИ ССССЕНИ СССЕНИ ССССЕНИ СССЕНИ СССЕНИ СССЕНИ ССССЕНИ СССЕНИ СССЕ
 Q ss pred
 Q Fri Mar 04 23: 365 IP-SLELSAEYLQMSLEAN-VVDITNDWEQPCVDIISGKIHSILPVMESL-----DSC--TAAFTAMICEAKGLIE 431 (744)
                         365 ~P-t~~l~~y~~~~~d~~~~E~~~~i~egd~~~vL~l~~l-----d~w---~aAHladLl~~~g~L~
                                                                                                                                            431 (744)
 O Consensus
                              T Consensus
                                                                                                                                             564 (925)
                         485 ANWTLEKVFEELQATDKKRVLEENQEHYHIVQKFLILGDIDGLMDEFSKWLSKSRNNLPGHLLRFMTHLILFFRTLGLQT
 T 5a9q_4
                                                                                                                                             564 (925)
                              T ss_dssp
 T ss pred
                               Q ss_pred
                              ссссссссссссссссьный делиний и делиний 
 Q Fri Mar 04_23: 432 NIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNSFAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPHY
                                                                                                                                             511 (744)
                         Q Consensus
                                                                                                                                             511 (744)
                                       565 ~-
 T Consensus
                                                                                                                                             612 (925)
 T 5a9q_4
                         565 K-----EEVSIEVLKTYIQLLIREKHTNLIAFYTCHLP--QDLAV----AQYALFLESV
                                                                                                                                             612 (925)
 T ss dssp
                              C-----HHHHHHHHHHHHHHHHHHHHHHHHHTCCGGGHHHHTTCG--GGGTC-----
                              T ss_pred
 Q ss_pred
                              ССССНИНИНИНИНИНЕССИНИНИНИНИНИНИНИНИСС------СИНИНИНИНИН-НСССИНИН
 Q Fri_Mar_04_23: 512 PFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAH-----NIIESIANFS-RAGKYELV
                                                                                                                                             568 (744)
                         O Consensus
                                                                                                                                            568 (744)
                         T Consensus
                                                                                                                                             688 (925)
                         613 T-EFEQRHHCLELAKEADLD-VATITKTVVENIRKKDNGEFSHHDLAPALDTGTTEEDRLKIDVIDWLVFDPAQRAEA
 T 5a9q 4
                                                                                                                                             688 (925)
                                                                          -----CHHHHHHHHHHHHSGGGHHHH
 T ss_dssp
                              T ss pred
 Q ss_pred
                              нниннинннин
                         569 KSYSWLLFEASCMEGQ
 Q Fri Mar 04 23:
                                                      584 (744)
                         569 ~~i~~~l~~~sl~~g~
 O Consensus
                                                      584 (744)
                             =..++.|+...+..|+
                         689 1~~~n~L~R~FL~~qk 704 (925)
 T Consensus
                         689 LKQGNAIMRKFLASKK
 T 5a9g 4
                                                      704 (925)
                              нининининиттс
 T ss dssp
                              нинининининесс
 T ss pred
 No 12
                                                                             Pub Med
>2pm7_A Protein WEB1, protein transport protein SEC31; beta propeller, alpha solenoid; 2.35A {Saccharomyces
 cerevisiae} PDB: 2pm6 _A 3mzl _B
 Probab=95.35 E-value=2.1 Score=47.66 Aligned_cols=212 Identities=9% Similarity=0.069 Sum_probs=0.0
                              синнининнинеснининниннессининниннинниннин
 Q ss pred
 Q Fri_Mar_04_23: 242 TQYFWKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQY-P-KDSSSTFREWKNLVLKLSQAFGS
                         O Consensus
                                                                                                                                            319 (744)
                              ++..=..|.++++.|+++.|+++-=..+.|.+
                                                                                             .-+|.++ - .
                                                                                                                   +. |+.-+.++....
                         143 ~~~~~i~~Ll~G~~~Av~~al~~~~a~~~~~ALlLA~~qd~~~~~l~~v~~y~~~~
 T Consensus
                                                                                                                                             201 (399)
 T 2pm7_A
                         143 SGNIEQTISKNLVSGNIKSAVKNSLENDLMME-----AMVIALDSNNE-----RLKESVKNAYFAKYGS
                                                                                                                                             201 (399)
                               T ss dssp
                               СНИНИНИНИННЕСССИНИНИНИНИНСССИИ
 T ss pred
                              cccCcHhHHHHHHHHHCCCHHHHHHHhh--hHHHHHHHhheeCCC---chhHHHHHHHHHCCCCCCCHHHHHH
 Q ss pred
 Q Fri Mar 04 23:
                         320 SATDISGELRDYIEDFLLVIGGNORKILQYSR--TWYESFCGFLLYYIPS---LELSAEYLOMSLEANVVDITNDWEQPC
                                                                                                                                             394 (744)
                                                                                                                                             394 (744)
                         Q Consensus
                         .. +.++.++.|+.|+-..+. +|.|.+...+-|..+. ....+-..+...+....+
202 ~-----1-11-v-----v---1--Wre-la-iltn-------1--LGdrL---g------aA--
202 KS------SLSRILYSISKREVDDLVENLDVSQWKFISKAIQNLYPNDIAQRNEMMIKLGDRMKENG----HRQDSLT
 T Consensus
                                                                                                                                             269 (399)
 T 2pm7 A
                                                                                                                                             269 (399)
                              SC------НИНИНИННТТССИНИНИНВСЭББИНИНИНИНИНИНИНИНИНИНИНИНИНИНИТТ----СИНИНИН
 T ss dssp
 T ss_pred
                               СС------hнинининесСинининесСининининининининининининининин
                              Q ss_pred
                         395 VDIISGKIHSILPVMES-L-----DSCTAAF---TAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRN
 O Fri Mar 04 23:
                                                                                                                                            459 (744)
 Q Consensus
                         459 (744)
                         T Consensus
                         270 LYLAAGSLDKVASIWLSEFPDLEDKLKKDNKTIYEAHSECMTEFIERFTVFSNFINGSSTIN-----NE
 T 2pm7_A
                                                                                                                                             333 (399)
                              T ss_dssp
                              T ss pred
                              снининининнининнин
 Q ss pred
 Q Fri Mar 04 23: 460 GMASYMLNSFAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPHY 511 (744)
```

```
Q Consensus
             460 ~lre~~Ll~YA~~l~l~~~~~LW~vai~YL~~c~~~g~~~~r~~i~elL~r~ 511 (744)
             .+-. +.++||.|| +.+...|..|+...+... .-+..++..|+
334 ~l~-~-l~yA~-LA--~-G~~~A~~Yl~i~~~~----l~Rl 376 (399)
T Consensus
             334 QLIA-KFLEFINLTT---STGNFELATEFLNSLPSDN----EEVKTEKARV 376 (399)
T 2pm7 A
                ННН-ННИНИНН---ТТТСНИННИНННЯSCTTC----ННИНИНН
T ss dssp
                ННН-ННИНННН---hCCCHHHHHHHHHHhhcCCCC-----ННИННННН
T ss pred
                         PDB"
                               Pub Med
No 13
Siko_C Nucleoporin NUP84; NPC, transport, WD repeat, autocatalytic cleavage, mRNA transport, nuclear pore
complex, nucleus, phosphoprotein; 3.20A {Saccharomyces cerevisiae} PDB: 4xmm F 4xmn F 3jro C Probab=95.17 E-value=0.12 Score=58.66 Aligned_cols=191 Identities=16% Similarity=0.169 Sum_probs=0.0
                Q ss_pred
Q Fri_Mar_04_23: 245 FWKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYPKDSSS------TFREWK 307 (744)
             O Consensus
T Consensus
T 3iko C
             180 FFKYIYELILAGAIDEALEEAKLSD-----NISI-----CMILCGIQEYLNPVIDTQIANEFNTQQGIKKHSLWR
                                                                         244 (460)
T ss dssp
                HHHHHHHHHTTCHHHHHHHHTT-----CHHH-----HHHHHTTSBCBCTTTSGGGTTTCSSCBSBTTHHHHH
                НИНИНИНИНСССИНИНИНИНИНСС------Chhi------HHHHeCeccccCcccccccccccccccchhi
T ss_pred
                нининининининининининининининин
Q ss pred
Q Fri_Mar_04_23: 308 NLVLKLSQAFGSSATDISGELRDYIEDFLLVIGGNQ-RKILQYSRTWYESFCGFL-----LY
                                                                         363 (744)
             363 (744)
Q Consensus
                  |.++.. +...+.+ =+-+|+||+||+...+.+|.+|-+.=+++
---la------d-y-----erAvY-L-g---s-l-v--swED-LW-l------d-l-----e---1 315 (460)
T Consensus
             245 ~~
             245 RTVYSLSQ---QAGLDPY-----ERAIYSYLSGAIPNQEVLQYSDWESDLHIHLNQILQTEIENYLLENNQVGTDELIL
T 3iko C
                                                                         315 (460)
T ss dssp
                НИНИНИН---CSSSCHH-----НИНИНИНИТSCCCHHHHTTCCHHHHHHHHHHHHHHHHHHHHHTTCSCGGGCCS
T ss_pred
                НИНИНИН---CCCcCHH------НИНИНИНННССеhhhheeecCCHHHHHHHHHHHHHHHHHHHHCCCCCeeecC
Q ss_pred
                Q Fri_Mar_04_23: 364 YIP-SLELSAEYLQMSLEANVVDITNDWEQPCVDIISGKIHSILP----VMESLD-------SCTAAFTAMI
                                                                         423 (744)
             Q Consensus
                                                                         423 (744)
T Consensus
                                                                         395 (460)
T 3iko C
T ss_dssp
                T ss pred
                Q ss_pred
                HHhcCccccccccccccccchhhhccccchнннннннннhhhccCCccchнн
Q Fri_Mar_04_23: 424 CEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNSFAFELCSLGDKELWPV 484 (744)
             O Consensus
                             ....+-+|..|...|...+...|-++
                |...|++..
             396 L---g-----il--Yi--L-----LI--
T Consensus
             396 LDIINPGSV-----EEVDKSKLITTYISLLKLQGLYENIPI 431 (460)
T 3iko C
T ss_dssp
                ннньссссс-----сьининининининин
T ss_pred
                        PDB NCBI Pub Med
No 14
->4bzj_A Protein transport protein SEC31; secretion, trafficking; 40.00A (Saccharomyces cerevisiae) PDB: 4bzk_A
Probab=95.15 E-value=0.75 Score=58.65 Aligned cols=205 Identities=8% Similarity=0.082 Sum probs=0.0
                Q ss pred
Q Fri_Mar_04_23: 247 KLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYP-KDSSSTFREWKNLVLKLSQAFGSSATDIS 325 (744)
             247 ~-V~-lvLrG~~~A~-lL~~~~~~l~~~~~v~~~~LL~~P~~~~w~Wk~~~~l~~~~~~~325 (744) +++++|+|.++|++..++
O Consensus
             T Consensus
                                                                         567 (1273)
T 4bzj_A
             512 QTISKNLVSGNIKSAVKNSLEND------LLMEAMVIALDSNNE-----RLKESVKNAYFA--KYGSKS-
                HHHHHHHHTTCHHHHHHHHTTT-----CHHHHHHHHTTCCCT-----THHHHTHHHHT---TTTTTC-
T ss dssp
                T ss pred
Q ss pred
                нынниннинннынсссининнин--hhниннинныныныессс--с--hhниннинннынсссссссининнинн
Q Fri_Mar_04_23:
             326 GELRDYIEDFLLVIGGNQRKILQYS--RTWYESFCGFLLYYIPS--L--ELSAEYLQMSLEANVVDITNDWEQPCVDIIS
                                                                         399 (744)
             399 (744)
T Consensus
                                                                         638 (1273)
T 4bzi A
                                                                         638 (1273)
T ss dssp
              ----нинининттсснининвсдддинининнысттснинининининттт----снининини
T ss_pred
                ----hнинининнноссинининоссининининнныннининининининининини
                Q ss_pred
O Fri Mar 04 23: 400 GKIHSILPVMES-L-----DSCTAAF---TAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASY
                                                                         464 (744)
O Consensus
             400 gd---vL--1---1----d-w-aAH---ladL1---g-L-------d-u-a-dl------lre-
                                                                         464 (744)
                T Consensus
             639
                                                                ____~~1~~~
                                                                         702 (1273)
             639 GSLDKVASIWLSEFPDLEDKLKKDNKTIYEAHSECLTEFIERFTVFSNFINGSSTIN-----NEQLIAK
T 4bzj A
                                                                         702 (1273)
T ss dssp
                T ss_pred
Q ss pred
                нинининриросссссининининроссссини--инин
Q Fri Mar 04 23: 465 MLNSFAFELCSLGDKELWPVAIGLIALSATGTRSA--KKMVI 504 (744)
```

```
Q Consensus
             465 ~Ll~YA~~l~l~~~~~LW~vai~YL~~c~~~g~~~-~r~~i 504 (744)
             740 (1273)
T Consensus
             703 F-LEFINLTT---STGNFELATEFLNSLPSDNEEVKTEKARV
T 4bzi A
                                              740 (1273)
                Н-ННИННН---ТТТСНИНННННННКСТТСИННННННН
T ss dssp
                Н-ННИНИН--- hCCCHHHHHHHHHHHCCCccHHHHHHHHH
T ss pred
                        PDB'
No 15
                                             Pub Med
>3mzk B Protein transport protein SEC16; alpha-helical-stack, beta-propeller; 2.69A (Saccharomyces cerevisiae)
Probab=90.81 E-value=5.8 Score=44.66 Aligned_cols=196 Identities=12% Similarity=0.062 Sum_probs=0.0
                нинининнессинининин
Q ss pred
Q Fri_Mar_04_23: 247 KLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYPKDSSSTFREWKNLVLKLSQAFGSSATDISG
                                                                        326 (744)
             247 ~~V~~lvLrG~~~A~~lL~~~~~l~~~~v~~~LL~~P~~~w~~Wk~~~~l~~~~~w~~
               +.|.++++.|+++.|+++==..+.|.+
                                            .=+|.++=.
                                                    =+. |+.-+.++...-
             155 ~-i~~Ll~G~~~Av~~al~~~lwa~------ALlLA~~~g-----e~~~v~~~y~~~~~~~
T Consensus
                                                                        214 (441)
             155 MRVLAFLOTGNHDEALRLALSKRDYAI------ALLVGSLMG----KDRWSEVIOKYLYEGFTAGPNDOK
T 3mzk B
                                                                        214 (441)
                T ss dssp
T ss_pred
                Q ss_pred
Q Fri Mar 04 23: 327 ELRDYIEDFLLVIGGNQRKILQYS-----R-TWYESFCGFLLYYIPSLEL----SAEYLQMSLEANVVD
                                                                        385 (744)
             Q Consensus
                                                                        385 (744)
             T Consensus
                                                                        292 (441)
T 3mzk B
             215 ELAHFLLLIFOVFVGNSKMAIKSFYTNNETSOWASENWKSIVAAVLINIPENNEDPLLIPPVVLEFLIEFGIFLTKKG--
                                                                        292 (441)
                T ss dssp
T ss pred
                Q ss_pred
                Q Fri Mar 04 23:
             386 ITNDWEOPCVDIISGK---IHSILPV-----MESLDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLF
                                                                        455 (744)
                ----E----i-egd-----vL-----ld-w-aAHladLl---g-L-----
Q Consensus
                                                                        455 (744)
               ...+...|+.|+ ...+... +.+-...++++++....++....
-----aA-iCYL-a--pl--------lgs------ltEi-E----l------
T Consensus
T 3mzk B
             293 --LTAAASTLFIIGNVPLSNEPVMADSDVIFESIGNMNTFESILWDEIYEYIFSYDPKFKG------
T ss_dssp
                T ss_pred
                ссссснинининннын
Q ss_pred
Q Fri_Mar_04_23: 456 SYRNGMASYMLNSFAFELCSLGDKELWPVAIGLIAL 491 (744)
O Consensus
             456 ~~~~lre~~Ll~YA~~l~l~~~~LW~vai~YL~~
                                          491 (744)
             ...+-.|.+ +||..|| +.+.-.|..|+..
352 ---~1~~kl-~yA~~LA---e~G~~~A~~Y~~~
T Consensus
                                         381 (441)
             352 --FSSILPQKI-YHASLLQ---EQGLNSLGTKYTDY 381 (441)
T 3mzk B
                --CGGGНННН-НННННН---НТТСНННННННН
T ss dssp
T ss_pred
                --СИНИНИНИ-НИНИНИН---ЪСССИНИНИНИНИ
                                             Pub Med
No 16
->4bzj_A Protein transport protein SEC31; secretion, trafficking; 40.00A (Saccharomyces cerevisiae) PDB: 4bzk_A
Probab=85.75 E-value=29 Score=44.24 Aligned_cols=201 Identities=13% Similarity=0.147 Sum_probs=0.0
                нининнесссинининнессьининнинненнинн
Q ss pred
             \textbf{391} \ \ \textbf{EQPCVDIISGKIH} \textbf{SILPVMESLDSCTAAFTAMICEAK} \textbf{GLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNSFA}
Q Fri_Mar_04_23:
                                                                        470 (744)
O Consensus
             +.+...+.||+.+++..|-+ |+..+|
512 ~-i---l--G--e-Av--cl------Al---lA---g-------y-
                                                                        560 (1273)
T Consensus
             512 QTISKNLVSGNIKSAVKNSLENDLLMEAMV-IALDSN------NERLKESVKNAYF
T 4bzi A
                                                                        560 (1273)
                T ss dssp
                T ss pred
                Q ss pred
Q Fri Mar 04 23:
             471 FELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDDIEWMLSICVEWRLPE--IAKEIYTTLGNQMLS
                                                                        548 (744)
             471 --l-l-----LW-vai-YL--c---g----r--i-elL-r-pl-t----ek-L-iC-----L----a--I-----g---l-
                                                                        548 (744)
             ...+.++++.++...+=...++...+-...|.+-..-.|.+-..+-...|.+|.|++.
561 ~~--~~p~rl-l~i~--~d~~---dv~~----l~wke-l~~-t~~~~-l~~lq-rl~
T Consensus
                                                                        624 (1273)
             561 AK--YGSKSSLSRI-LYSIS--KREVD----DLVEN------LDVSQWKFISKAIQNLYPNDIAQRNEMLIKLGDRLKE
T 4bzj A
                                                                        624 (1273)
T ss dssp
                ТТ--ТТТСНИНН-HHHH--ТТССН----НИНН--------BCGGGHHHHHHHHHHHHHHHHHHHHHH
T ss pred
                НЬ--сссССЬНИН--НИНИ--ЬССИ----НИНЬс-----ССИНИНИНИНИНННЫН В СССИНИНИНИНИНИНИНИНИ
Q ss_pred
                Q Fri Mar 04 23: 549 AHNIIESIANFSRAGKYELVKSYSWLLFEASC----MEGQKLD--DPVLNAIVSKNSPAEDDVIIPQDILDCVVTNSMR
                                                                        621 (744)
             549 -g--g-AL----rA-d---V--i---l---sl-----g-----D--L--iv--------p---le------l-
                                                                        621 (744)
O Consensus
             693 (1273)
T Consensus
T 4bzj A
             625 NGHRODSLTLYLAAGSLDKVASIWLSEFPDLEDKLKKDNKTIYEAHSECLTEFIER-----FTVFSNFINGSST
                                                                        693 (1273)
T ss_dssp
                T ss pred
                Q ss pred
                ннин-нининнинн
Q Fri Mar 04 23: 622 QTLAP-YAVLSQFYELRDR-EDWGQALRLL 649 (744)
O Consensus
             622 ~~Ls~-ya~lreF~~~~-q~~~Aa~~L 649 (744)
```

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T Consensus
                      694 INNEQLIAKFLEFINLTTSTGNFELATEFL 723 (1273)
 T 4bzi A
                          СССИНИНИНИНИНИНИТТТСИНИНИНИ
 T ss dssp
 T ss_pred
                          ССНИНИНИНИНИНИНИНИСССИНИНИНИН
                                        PDB"
                                                    NCBI
                                                                 Pub Med
 No 17
>2pm7_A Protein WEB1, protein transport protein SEC31; beta propeller, alpha solenoid; 2.35A {Saccharomyces
                           _A 3mz1 _B
 cerevisiae} PDB: 2pm6
 Probab=70.32 E-value=61 Score=35.88 Aligned_cols=139 Identities=15% Similarity=0.108 Sum_probs=0.0
                          ССНИНИНИННЕССИНИННИНННЕССИНИННИНННИНННЕССИССЕССИССЕССИНННЕНН
 Q ss pred
 Q Fri_Mar_04_23: 387 TNDWEQPCVDIISGKIHSILPVMESLDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYML
                                                                                                                       466 (744)
                      387 ----E----i-egd---vL--l--ld-w-aAHladLl---g-L-----
                     T Consensus
                                                                                                                       192 (399)
                      144 GNIEOTISKNLVSGNIKSAVKNSLENDLM--MEAMVIALDSN------NERLKESVK
 T 2pm7 A
                                                                                                                       192 (399)
                          T ss dssp
 T ss_pred
                          ННИНИНИННИНСССИНИНИНИННИНСССИ---------
                          нининрриссСсссинининин и Ссссинининин и Ссссинининин и Ссссининин и Сссининини и Сссинини и Сссинини и Сссини и
 Q ss pred
 Q Fri Mar 04 23: 467 NSFAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDDIEWMLSICVEWRLPE-IAKEIYTTLGNQ
                                                                                                                       545 (744)
                     Q Consensus
                                                                                                                       545 (744)
                                                                                                                      257 (399)
 T Consensus
                      193 NAYFAK--YGSKSSLSRILYSISK------REVDDLVENLDVSQWKFISK--AIQNLYPNDIAQRNEMMIKLGDR
 T 2pm7_A
                                                                                                                       257 (399)
                          HHHHHH--HTTSCHHHHHHHHHT-----TCCHHHHHHBBCGGGHHHHHH-HHHHHHHHHHHHHHHHH
 T ss dssp
 T ss pred
                          Q ss_pred
                          нинсссининининисссининин
 Q Fri_Mar_04_23: 546 MLSAHNIIESIANFSRAGKYELVKSY 571 (744)
                      546 ~l~~g~~g~AL~~~rA~d~~~V~~i 571 (744)
 Q Consensus
                         +..+|+.-.|..+|.-||+..++-.+
                      258 L---g---aA--CYL-a----k-v-i 283 (399)
 T Consensus
 T 2pm7 A
                      258 MKENGHRQDSLTLYLAAGSLDKVASI
                                                         283 (399)
 T ss_dssp
                          ниттсининининитсинини
 T ss_pred
                          HHhCCChhhhhHhHhhcCChHHHHHH
                                                    S NCBI
                                                                          Pub Med
                                                                 >4lct_A COP9 signalosome complex subunit 1; signaling protein; 2.70A {Arabidopsis thaliana}
 Probab=65.39 E-value=1.7e+02 Score=31.37 Aligned_cols=205 Identities=15% Similarity=0.146 Sum_probs=0.0
 Q ss_pred
                          Q Fri_Mar_04_23: 517 DDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRAGKY----ELVKSYSWLLFEASCMEGQKLDDPVLN 592 (744)
                     O Consensus
                                                                                                                       592 (744)
                                                                                                                       165 (348)
 T Consensus
                      89 VKLENELSSYRTNLIKESIRMGYNDFGDFYYACGMLGDAFKNYIRTRDYCTTTKHIIHMCMNAILVSIEMG---QFTHVT
 T 4lct_A
                                                                                                                       165 (348)
                          T ss_dssp
                          T ss pred
                          Q ss pred
 Q Fri_Mar_04_23: 593 AIVSKNSPAEDDVIIPQDILDCVVTNSMRQTLAPYAVLSQFYELRDREDWGQALRLLLLL---IEF----PYLPKHYLVL
                                                                                                                       665 (744)
 O Consensus
                     ..+.+ ...+++++..+--+.-+... .+++|..|+++..- +++ -..|+++..-

166 ~-1~k------a~~1~~-~a~~1~~-~q~~x-a~~f~a~~f~a~~f~a~~e~s~~-~y
                                                                                                                       230 (348)
 T Consensus
 T 4lct_A
                     166 SYVNK------AEQNPET-LEPMVNAKLRCASGLAHL---ELKKYKLAARKFLDVNPELGNSYNEVIAPQDIATY
                                                                                                                       230 (348)
                          HHHHH-----HTTCSSC-CCHHHHHHHHHHHHHHHHH----HTTCHHHHHHHHTCCGGGTTTTTTCCHHHHHHH
 T ss dssp
                          T ss_pred
                          Q ss_pred
 Q Fri Mar 04 23:
                      666 LVAKFLYPIFLL--D-DKKLMDEDSVATVIEVIETKWDDAD-----EKSSNLYETI---IEADKSLPSSMATLLKN
                                                                                                                       730 (744)
                      Q Consensus
                                                                                                                       730 (744)
                     T Consensus
                                                                                                                       306 (348)
                          GGLCALA--SFDRSELKOKVIDNINFRNFLELVPDV--RELINDFYSSRYASCLEYLASLKSNLLLDIHLHDHVDTLYDQ
 T 41ct A
                                                                                                                       306 (348)
 T ss dssp
                          НИНИНИ--HCCHHHCCCCCSCHHHHHHHHHTCHHH--НИНИННННТТСНИНННННННННННТСТТТGGGHHHHHH
 T ss pred
                          НИНИНИН--cCCHHHHHHHhcCCHHHHHhccCChHH--нинининисССНННННННННННННННННННН
 Q ss_pred
                          нининининин
 Q Fri Mar 04 23: 731 LRKKLNFKLCQAF 743 (744)
                     731 lR~~la~~l~~~~
 O Consensus
                                          743 (744)
                          + | . + . = . ++++ . |
 T Consensus
                      307 ir~~~l~q~~~py 319 (348)
 T 4lct_A
                     307 IRKKALIOYTLPF
                                          319 (348)
 T ss_dssp
                          нининининсс-
 T ss pred
                          ННННННННСССС
                                                    NCBI
                                                                 Pub Med
>4ady A RPN2, 26S proteasome regulatory subunit RPN2; protein binding, PC repeat; 2.70A {Saccharomyces
```

```
cerevisiae} PDB: 4cr2 _N 4cr3 _N 4cr4 _N 5a5b _N*
  Probab=60.32 E-value=1.6e+02 Score=36.53 Aligned cols=226 Identities=13% Similarity=0.142 Sum probs=0.0
                                       Q ss pred
  Q Fri_Mar_04_23: 485 AIGLIALSATGTRSAKKMVIAELLPHYPF---VTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSR
                                                                                                                                                                                   561 (744)
                                Q Consensus
                                                                                                                                                                                   561 (744)
  T Consensus
                                                                                                                                                                                     95 (963)
                                  17 AAPLLALLRENQDSVKTYALESINNVVDQLWSEISNELPDIEALYDDDTFS-DREMAALIASKVYYNLGEYESAVKYALA
  T 4ady A
                                                                                                                                                                                     95 (963)
                                       SHEHHHTTSSCHEHHHHHHHHHHHHHHHHHHHTTHHHHHHHSCTTCT-ТНИННННННННН
  T ss_dssp
  T ss_pred
                                       сССНИНН----нининининнесССССИНИНИННН
  Q ss pred
  Q Fri Mar 04 23: 562 AGKYELVK---SYSWLLFEASCMEGQKLDDPVLNAIVSKNSP----AED----DVIIPQDILDCVVTNSMRQTLAP----
                                                                                                                                                                                   626 (744)
  O Consensus
                                 562 A-d---V----i---l---sl--g----L--iv----------p---le------l----ls-----
                                                                                                                                                                                   626 (744)
                                  T Consensus
                                                                                                                                          ---L--lv--iv----n-e-
                                                                                                                                                                                   162 (963)
                                  96 AKDRFDIDEKSQFVETIVSKS-----IEMYVQEASKQYTKDEQFYTKDIIDPK-LTSIFERMIEKCLKASELK 162 (963)
  T 4ady_A
                                       T ss_dssp
  T ss pred
                                       Q ss_pred
                                       Q Fri_Mar_04_23: 627 ------YAVLSQFYELRD-RED---WGQALRLLLLLIEFFYLPKHYLVLLVAKFLYPIFLLDDKKLMDEDSVATV
                                                                                                                                                                                   691 (744)
                                 Q Consensus
                                 ++.+.+.+... +.+....+.-...-|+.|...|+..+.+ ++ ...

163 -AvglalE--rLD-1---v-------rv--Yl1------------r--iL--1----iy-----
  T Consensus
                                                                                                                                                                                   236 (963)
                                 163 LALGIALEGYRLDIIESALKSKLDQDSTSENVKIINYLLTLAITTVTNSKFRSSILRKSFD--FL---MNMPNCDYLTL 236 (963)
  T 4ady_A
  T ss dssp
                                       T ss_pred
                                       ннининниннинниннинн
  Q ss_pred
  Q Fri_Mar_04_23:
                                692 IEVIETKWDDADEKSSNLYETIIEADKSLPSSMATLLKNLRKKLNFKLCOA 742 (744)
  O Consensus
                                 692 L--Lee----y---lp------lR--la--l---
                                                                                                                                 742 (744)
                                T Consensus
                                                                                                                                 275 (963)
                                237 NKVVVNL--NDAGLALQLFKKLKEEND-----EGLSAQIAFDLVSS 275 (963)
  T 4ady A
                                       T ss_dssp
  T ss_pred
                                                          PDB<sup>N</sup>
PROTEIN DATA BANK

NCBI
  No 20
                                                                                                  Pub Med
>4d10_D COP9 signalosome complex subunit 4; signaling protein; 3.80A {Homo sapiens} PDB: 4d18_D
  Probab=59.77 E-value=2.3e+02 Score=31.02 Aligned cols=156 Identities=8% Similarity=0.038 Sum probs=0.0
                                       Q ss_pred
  Q Fri_Mar_04_23: 500 KKMVIAELLPHYPFVTNDDIEWMLSICVE-----WRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRAG------KY 565 (744)
                                500 ~r~i~elL~r~pl~t~~~ek~L~iC~~~~~~~L~~~a~~I~~~~g~~~l~~g~~q~AL~~~rA~~~~~d~~+|.+|.++..++...+|...+..+|...+.|.+..+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+.
  O Consensus
                                                                                                                                                                                   565 (744)
  T Consensus
                                                                                                                                                                                   145 (410)
  T 4d10 D
                                  66 SRQLLTDFCTHLPNLPDSTAKEIYHFTLEKIQPRVISFEEQVASIRQHLASIYEKEEDWRNAAQVLVGIPLETGQKQYNV
                                                                                                                                                                                   145 (410)
                                       НИНИНИНИНИ GGGSCHИНИНИНИНИНИН GGGGGGGHИНИНИНИНИНИТТСИНИНИНИН TSCTTTSSSCCCH
  T ss_dssp
                                       нининининненнисссенинининниннин
  T ss_pred
                                       нининининининининининин
  Q ss pred
  Q Fri_Mar_04_23: 566 ELVKSYSWLLFEASCMEGQKLDDPVLNAIVSKNSPAEDDVIIPQDILDCVVTNSMRQTLAPYAVLSQFYELRDREDWGQA 645 (744)
                                566 \hspace{0.1cm} \text{--V--i---l---sl---g-----L--iv--------p---le------l---Ls-ya-lreF------g-----A}
                                                                                                             .....++...++..+ .....|.....|.. +++|.+|
                                       ...-.+...+ +=....+++
                                 146 \, \, \cdots \, 1 - \cdots \, 1 - \cdots \, 1 - 1 - \cdots - - - d - \cdots \, a - \cdots \, 1 - \cdots - - - - - k - \cdots - - - - \cdots \, y - \cdots - - - - - y - \cdots \, 2 - \cdots \, - \cdots 
  T Consensus
                                                                                                                                                                                   208 (410)
                                 146 DYKLETYLKIARLYLEDD---DPVQAEAYIN------RASLLQNESTNEQL--QIHYKVCYARVLDY--RRKFIEA
  T 4d10 D
                                                                                                                                                                                   208 (410)
  T ss_dssp
                                       T ss pred
                                       ннининнессссьныминининным
  Q ss pred
  Q Fri Mar 04 23: 646 LRLLLLLEFPYLPKHYLVLLVAKFLY 672 (744)
                                 646 a~~Lv~Ll~s~~~Pk~f~~~LL~dalp 672 (744)
  Q Consensus
                                ++.+..++..+...+...+...+..+++
209 -----a-----l--lv-
                                                                                        235 (410)
  T Consensus
                                 209 AQRYNELSYKTIVHESERLEALKHALH 235 (410)
  T 4d10 D
                                       нининнттсттѕсининининини
  T ss dssp
                                       ннининнесссссьнининининин
  T ss pred
  No 21
                                                                                                                Pub Med
□ >5cqr_A Elongator complex protein 1; familial dysautonomia, ELP1 subunit, DIME protein binding; 3.02A {Homo
  sapiens }
  Probab=58.59 E-value=1.2e+02 Score=35.61 Aligned cols=145 Identities=10% Similarity=0.091 Sum probs=0.0
  Q ss_pred
                                       нининнессинининныесьнининнынныесессссссссссссссссссьныесьный
  Q Fri_Mar_04_23: 392 QPCVDIISGKIHSILPVMESLDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNSFAF 471 (744)
                                Q Consensus
                                T 5cqr_A
  T ss dssp
```

```
T ss_pred
                  hhheeCCeechнининннhhCeechниннннннннннннннннннннннннннннннннн
0 ss pred
 Q Fri_Mar_04_23: 472 ELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDDIEWMLSICVEWR-LPEIAKEIYTTLGNQMLSAH
                                                                                   550 (744)
               Q Consensus
                                                                                   550 (744)
               T Consensus
                                                                                   350 (622)
               285 HLM---QEHMYEPAGLMFARCGAHE-----KALSAFLTC-----GNWKQALCVAAQLNFTKDQLVGLGRTLAGKLVEQR
T 5cgr A
                                                                                   350 (622)
                  ННН---ТТТСИНИНИНИНТТСИН-----НИНИНИНТ-----ТСИНИНИНИНТТССИНИНИНИНИНИНИНИТТТ
T ss_dssp
                  T ss_pred
                  СИНИНИНИННЫ—сССИНИН
Q ss pred
Q Fri Mar 04 23: 551 NIIESIANFSR-AGKYELV 568 (744)
O Consensus
               551 ~~g~AL~~~r-A~d~~~V 568 (744)
               +|.+|...|.+ +|++...
351 ~~eA~~~~1~d~~A 369 (622)
T Consensus
               351 KHIDAAMVLEECAQDYEEA 369 (622)
T 5cqr_A
                  СНИННИННИН
T ss_dssp
T ss_pred
                  СНИНИНИНИНИСССИИНИ
                            PDB"
No 22
□ >5cqr_A Elongator complex protein 1; familial dysautonomia, ELP1 subunit, DIME protein binding; 3.02A {Homo
 sapiens}
 Probab=55.77 E-value=1.1e+02 Score=35.89 Aligned cols=140 Identities=16% Similarity=0.169 Sum probs=0.0
                  hнинининhccccchининининныесссссенинининныесссинининининининининининининин
Q ss pred
Q Fri Mar 04 23: 482 WPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSR
                                                                                   561 (744)
O Consensus
               482 W-vai-YL--c---g----r-i-elL-r-pl-t----ek-L-iC----L---a--I----g---l---g--AL----r
                                                                                   561 (744)
                  T Consensus
               233 -eeAl--y---g-----Ai-l--------g-y--ALeLa------i----A--L---g---eAa--Y-k
                                                                                   301 (622)
               233 YEKAIGHLSKCGPEYFPECLNLIKD-----KNLYNEALKLYSP-SSQQYQDISIAYGEHLMQEHMYEPAGLMFAR
T 5cqr_A
                                                                                   301 (622)
                  T ss_dssp
T ss pred
                  Q ss_pred
                  Q Fri_Mar_04_23: 562 AGKYELVKSYSWLLFEASCMEGQKLD-DPVLNAIVSKNSPAEDDVIIPQDILDCVVTNSMRQTLAPYAVLSQFYELRDR-
                                                                                   639 (744)
Q Consensus
               562 A-d---V--i---l---sl--q-----D--L--iv----------p---le------l---Ls-ya-lreF-----
                                                                                   639 (744)
                  +|+..+. ++-|...| . ++.+.-.-+. +|+++-+ +...+...|..-+.+.++.+
               302 ag~~~kA----ie~y~~a
                                   ----w~~A~~la~~l~~----
                                                        ----g---eA----
T Consensus
                                                                                   362 (622)
T 5cqr_A
               302 CGAHEKA-----LSAFLTCG--NWKOALCVAAOLNF-----TKDOLVG-LGRTLAGKLVEORKHIDAAMVLEEC
                                                                                   362 (622)
T ss dssp
                  ТТСИНИН------ИНИНИНТТ---СИНИНИНИНТТС-----СИНИНИН--ИНИНИНИНИНТТТСНИНИНИНИ
T ss_pred
                  сссинин------нининисс---сининининиссс------сьинини--ининининин
                  -Сснинниннин
Q ss_pred
Q Fri_Mar_04_23:
               640 -EDWGQALRLLLL 651 (744)
Q Consensus
               640 -q~~~Aa~~Lv~
                              651 (744)
                   |+...|+..++.
               363 l~d~~~AI~ll~~
                              375 (622)
T Consensus
               363 AQDYEEAVLLLLE 375 (622)
T 5cqr_A
                  SCCHHHHHHHHH
T ss_dssp
T ss_pred
                  сССНИНИНИНИН
No 23
                                     NCBI
                                                    Pub Med
□ >3mkq_B Coatomer subunit alpha; beta-propeller, alpha-solenoid, transport protein; 2.50A {Saccharomyces
cerevisiae}
Probab=53.31 E-value=20 Score=35.00 Aliqned cols=50 Identities=8% Similarity=0.058 Sum probs=0.0
                  ннининнинессинининнининнин
Q ss_pred
 Q Fri_Mar_04_23: 518 DIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRAGKYELVKSY
                                                              571 (744)
               518 ~~ek~L-iC~~~L~~~a~I~~~g~~l~~g~~g~AL~~~rA~d~~V~i
+.+..++|......+..+.+|..+++.|++..|-.|.++||..++..+
20 ~l~~A~~a~~~----W~La~~AL~~~l~iAe~~y~~~d~~l~L
O Consensus
                                                              571 (744)
T Consensus
                                                               69 (177)
T 3mkq_B
                20 NLDAALDEAKKL----NDSITWERLIQEALAQGNASLAEMIYQTQHSFDKLSFL
                                                               69 (177)
                  СНИНИНИНИН----ССИНИНИНИНИНИТТСИНИНИНИНИТТСИНИНИНИ
T ss_dssp
                  СНИНИНИННЕ----ССИНИНИНИНИННИНСССИНИНИНИННЕСССИНИНИН
T ss pred
No 24
                                              Pub Med
>2wpv_A GET4, UPF0363 protein YOR164C; golgi-ER trafficking, tail-anchored protein, protein binding GET4; 1.99A
{Saccharomyces cerevisiae} PDB: 5bwk _E 31ku _A 5bw8 _C 4pwx _E*
Probab=53.15 E-value=2.7e+02 Score=29.70 Aligned cols=161 Identities=12% Similarity=0.122 Sum probs=0.0
Q ss_pred
                  Q Fri_Mar_04_23: 389 DWEQPCVDIISGKIHSILPVMESLDSC-----TAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFS 456 (744)
 Q Consensus
               389 ~~E~~~~i~egd~~~vL~-l~~ld~w------aAHladLl~~~g~L~~~~~~~~~~dl~~ 456 (744)
                  .+..+-..|=+||+...+.+..++-.= +..+-|..+-+.||.-..
                16 ~l~rl~~i~~G~yYEAhQ~~RT~~~Ry~~~~~eAidlL~~gA~~ll~~~Q~~s-------
T Consensus
                                                                                    71 (312)
                16 TLQRFENKIKAGDYYEAHQTLRTIANRYVRSKSYEHAIELISQGALSFLKAKQGGS-----
T 2wpv_A
                                                                                    71 (312)
T ss dssp
                  T ss pred
```

```
Q ss pred
                         сссенининининнын
 Q Fri_Mar_04_23: 457 YRNGMASYMLNSFAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDD---IEWMLSICVEWR-LP
                                                                                                                 532 (744)
 O Consensus
                     457 ----lre--Ll-YA--l-l------LW-vai-YL--c---g----r--i-elL-r-pl-t-----ek-L-iC-----L-
                                                                                                                 532 (744)
                     +.+++...+.| -+
                     72 -GTDLIFYLLEVYDLA------EVKVDDISVARLVRLIAELDPSEPNLKDVITGMNNWSIKFSEYK
 T 2wpv A
                                                                                                                 130 (312)
                         T ss_dssp
                         T ss_pred
                         нининининининининисссининининин
 Q ss_pred
 Q Fri_Mar_04_23: 533 EIAKEIYTTLGNQMLSAHNIIESIANFSRAGKYELVKSYSWLLFEASCMEGQK--LD-DPVLNAIV 595 (744)
 O Consensus
                    533 ~~a~~I~~~g~~l~~g~AL~~~rA~d~~V~~i~~l~~sl~~g~~-~~L~~iv 595 (744)
                    T Consensus
                     131 FGDPYLHNTIGSKLLEGDFVYEAERYFML-GTHDSMIKYVDLLWDWLCQVDDIEDSTVAEFFSRLV
 T 2wpv_A
                         ТССИНИНИНИННИТТСИНИНИННИТ-SCHHHHHHHHHHHHHHHHHH
 T ss dssp
 T ss pred
                         СССИНИНИНИННЕСССИНИНИНИННЬ-сССссининининннинин
                                      PDB"
 No 25
                                                 NCBI
                                                                      Pub Med
>2n8i_A Designed protein DA05; de novo protein; NMR {Synthetic construct}
 Probab=50.92 E-value=42 Score=27.03 Aligned_cols=46 Identities=20% Similarity=0.167 Sum_probs=0.0
                         ннинининнессинининнининнинин
 Q ss pred
 Q Fri_Mar_04_23: 517 DDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRA
                    517 ---ek-L-iC----L---a--I----g---l--g--g-AL----rA
                      +-..+.+++.+.+-...-.++..+|.-...|++..+|+..+|+..+|
9 ----al------a
 T Consensus
                                                                              54 (100)
                      9 AKFEKAYKKAEELNQGELMGRALYNIGLEKNKMGKVKEAIEYFLRA
 T 2n8i_A
                                                                              54 (100)
 T ss dssp
                         нининининиттеннининининининитеннининин
 T ss pred
                         ннинининнессенининининининин
                                      PDB"
PROTEIN DATA BANK
 No 26
                                                  NCBI
                                                              Pub Med
>5cqs_A Elongator complex protein 1; familial dysautonomia, ELP1 subunit, DIME protein binding; 2.70A
 {Saccharomyces cerevisiae}
 Probab=50.90 E-value=59
                            Score=36.36 Aligned cols=108 Identities=11% Similarity=0.100 Sum probs=0.0
                         нинининессинининининининин
 Q ss pred
 Q Fri_Mar_04_23: 520 EWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRAGKYELVKSYSWLLFEASCMEGQKLD-DPVLNAIVSKN
                                                                                                                 598 (744)
                    598 (744)
                                                                                                                 160 (435)
 T Consensus
 T 5cqs_A
                                                                                                                 160 (435)
                         НИНИННЕССС -- СИНИНИНИНИНИНИНТТТТСИНИНИНИНТТСИНИНИНИ.-----НИНТТСИНИНИНИНИНТ----
 T ss dssp
 T ss_pred
                         сссссссСhннннhhheсннннннннннннннннн---Сснннннннн
 Q ss pred
 Q Fri Mar 04 23:
                     599 SPAEDDVIIPQDILDCVVTNSMRQTLAPYAVLSQFYELRDR--EDWGQALRLLL
                                                                                     650 (744)
                                ---p---le-----ls-ya-lreF-----g---Aa--Lv
                                                                                     650 (744)
                     +|.++-. +...+...|-+...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|++...|+
 T Consensus
                                                                                     204 (435)
                     161 -----FPEEVES--VAEELISSLTFEHRYVDAADIQLEYLDNVKEAVALYC
 T 5cqs_A
                                                                                     204 (435)
                         -----СТТТНН--ННИННИННТТСНИННИННИННИНССИННИННИН
 T ss_dssp
                         -----Сhнини--ининининининининининининин
 T ss_pred
 No 27
                                                              S
                                                                      Pub Med
>4dOp_A COP9 signalosome complex subunit 4; signaling protein, PCI; HET: EDO; 1.60A {Homo sapiens}
 Probab=47.52 E-value=3.5e+02 Score=29.40 Aligned_cols=155 Identities=7% Similarity=0.046 Sum probs=0.0
 Q ss_pred
                         нининининосссссинининининини
 Q Fri Mar 04 23: 500 KKMVIAELLPHYPFVTNDDIEWMLSICVE-----WRLPEIAKEIYTTLGNQMLSAHNIIESIANFS------RAGKY
                                                                                                                 565 (744)
                     565 (744)
 Q Consensus
                     T Consensus
                                                                                                                  165 (387)
                      86 SRQLLTDFCTHLPNLPDSTAKEIYHFTLEKIQPRVISFEEQVASIRQHLASIYEKEEDWRNAAQVLVGIPLETGQKQYNV
 T 4d0p_A
                                                                                                                 165 (387)
 T ss_dssp
                         T ss_pred
                         Q ss pred
 Q Fri Mar 04 23: 566 ELVKSYSWLLFEASCMEGQKLD-DPVLNAIVSKNSPAEDDVIIPQDILDCVVTNSMRQTLAPYAVLSQFYELRDREDWGQ
                                                                                                                 644 (744)
                     566 ~-V~-i~~l~-~sl~-g~-~-D~-L~-iv~-~-~-p~~le~-~~-l~-~Ls-ya~lreF~-~-~g~-~-
 O Consensus
                                                                                                                 644 (744)
                        166 ~~~l~i~l~~irl~l~~~d~~~a~~~l~k~~~~~
 T Consensus
                                                                                                                 227 (387)
                     166 DYKLETYLKIARLYLEDDDPVQAEAYINRASLL-----QNESTNEQL--QIHYKVCYARVLDY--RRKFIE 227 (387)
 T 4d0p A
                         T ss dssp
 T ss_pred
                         ННННННННССССchНhНННННННН
 Q ss pred
 Q Fri_Mar_04_23:
                    645 ALRLLLLIEFPYLPKHYLVLLVAKFLY
                                                         672 (744)
                     645 Aa~~Lv~Ll~s~~~Pk~f~~~LL~dalp 672 (744)
 Q Consensus
                    |++.+..+..+..+..+..+..
228 A---f-----e----lk--vl 255 (387)
 T Consensus
```

```
T 4d0p_A
             228 AAQRYNELSYKTIVHESERLEALKHALH 255 (387)
T ss_dssp
               нинининттсттѕсининининини
T ss pred
               НИНИНИНИНСССССЬНИНИНИНИНИ
No 28
                                             Pub Med
>5cqs A Elongator complex protein 1; familial dysautonomia, ELP1 subunit, DIME protein binding; 2.70A
 {Saccharomyces cerevisiae}
 Probab=45.30 E-value=2.6e+02 Score=31.12 Aligned_cols=146 Identities=11% Similarity=0.100 Sum_probs=0.0
               Q Fri_Mar_04_23: 389 DWEQPCVDIISGKIHSILPVMESLDS---CTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYM 465 (744)
             389 --E----i-eqd---vL--l--ld----w-aAHladLl---q-L----
                                                  -----lre-- 465 (744)
Q Consensus
             ---1~~~~~i 110 (435)
T 5cqs A
             50 LRRKFLIDDYLGNYEKALEHLSEIDKDGNVSEEVIDYVESHDLYKHGL-----ALYRYDSEKONVI
                                                                        110 (435)
T ss_dssp
               T ss_pred
               Q ss pred
Q Fri_Mar_04_23:
             466 LNSFAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQ
                                                                        545 (744)
Q Consensus
             466 Ll-YA--l-l-----LW-vai-YL--c---g----r-i-elL-r-pl-t----ek-L-iC----L---a--I-----g--
                                                                        545 (744)
             T Consensus
                                                                        175 (435)
T 5cqs_A
             111 YNIYAKHLS---SNQMYTDAAVAYEMLGKLK-----EAMGAYQSA------KRWREAMSIAVQKFPEEVE-SVAEELISS
                                                                        175 (435)
               T ss dssp
T ss_pred
Q ss pred
               нинсссинининин-сссинин
Q Fri_Mar_04_23: 546 MLSAHNIIESIANFSR-AGKYELV 568 (744)
             546 ~l~~g~~g~AL~~~r~A~d~~~V 568 (744)
+.+.|+|..|..|.+ +||+...
176 l~~~g~~~A~ly~~~~d~~~A 199 (435)
O Consensus
T Consensus
             176 LTFEHRYVDAADIQLEYLDNVKEA 199 (435)
T 5cgs A
T ss_dssp
                нинттеннинниннин
T ss_pred
                нннсссининнинннин
                        PDB"
PROTEIN DATA BANK
No 29
                                NCBI
                                            Pub Med
->2rkl_A Vacuolar protein sorting-associated protein VTA1; dimerization motif, cytoplasm, endosome, lipid
transport, membrane, protein transport; 1.50A {Saccharomyces cerevisiae} PDB: 3mhv _A
Probab=42.20 E-value=95 Score=24.50 Aligned_cols=46 Identities=20% Similarity=0.324 Sum_probs=0.0
               сСининининининининининининининин
Q ss pred
Q Fri_Mar_04_23: 683 MDEDSVATVIEVIETKWDDADEKSSNLYETIIEA-D-KSLPSSMATLLKNLRKKLNF
                                                        737 (744)
             683 fs-----lL--Lee-----y---l----lp------lR--la-
O Consensus
                                                        737 (744)
              T Consensus
                                                         49 (53)
              2 STKDELTKIMDRASKI----EQIQKLAKYAISALNYE----DLPTAKDELTKALDL
T 2rkl A
                                                         49 (53)
               СНИНИНИНИНИНИ
T ss_dssp
                Ссинининесссинин-----ининининининессс---синининининин
T ss pred
                       PDB™
PROTEIN DATA BANK
     No 30
                               NCBI
                                            Pub Med
                                       重
🗌 >5ft9_A Proteinaceous RNAse P 2; hydrolase, prorp, PPR, tRNA 5' matura; 3.05A {Arabidopsis thaliana} PDB: 5diz _A
  Probab=41.15 E-value=2.6e+02 Score=31.49 Aligned_cols=164 Identities=10% Similarity=-0.015 Sum_probs=0.0
               0 ss pred
Q Fri_Mar_04_23: 482 WPVAIGLIALSATGTRSAKKMVIAELLPH--YPFVTNDDIEWMLSICVEWR------LPEIAKEIYTTL----- 542 (744)
             482 W-vai-YL-cc---g---r--i-elL-r---pl-t----ek-L-iC------L---a--I------ 542 (744)
             T Consensus
T 5ft9 A
               T ss dssp
T ss_pred
                Q ss_pred
O Fri Mar 04 23:
             543 -----GNQMLSAHNIIESIANFSRAG----KYELVKSYSWLLFEASCMEGQKLD-DPVLNAIVSKNSPAEDDVIIPQDI
                                                                        611 (744)
             543 -----g---l--g--g-AL----rA-----d---V--i---l---sl--g-----D--L--iv------
Q Consensus
                                                                        611 (744)
             T Consensus
                                                                        181 (537)
T 5ft9 A
             111 ASVTSVARLAAAKGNGDYAFKVVKEFVSVGGVSIPRLRTYAPALLCFCEKLEAEKGYEVEEHMEAAGI------ALE--
                                                                        181 (537)
T ss dssp
               НИНИНИНИНТSCHИНИНИНИНИНИНСSSCCCCИНИНИНИНИНТТСИНИНИНИНИНИНИСС-----CCC--
               T ss_pred
               нинестинининининининин
Q ss pred
Q Fri_Mar_04_23:
             612 LDCVVTNSMRQTLAPYAVLSQFYELRDREDWGQALRLLLLLIEFPYLPKHYLVLLVAKFL
                                                          671 (744)
             612 le~~~~Ls~ya~lreF~~~~g~~~Aa~~Lv~Ll~s~~Pk~f~~~LL~dal
Q Consensus
                                                          671 (744)
             T Consensus
T 5ft9 A
             182 ----EAEISALLKVSAAT-----GRENKVYRYLHKLREYVGCVSEETLKIIEEWF
                                                          227 (537)
               T ss_dssp
T ss_pred
```

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No 31
                                                                                                    PDB"
                                                                                                                                                                                    Pub Med
>2wpv_A GET4, UPF0363 protein YOR164C; golgi-ER trafficking, tail-anchored protein, protein binding GET4; 1.99A
    {Saccharomyces cerevisiae} PDB: 5bwk _E 31ku _A 5bw8 _C 4pwx _E*
   Probab=39.32 E-value=2.9e+02 Score=29.41 Aligned_cols=80 Identities=15% Similarity=0.072 Sum_probs=0.0
                                                                нинининининессининининининининин
   Q ss pred
   Q Fri Mar 04 23: 517 DDIEWMLSICVEWRLPEIAKEIYTLGNQMLSAHNIIESIANFSR-----AGKYELVKSYSWLLFEASCMEGQKLDDP
                                                                                                                                                                                                                                                                                                     589 (744)
                                                     589 (744)
   Q Consensus
   T Consensus
                                                                                                                                                                                                                                                                                                         93 (312)
   T 2wpv_A
                                                                                                                                                                                                                                                                                                        93 (312)
   T ss_dssp
                                                                T ss_pred
                                                                 нининининининсссининининининининин
   Q ss_pred
                                                                ниннинь
   Q Fri Mar 04 23: 590 VLNAIVS 596 (744)
                                                     590 ~L~~iv~ 596 (744)
   O Consensus
                                                        .++.++.
94 ~~~rl~~
                                                                                          100 (312)
   T Consensus
   T 2wpv_A
                                                        94 SVARLVR 100 (312)
   T ss_dssp
                                                                нининин
   T ss pred
                                                                нннннн
   No 32
33jck D 265 proteasome regulatory subunit RPN7; deubiquitinase, RPN11, protein homeostasis, HYDR; 3.50A
    {Saccharomyces cerevisiae S288C} PDB: 4cr2 R 4cr3 R 4cr4 R 5a5b R* 3j47 R
   Probab=39.06 E-value=4.9e+02 Score=28.63 Aligned_cols=201 Identities=10% Similarity=0.054 Sum_probs=0.0
                                                                Q ss_pred
   Q Fri Mar 04 23: 517 DDIEWMLSICVEWR-LPEIAKEIYTTLGNQMLSAHNIIESIANFSRAGKYE----LVKSYSWLLFEASCMEGQKLD-DPV
                                                                                                                                                                                                                                                                                                     590 (744)
                                                     517 ---ek-L-iC-----L---a--I-----g---g-AL-----R-d------V--i----I----sl---g-----D--
   O Consensus
                                                                                                                                                                                                                                                                                                     590 (744)
                                                                +.++.-+.-.+...
                                                      111 \ \text{$\sim$L$} \sim \text{$l$} \sim \text{$a$} \sim \text{$i$} \sim \text{$i$} \sim \text{$a$} \sim \text{$a$} \sim \text{$a$} \sim \text{$a$} \sim \text{$k$} \sim \text{$c$} \sim \text{$k$} \sim \text{$c$} \sim \text{$i$} \sim \text{$a$} \sim \text{
   T Consensus
                                                                                                                                                                                                                                                                                                     190 (429)
                                                      111 KELNEKIQKLEEDDEGELEQAQAWINLGEYYAQIGDKDNAEKTLGKSLSKAISTGAKIDVMLTIARLGFFYNDQLYVKEK
   T 3jck_D
                                                                                                                                                                                                                                                                                                     190 (429)
   T ss_dssp
                                                                 T ss pred
                                                                 нининининесссенининининининининин
   Q ss_pred
                                                                НИНИН ССССССССС С С НЕНИНИ НЕНИВИНИНИ НИНИНИ НЕНИВИНИ НЕНИВИ НЕНИВИ НЕНИВИНИ НЕНИВИ НЕН
   Q Fri Mar 04 23:
                                                     591 LNAIVSKNSPAEDDVIIPQDILDCVVTNSMRQTLAPYAVLSQFYELRDREDWGQALRLLLLLIEFPY-----LPKHYLV
                                                                                                                                                                                                                                                                                                     664 (744)
                                                      591 L--iv-----p---le-----ls-ya-lreF-----g----Aa--Lv-Ll-s------Pk-f--
   O Consensus
                                                                                                                                                                                                                                                                                                     664 (744)
                                                                                                                ..++++..++..+..--
                                                      191 l~k~-----y~A~~~f~e~~~~
                                                                                                                                                                                                                                                                                                     252 (429)
   T Consensus
                                                                                                                                                                                                                                                                                           ~v
                                                      191 LEAV-----NSMIEKGGDWERRNRYKTYYGIHCLAV---RNFKEAAKLLVDSLATFTSIELTSYESIATY
   T 3jck_D
                                                                                                                                                                                                                                                                                                     252 (429)
                                                                T ss dssp
                                                                 T ss_pred
   Q ss_pred
                                                                665 LLVA-----KFLYPIFLLDDKKLMDEDSVATVIEVIETKWDDADEKSSNLYETI----IEADKSLPS
   Q Fri Mar 04 23:
                                                      Q Consensus
                                                                                                                                                                                                                                                                                                     722 (744)
                                                     T Consensus
                                                                                                                                                                                                                                                                                                     324 (429)
                                                      253 ASVTGLFTLERTDLKSKVIDSPELLS--LISTTA---ALQSISSLTISLYAS--DYA-SYFPYLLETYANVLIPCKYLNR
   T 3jck D
                                                                                                                                                                                                                                                                                                     324 (429)
                                                                 HHHHHHHHCCHHHHCCCCCSCTTHHH--HGGGSS---SHHHHHHHHHHHHTT--CHH-HHHHHHHHCCCCCTTCTTTGG
   T ss dssp
   T ss pred
                                                                снининининининин
   0 ss pred
   Q Fri_Mar_04_23: 723 SMATLLKNLRKKLNFKLCQAF 743 (744)
                                                      723 ~~~~~1R~~la~~l~~~~
                                                                  ....+.+.+|...-.++++.|
   T Consensus
                                                      345 (429)
                                                      325 HADFFVREMRRKVYAQLLESY
   T 3jck D
                                                                                                                                345 (429)
   T ss dssp
                                                                GHHHHHHHHHHHHHHTTE
   T ss_pred
                                                                                                    PDB"
   No. 33
                                                                                                                                                                                       Pub Med
                                                                                                                                   NCBI
                                        signalosome complex subunit 1; signaling protein; 3.80A {Homo sapiens} PDB: 4d18 _A
   Probab=38.77 E-value=5.2e+02 Score=28.91 Aligned_cols=202 Identities=15% Similarity=0.163 Sum_probs=0.0
   Q ss pred
                                                                НИНИНИНИНЕССИВЕННИИ НЕНИВИНЕНИИ НЕНИВИЕССИ НЕНИВИНЕССИ ———— НЕНИВИНИНИ НЕНИВИНИТЕЛЬНИЕ НЕНИВИЕССИ НЕНИВИВИТЕЛЬНИЕ НЕНИВИВИТЕЛЬНИЕ НЕНИВИТЕЛЬНИЕ НЕНИВИТЕЛЬНИЕ НЕНИВИТЕЛЬНИВИ НЕНИВИВИТЕЛЬНИЕ НЕНИВИТЕЛЬНИЕ НЕНИВИТЕЛЬНИЕ
   Q Fri Mar 04 23: 517 DDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRAGKY----ELVKSYSWLLFEASCMEGQKLDDPVLN
                                                                                                                                                                                                                                                                                                     592 (744)
                                                      517 ---ek-L-iC----L---a--I----g--g--l--g--g-AL----rA-d------V--i---l---sl--g----D--L-
   Q Consensus
                                                                                                                                                                                                                                                                                                     592 (744)
                                                                 +.++.-+.-.+....+|....+|+|.+|+.+.+.+.
                                                                {\overset{\text{--}}{\text{--}}} - {\overset{--}}} - {\overset{\text{--}}{\text{--}}} - {\overset{\text{--}}{\text{--}}} - {\overset{\text{--}}{\text{--}}} - {\overset{\text{--}}{\text{--}}} - {\overset{\text{--}}{\text{--}}} - {\overset{\text{--}}{\text{---}}} - {\overset{\text{--}}{\text{---}}} - {\overset{\text{--}}{\text{---}}} - {\overset{\text{--}}{\text{---}}} - {\overset{\text{---}}{\text{---}}} - {\overset{\text{----}}{\text{----}}} - {\overset{\text{---}}{\text{----}}} - {\overset{\text{----}}{\text{----}}} - {\overset{\text{----}}{\text{-----}}} - {\overset{\text{----}}{\text{-----}}} 
   T Consensus
                                                                                                                                                                                                                                                                                                     208 (480)
                                                      132 EKLDTDLKNYKGNSIKESIRRGHDDLGDHYLDCGDLSNALKCYSRARDYCTSAKHVINMCLNVIKVSVYLQ---NWSHVL
   T 4d10 A
                                                                                                                                                                                                                                                                                                     208 (480)
                                                                T ss dssp
                                                                 ниннинининессининининининининин
   T ss_pred
   655 (744)
                                                                                         -----p--le----Aa--Lv-L-l-s-ya-lreF----q---Aa--Lv-L-l-s---
                                                     593 ~iv~~~
   O Consensus
                                                                                                                                                                                                                                                                                                    655 (744)
```

```
+.+...+-.|.-+..+++
                                                            ++|.+|++.++.. +..
              T Consensus
                                                                             270 (480)
              209 SYVSK-----AESTPEIAEQRGERDSQTQAILTKLKCAAGLAELAA---RKYKQAAKCLLLASFDHCDFP
T 4d10 A
                                                                             270 (480)
                 T ss dssp
 T ss_pred
                 Q ss pred
              656 -PYLPKHYLVLLVAKFLYPIFLLDDK---KLMDEDSVATVIEVIETKWDDAD------EKSSNL---YETIIEADKS
Q Fri Mar 04 23:
                                                                             719 (744)
              Q Consensus
                                                                             719 (744)
              T Consensus
                                                                             346 (480)
T 4d10 A
                                                                             346 (480)
                 ТЅССНИНИНИНИН--НССИНИНСССССЅСИНИНИННИН--НИНИНИТТСИНИННИНИННИНИН ТСТТ
T ss dssp
                 T ss pred
Q ss pred
                 ССссиннинниннинниннин
Q Fri Mar 04 23:
              720 LPSSMATLLKNLRKKLNFKLCQAF 743 (744)
              720 lp-----lR--la--l----
Q Consensus
                                    743 (744)
                 |-....+.+.||...-.++++.|
              347 L--h---l----Y
T Consensus
T 4d10_A
              347 LAPHVRTLYTQIRNRALIQYFSPY
                                    370 (480)
T ss_dssp
                 ТGGGHHHHHHHHHHHHHHHH
T ss_pred
                 нининининининини
                          PDB"
PROTEIN DATA BANK
                                  NCBI
                                                Pub Med
>3mkq_A Coatomer beta'-subunit; beta-propeller, alpha-solenoid, transport protein; 2.50A {Saccharomyces
cerevisiael PDB: 2vnp A
Probab=36.74 E-value=95 Score=36.65 Aligned_cols=60 Identities=18% Similarity=0.149 Sum_probs=0.0
                 Q Fri Mar 04 23: 512 PFVTNDDIEWMLSICVEWRLPEIA------KEIYTTLGNQMLSAHNIIESIANF
                                                                             559 (744)
              512 pl-t---ek-L-iC----L---a------------I----g---l--g--g-AL--
Q Consensus
                                                                             559 (744)
                 .++++....++.+.|.+.|+.++|
                                                        +...+.+|+.++++|++-.|..+|
              T Consensus
                                                                             704 (814)
T 3mkq A
              \mathbf{625} \ \ \mathsf{NVEGKDSLTKIARFLEGQEYYEEALNISPDQDQKFELALKVGQLTLARDLLTDESAEMKWRALGDASLQRFNFKLAIEAF}
                                                                             704 (814)
T ss_dssp
                 T ss_pred
                 ННСССИННИННИ
Q ss_pred
Q Fri_Mar_04_23: 560 SRAGKYELVKSY 571 (744)
O Consensus
              560 ~rA~d~~~V~~i 571 (744)
                .+++|+.++..+
                 ~~~d~~~l~~l 716 (814)
T Consensus
T 3mkq_A
              705 TNAHDLESLFLL 716 (814)
                 ннитсининин
T ss dssp
                 HHCcChhhhHHH
T ss pred
                                          Pub Med
No 35
                                  NCBI
->4yvo_A Protein fluorescent in blue light, chloroplastic; TPR, fluorescent protein; 1.45A {Arabidopsis thaliana}
  Probab=35.32 E-value=98 Score=27.79 Aligned_cols=46 Identities=17% Similarity=0.195 Sum_probs=0.0
                 ннинининнессинининнининнинин
Q ss pred
Q Fri_Mar_04_23: 517 DDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRA
             517 ---ek-L-iC----L---a--I----g--l--g--g-AL----rA
O Consensus
              +-.++.+++.+.+-...-.+|.-...|+|.+|.+|.+|
73 ~~~~al~~~~~a
                                                   118 (165)
T Consensus
T 4vvo A
              73 TEFKIALELAQSLKDPTEEKKAARGLGASLQRQGKYREAIQYHSMV
                                                   118 (165)
                 нининининиттеннинининининитеннинини
T ss dssp
T ss_pred
                 PDB<sup>N</sup>
PROTEIN DATA BANK

NCBI
No 36
                                          Pub Med
>4yvq_C Protein fluorescent in blue light, chloroplastic, glutamyl-tRNA reductase 1, chloroplastic; TPR,
protein-protein interaction; 2.40A {Arabidopsis thaliana}
Probab=34.57 E-value=89 Score=27.94 Aligned_cols=46 Identities=17% Similarity=0.195 Sum_probs=0.0
                 ннинининнессинининнининнинин
Q ss pred
Q Fri_Mar_04_23: 517 DDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRA 562 (744)
              517 ---ek-L-iC----L---a--I----g---l--g--g-AL----rA 562 (744)
              +-.++.++++.+-.....++..+|.-...|+|.+|+.+|.+|
67 ----al-----a
T Consensus
                                                   112 (159)
              67 TEFKIALELAQSLKDPTEEKKAARGLGASLQRQGKYREAIQYHSMV
T 4vva C
                                                    112 (159)
                 нининининттеннининининининининининини
T ss_dssp
T ss_pred
                 PDB"
No 37
                                  NCBI Pub Med

☐ >31pz_A GET4 (YOR164C homolog); protein targeting, tail-anchored protein biogenesis, GET PAT GET5 binding,

protein transport; 1.98A {Chaetomium thermophilum}
 Probab=32.94 E-value=3.8e+02 Score=28.93 Aligned_cols=80 Identities=14% Similarity=0.094 Sum_probs=0.0
```

```
Q ss pred
                              Q Fri Mar 04 23: 517 DDIEWMLSICVEWRLP---EIAKEIYTTLGNQMLSAHNIIESIANFSR------AGKYELVKSYSWLLFEASCMEGQKL
                                                                                                                                           586 (744)
 O Consensus
                         517 ~~~ek~L~iC~~~~L~~--~~a~~I~~~g~~g~AL~~~~r----A~d~~~V~~i~~l~~~sl~~g~~~
                                                                                                                                           586 (744)
                          +++..=++-+-|=- -+|...+|.++-|.++-+--. +|...-+++++--.

13 ~k-l-rl-~G-y-~YEAhQ-~RTi-~Ry-~-y-eAidlL-~gA-~llk-~Q-~sg-DLa-~lvevy-~-
                                                                                                       92 (336)
                           T 3lpz A
                                                                                                                                             92 (336)
 T ss_dssp
                              нинининининессинининининининининитскинининининининиттскинининининининини
 T ss_pred
                              Q ss_pred
                              СНИННИННН
 Q Fri_Mar_04_23: 587 DDPVLNAIVS 596 (744)
 O Consensus
                         587 ~D~~T.~~iv~
                                              596 (744)
                              +++.++.++.
                          93 ~~~~rl~~
 T Consensus
                                             102 (336)
 T 3lpz_A
                          93 DGASRGKLLG 102 (336)
 T ss_dssp
                              СНИНИНИНИ
 T ss pred
                              СНИНИНИНИ
                                               PDB
 No 38
                                                              NCBI
🗌 >3ro3_A PINS homolog, G-protein-signaling modulator 2; asymmetric cell division, protein binding; 1.10A {Mus
 musculusl
 Probab=32.83 E-value=3.1e+02 Score=24.47 Aligned cols=68 Identities=13% Similarity=0.072 Sum probs=0.0
                              Q ss pred
 Q Fri_Mar_04_23: 517 DDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSR-----AGKYELVKSYSWLLFEASCMEGQ
                                                                                                                                     584 (744)
                         O Consensus
                                                                                                                                     584 (744)
                             T Consensus
                                                                                                                                    144 (164)
 T 3ro3 A
                          70 EYYKKTLLLARQLKDRAVEAQSCYSLGNTYTLLQDYEKAIDYHLKHLAIAQELKDRIGEGRACWSLGNAYTALGN
                                                                                                                                    144 (164)
 T ss dssp
                               T ss pred
                               нинининининоссининининининининин
                                               PDB
 No 39
                                                                                       Pub Med

☐ >31pz_A GET4 (YOR164C homolog); protein targeting, tail-anchored protein biogenesis, GET PAT GET5 binding,

 protein transport; 1.98A {Chaetomium thermophilum}
 Probab=32.22 E-value=5.8e+02 Score=27.49 Aligned cols=161 Identities=9% Similarity=0.015 Sum probs=0.0
                              Q ss pred
 Q Fri_Mar_04_23: 389 DWEQPCVDIISGKI--HSILPVMESLDSC-----TAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLED 453 (744)
                         389 ~-E~~~i~egd~--~~vL~l~ld~w----~aAHladLl~~g~L~~~~~d 453 (744)
 O Consensus
                          15 ~l~rl~~i~~g~y~~YEAhQ~~RTi~~Ry~~~~y~eAidlL~~qA~~1lk~Q~~s------
 T Consensus
                                                                                                                                            73 (336)
 T 3lpz_A
                          15 IIARLQRRIAEGQPEEQYEAAQETRLVAARYSKQGNWAAAVDILASVSQTLLRSGQGGS------
                                                                                                                                            73 (336)
 T ss_dssp
                               T ss pred
                              hccccchниннинниннhhhccCccchнинниннhCccchнинниннннносСССССНИН---нниннинннысС
 Q ss pred
                         454 LFSYRNGMASYMLNSFAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPHYPFVTNDD---IEWMLSICVEWR
 Q Fri_Mar_04_23:
                                                                                                                                           530 (744)
                         454 l~~~~~lre~~Ll~YA~~l~l~~~~LW~vai~YL~~c~~g~~~~r~~i~elL~r~pl~t~~~~--~ek~L~iC~~~~
                                                                                                                                           530 (744)
                          T Consensus
                                                                                                                                           129 (336)
                          74 ---GGDLAVLLVDTFROA------GORVDGASRGKLLGCLRLFOPGEPVRKRFVKEMIDWSKKFG
 T 31pz A
                                                                                                                                           129 (336)
                              ----нининининин
 T ss dssp
  T ss_pred
                               Q ss pred
 O Fri Mar 04 23: 531 -LPEIAKEIYTTLGNOMLSAHNIIESIANFSRAGKYELVKSYSWLLFEASCMEGOKLDDPVLNAIV 595 (744)
                         O Consensus
 T Consensus
 T 31pz A
 T ss dssp
                              ССССССНИНИНИНИНННИНСССИНИНИНИНННИН ССССС-ИНИНИНИНИНННИН СССССОНИНИНИНИН Н
 T ss pred
 No 40
                                                                                       Pub Med
🗌 >3ro3_A PINS homolog, G-protein-signaling modulator 2; asymmetric cell division, protein binding; 1.10A {Mus
 Probab=31.82 E-value=3.2e+02 Score=24.35 Aligned_cols=68 Identities=13% Similarity=0.089 Sum_probs=0.0
 Q ss pred
                              НИНИНИНИНЕССИВЕННИИ НИНИНИНИ НИНИНИНИ НИНИНИ -----сССИНИНИНИНИНИНИНИНИНИ НИСС
 O Fri Mar 04 23: 517 DDIEWMLSICVEWRLPEIAKEIYTTIGNOMLSAHNIIESIANFSR-----AGKYELVKSYSWLLFEASCMEGO 584 (744)
                         517 \;\; \cdots \; ek \cdot L - iC - \cdots - L - \cdots - a - \cdots I - \cdots - g - \cdots - 1 - \cdots - g - - g - AL - \cdots - r - \cdots - A - d - \cdots - V - i - \cdots - 1 - \cdots - s1 - \cdots - g - \cdots - 1 - \cdots - g - \cdots - g - \cdots - 1 - \cdots - g - \cdots
                                                                                                                                    584 (744)
 Q Consensus
                               30 ----al-----ig-----ig-----ig-----ig-----
 T Consensus
                                                                                                                                     104 (164)
                          30 IAHEQRLLIAKEFGDKAAERIAYSNLGNAYIFLGEFETASEYYKKTLLLARQLKDRAVEAQSCYSLGNTYTLLQD 104 (164)
 T 3ro3 A
                              T ss dssp
                               T ss pred
                                                                                        Pub Med
```

```
🗌 >3mzk_B Protein transport protein SEC16; alpha-helical-stack, beta-propeller; 2.69A {Saccharomyces cerevisiae}
 Probab=30.84 E-value=3.5e+02 Score=30.23 Aligned cols=134 Identities=14% Similarity=0.122 Sum probs=0.0
                                НИНИНИННЕССИНИНИНИННЕССИНИНИНИННИННИННЕССИСИИ СОСИСИСИИ СОСИСИСИИ СОСИСИИ СТАТИТЕЛЬНИИ СОСИСИИ СТАТИТЕЛЬНИИ СОСИСИИ СТАТИТЕЛЬНИИ СОСИСИИ СТАТИТЕЛЬНИИ СОСИСИИ СТАТИТЕЛЬНИИ СТА
 Q ss pred
 Q Fri_Mar_04_23: 390 WEQPCVDIISGKIHSILPVMESLDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYML--- 466 (744)
                           390 ~E~~~~i~egd~~~vL~~l~~ld~w~aAHladLl~~~g~L~~~~~~~~~~~
                                                                                                                   ~~~~dl~~~~lre~~L--- 466 (744)
 Q Consensus
                           T Consensus
 T 3mzk B
                                T ss dssp
 T ss_pred
                                Q ss pred
 Q Fri Mar 04 23: 467 -----NSFAFELCSLGDKELWPVAIGLIALSATG----TRSAKKMVIAELLPHYPFVTNDDIEWMLSICVEWR 530 (744)
                           467 -----l-YA--l-l-----LW-vai-YL--c-----g----r-i-elL-r-pl-t----ek-L-iC---- 530 (744)
 O Consensus
                          T Consensus
                           207 TAGPNDOKELAHFLLLIFQVFYGNSKMA----IKSFYTNNETSQWASENWKSIVAAVLINIPENNEDPLL------ 272 (441)
 T 3mzk B
                                T ss_dssp
 T ss pred
                                Q ss_pred
                                СИНИНИНИНИНИНИНИНИСССИИНИНИНИНИССС
 Q Fri_Mar_04_23: 531 LPEIAKEIYTTLGNQMLSAHNIIESIANFSRAGK 564 (744)
                           531 L---a--I---g---l--g--g-AL----rA-d 564 (744)
 Q Consensus
                           ++..+..+|..+|..+|..+|..+|..+|..+|273 ~p~~~~1~~LGd~L~~~g~~~aA~iCYL~a~~
                                                                                   306 (441)
 T Consensus
                           273 IPPVVLEFLIEFGIFLTKKGLTAAASTLFIIGNV 306 (441)
 T 3mzk B
 T ss dssp
                                ССИНИНИНИНИНИНИНИТТСИНИНИНИНИТТС
                                ссhhнннннннннннннсССсhhнннннннсС
 T ss_pred
 No 42
                                                                                             Pub Med
>4a5p_A Protein MXIA, protein VIRH; protein transport, type three secretion, export apparatus; HET: MLY; 3.15A
  {Shigella flexneri}
  Probab=30.06 E-value=1.6e+02 Score=32.46 Aligned_cols=82 Identities=12% Similarity=0.287 Sum_probs=0.0
 Q ss pred
                                Q Fri_Mar_04_23: 657 YLPKHYLVLLVAKFLYPIFLLDDKKLMDEDSVATVIEVIETKWDDAD-----EKSSNLYETIIEAD---KSLPS 722 (744)
                           657 ~~Pk~f~~~LL~dalp~~lL~~~~~fs~~~~~LL~Lee~~~~~~~y~~~l~~~~~y~~~l~~~~~lp~
 Q Consensus
                                                                                                                                                   722 (744)
                           +.|....+|..|+.++ ...|.++++...||..+++ ...|.++|..|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+..
 T Consensus
                                                                                                                                                   246 (383)
 T 4a5p_A
                           173 XSAQDEFYHQLSQALL----NNINEIFGIQETKNMLDQFENR--YPDLLXEVFRHVTIQRISEVLQRLLGENISVRNLKL
                                                                                                                                                   246 (383)
 T ss dssp
                                T ss_pred
                                ССИНИНИНИНИНИН----НЪНИНИНЬСИНИНИНИНИНЬ--СЪНИНИНИНЬТЬССИСССИНИНИНИНЬ
 Q ss_pred
                                -----снининининининин
 Q Fri_Mar_04_23:
                           723 ----SMATLLKNLRKKLNFKLCQAFM
                                                                                    744 (744)
 O Consensus
                           744 (744)
                                                  |...+...+|.+|++.||+.|.
                           247 IlEtLad~a~~~kD~~~LtE~VR~aL~R~I~
 T Consensus
                                                                                    281 (383)
                           247 IMESLALWAPREXDVITLVEHVRASLSRYICSKIA 281 (383)
 T 4a5p_A
                                нинининтттсссинининининининин
 T ss_dssp
                                нинининне
 T ss pred
                                                  PDB"
 No 43
                                                                NCBI
                                                                                            Pub Med
->4ui9_ Anaphase-promoting complex subunit 5; ubiquitination, cell cycle, APC/C; 3.60A {Homo sapiens}
 Probab=28.56 E-value=3.3e+02 Score=31.87 Aligned_cols=122 Identities=11% Similarity=0.041 Sum_probs=0.0
                                Q ss_pred
 Q Fri_Mar_04_23: 517 DDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRA------GKYELVKSYSWLLFEASCMEGQKLD-D 588 (744)
                          Q Consensus
 T Consensus
 T 4ui9 O
                           563 KLLQKLLVHCQKLKNTEMVISVLLSVAELYWRSSSPTIALPMLLQALALSKEYRLQYLASETVLNLAFAQLILGIPEQAL 642 (756)
 T ss_dssp
                                T ss_pred
 0 ss pred
                                Q Fri_Mar_04_23:
                           589 PVLNAIVSKNSPAEDDVIIPQDILDCVVTNSMRQTLAPYAVLSQFYELR-----DREDWGQALRLLLLLIE
                                                                                                                                           654 (744)
 Q Consensus
                           589 ~-L~iv~~~~~p~~le~~~~le~~Ls~ya~lreF~~~~g~~~Aa~-Lv~Ll~
                                                                                                                                           654 (744)
                           T Consensus
                                                                                                                                           700 (756)
                           643 SLLHMATEP-----ILA-----DGAILDKGRAMFLVAKCQVASAASYDQPKKAEALEAATENLNEAKN
 T 4ui9 O
                                                                                                                                           700 (756)
 T ss_dssp
                                ННИНИНИН——————ННН—————SCCSНИНИНИНИНИНИНИНИНИНССЭТТИНИНИНИНИНИНИНИН
 T ss pred
                                PDB"
 No 44
                                                                NCBI
                                                                                 Pub Med
>3iko_C Nucleoporin NUP84; NPC, transport, WD repeat, autocatalytic cleavage, mRNA transport, nuclear pore
  complex, nucleus, phosphoprotein; 3.20A {Saccharomyces cerevisiae} PDB: 4xmm _F 4xmn _F 3jro _C
 Probab=28.33 E-value=1e+02 Score=34.72 Aligned_cols=90 Identities=13% Similarity=0.146 Sum_probs=0.0
                                НННhCCCHHHHHHhh----hHHHHH-HHhheeCC-------CchhHHHHHHHHHhCCCCCCCHHHHHHHH
 0 ss pred
```

```
Q Fri_Mar_04_23: 336 LLVIGGNQRKILQYSR----TWYESFC-GFLLYYIP------SLELSAEYLQMSLEANVVDITNDWEQPCVD 396 (744)
                        O Consensus
 T Consensus
                                                                                                                                      265 (460)
                        186 ELILAGAIDEALEEAKLSDNISICMILCGIQEYLNPVIDTQIANEFNTQQGIKKHSLWRRTVYSLSQQAGLDPYERAIYS
 T 3iko C
                                                                                                                                      265 (460)
                             НИНИТТСИНИНИВИНИТТСИНИВИВИТЕ SCECTTTSGGGTTTCSSCBSBTTHHHHHHHHHHHCSSSCHHHHHHHH
 T ss_dssp
                             T ss pred
                             ннсссн-инининннссьинининин
 Q ss pred
                        397 IISGKI-HSILPVMESLDSCTAAFTAMICE
 Q Fri_Mar_04_23:
                                                                     425 (744)
                        397 i~egd~-~~vL~~l~~ld~w~aAHladLl~
                             ++. | +- | +- | +- | +- | +- |
                        266 ~L~q~~~s~~l~v~~swED~LW~~l~~~~~
                                                                      295 (460)
 T Consensus
 T 3iko C
                        266 YLSGAIPNQEVLQYSDWESDLHIHLNQILQ 295 (460)
 T ss_dssp
                             ннитессининттссинининининин
 T ss_pred
                             ННhCCchhhhccccCCНННННННННН
                                              PDB'
 No 45
                                                                                    Pub Med
             Nuclear pore complex protein NUP107; transport protein; 23.00A {Homo sapiens}
 Probab=27.71 E-value=84 Score=38.78 Aligned_cols=95 Identities=15% Similarity=0.353 Sum_probs=0.0
                             Q ss pred
 Q Fri Mar 04 23: 332 IEDFLL-VIGGNQRKILQYS----RTWYES-FCGFLLYYIPSLE------LSAEYLQMSLEANVVDITNDWEQP
                                                                                                                                      393 (744)
                        393 (744)
 Q Consensus
                        ++.+++ |.+|.-+.+.| +.|.=+.++|.+|.+|... ...-+-..|...-+...|.+

347 ---if-llr-g---eA-elc---gg-WRAasL-g--l--dp------------------gn--r-LWK--c--la------yERA

347 LKYLFTLIRAGMTEEAQRLCKRCGQAWRAATLEGWKLYHDPNVNGGTELEPVEGNPYRRIWKISCWRMAEDELFNRYERA
 T Consensus
                                                                                                                                      426 (925)
 T 5a9g 4
                                                                                                                                      426 (925)
 T ss_dssp
                             НИНИНИНИТСИНИНИНИНИТСИНИНИНИТТSBCBCTTTCCTTCCSSCBSBSCHHHHHHHHHHHHHCSSSCHHHHH
 T ss_pred
                             Q ss_pred
                             нининсссининининныесьнинининин
 Q Fri Mar 04 23: 394 CVDIISGKIHSILPVMESLDSCTAAFTAMICEA
                                                                          426 (744)
 Q Consensus
                        394 ~~~i~egd~~~vL~~l~~ld~w~aAHladLl~~
                                                                          426 (744)
                             +-++. | | + . . + + . | . + | + - . + = | | + - - + + . .
 T Consensus
                        427 IYg~LsGdl~~~l~vc~sWeD~LwA~~n~~ld~
                                                                          459 (925)
                        427 IYAALSGNLKQLLPVCDTWEDTVWAYFRVMVDS
 T 5a9q_4
                                                                          459 (925)
 T ss_dssp
                             нининтсссянинтссинининининини
 T ss pred
                             ННННННСССННННННННННННН
 No 46
                                                                                     Pub Med
>3mix A Flagellar biosynthesis protein FLHA: flagella biosynthesis, protein transport, type III secretion: 2.30A
  {Bacillus subtilis}
 Probab=27.16 E-value=3e+02 Score=30.33 Aligned_cols=110 Identities=15% Similarity=0.182 Sum_probs=0.0
                             сСинниний рассиний и получений 
 Q ss_pred
 Q Fri Mar 04 23:
                        606 IIPODILDCVVTNSMRQTLAPYAVLSQFYELRDREDWGQALRLLLLLIEFPYLPKHYLVLLVAKFLYPIFLLDDKKLMDE
                                                                                                                                      685 (744)
                        Q Consensus
                                                                                                                                      685 (744)
                        T Consensus
 T 3mix_A
                                                                                                                                      237 (382)
 T ss_dssp
                             T ss pred
 Q ss_pred
                             ннинининининининининин
 Q Fri Mar 04 23:
                        686 DSVATVIEVIETKWDDADEKSSNLYETIIEADKSLPSSMATLLKNLRKKLNFKLCQAFM 744 (744)
 O Consensus
                         \texttt{686} \quad \texttt{-----} \texttt{LL} \texttt{--Lee} \texttt{-----} \texttt{y} \texttt{---} \texttt{1} \texttt{p} \texttt{-----} \texttt{1} \texttt{R} \texttt{--1} \texttt{a} \texttt{--1} \texttt{----} 
                                                                                                           744 (744)
                              .++..|+++|-+.
                                                                     ...-+|...+|.+|++.||+.|.
                        238 Rdl~tilEaLae~-----a~~kD~~~LtE~VR~aL~R~I~
 T Consensus
                                                                                                           277 (382)
                        238 RNLVTIFETLADY------GKLTTDSDLLTEYTRQALAKQITAQFA
 T 3mix A
                                                                                                           277 (382)
                             ССНИНИНИНИН-----ТТТСССИНИНИНИНИННИНИНН
 T ss dssp
 T ss_pred
                             ссинининини
                                              PDB"
 No 47
                                                           NCBI
                                                                                    Pub Med
->4yvo_A Protein fluorescent in blue light, chloroplastic; TPR, fluorescent protein; 1.45A {Arabidopsis thaliana}
    Probab=26.90 E-value=99 Score=27.77 Aligned cols=46 Identities=9% Similarity=0.008 Sum probs=0.0
 Q ss pred
                             Q Fri_Mar_04_23: 517 DDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRA
                                                                                           562 (744)
 O Consensus
                        517 \;\; \text{---ek-L-iC----L---a--I----g---l--g--g-AL-----rA}
                                                                                           562 (744)
                        +-.++.+++.+-...-.++..+|.-+...|++..+|+..+|-+|
113 ----al-----al-----al-----a
 T Consensus
                                                                                          158 (165)
                        113 QYHSMVLAISKRESEDSGITEAYGAIADCYTELGDLEKAGKFYDTY
                                                                                          158 (165)
 T 4yvo A
 T ss dssp
                             нинининининтссттинининининиттсинининини
                             T ss pred
                                            PDB<sup>™</sup>
PROTEIN DATA BANK
 No 48
                                                          NCBI (S)
                                                                                  Pub Med
🗌 >3a5i_A Flagellar biosynthesis protein FLHA; four domains, thioredoxin-like fold, bacterial flagellum BIO
 bacterial flagellum protein export; 2.80A {Salmonella typhimurium}
 Probab=26.08 E-value=2e+02 Score=31.85 Aligned_cols=80 Identities=6% Similarity=0.161 Sum_probs=0.0
```

```
Q ss_pred
               Q Fri Mar 04 23: 659 PKHYLVLLVAKFLYPIFLLDDKKLMDEDSVATVIEVIETKWDDAD------EKSSNLYETIIEAD---KSLPS-
                                                                      722 (744)
             659 Pk-f---LL-dalp--lL------fs------LL--Lee----------y----l------lp--
O Consensus
                                                                      722 (744)
               T Consensus
                                                                      254 (389)
T 3a5i A
             181\ \text{ASTVVATHLNHLIG----QFSAELFGRQEAQQLLDRVSQE--MPKLTEDLVPGVVTLTTLHKVLQNLLAEKVPIRDMRTI}
                                                                      254 (389)
               T ss_dssp
               T ss pred
                -----снинининининининин
Q ss_pred
Q Fri_Mar_04_23: 723 -----SMATLLKNLRKKLNFKLCQAFM 744 (744)
            723 -----1R~~la~~l~~~~
O Consensus
                                       744 (744)
                       |...+...+|.+|++.||+.|.
             255 lEaLae~a~~~kD~~~LtE~VR~aL~R~I~
T Consensus
                                        288 (389)
             255 LETLAEHAPLQSDPHELTAVVRVALGRAITQQWF 288 (389)
T 3a5i A
T ss_dssp
               НИННИННЕССССИННИННИННИННИННИН
T ss_pred
               нининина
                        PDB™
PROTEIN DATA BANK
                               NCBI
No 49
                                            Pub Med
🗌 >2x49_A INVA, invasion protein INVA; protein transport, transport, pathogenesis; 1.50A {Salmonella enterica
subsp} PDB: 2x4a A* 31w9 A
Probab=26.01 E-value=1.7e+02 Score=31.51 Aligned cols=79 Identities=14% Similarity=0.279 Sum probs=0.0
               Q Fri_Mar_04_23: 659 PKHYLVLLVAKFLYPIFLLDDKKLMDEDSVATVIEVIETKWDDAD-----EKSSNLYETIIEAD--KSLPS-- 722 (744)
            O Consensus
               |..-..+|.+.+- ...||..+++- ...
                                                     ..-.+.+|..|+.. ++++.
                -tvi-thl-evi-----a-ellg-qEv--Lld-l----p-LV-El---l-l--i--VLq-LL-E-VsIRdl-tIl 198 (333)
T Consensus
T 2x49 A
            125 ALDELYHCLAVTLA----RNVNEYFGIQETKHMLDQLEAK--FPDLLKEVLRHATVQRISEVLQRLLSERVSVRNMKLIM 198 (333)
T ss_dssp
               T ss_pred
               Q ss_pred
               ----снинининининининин
Q Fri Mar 04 23: 723 -----SMATLLKNLRKKLNFKLCQAF 743 (744)
O Consensus
             723 ----lR~~la~~l~~~
                                      743 (744)
                  |...+...+|.+|++.||+.|
             199 EtLa~~~~kD~~~LtE~VR~aL~r~I~~
T Consensus
                                      230 (333)
             199 EALALWAPREKDVINLVEHIRGAMARYICHKF
T 2x49 A
                                     230 (333)
               нининтттсссинининининининини
T ss_dssp
T ss pred
               нининнессссинининнининнинин
                        PDB'
                                       Pub Med
No 50
      Protein fluorescent in blue light, chloroplastic, glutamyl-tRNA reductase 1, chloroplastic; TPR,
protein-protein interaction; 2.40A {Arabidopsis thaliana}
Probab=23.66 E-value=1.1e+02 Score=27.39 Aligned_cols=46 Identities=9% Similarity=0.008 Sum probs=0.0
               Q ss pred
Q Fri Mar 04 23: 517 DDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRA
             517 ---ek-L-iC----L---a--I---g--g-AL----rA 562 (744)
Q Consensus
            +-.++.++++.+-.....++..+|.-..+.|++.+|+.||.+|
107 ----al-----al-----alg-----g---A-----a
T Consensus
                                               152 (159)
             107 QYHSMVLAISKRESEDSGITEAYGAIADCYTELGDLEKAGKFYDTY
T 4yvq C
                                               152 (159)
               ннининининитссттинининининитсинининин
T ss dssp
T ss pred
               PDB"
No 51
           NCBI
                                       Pub Med
      Proteinaceous RNAse P 2; hydrolase, prorp, PPR, tRNA 5' matura; 3.05A {Arabidopsis thaliana} PDB: 5diz _A
  Probab=21.83 E-value=5.3e+02 Score=28.89 Aligned_cols=196 Identities=9% Similarity=0.006 Sum_probs=0.0
               Q ss pred
Q Fri_Mar_04_23: 517 DDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAHNIIESIANFSRAGKY--ELVKSYSW-LLFEASCMEG------QK
                                                                      585 (744)
             585 (744)
T Consensus
                                                                       91 (537)
             14 DESSSRPNKKKKVSRNPETN--LLFNLNSCSKSKDLSAALALYDAAITSSEVRLSQOHFOTLLYLCSASITDISLOYLAI
T 5ft9 A
                                                                       91 (537)
                T ss_dssp
               T ss_pred
               Q ss pred
O Fri Mar 04 23: 586 LD-DPVLNAIVSKNSPAEDDVIIPODILDCVVTNSMROTLAPYAVLSOFYELRDREDWGOALRLLLLLI -- EFPYLPKHY
                                                                      662 (744)
             586 ~~-D~~L~~iv~~~~~
                              --p---le-----l---Ls-ya-lreF--
                                                    ~g~~~~Aa~~Lv~Ll--~s~~~Pk~f
Q Consensus
                                                                      662 (744)
             92 ~~A~~~~m~~~g~--
                                ~____L~~~L
T Consensus
                                                                      148 (537)
             92 DRGFETFDRMVSSGI-----SPN-----EASVTSVARIAA-----AKGNGDYAFKVVKEFVSVGGVSIPRLR
T 5ft9 A
                                                                      148 (537)
               T ss dssp
               T ss_pred
728 (744)
             663 ~~LL~dalp~lL~~~---------fs~~~~LL~Lee~~~~~y~~l~~~--lp~
O Consensus
                                                                      728 (744)
```

```
..-+..-..++.++-.. ...+++.++|+..++..++..++
                 149 ----li----g----A-----m-----p------li--------g---eA-----m-----p----t---11
 T Consensus
                                                                                               224 (537)
                 149 TYAPALLCFC--EKLEAEKGYEVEEHMEAAGIALEEAEISALLKVSAAT--GRENKVYRYLHKLREYVGCVSEETLKIIE
 T 5ft9 A
                                                                                               224 (537)
                     T ss dssp
                     T ss_pred
                     нининининини
 Q ss_pred
 Q Fri Mar_04_23: 729 KNLRKKLNFKLCQ 741 (744)
                 729 ~~lR~~la~~l~~ 741 (744)
 Q Consensus
                     ....+.=+...|+
                 225 ~~~~g~~~g~~ 237 (537)
225 EWFCGEKAGEVGD 237 (537)
 T Consensus
 T 5ft9 A
                     ннитеннинисс
 T ss dssp
 T ss pred
                     HHHhhcchhhcCC
 No 52
                                                            Pub Med
>3fxd A Protein ICMQ; helix bundle, helix-turn-helix, unknown function; 2.10A {Legionella pneumophila} PDB:
 Probab=20.99 E-value=1.8e+02 Score=23.14 Aligned_cols=42 Identities=14% Similarity=0.500 Sum_probs=0.0
                     ссининининини-----нырынинининининин
 Q ss pred
 Q Fri Mar 04_23: 683 MDEDSVATVIEVIETK-----WDDADEKSSNLYETIIEADKSLPSSMATLLKNLRKKLNFKLC
                                                                               740 (744)
 Q Consensus
                  683 fs-----LL--Lee-----
                                                 ~y~~~1~~~~1p~~
                                                                   ---lR--la--l-
                                                                                740 (744)
                     ++.+|...||++|++-
                                      |++.+
                                                                  |..||...+.+|+
 T Consensus
                   5 lt~eq~~aILkaLdeaIe~GPWe~SN-----FLRvIGKn----
                                                                 --L~eIRd~F~~~i~
                                                                                 51 (57)
 T 3fxd A
                   5 LSDEOKETILKALNDAIEKGPWDKSN-----FLRVIGKK-----LIAIRDRFLKRIG
                                                                                51 (57)
                     ССИНИНИНИНИНИНИНИН СТТЅСИ-----НИНИНИНИ
 T ss dssp
 T ss pred
                     ссининининининининин
Done!
Please cite as appropriate:
HHpred: Söding, J. (2005) Protein homology detection by HMM-HMM comparison. Bioinformatics 21: 951-960.
PSIPRED: Jones, D.T. (1999) Protein secondary structure prediction based on position-specific scoring matrices. JMB 292: 195-202.
PDB: Bourne, PE. et al. (2004) The distribution and query systems of the RCSB Protein Data Bank. NAR 32: D223.
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                                                                                                     Release-2.18.5
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