

```
T ss_pred
             CCCHHHHhhhccCCCCCccCCHHHHHHHCCCcccccCCCCcccCHHhhccccchhHHHhhccccccCCcccc
             0 ss pred
Q Fri_Mar_04_23: 152 AKFSTGSMLLTKDIVGKSGVSIKRLPTELQRKFLFDDVYLDKEIEKVTIEARKSNPYPQISESSLLFKDALDYMEKTSSD 231 (712)
           Q Consensus
                                                           231 (712)
             92 ~ f~~~11~~~~~~e 171 (652)
T Consensus
           92 AKFSTGSMLLTKDIVGKSGVSIKRLPTELQRKFLFDDVYLDKEIEKVTIEARKSNPYPQISESSLLFKDALDYMEKTSSD
T 4xmm B
                                                           171 (652)
             EEECSSSCEEEECSSSSSEEEECCCCSCCCGGGGSHHHHHHHHHTTEEEEECSSSSCEEEEEECCCGGGGGGGGGCTTSHH
T ss_dssp
T ss_pred
             Q ss pred
Q Fri Mar 04 23: 232 YNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERHCRLTSWIVSQIGPEIEEKIRNSSNEIEQIFLYLLLNDVVRASKLA 311 (712)
          311 (712)
O Consensus
             172 ~~vW~L~saLfd~~~~~~~~~~~~Rr~~ls~WL~~~v~~~v~~~~~e~if~~L~
T Consensus
                                                            251 (652)
          172 YNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERHCRLTSWIVSQIGPEIEEKIRNSSNEIEQIFLYLLLNDVVRASKLA
T 4xmm B
                                                            251 (652)
             T ss_dssp
T ss pred
             НИНИНИНННОСС
Q ss_pred
             ннссссеннининнессссыннинининнинн
                                                            391 (712)
Q Fri Mar 04 23: 312 IESKNGHLSVLISYLGSNDPRIRDLAELQLQKWSTGGCSIDKNISKIYKLLSGSPFEGLFSLKELESEFSWLCLLNLTLC
           312 i--gn-rLA-Llsq-gs----r----QL--W------I-----kIY-LLAG---e----i-e-LdW-ralgL-LW
                                                            391 (712)
Q Consensus
          T Consensus
                                                            331 (652)
T 4xmm B
          252 IESKNGHLSVLISYLGSNDPRIRDLAELQLQKWSTGGCSIDKNISKIYKLLSGSPFEGLFSLKELESEFSWLCLLNLTLC
                                                            331 (652)
T ss dssp
             T ss_pred
             Q ss_pred
Q Fri_Mar_04_23: 392 YGQIDEYSLESLVQSHLDKFSLPYDDPIGVIFQLYAANENTEKLYKEVRQRTNALDVQFCWYLIQTLRFNGTRVFSKETS
                                                           471 (712)
          O Consensus
                                                            471 (712)
T Consensus
                                                            411 (652)
           332 YGQIDEYSLESLVQSHLDKFSLPYDDPIGVIFQLYAANENTEKLYKEVRQRTNALDVQFCWYLIQTLRFNGTRVFSKETS
T 4xmm_B
                                                            411 (652)
             T ss_dssp
             T ss pred
Q ss_pred
             ннининининсссенининин
Q Fri_Mar_04_23: 472 DEATFAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDTIKRLVMREITLLRASTNDHILNRLKIPSQLIFNAQALKDRYEGN
                                                            551 (712)
          O Consensus
                                                            551 (712)
                                                            491 (652)
T Consensus
T 4xmm B
           412 DEATFAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDTIKRLVMREITLLRASTNDHILNRLKIPSQLIFNAQALKDRYEGN
                                                            491 (652)
             НИНИНИНИНИТСИНИНИНИТСССИНИНИНИНИНИНИТТТSSSHHHHHHHTTCCHHHHHHHHHHHHHHH-
T ss dssp
             T ss_pred
             нинининнесссининининниннинн
Q ss pred
Q Fri Mar 04 23: 552 YLSEVQNLLLGSSYDLAEMAIVTSLGPRLLLSNNPVQNNELKTLREILNEFPDSERDKWSVSINVFEVYLKLVLDNVETQ
                                                            631 (712)
          552 ---e--Ll-A----eAH-v-v--laP--II-----d---L--fp---I--W--Gg-Vy-dYl-l----
                                                            631 (712)
Q Consensus
          T Consensus
                                                            571 (652)
T 4xmm B
                                                            571 (652)
             T ss dssp
T ss pred
             нинининнессининининининин
Q ss_pred
             O Fri Mar 04 23: 632 ETIDSLISGMKIFYDOYKHCREVAACCNVMSOEIVSKILEKNNPSIGDSKAKLLELPLGOPEKAYLRGEFAODLMKCTYK
                                                            711 (712)
Q Consensus
           632 --l--L---L--l----va--ems--v--l------il-LPL-ed---Y----l--
                                                            711 (712)
            T Consensus
           651 (652)
           572 ETIDSLISGMKIFYDQYKHCREVAACCNVMSQEIVSKILEKNNPSIGDSKAKLLELPLGQPEKAYLRGEFAQDLMKCTYK
T 4xmm B
                                                            651 (652)
T ss_dssp
             ННИНИНИНИТС-----СИНИНИНИНИНИНИНИ
             нининининны
T ss pred
Q ss_pred
Q Fri_Mar_04_23: 712 I 712 (712)
O Consensus
          712 ~
              712 (712)
T Consensus
           652 ~
              652 (652)
          652 I
T 4xmm B
              652 (652)
T ss_dssp
             C
T ss_pred
                          NCBI
                                 Pub Med
>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=100.00 E-value=9.7e-105 Score=884.32 Aligned cols=427 Identities=100% Similarity=1.448 Sum probs=0.0
             Q Fri_Mar_04_23: 126 FSECNDEIDNAKLIMKERRFTASYTFAKFSTGSMLLTKDIVGKSGVSIKRLPTELQRKFLFDDVYLDKEIEKVTIEARKS 205 (712)
```

```
Q Consensus
                                         205 (712)
                                                 T Consensus
                                                                                                                                                                                                                                                94 (442)
                                           15 FSECNDEIDNAKLIMKERRFTASYTFAKFSTGSMLLTKDIVGKSGVSIKRLPTELORKFLFDDVYLDKEIEKVTIEARKS
T 3bal B
                                                                                                                                                                                                                                                94 (442)
                                                   T ss dssp
                                                  T ss pred
                                                  Q ss pred
Q Fri_Mar_04_23: 206 NPYPQISESSLLFKDALDYMEKTSSDYNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERHCRLTSWIVSQIGPEIEEKI
                                                                                                                                                                                                                                              285 (712)
Q Consensus
                                         206 ng~P~~~~l~f~d~~~~e~~vW~L~saLFd~~~
                                                                                                                                                                                                                                              285 (712)
                                           T Consensus
                                                                                                                                                                                                                                              174 (442)
                                           95 NPYPQISESSLLFKDALDYMEKTSSDYNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERHCRLTSWIVSQIGPEIEEKI
T 3bg1 B
                                                                                                                                                                                                                                              174 (442)
T ss_dssp
                                                  T ss_pred
                                                  Q ss_pred
                                                  рессенинининные ссетинининин в ссетинининин в ссетинининини в ссетинининини в ссетининини в ссетининини в ссетинини в в ссетини в ссетини в ссетини в в ссетини в в ссетини в ссетини в в ссетини в с
Q Frī_Mar_04_23: 286 RNSSNEIEQIFLYLLLNDVVRASKLAIESKNGHLSVLISYLGSNDPRIRDLAELQLQKWSTGGCSIDKNISKIYKLLSGS
                                                                                                                                                                                                                                              365 (712)
Q Consensus
                                                  ~~~~e~if~~L~g~~I~~A~~Ai~~gn~rLA~Llsq~gs~~~~~~QL~~W~~~~~I~~~~kIY~LLAG~
                                                                                                                                                                                                                                              365 (712)
                                         T Consensus
                                                                                                                                                                                                                                              254 (442)
T 3bg1_B
                                                                                                                                                                                                                                              254 (442)
                                                  T ss_dssp
                                                  T ss pred
Q ss_pred
                                                  сеесссеррусский и получить полу
Q Fri Mar 04 23: 366 PFEGLFSLKELESEFSWLCLLNLTLCYGQIDEYSLESLVQSHLDKFSLPYDDPIGVIFQLYAANENTEKLYKEVRQRTNA
                                                                                                                                                                                                                                              445 (712)
                                         366 ~~e~~~~i~e~LdW~ralgL~LWYg~~~~sl~~av~~v~~~~P~~D~~~LLkLva~~~~le~vL~p~s~t~~~
O Consensus
                                                                                                                                                                                                                                              445 (712)
                                                  +++++.+.+++|+|||+|+||||||++++.|++|+||.|++++|+||.|++++|+||.|+++|+||.|++++|+||.|+++|+||.|++++|+||.|+++|+||.|+++|+||.|+++|+||.|+++|+||.|+++|+||.|+++|+||.|++|+||.|++|+||.|++|+||.|++|+||.|++|+||.|++|+||.|++|+||.|+|+||.|+|+||.|+|+||.|+|+||.|+|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+|||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+|||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+||.|+|
T Consensus
                                                                                                                                                                                                                                               334 (442)
                                         255 PFEGLFSLKELESEFSWLCLLNLTLCYGQIDEYSLESLVQSHLDKFSLPYDDPIGVIFQLYAANENTEKLYKEVRQRTNA
{\tt T} 3bg1_B
                                                                                                                                                                                                                                              334 (442)
T ss_dssp
                                                  T ss_pred
                                                  ссссссь рассисствия и политирующий политирующ
                                                  Q ss_pred
Q Fri Mar 04 23:
                                         {\tt 446\ LDVQFCWYLIQTLRFNGTR} {\tt VFSKETSDEATFAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDTIKRLVMREITLLRASTND}
                                                                                                                                                                                                                                              525 (712)
                                         Q Consensus
                                                                                                                                                                                                                                              525 (712)
                                         T Consensus
                                                                                                                                                                                                                                              414 (442)
T 3bg1_B
                                         {\tt 335~LDVQFCWYLIQTLRFNGTR}{\tt VFSKETSDEATFAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDTIKRLVMREITLLRASTND}
                                                                                                                                                                                                                                              414 (442)
                                                  T ss dssp
                                                  сссиннининне
T ss pred
                                                  ннинньссси
0 ss pred
Q Fri_Mar_04_23: 526 HILNRLKIPSQLIFNAQALKDRYEGNY
                                         526 ~L~e~L~IP~~WI~eAkAl~ar~~gd~
                                         ||+++||||++||||||+|||+||+
415 ~L~e~L~IP~~WI~eAkAl~a~~~qd~
T Consensus
                                                                                                                    441 (442)
                                         415 HILNRLKIPSQLIFNAQALKDRYEGNY
T 3bg1_B
                                                                                                                    441 (442)
                                                  СНИНТТССИНИННИНИННИННИН
T ss dssp
T ss_pred
                                                  ННННННСССИННННННННННННННСССС
                                                                                PDB<sup>™</sup>
No 3
                                    NCBI
                                                                                                                                                     Pub Med
                    Nuclear pore complex protein NUP96; transport protein; 23.00A {Homo sapiens}
Probab=100.00 E-value=1.6e-104 Score=946.21 Aligned_cols=538 Identities=18% Similarity=0.296 Sum_probs=0.0
                                                  ccCCcceeecccccceeeccccc-hhHHHH-HHHHHHHHHhcCeeeccCCCCCceeeCC-CCC----HHHHHhhc
0 ss pred
Q Fri Mar 04 23: 154 FSTGSMLLTKDIVGKSGVSIKRLPTELQ--RKFLFD-DVYLDKEIEKVTIEARKSNPYPQISES-SLL----FKDALDYM 225 (712)
                                         O Consensus
                                                                                                                                                                                                                                              225 (712)
                                                   T Consensus
T 5a9q 5
                                                  CSSSCEECCC-CCSSSCEECCCCCC---CHHHHSHHHHHHHHHCCBCCCS--SSCCBCCC--CCCHHHHHHHC----
T ss dssp
                                                  ccccccccccchhhнннннhhcccCcchhhнhhhннннннcccccC--CCCCccCCchhннннннннн
T ss pred
Q ss_pred
                                                  Q Fri Mar 04 23: 226 EKT-----SSDYNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERHCRLTSWIVSQIGPEIEEKIRNS-SNEIEQIF
                                                                                                                                                                                                                                              296 (712)
                                         Q Consensus
                                                                                                                                                                                                                                              296 (712)
                                                            ~~~~~~~~vw·L·saLfd-~~~~~~~l-Rr-aLS-WL~~v~~v~ev~~~~s~e~if
                                                                                                                                                                                                                                              455 (937)
T 5a9q 5
                                         377 SGDLPEAOIVKHWSLTWTLCEALWGHLKELDSOLNEP-REYIOILERRRAFSRWLSCTATPOIEEEVSLTOKNSPVEAVF
                                                                                                                                                                                                                                              455 (937)
T ss dssp
                                                  T ss_pred
                                                  НННСССНИНИНИНННСССссининининесССС ННННИНИНИННННН ССС--сСС ННИНИНИН НСССсссссс
Q ss_pred
Q Fri_Mar_04_23: 297 LYLLLNDVVRASKLAIESKNGHLSVLISYLGSNDPRIRDLAELQLQKWSTGGC--SIDKNISKIYKLLSGSPFEGLFS--
                                                                                                                                                                                                                                              372 (712)
                                         297 ~~L~q~~I~~A~~~Ai~~qn~rLA~Llsq~qs~~~~~~OL~~W~~~~~~~I~~~~kiY~LLAG~~~e~~~~~
Q Consensus
                                                                                                                                                                                                                                              372 (712)
                                                  534 (937)
T Consensus
                                         456 SYLTGKRISEACSLAQQSGDHRLALLLSQFVGSQ-SVRELLTMQLVDWHQLQADSFIQDERLRIFALLAGKPVWQLSEKK
                                                                                                                                                                                                                                              534 (937)
T 5a9q_5
T ss_dssp
                                                  НИНИНТСИНИНИНИНИНТСИНИНИНИНТТССS-ТИНИНИНИНИТТSCC--CCCHHHHHHHHHHSCCC-CCSCC-
T ss pred
                                                  ниньсссининининнесссинининны в составления в при в при в составления в при в при в составления в при в составления в при в составления в при в составления в при в
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сhhhccCCCнининининсССССССининининн
 Q ss_pred
 Q Fri Mar 04 23: 373 LKELESEFSWLCLLNLTLCYGQIDEYSLESLVQSHLDKF-----SLPYDDPIGV
                                                                                                                                                  421 (712)
                          373 ~~~i~e~LdW~ralgL~LWYg~~~~sl~~av~~y~~~~~
                                                                                                                                                  421 (712)
 Q Consensus
                               .+++++||||+|+||||||||++++.||++||..|++++
                           535 ~i~~~~LdWkralGL~LWYg~~~~sl~~av~~y~~~~~a~~P~P~Y~e~~~~~~~Dl~~~
 T Consensus
                                                                                                                                                  614 (937)
                          535 QINVCSQLDWKRSLAIHLWYLLPPTASISRALSMYEEAFQNTSDSDRYACSPLPSYLEGSGCVIAEEQNSQTPLRDVCFH
 T 5a9q 5
                                                                                                                                                  614 (937)
                                CCTHHHHSCHHHHHHHHHSCTTTSCHHHHHHHHHHSCC-----CCSCHHHH
 T ss dssp
                                T ss_pred
                                Q ss_pred
 Q Fri Mar 04 23: 422 IFQLYAANE-NTEKLYKEVRQRTNALDVQFCWYLIQTLRFNGTRVFSKETSDEATFAFAAQLEFAQLHGHSLFVSCFLND
                                                                                                                                                  500 (712)
                           Q Consensus
                                                                                                                                                  500 (712)
                                615 LLKLya~~~~Le~vL~P~s~t~~plD~rLsW~L~~vL~alg~~~~s~~~d~L~~sfA~QLe~~GlW~wAiFVLLHL~d
 T Consensus
                                                                                                                                                  694 (937)
 T 5a9q 5
                           615 LLKLYSDRHYDLNOLLEPRSITADPLDYRLSWHLWEVLRALNYTHLSAOCEGVLOASYAGOLESEGLWEWAIFVLLHIDN
                                                                                                                                                  694 (937)
 T ss_dssp
                                НИНИНЕТСС-СИНИНИНИЕТТСССSСИНИНИНИНИНИТSSCCCHИНИНИНИНИНИНИНИНИТСЯНИНИНИНИТСЯС
                                T ss pred
                                Q ss pred
 Q Fri_Mar_04_23:
                          501 \ \texttt{DKAAEDTIKRLVMREITLLRAST----NDHILNRLKIPSQLIFNAQALKDRYEGNYLSEVQNLLLGSSYDLAEMAIVTSL}
                                                                                                                                                  576 (712)
 Q Consensus
                           501 ~~R~aIr~lL~R~~~~~L~e~L~IP~~WI~eAkAl~ar~~qd~~e~~~Ll~A~~~~eAH~v~v~l
                                                                                                                                                  576 (712)
                               774 (937)
 T Consensus
                           695 SGIREKAVRELLTRHCQLLETPESWAKETFLTQKLRVPAKWIHEAKAVRAHMESDKHLEALCLFKAEHWNRCHKLIIRHL
 T 5a9q 5
                                                                                                                                                  774 (937)
 T ss_dssp
                                НИНИНИНИНИНИНИНИНИСС----СИНИНИНИТТССИНИНИНИНИНИТССС------
 T ss_pred
                                ниннининнинный рессесству в начининний в начиний в начини
 Q ss_pred
                                hнининнессСсссенининининс--ссс--сСССhhcchнининининс-----ССссинининининин
 Q Fri_Mar_04_23: 577 GPRLLLSNNPVQNNELKTLREILNEF--PDS--ERDKWSVSINVFEVYLKLVLD-----NVETQETIDSLISGMKIFYD
                                                                                                                                                  646 (712)
 Q Consensus
                           577 aP~~II~~~~~d~~L~~Ll~~f--p~~-~I~~W~~Gg~Vy~dYl~l~~~--------~~~~l~~L~~~L~~L~~l~~
                                                                                                                                                  646 (712)
                          848 (937)
 T Consensus
 T 5a9q 5
                           775 ASDAIIN---E---NYDYLKGFLEDLAPPERSSLIQDWETSGLVYLDYIRVIEMLRHIQQVDCSGNDLEQLHIKVTSLCS
                                                                                                                                                  848 (937)
 T ss_dssp
                                hhннннс---С---Сниннинннннннне
 T ss pred
 Q ss pred
                                С------ССЬННИНИНИНИНИНИНИНИН
 Q Fri_Mar_04_23:
                           647 Q----YKHCREVAACCNVMSQEIVSKIL-----EKNNPSIGD--SKAKLLELPLGQPE-----K
 Q Consensus
                           647 ~-----va~ems~v~l~-------il~LPL~ed~-----
                                         .++++| +|+++||++|++++.
                                                                                    ...+....+ ..+.|++|||||
                           T Consensus
                                                                                                                                                  926 (937)
                          849 RIEOTOCYSAKDR--LAOSDMAKRVANLLRVVLSLHHPPDRTSDSTPDPORVPLRLLAPHIGRLPMPEDYAMDELRSLTO
 T 5a9g 5
                                                                                                                                                  926 (937)
 T ss dssp
                                ______
                                НИССССССНИН -- НИНИНИНИНИНИНИНИНИНИНИНИНИ
 T ss pred
                                нниннны
 Q ss pred
 Q Fri_Mar_04_23: 695 AYLRGEFAQ 703 (712)
 Q Consensus
                          695 ~Y~~~~1~~
                                               703 (712)
                               .||+..++.
                          927 ~y
 T Consensus
                                               935 (937)
                          927 SYLRELAVG 935 (937)
 T 5a9q_5
 T ss dssp
                                HHHHHHHhh
 T ss pred
                                                                              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}
                                            Score=755.86 Aligned_cols=449 Identities=100% Similarity=1.435 Sum_probs=0.0
                    E-value=2.4e-83
 Q ss_pred
                                ccCCCcccCCccccHHhhccccchhHHHhhccccccCCCcchhhccCCcceeecccccccceeeccccchhHHH
 Q Fri_Mar_04_23: 107 VFATSKEFDGPCQNEIDLLFSECNDEIDNAKLIMKERRFTASYTFAKFSTGSMLLTKDIVGKSGVSIKRLPTELQRKFLF 186 (712)
                           Q Consensus
                                                                                                                                                 186 (712)
                          T Consensus
                                                                                                                                                  384 (753)
                          305 GGATSKEFDGPCQNEIDLLFSECNDEIDNAKLIMKERRFTASYTFAKFSTGSMLLTKDIVGKSGVSIKRLPTELQRKFLF
 T 3jro_A
                                                                                                                                                  384 (753)
 T ss dssp
                                -----CCSHHHHHHTTTCCSCCCCCCCCTTSCBCEECSSSTTSEECCCCCCCCTTGGG
                                {\tt EecCccceeccCCccceehhhhhhhhhcccceeecccCCceeEEEEcCCCceEEeecCCCcceEEEecccchhhhhhhh}
 T ss pred
 Q ss_pred
                                НИНИНИНННОСееессСССССеееСССССНИННИН носсоний нинин не постоя пос
 Q Fri_Mar_04_23: 187 DDVYLDKEIEKVTIEARKSNPYPQISESSLLFKDALDYMEKTSSDYNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERH 266 (712)
                          O Consensus
                                                                                                                                                  266 (712)
 T Consensus
                                                                                                                                                  464 (753)
                           385 DDVYLDKEIEKVTIEARKSNPYPQISESSLLFKDALDYMEKTSSDYNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERH
 T 3jro A
                                                                                                                                                  464 (753)
 T ss_dssp
                                T ss_pred
                                Q ss pred
 Q Fri_Mar_04_23: 267 CRLTSWIVSQIGPEIEEKIRNSSNEIEQIFLYLLLNDVVRASKLAIESKNGHLSVLISYLGSNDPRIRDLAELQLQKWST 346 (712)
                          267 ~~Ls~WL~~~v~~~v~~~l~~~~e~if~~L~g~~I~~A~~Ai~qn~rLA~Llsq~qs~~~~r~~~~QL~~W~~ 346 (712)
```

```
T Consensus
                                                              544 (753)
           465 CRLTSWIVSQIGPEIEEKIRNSSNEIEQIFLYLLLNDVVRASKLAIESKNGHLSVLISYLGSNDPRIRDLAELQLQKWST
T 3jro A
                                                              544 (753)
             T ss dssp
T ss_pred
             Q ss pred
Q Fri_Mar_04_23: 347 GGCSIDKNISKIYKLLSGSPFEGLFSLKELESEFSWLCLLNLTLCYGQIDEYSLESLVQSHLDKFSLPYDDPIGVIFQLY
                                                              426 (712)
           347 ----kiy-LlAG--e----i-e-LdW-ralgL-LWYg----sl--av-y----P---D----LLkLy
Q Consensus
                                                              426 (712)
           T Consensus
                                                              624 (753)
T 3jro_A
                                                              624 (753)
             T ss dssp
             T ss pred
Q ss pred
             Q Fri_Mar_04_23:
           427 AANENTEKLYKEVRORTNALDVOFCWYLIOTLRFNGTRVFSKETSDEATFAFAAOLEFAOLHGHSLFVSCFLNDDKAAED
                                                              506 (712)
           427 a----le-vL-p-s-t---lD-rLsW-L---vL-a-g----s----d-Lt-sfA-QLe--Glw--AvFVllHl-d----R--
Q Consensus
                                                              506 (712)
           T Consensus
           \textbf{625} \quad \texttt{AANENTEKLYKEVRQRTNALDVQFCWYLIQTLRFNGTRVFSKETSDEATFAFAQLEFAQLHGHSLFVSCFLNDDKAAED}
T 3jro A
                                                              704 (753)
T ss_dssp
             T ss_pred
             нниннинннинннинннинннинннинннинн
Q ss pred
Q Fri_Mar_04_23: 507 TIKRLVMREITLLRASTNDHILNRLKIPSQLIFNAQALKDRYEGNYLSE 555 (712)
O Consensus
           507 aIr-lL-R-----L-e-L-IP--WI-eAkAl-ar--gd---e
                                           555 (712)
           T Consensus
                                           753 (753)
           705 TIKRLVMREITLLRASTNDHILNRLKIPSQLIFNAQALKDRYEGNYLSE 753 (753)
T 3jro_A
             НННННННSCTTSSTTTTTTTTTTCCHHHHHHHHHHHHHHHHHC--
T ss dssp
T ss_pred
             PDB<sup>™</sup>
PROTEIN DATA BANK
                          NCBI
No 5
                                      Pub Med
>4ycz_A Fusion protein of SEC13 and NUP145C; structural protein complex, nuclear pore complex, macromolec
assemblies, structural protein; 4.10A {Thielavia heterothallica}
Probab=100.00 E-value=2.8e-84 Score=778.94 Aligned_cols=484 Identities=18% Similarity=0.247 Sum probs=0.0
             hhccCcceeecccccceeeccccchhнннннннннннhcceeeccCCCCCeeeCCCCCHннннhhcccchнн
Q ss pred
Q Fri_Mar_04_23: 152 AKFSTGSMLLTKDIVGKSGVSIKRLPTELQRKFLFDDVYLDKEIEKVTIEARKSNPYPQISESSLLFKDALDYMEKTSSD 231 (712)
O Consensus
           231 (712)
             T Consensus
                                                     ----e~~~~e 423 (876)
           356 TNWGPNGLLVTTHHGEPSLQPADGTLAASEESVGSPENLARLQRYIDSVSFKE--GQPIASP------EFRELAQG
                                                             423 (876)
T 4ycz A
             CCCCCCCBTTTBBCCCC----CCCCBCCCCCCSCSHHHHHHHHHHHHHTTCSCC-----CCC-----CSTTSCTT
T ss_dssp
T ss_pred
             CccCCCcEEEecCCCcceeccchhhhcccCcCChHHHHHHHHHhhhhhhhccc--cCcccch------hHHHHHHH
             Q ss pred
Q Fri_Mar_04_23: 232 YNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERHCRLTSWIVSQIGPEIEEKIRNSSNEIEQIFLYLLLNDVVRASKLA
                                                              311 (712)
                             Q Consensus
           232 ~~vW~L~saLFd~~~~
                                                              311 (712)
           +.||+||++||++
424 ~~~W~1~~~Lf~~--
T Consensus
                                                              483 (876)
           424 DPSWELASLLFDD-----NGYGLPAFWRQLVSEATDRALAQEPGLEEKAIICLAGNRVADACGYL
T 4ycz A
                                                              483 (876)
T ss dssp
             CHHHHHHHTTSSS-----STTCHHHHHHHHHHHTTTTTTTTCC--CHHHHHHHSSSCCHHHHHHH
T ss_pred
             Q ss pred
Q Fri Mar 04 23: 312 IESKNGHLSVLISYLGSNDPRIRDLAELQLQKWSTGGC--SIDKNISKIYKLLSGSPFE------GLFSLKELE
                                                              377 (712)
           O Consensus
                                                              377 (712)
           T Consensus
                                                              559 (876)
           484 LAAGNFRLATLVSGIGMQ----DGDMKAQLKDWRESNVLAEFSQPVRAIYELLAGNAGVCAGVKNVPIENRVDSFTISQR
T 4ycz A
                                                              559 (876)
             T ss dssp
             T ss pred
Q ss_pred
             Q Fri Mar_04_23: 378 SEFSWLCLLNLTLCYGQIDEYSLESLVQSHLDKFS---LPYDDPIGVIFQLYAANENTEKLYKEVRQRTNALDVQFCWY
Q Consensus 378 e-LdW-ralgL-LWYg----sl--av--y------P---D----LLkLya----le-vL-p-s-t---lD-rLsW-
                                                              453 (712)
                                                              453 (712)
           627 (876)
T 4ycz A
           560 FGLDWMRSFGLRLFYTTGATANVAEAVRSFOADIEODKEPEPDSALWSLLKAFANOE-----FDWSDTRLGWL
                                                              627 (876)
T ss dssp
             T ss_pred
             ccccнинининнесссссссининининнын
             Q ss_pred
Q Fri_Mar_04_23:
           526 (712)
           454 L--vL-a-g---s----d-Lt-sfA-QLe--Glw--AvFVllHl-d---R--aIr-lL-R--------
                                                              526 (712)
Q Consensus
             707 (876)
           628
T Consensus
           628 LTKAIYATGKVSFGQDAAEKLDKASLAYASALTAQSQWVPATFVLLQLSDAASREAAVRDHLGRHARRIGSPRNPNSAFS
                                                              707 (876)
T 4ycz_A
T ss_dssp
             T ss pred
             HHHHHHHHDCCCCCCCChhhHHHHHHHHHHHHHHHCCCchhhhbeeeecCChHHHHHHHHHHHHhhhhhhccCcccchhHHH
```

```
Q ss_pred
 Q Fri Mar 04 23: 527 ILNRLKIPSQLIFNAQALKDRYEGNYLSEVQNLLLGSSYDLAEMAIVTSLGPRLLLSNNPVQNNELKTLREILNEF--PD
                                                                                                       604 (712)
                   527 L-e-L-IP--WI-eAkAl-ar--gd---e---Ll-A----eAH-v-v-laP--II-----d---L--Ll--f--p-
                                                                                                        604 (712)
 Q Consensus
                  T Consensus
                                                                                                       781 (876)
 T 4ycz A
                                                                                                       781 (876)
                      ННТТТССТТНИНИНИНННС--ССТНИНННТТССТНИНТТНИНGGGCC------CCHHHHHHHHHHHHHCC
 T ss_dssp
                       T ss_pred
                      Q ss_pred
 Q Fri Mar 04 23:
                  605 SERDKWSVSINVFEVYLKLVLD-NVETOETID-SLISGMKIFYDO--YKHCREVAACCNVMSOEIVSKILEKNNPSIGDS
                                                                                                       680 (712)
                   605 ~-I~-W~-Gq~Vy~dYl~l~----l~--L~-L--l-----va--ems--v--l---
 Q Consensus
                                                                                                       680 (712)
                      782 --i-W--gg-vy------i----
 T Consensus
                                                                                                       854 (876)
 T 4ycz A
                   782 GKLODWDRGAAVYLLYPMARLOGKOHGLDKFDHOLFDGLVALRGOTHGDIROE--AAIADMAEDLIRCRGGDPRL----
                                                                                                       854 (876)
 T ss_dssp
                      T ss pred
                      ниннессссинин-нинини
 Q ss pred
 Q Fri_Mar_04_23:
                  681 KAKLLELPLGOPEK-AYLRGEF
                                              701 (712)
 Q Consensus
                  ...+|+|...|+...|
                   681 ~~~il~LPL~ed~~-~Y~~~~l
                                              701 (712)
                                              871 (876)
 T Consensus
                   855 ----FGLLPEDVRSKYMRAQA
 T 4ycz A
                                              871 (876)
 T ss_dssp
                      ----ССНИННИННИНННСС--
 T ss_pred
                      ---- hCCCCHHHHHHHHHH
                                 PDB™
PROTEIN DATA BANK
                                              NCBI
                                                                Pub Med
                                                         >5a9q_8 Nuclear pore complex protein NUP85; transport protein; 23.00A {Homo sapiens}
 Probab=98.21 E-value=1.8e-05 Score=93.03 Aligned_cols=311 Identities=14% Similarity=0.172 Sum_probs=0.0
 Q ss pred
                      НННННННСССсссссСССНННННННННННННННННН
 Q Fri_Mar_04_23: 234 LWKLSSILFDPVSYPYKTDNDQVKMALLKKERHCRLTSWIVSQ---IGPEIEEKIRN-----SSNEIEQIFLYLLLNDVV
                                                                                                       305 (712)
                  234 vW-L-saLFd------e-if--L-g--I-
 O Consensus
                                                                                                       305 (712)
                  T Consensus
                                                                                                       210 (656)
                   145 IWNLCEILFIEVAPAGPLLL------HLLDWVRLHVCEVDSLSADVLGSENPSKHDSFWNLVTILVLQGRLD
 T 5a9q 8
                                                                                                       210 (656)
                       T ss_dssp
 T ss pred
                      Q ss pred
                      Q Fri Mar_04_23: 306 RASKLAIESKNGH-----LSVLISYLGSNDPRIR------DLAELQLQKWST------GGC-SIDKNISKIYKLLSG
                                                                                                       364 (712)
                  364 (712)
                                                                                                       289 (656)
 T Consensus
                  T 5a9q 8
                                                                                                       289 (656)
 T ss dssp
                       T ss pred
                      Сосососсь рругического достигний и достигн
 Q ss_pred
 Q Fri Mar 04 23: 365 SPFEGLFSLKEL--ESEFS-WLCLLNLTLCYGQID--EYSLESLVQSHLDKFS---LPYDDPIGVIFQLYAANENTEKL
                                                                                                       435 (712)
                      ---e-Ld-W-ralgL-LWYg-----sl--av--y-----P---D----LLkLya----le-v
                                                                                                       435 (712)
                  T Consensus
                   290 DE-----AALLEOKELLSNWYHFLVTRLLYSNPTVKPIDLHYYAOSSLDLFLGGESSPEPLDNILLAAFEF--DIHOV
 T 5a9q 8
                                                                                                       360 (656)
                      T ss dssp
                      СН------НИНИНИНННОССИНИНИНННИННННОССССССАНИНИНННИНННОСССССССАНИНИННИНННОСССССССАНИНН
 T ss_pred
 Q ss_pred
                      hCcccCCCcccchнининнньcCccc-----cCchhнининннннн-ннсСссинининнн
                  436 YKEVRQRTNALDVQFCWYLIQTLRFNGTRV----FSKETSDEATFAFAAQL-EFAQLHGHSLFVSCFLNDDKAAEDTIK
 Q Fri_Mar_04_23:
                                                                                                       509 (712)
                   436 L-p-s-t---lD-rLsW-L--vL-a-g------s----d-Lt-sfA-QL-e--Glw--AvFVllHl-d---R--aIr
 Q Consensus
                                                                                                       509 (712)
                   T Consensus
                   361 IKE--CSIALSNWWFVAHLTDLLDHCKLLQSHNLYFGSNMREFLLLEYASGLFAHPSLWQLGVDYFDYCPELG--RVSLE
 T 5a9q 8
                                                                                                       436 (656)
 T ss dssp
                      T ss_pred
                      Q ss_pred
 Q Fri_Mar_04_23: 510 RLVMREITLLRASTND--HILNRLKIP--SQLIFNAQALKDRYEGNYLSEVQNLLLGSSYDLAEMAI 572 (712)
 O Consensus
                   572 (712)
                   T Consensus
                   437 LHIERIPLNTEQKALKVLRICEQRQMTEQVRSICKILAMKAVRNNRLGSALSWSIRAKDAAFATLVS 503 (656)
 T 5a9q_8
                      HHGGGCCCCSSTTHHHHHHHHHHHTTCHHHHHHHHHHHC-----
 T ss_dssp
 T ss_pred
                      нньссСССсининининнессинининнинниннин
                                   PDB
                                             NCBI
 No 7
                                                                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 _B
```

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Probab=98.05 E-value=0.00021 Score=82.70 Aligned_cols=312 Identities=13% Similarity=0.107 Sum_probs=0.0
                       ННЫННИННЫНСССсссссСССЫННИНИННИННЫН ---- НИНИННИН ---- НИНИННИН ----- ССИН-----
 Q ss pred
 Q Fri Mar 04 23: 230 SDYNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERHC---RLTSWIVSQIG----PEIEEKIRN--S---SNEI----- 292 (712)
                   T Consensus
                   177 ESLTVLNCLRTMYFILDGQDVEEN-----RSEFIESLLNWINRSDGEPDEEYIEQVFSVKDSTAGKKVFETQYF 245 (570)
 T 3f3f C
                       НИНИНИНИНИSSTTSCGGGG-------HИНИНИНИНИНИНИНИНИТС---CCSSSCSHHH
 T ss dssp
                       T ss_pred
                       -нининньсссинининнинсс------Сссининни---ньссссынинниннинниннин------------------
 Q ss_pred
 Q Fri_Mar_04_23: 293 -EQIFLYLLLNDVVRASKLAIESK-------NGHLSVLIS---YLGSNDPRIRDLAELQLQKWST--------G 347 (712)
                   293 -e~if~~L~g~~I~~A~~~Ai~~g-----n~rLA~Lls---q~gs~~~~r~~~~QL~~W~~------
 Q Consensus
                                                                                                         347 (712)
                   T Consensus
 T 3f3f C
                   246 WKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYPKDS---SSTFREWKNLVLKLSQAFGSSAT
                                                                                                         322 (570)
 T ss_dssp
                       T ss pred
                       СС--сССНИННИНИНННСССссссссеннын нининнын нессссссеннын нининнын нессссссенны нининнын нессссссенны нининнын нессссссенны нининны нессссссенны нининны нессссссенны не несстанивающих несст
 Q ss_pred
 Q Fri_Mar_04_23: 348 GC--SIDKNISKIYKLLSGSPFEGLFSLKELES-EFSWLCLLNLTLCYGQIDEYSLESLVQSHLDKFSLPYDDPIGV-IF
                                                                                                         423 (712)
 Q Consensus
                   348 ----I----kIY-LLAG---e----i-e--LdW-ralgL-LWYg----sl--av--y----P---D-----LL
                                                                                                         423 (712)
                      395 (570)
 T Consensus
                   323 DISGELRDYIEDFLLVIGGNQ-----RKILQYSRTWYESFCGFLLYYIPSLELSAEYLQMSLEANVVDITNDWEQPCV
 T 3f3f C
                                                                                                         395 (570)
 T ss_dssp
                       CSCHHHHHHHHHHHHHHTCH-----HHHHHTCSSHHHHHHHHCCCCCCCCGGGHHHHHHHHHHSCCCTTSSSHHHHH
 T ss_pred
                       Q ss_pred
                       ННhcCCC-CHHHhhCcccCCCCcccchнининниннносссс-------Cchhнинини
 Q Fri_Mar_04_23: 424 QLYAANE-NTEKLYKEVRQRTNALDVQFCWYLLQTLRFNGTRVF-----SKETSDEATFA
                                                                                                         477 (712)
 Q Consensus
                   424 kLya~~~-le~vL~p~s~t~~~lD~rLsW~L~~vL~a~g~~~~------s~~~d~Lt~s
                                                                                                         477 (712)
                       468 (570)
 T Consensus
                   396 DIISGKIHSILPVMES-----LDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNS
 T 3f3f C
                                                                                                         468 (570)
                       T ss_dssp
                       НННСССИНИНИНИНН-----hCHHHHHHHHHHHHHHHHCccccccccccccccchhhhhhhcchhhHHHHHHH
 T ss pred
                       Q ss pred
 Q Fri Mar_04_23: 478 FAAQLE---FAQLHGHSLFVSCFLN--DDKAAEDTIKRLVMREITLLRAST-ND--HILNRLKIP--SQLIFNAQALKDR
                   478 fA-QLe----Glw--AvFVllHl---d---R--aIr-lL-R------L-e-L-IP----WI-eAkAl-ar
 Q Consensus
                                                                                                         547 (712)
                   T Consensus
                                                                                                         547 (570)
                   469 FAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELL-PHYPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQML
 T 3f3f C
                                                                                                         547 (570)
 T ss_dssp
                       T ss pred
                       hСССИНИНИНИНННСССИНИНИН
 Q ss pred
 Q Fri_Mar_04_23: 548 YEGNYLSEVQNLLLGSSYDLAEM 570 (712)
 Q Consensus
                   548 ~~gd~~~e~~Ll~A~~~eAH~ 570 (712)
                      .+|++..++.+||+.+.-+.
                   548 ~~g~~g~AL~~~~rA~~~~Vk~
 T Consensus
 T 3f3f C
                   548 SAHNIIESIANFSRAGKYELVKS 570 (570)
 T ss dssp
                       _____
                       НСССИННИНИНИННСССЫ
 T ss pred
                                                        Pub Med
>4xmm D Nucleoporin NUP85; structural protein, immune system, transport protein-immune complex: 7.38A
 {Saccharomyces cerevisiae S288C} PDB: 4xmn _D
 Probab=98.04 E-value=0.00012 Score=86.74 Aligned_cols=341 Identities=13% Similarity=0.079 Sum_probs=0.0
                       Q ss_pred
 T Consensus
 T 4xmm D
                       HHHHHHHHHHHSSSTTSCGGC-----HHHHHHHHHHHHHHHHHHCCCSCHHHHHHHHTTC----CCSSSSCSHHH
 T ss dssp
                       НИНИНИНИНННЫ CCCCCcccc------chинининин hhttp://www.ncccccccccccchhi
 T ss pred
 Q ss_pred
                       Q Fri_Mar_04_23: 293 -EQIFLYLLLNDVVRASKLAIESK------NGHLSVLIS--YLGSNDPRIRDLAELQLQKWST------GGC- 349 (712)
                  O Consensus
 T Consensus
                   217 WKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYPK---DSSSTFREWKNLVLKLSQAFGSSAT
 T 4xmm D
 T ss_dssp
                       НИНИНИННЕССИНИНИНИННЕННИННЕННИННЕННИННЕННИННЕННИННЕННИННЕННИННЕННИННЕННИННЕННИННЕННИННЕ
 T ss_pred
                       сСС----ННИНИННННСССсссссссенные-СССИНИНИННННЕСССССССИНИННННННН
 Q ss pred
 Q Fri_Mar_04_23: 350 SID----KNISKIYKLLSGSPFEGLFSLKELES-EFSWLCLLNLTLCYGQIDEYSLESLVQSHLDKFSLPYDDPIGVIFQ 424 (712)
                  350 ~I~---~kIY~LLAG~~e~~~~i~e~LdW~ralqL~LWYq~~~~sl~av~~y~~~~P~~~D~~~~LLk 424 (712)
```

```
.++ +.+..||++|+|. ..|++ .=+|..+++-+-|-.|...+.+.+.+.+.+.+.+ |+...++.+-294 -----i---L-1-Gd-------I---s--WyE--va--ly--Pt---l--y-------d-----e---
 T Consensus
                                                                                                                 365 (715)
                    294 DISGELRDYIEDFLLVIGGNQ-----RKILQYSRTWYESFCGFLLYYIPSLELSAEYLQMSLEAN-VVDITNDWEQPC 365 (715)
 T 4xmm D
                        CSCHHHHHHHHHHHHTCH------НННННTCSSHHHHHHHHCCCCCCCCGGGHHHHHHHHHHS-CCCTTSSSHHHH
 T ss dssp
 T ss_pred
                         сСсНhнннннннннннннннсссн-----ннннннhhhннннннhhheeCCCchhннннннннс-сссссннннн
                        НьсССССНИНььСсссСССсссссьнининнньсСс-----ссс------Ссььининин
 Q ss pred
 Q Fri Mar 04 23: 425 LYAANENTEKLYKEVRORTNALDVOFCWYLIQTLRFNGT------RVF------SKETSDEATFAFA 479 (712)
                    Q Consensus
                    +..-.++..+|.-... +|--++=|+.-+|.+.|. ...+ ....+..+.+.+.|. 366 ~-i-egd--vL--l---ld-w-aAhladLl---g-L------dl-s----ld-s---lre--Ll-YA
                    366 VDIISGKIHSILPVMES----LDSCTAAFTAMICEAKGLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNSFA
 T 4xmm D
                                                                                                                 441 (715)
                        T ss dssp
                        НИННСССИНИНИНИНН----сСhининининин
 T ss pred
 Q ss pred
                        Q Fri_Mar_04_23: 480 AQLE---FAQLHGHSLFVSCFLN--DDKAAEDTIKRLVMREITLLRAST-ND--HILNRLKIP--SQLIFNAQALKDRYE
                                                                                                                 549 (712)
                    480 ~QLe---~Glw~~AvFVllHl~--d~~R~aIr~lL~R~~~~~~---L~e~L~IP--~~WI~eAkAl~ar~~
 Q Consensus
                                                                                                                 549 (712)
                    .|- ..+|+-|+=+|.+.+ +...+..|.++|.+++++++++++|...=|++..|...=|++..|.+42 --|-1------|W-vai-yL-c----g------i-elL-r--Pl-t------k-l-iC----L---a--I-----g------
 T Consensus
                    {\tt 442} \ \ {\tt FELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSATGTRSAKKMVIAELLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSICVEWRLPH-YPFVTNDDIEWMLSTATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTRSATGTR
 T 4xmm D
                                                                                                                 520 (715)
 T ss_dssp
                        T ss_pred
                        HhhhcccCcchнинниннCccchниннинннинсс-ССССсниннинниннинссСининниннинниннин
                        ССНИНИННИННСССИННИННИНННЫНННННН
 Q ss pred
 Q Fri_Mar_04_23: 550 GNYLSEVQNLLLGSSYDLAEMAIVTSLGPRLLLSNNPVQNNELKTLREILNE 601 (712)
 O Consensus
                    550 qd---e--Ll-A----eAH-v-v-laP--II-----d---L--Ll--
                                                                                  601 (712)
                    T Consensus
                    521 HNIIESIANFSRAGKYELVKSYSW-LLFEASCME---GQKLDDPVLNAIVSK 568 (715)
 T 4xmm D
                         ---СНИНИНИС-----СНИНИНИ-ИНИНИНИНИ---ИНС----СНИНИНИС
 T ss dssp
 T ss_pred
                        ССНИНИНИННЕССИНИНИННИН-НИНИННЫ --- СССССИНИННИННЫ
                                     PDB™
PROTEIN DATA BANK
 No 9
                                               NCBI Pub Med
->3jrp_A Fusion protein of protein transport protein SEC13 nucleoporin NUP145; protein complex, cytoplasmic
 vesicle, endoplasmic reticulum; 2.60A {Saccharomyces cerevisiae}
 Probab=97.47 E-value=2.8e-05 Score=84.14 Aligned_cols=58 Identities=100% Similarity=1.383 Sum_probs=0.0
 Q ss pred
                        HHhhccccchhHHHhhcccccccCCccchhhccCCcceeecccccceeecccc
 Q Fri_Mar_04_23: 122 IDLLFSECNDEIDNAKLIMKERRFTASYTFAKFSTGSMLLTKDIVGKSGVSIKRLPTE 179 (712)
 O Consensus
                    122 --|I.F--fn----k----r|-----f-----||-------
                                                                                         179 (712)
                    T Consensus
                    322 IDLLFSECNDEIDNAKLIMKERRFTASYTFAKFSTGSMLLTKDIVGKSGVSIKRLPTE 379 (379)
 T 3jrp A
                         -----CTHHHHHHHTTCCTTCCCEEEETTTEEEEECTTSSSSEEEEECCCC
 T ss_dssp
 T ss_pred
                         hhhhHHHHHHHHHHHHHHhhhhhccCCccEEEEcCCceEEeccCCC
                                      PDB
                                                 NCBI
 No 10
                                                            Pub Med
>3iko_c Nucleoporin NUP84; NFC, transport, WD repeat, autocatalytic cleavage, mRNA transport, nuclear pore
 complex, nucleus, phosphoprotein; 3.20A {Saccharomyces cerevisiae} PDB: 4xmm _F 4xmm _F 3jro _C
Probab=96.24 E-value=0.05 Score=61.34 Aligned_cols=267 Identities=13% Similarity=0.135 Sum_probs=0.0
 Q ss pred
                        Q Consensus
 T Consensus
 T 3iko_C
                     71 EARFWHLVELLLVFRNADLDLDEMELHPYNSRGLFEKKLMQDNKQLYQIWIVMVWLKENTYVMERPKNVPTSKWLNSITS 150 (460)
 T ss_dssp
                        ннининининныесСссссссссссссссссснинининныннынныннынны
 T ss pred
                        ------ннининнныесссинининнныесссининниннн
 Q ss pred
 T Consensus
 T 3iko C
 T ss_dssp
                        T ss_pred
                         --ннесссенининининининсс----с-ссенинининнесссесссенынининин----
 Q ss_pred
 Q Fri Mar 04 23: 324 --SYLGSNDPRIRDLAELQLQKWSTGG----C-SIDKNISKIYKLLSGSPFEGLFSLKELESEFSWLCLLNLTL----
                                                                                                                 390 (712)
                    O Consensus
 T Consensus
                    231 FNTQQGIKK------HSLWRRTVYSLSQQAGLDPYERAIYSYLSGAI----PNQEVLQYSDWESDLHIHLNQILQ 295 (460)
 T 3iko C
                        T ss dssp
                        ccccCchh------hhhhccccСнининннннннн
 T ss_pred
 Q ss pred
                        Q Fri_Mar_04_23: 391 ------CYGQI-DEY-SLESLVQSHLDKFSLPYDDDIGVIFQLYAANENTEKLYKEVRQRTNALD--- 447 (712)
```

```
Q Consensus
                    391 ------WYg~-~~-sl~av~y~~~P~~P~~LkkLya~~~le~vL~p~s~t~~lD---- 447 (712)
                    T Consensus
                     296 TEIENYLLENNQVGTDELILPLPSHALTVQEVLNRVASRHPSESEHPIRVLMASVILD-SLPSVIHSSVEMLLDVVKGTE 374 (460)
 T 3iko C
                         T ss_dssp
                         T ss pred
                         -----ссhинининине
 Q ss pred
 Q Fri_Mar_04_23:
                    448 -----VQFCWYLIQTLRFNGTRVFSKETSDEATFAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDTIKRLVM
                                                                                                              513 (712)
 Q Consensus
                     448 \hspace{0.1in} -----rLsW-L\sim vL-a-g\sim -s\sim -d-Lt\sim sfA-QLe\sim -Glw\sim AvFVllHl\sim d\sim -R\sim alr\sim lL\sim -d-Lt\sim -d-Lt
                                                                                                              513 (712)
                     T Consensus
                                                                                                             451 (460)
                     375 ASNDIIDKPYLLRIVTHLAICLDIINPGSVEEVDKSKLITTYISLLKLQGLYENIPIYATFLNESDCLEACSFILSS 451 (460)
 T 3iko C
 T ss_dssp
                         T ss_pred
                         PDB"
                                                  NCBI
                                                              Pub Med
 No 11
>2pm7_A Protein WEB1, protein transport protein SEC31; beta propeller, alpha solenoid; 2.35A {Saccharomyces
 cerevisiae} PDB: 2pm6
                          _A 3mzl _B
 Probab=96.23 E-value=0.066 Score=59.33 Aligned_cols=219 Identities=12% Similarity=0.005 Sum_probs=0.0
                         Q ss pred
 Q Fri_Mar_04_23: 289 SNEIEQIFLYLLLNDVVRASKLAIESKNGHLSVLISYLGSNDPRIRDLAELQLQKWSTGGCSIDKNISKIYKLLSGSPFE 368 (712)
                     Q Consensus
                    T Consensus
                                                                                                                  217 (399)
 T 2pm7 A
                                                                                                                 217 (399)
 T ss_dssp
                         SHHHHHHHHHHTTCHHHHHHHHTTCCH----НННННННН
 T ss_pred
                         Q ss_pred
                         Q Fri Mar 04 23: 369 GLFSLKELESEF-SWLCLLNLTLCYGQIDEYSLESLVQSHLDKFSLPYDDPIGVIFQLYAANENTEKL----- 435 (712)
 Q Consensus
                     369 ~~~~~i~e~L-dW~ralgL~LWYg~~~~sl~av~~y~~~~P~~~D~~~LLkLya~~~~le~v------
                                                                                                                 435 (712)
                    T Consensus
 T 2pm7_A
 T ss_dssp
                         T ss pred
                         ---ННННhcCCHHHHHHHHHHHCCCCchhHHHHHHHHHHHHH--HhCCChhhhhhHhhhccChHHHHHHHhhhhcccc
 Q ss_pred
                        -----hCcccCCCcccchнининин---СсссСссьнинининининин
 Q Fri_Mar_04_23: 436 -----YKEVRQRTNALDVQFCWYLIQTLRFN--GTRVFSKETSDEATFAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDTI
                                                                                                                 508 (712)
                     436 ----L-p-s-t-~-lD-rLsW-L-~vL-a--g~~~s~~-d-Lt-sfA-QLe-~Glw~~AvFVllHl-d~~~R~aI 508 (712)
 O Consensus
                    T Consensus
                     293 DKLKKDNKTIYEAHSECMTEFIERFTVFSNFINGSSTINNEQLIAKFLEFINLTTSTGNFELATEFLNSLPSDNEEVKTE
 T 2pm7_A
 T ss_dssp
                         T ss_pred
 Q ss_pred
                        НННННhhccc
 Q Fri_Mar_04_23: 509 KRLVMREITL 518 (712)
                     509 r~lL~R~~~ 518 (712)
 Q Consensus
                        |+=|.++...
~~Rl~~a~~~
 T Consensus
                    373
                                     382 (399)
                    373 KARVLIASGK 382 (399)
 T 2pm7_A
                         нининннс-
 T ss_dssp
 T ss pred
                         HHHHHhCcCC
 No 12
                                       PDB"
                                                  NCBI
                                                                       Pub Med
>4ycz_8 NUP85; structural protein complex, nuclear pore complex, macromolec assemblies, structural protein; 4.10A
 {Thielavia heterothallica}
 Probab=96.11 E-value=0.019 Score=69.31 Aligned cols=276 Identities=12% Similarity=0.046 Sum probs=0.0
                         Q ss pred
 Q Fri Mar 04 23: 289 SNEIEQIFLYLLLNDVVRASKLAIESKNG------HLSVLISYLGSNDPRIRDLAELQLQK
                                                                                                                  343 (712)
                    Q Consensus
                                                                                                                 343 (712)
                    T Consensus
                                                                                                                 299 (933)
                     221 SLFWQAVFIALLRGKVGDAARLLDQAGWGHVRRGQRGEYAYVGQALENVQRAVDETIAVLESCPGFD-GNWEIWSSDWTL
 T 4ycz_B
                                                                                                                 299 (933)
 T ss dssp
                         T ss pred
                         HHHC------HHHHHHHHhhCCCccccccchh
 0 ss pred
 Q Fri_Mar_04_23:
                        WSTG-----KNISKIYKLLSGSPFEGLFSLKE
                                                                                                                 375 (712)
                     344 W~~~~kIY~LLAG~~e~~~~
                                                   +. -.+
                                                                                      +.+..||++|.|+.
                     300 wR--v-al--L---aeg----l----F--s-----r-aes-vpw-i---L--l--IllGd------
 T Consensus
                                                                                                                 372 (933)
                     300 FRVRARGLLEHLRRFAEGKDSAFGASAFSASAASAQSRQSMAGLARRAESQVPWEIYENLNIVFDIVLGQQ------GA 372 (933)
 T 4ycz B
                         нининининининин
 T ss dssp
 T ss pred
                         Q ss_pred
```

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Q Fri_Mar_04_23: 376 LES-EFSWLCLLNLTLCYGQIDE-------YSLESLVQSHLDKFS------LPYDDPIGVI 422 (712)
O Consensus
            376 i~e--LdW~ralgL~LWYg~~~~---P~~~L
            ~n~~~~E~
T Consensus
                                                                       452 (933)
             373 ILEAAQDWLEATVGLFGWWDERASRTEKPLSTSQSLSRSQALVLASAPANSESYLDRLARAFHTAVESDFHFNSQNAVEI
T 4ycz_B
               HTTCCSSHHHHHHCC-----CHH
T ss_dssp
               НИНИССЕНИИНИНИНИНИН
T ss pred
               ннньсссснинь
Q ss pred
Q Fri_Mar_04_23:
             423 FQLYAANENTEKLYKEVRQRTN------ALDVQFCWYLIQTLRFNGTRVFSK------ETSDEATFA
                                                                       477 (712)
            532 (933)
T Consensus
             453 GMACVFEDNIKGVIGLLRGWSLPIAAAVAEIASLGKWLPPHRPSGVYGLEDLDMDDLEVLGMDPGAPDEVDGIKDSTLVQ
T 4ycz B
                                                                       532 (933)
T ss_dssp
               HHHHHHSSCCHHHHHHHHHSSCTHHHHHHHHHTTTSCC------CCSSSSSHHHH
               ниннинессининининнессининниннинн
T ss_pred
               Q ss pred
Q Fri Mar 04 23: 478 FAAQLEF------AQLHGHSLFVSCFLNDDKAAEDTIKRLVMREITLLRASTNDHILNRLKIPSQL-----
                                                                       537 (712)
             478 fA-QLe-----Glw-AvFVllHl-d---R--aIr-lL-R------L-e-L-IP--W-----
Q Consensus
                           .++|+-|+=||.++.+....|+++|..++..++.+.+.+.+.-+.|-..|
             533 YA--L-s---l-----l---r-lWevai-yL--c---g------elLe-lL-r-Pl-t---vdkvl-iC-elgL---a 612 (933)
T Consensus
             533 YAQALADYEGLSSVQDRSGTSKDGWELSISVLGRMDSPERSEEMVRDLVEHLVQQLHVDSNATVDRLWFLLNELGMIEFA 612 (933)
T 4ycz B
               T ss_dssp
               T ss_pred
               --нининининьс-ссининининисссининини
Q ss_pred
Q Fri_Mar_04_23: 538 --IFNAQALKDRYE-GNYLSEVQNLLLGSSYDLAEMAI 572 (712)
            538 --I~eAkAl~ar~~-qd~~~e~~~Ll~A~~~~eAH~v~
Q Consensus
                                          572 (712)
                 |++-.|.+...+ |+|-.++.+++|+++...++|.
             613 r~I~k~~g~~l~~~s~ryGeAL~~~arA~d~~~V~~V~
T Consensus
                                          650 (933)
T 4ycz_B
             613 EDTTETYGDILARDSHRYGEAMWYYALAHRPNKVREVM
                                          650 (933)
               НИНИНИННТТSSSCSTHHHHHHHHSSSCHHHHHHHH
T ss_dssp
               НИНИНИНИННИНННИН
T ss pred
                                            Pub Med
>3mzk B Protein transport protein SEC16; alpha-helical-stack, beta-propeller; 2.69A {Saccharomyces cerevisiae}
Probab=95.73 E-value=0.029 Score=62.93 Aligned cols=112 Identities=14% Similarity=0.234 Sum probs=0.0
               Q Fri Mar 04 23: 292 IEQIFLYLLLNDVVRASKLAIESKNGHLSVLISYLGSNDPRIRDLAELQLQ-KWSTGGC---SIDKNISKIYKLLSGSPF 367 (712)
            292 \ \text{-e-if--L-g--I--A---Ai--gn-rLA-Llsq-gs-----r----QL---W------I-----kIY-LLAG----}
O Consensus
                                                                       367 (712)
            231 (441)
T Consensus
            154 QMRVLAFLQTGNHDEALRLALSKRDYAIALLVGSLMGKD-RWSEVIQKYLYEGFTAGPNDQKELAHFLLLIFQVFVGNS-
T 3mzk B
               НИНИНИНИТСИНИНИНИНИТСИНИНИНИНИТСИН-ИНИНИНИНИСС-----СТИНИНИНИНИНИТТСИ-
T ss_dssp
               нинининессининининессининининесси-ининининесси-ининининесси-ининининесси-
T ss_pred
Q ss_pred
               ссссссhhhccCC------СНИНИННИННСССССССС------НИНИННИНН
Q Fri Mar 04 23: 368 EGLFSLKELESEF-----SWLCLLNLTLCYGQIDEYS-----LESLVQSHLDKF 411 (712)
             T Consensus
            232 -----KMAIKSFYTNNETSQWASENWKSIVAAVLINIPENNEDPLLIPPVVLEFLIEFGIFL 288 (441)
T 3mzk B
               T ss_dssp
T ss pred
               -----ННИНН
No 14
                                            Pub Med
->4bzj_A Protein transport protein SEC31; secretion, trafficking; 40.00A (Saccharomyces cerevisiae) PDB: 4bzk_A
Probab=95.63 E-value=0.061 Score=68.02 Aligned_cols=215 Identities=12% Similarity=0.037 Sum_probs=0.0
               «ССНИНИННИННОССИНИНИНИННОСС««НИНИНИНН» СССЬНИНИНИННИННЕСС«ССИНИНИННИННОСС«
Q ss pred
Q Fri_Mar_04_23:
            288 SSNEIEQIFLYLLLNDVVRASKLAIESKNGHLSVLISYLGSNDPRIRDLAELQLQKWSTGGCSIDKNISKIYKLLSGSPF
                                                                       367 (712)
             288 ----e-if--L-g--I--A---Ai--gn-rLA-Llsq-gs----r----QL--W-----I-----kIY-LLAG---
                                                                       367 (712)
            T Consensus
                                                                       581 (1273)
             507 SGNIEQTISKNLVSGNIKSAVKNSLENDLLMEAMVIALDSNNE-RLKESVKNAYFAKYGSK----SLSRILYSISKREV
T 4bzi A
                                                                       581 (1273)
T ss dssp
               T ss_pred
               Ссьининининесссининининессинининин
               Q ss_pred
Q Fri Mar 04 23: 368 EGLFSLKELESEF-SWLCLLNLTLCYGQIDEYSLESLVQSHLDKFSLPYDDPIGVIFQLYAANENTEKL----- 435 (712)
            O Consensus
T Consensus
                                                                       655 (1273)
             582 DD----LVENLDVSQWKFISKAIQNLYPNDIAQRNEMLIKLGDRL--KENGHRQDSLTLYLAAGSLDKVASIWLSEFPDL
T 4bzj A
                                                                       655 (1273)
T ss dssp
               HH----HhccCнинининининининининининининин--ннсссьнынынынининининыныныныныны
T ss_pred
Q ss pred
               ------hCcccCCCcccchнинининнь---СсссСсьнининининнин
Q Fri Mar 04 23: 436 -----YKEVRORTNALDVQFCWYLIQTLRFN---GTRVFSKETSDEATFAFAAQLEFAQLHGHSLFVSCFLNDDKAAED 506 (712)
```

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Q Consensus
                           436 ----L-p-s-t---lD-rLsW-L--vL-a---g----s----d-Lt-sfA-QLe--Glw--AvFVllHl-d---R-- 506 (712)
                           T Consensus
                                                                                                                                                       734 (1273)
                            656 EDKLKKDNKTIYEAHSECLTEFIERFTVFSNFINGSSTINNEQLIAKF-LEFINLTTSTGNFELATEFLNSLPSDNEEVK 734 (1273)
 T 4bzi A
                                 НИНИНТТТССИНИНИНИНИНИНИНИНТТSCC---СССИНИНИН-ИНИНИНТТТСИНИНИНИНН SCTTCHHH
 T ss dssp
                                 hhhccccCccchhнинининининининин
 T ss pred
                                 ннннннн
 Q ss pred
 Q Fri_Mar_04_23: 507 TIKRLVMR 514 (712)
 Q Consensus
                           507 aIr~lL~R 514 (712)
                           ..|+=|.+
735 ~~r~r~~ 742 (1273)
 T Consensus
                           735 TEKARVLI 742 (1273)
 T 4bzj_A
 T ss_dssp
                                 нининин
 T ss_pred
 No 15
                                                    PDB"
                        S
                                                                                             Pub Med
              Nuclear pore complex protein NUP107; transport protein; 23.00A {Homo sapiens}
  Probab=94.68 E-value=0.67 Score=56.68 Aligned_cols=268 Identities=13% Similarity=0.169 Sum_probs=0.0
 Q ss_pred
                                 Q Fri Mar 04 23: 292 IEQIFLYLLLNDVVRASKLAIESKNGHLSVLISY------LGSNDPRIRDLAELQLQKWSTGGC----- 349 (712)
                           292 -e-if--L-g--I--A---Ai--gn-rLA-Llsq------------gs-----r----QL--W------------ 349 (712)
 Q Consensus
                           T Consensus
 T 5a9q_4
                           347 LKYLFTLIRAGMTEEAQRLCKRCGQAWRAATLEGWKLYHDPNVNGGTELEPVEGN-PYRRI------WKISCWRMAEDE 418 (925)
                                 HHHHHHHHHTCHHHHHHHHHTCHHHHHHHTTSBCBCTTTCCTTCCSSCBSB-SCHH------HHHHHHHHHHHCS
 T ss dssp
 T ss_pred
                                 Q ss_pred
                                 Q Fri_Mar_04_23: 350 SIDKNISKIYKLLSGSPFEGLFSLKELESEFSW------LCLLNLTLC------YGQIDE-----YSLESL
                                                                                                                                                       403 (712)
                           Q Consensus
                                                                                                                                                        403 (712)
 T Consensus
                                                                                                                                                        492 (925)
 T 5a9q 4
                            419 LFNRYERAIYAALSGNL----KQLLPVCD--TWEDTVWAYFRVMVDSLVEQEIQTSVATLDETEELPREYLGANWTLEKV
                                                                                                                                                        492 (925)
 T ss_dssp
                                 T ss_pred
                                 CCCHHHHHHHHHHCCc----HHhhhccC--СНИНННИНННИНННННННННННННОССссссссСсhhhccCccCHHHH
                                 ННННННhhCCC----ccCHHHHHHHHhcCCC-----CHHHhhCcccCCCCcccchHHHHHHHHHhcCccccCchhHHH
 Q ss_pred
 Q Fri_Mar_04_23: 404 VQSHLDKFSLP----YDDPIGVIFQLYAANE-----NTEKLYKEVRQRTNALDVQFCWYLIQTLRFNGTRVFSKETSDE
                                                                                                                                                       473 (712)
 O Consensus
                            404 v--y----P-----D----LLkLya-------le-vL-p-s-t---lD-rLsW-L--vL-a-g----s---d-
                                                                                                                                                        473 (712)
                           T Consensus
 T 5a9g 4
                            493 FEELQATDKKRVLEENQEHYHIVQKFLILGDIDGLMDEFSKWLSKSRNNLPGHLLRFMTHLILFFRTLG-LQTKEEVSIE 571 (925)
                                 T ss_dssp
 T ss_pred
                                 нинннееССссеррирования и выпуска в при в п
                                 нининининиссенининин
 Q ss pred
 Q Fri_Mar_04_23: 474 ATFAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDT------IKRLVMREITLLRASTNDHI
                           474 Lt~sfA~QLe~~Glw~~AvFVllHl~d~~~R~~a-------Ir~lL~R~~~~~~~L
  Q Consensus
                                                                                                                                                        527 (712)
                            +-..|+.-|...|+.+.-.|-..+|+.+...+...

572 II--YI--L-----eLIplYaS-Lp----e-Ys--L--i-d--eR---L-la---glDv--i-k--ve-i------
 T Consensus
                                                                                                                                                        651 (925)
                            572 VLKTYIQLLIREKHTNLIAFYTCHLPQDLAVAQYALFLESVTEFEQRHHCLELAKEADLDVATITKTVVENIRKKDNGEF
 T 5a9q 4
                                                                                                                                                       651 (925)
 T ss dssp
                                 HHHHHHHHHHHTCCGGGHHHHTTCGGGGTC------
 T ss_pred
                                 НН------НhСсСнининининин-hСССнин-------ннининссСнинининин
 Q ss pred
 O Fri Mar 04 23: 528 LN------RLKIPSOLIFNAOALKDR-YEGNYLSE-------VONLLLGSSYDLAEMAIVT 574 (712)
                           528 ~e-----L-IP--WI-eAkAl-ar---gd---e---Ll-A----eAH-v-v-
 O Consensus
                            T Consensus
                            652 SHHDLAPALDTGTTEEDRLKIDVIDWLVFDPAQRAEALKQGNAIMRKFLASKKHEAAKEVFVK 714 (925)
 T 5a9q 4
                                 T ss dssp
                                 T ss pred
                                                    PDB"
 No 16
                                                                                   Pub Med
>5cqr_A Elongator complex protein 1; familial dysautonomia, ELP1 subunit, DIME protein binding; 3.02A {Homo
  sapiens}
 Probab=84.41 E-value=7.1 Score=45.71 Aligned_cols=102 Identities=11% Similarity=0.102 Sum_probs=0.0
                                 Q ss_pred
 O Fri Mar 04 23: 473 EATFAFAAOLEFAOLHGHSLFVSCFLNDDKAAEDTIKRLVMREITLLRASTNDHILNRLKIPSOLI------ 538 (712)
                           O Consensus
                           17.5 Bt SIA gibe diw AVVVIII to the transfer of transfer of the transfer of transfer o
 T Consensus
 T 5cqr_A
 T ss dssp
                                 НИНИНИНИНТТСИНИНИНИННТС-----ИНИНИНИНТТСНИНИНИНТТССИНИНИНИНИННИН
                                 T ss_pred
 Q ss pred
                                 ---нининининосссининининисссининининины
 Q Fri_Mar_04_23: 539 ---FNAQALKDRYEGNYLSEVQNLLLGSSYDLAEMAIVTSLGPRLL 581 (712)
```

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O Consensus
                     539 ---~eAkAl~ar~~gd~~~e~~~Ll~A~~~~eAH~v~v~laP~~I 581 (712)
                     .+|..++.+|-||+...+++|.|++|-+++--|+++
350 g~~eA~~~~l-d~~AI-ll~~a~~~eA~-La~~~~dl~ 395 (622)
 T Consensus
                      350 RKHIDAAMVLEECAQDYEEAVLLLLEGAAWEEALRLVYKYNRLDII
 T 5car A
                                                                                 395 (622)
                          тснининнинн
 T ss dssp
                          T ss pred
                                         PDB"
                                                                           Pub Med
 No 17
->5cqs A Elongator complex protein 1; familial dysautonomia, ELP1 subunit, DIME protein binding; 2.70A
  {Saccharomyces cerevisiae}
 Probab=76.91 E-value=8 Score=43.15 Aligned cols=109 Identities=16% Similarity=0.113 Sum probs=0.0
                          Q ss_pred
 Q Fri_Mar_04_23: 473 EATFAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDTIKRL----VMREITLLRASTNDHILNRLKIP---SQLIFNAQAL
                                                                                                                        544 (712)
 O Consensus
                     473 \text{ $\sim$Lt$-sfa-QLe} - \text{Glw}-\text{AvFVllHl}-\text{d}---\text{R}-\text{alr}-\text{l}-----\text{L}-\text{R}------\text{L}-\text{e}-\text{L}-\text{iP}-----\text{WI}-\text{eAkAl}}
                                                                                                                        544 (712)
                     T Consensus
                                                                                                                        188 (435)
                      109 VIYNIYAKHLSSNOMYTDAAVAYEMLGKLKEAMGAYQSAKRWREAMSIAVQKFPEEVESVAEELISSLTFEHRYVDAADI
 T 5cas A
                                                                                                                        188 (435)
 T ss_dssp
                          НИНИНИНИТТТТСИНИНИНИНТТСИНИНИНИТТСИНИНИНИТСТИТИНИТТСИТИТЕТ
                          T ss_pred
                          ннннсссининнинннессининнинннинн
 Q ss pred
 Q Fri_Mar_04_23: 545 KDRYEGNYLSEVQNLLLGSSYDLAEMAIVTSLGPRLL
                                                                      581 (712)
                      545 ~ar~~gd~~~e~~~Ll~A~~~~eAH~v~v~~laP~~I
 Q Consensus
                          +..|.||+-..+..|+++.|++|-++.-++-|+.+
v----d---AI--1------eA--La-----d1-
 T Consensus
                     189 y~~
                                                                      225 (435)
                      189 QLEYLDNVKEAVALYCKAYRYDIASLVAIKAKKDELL
 T 5cqs A
                                                                      225 (435)
 T ss_dssp
                          ниннессинининнинттсинининнинттсттин
 T ss_pred
                          ннньссениннинннессиннинннинн
                                         PDB"
 No 18
                                                                           Pub Med
>2qx5 A Nucleoporin NIC96; mRNA transport, nuclear pore complex, nucleus, protein transport, translocation,
 transport, transport protein; 2.50A {Saccharomyces cerevisiae} PDB: 2rfo
 Probab=70.71 E-value=1.1e+02 Score=36.23 Aligned_cols=271 Identities=10% Similarity=0.036 Sum_probs=0.0
                          НННННhCCCннннннннннсссе-----енннн-----ннесссьнинннннннннннннсссессниннннннh
 Q ss pred
 Q Fri Mar 04 23: 295 IFLYLLLNDVVRASKLAIESKNG-----HLSVLI-----SYLGSNDPRIRDLAELQLQKWSTGGCSIDKNISKIYKLLS
                                                                                                                        363 (712)
                      Q Consensus
                      T Consensus
                                                                                                                       238 (661)
                      159 IFYLLRAGLIKEALQVLVENKANIKKVEQSFLTYFKAYASSKDHGLPVEYSTKLHTEYNQHIKSSLDGDPYRLAVYKLIG
 T 2qx5 A
                                                                                                                        238 (661)
                          T ss dssp
                          нининессинининины
 T ss pred
 Q ss_pred
                          ССесесесентиненнин и получения и получения
 Q Fri_Mar_04_23: 364 GSPFEGLFSLKELESEFSWLCLLNLTLCYGQIDEYSLES----LVQSHLDKFS---LPYDDPIGVIFQLYAANENTEKL
                                                                                                                        435 (712)
                      364 G---e---i-e-LdW-ralgL-LWYg-----sl----av--y-----P---P----LLkLya----le-v
 Q Consensus
                                                                                                                        435 (712)
                          T Consensus
                                                                                                                        313 (661)
                      239 RCDLSRKNIPAVTLSIEDWL---WMHLMLIKEKDAENDPVYERYSLEDFQNIIISYGPSRFSNYYLQTLLLSG--LYGLA
 T 2qx5 A
                                                                                                                        313 (661)
 T ss_dssp
                          T ss pred
 Q ss_pred
                          hCcccCCCcccchнинининньсссссСс-----hhнинининннинисСссинининн
 Q Fri Mar 04 23: 436 YKEVRQRTNALDVQFCWYLIQTLRFNGTRVFSK------ETSDEATFAFAAQLEFAQLHGHSLFVSCFLNDD---
                                                                                                                        501 (712)
                      436 L~p~s~t~~lD~rLsW~L~~vL~a~g~~~s~-----d~Lt~sfA~QLe~~Glw~~AvFVllHl~d~---
 O Consensus
                                                                                                                        501 (712)
                          --..++...|+...+....-..|+.-+..|..-
                      314 I--L-----vd---AVH-AIaL---gLL-----lls------lnfarLI--Yt--F----d---Al-Y--li----d-
 T Consensus
                                                                                                                        388 (661)
                      314 IDYTYTF-SEMD---AVHLAIGLASLKLFKIDSSTRLTKKPKRDIRFANILANYTKSFRYS-DPRVAVEYLVLITLNEGP
 T 2qx5_A
                                                                                                                        388 (661)
 T ss_dssp
                          T ss_pred
                          ---НИНИНИНИНННЫМ-----ссссенн------нинин------нинин------
 Q ss pred
                      502 ---KAAEDTIKRLVMREI-----TLLRAST-----NDHIL-----NRLKIPSQLIFNAQALKDRYEGNYLSEVQN
 Q Fri Mar 04 23:
                                                                                                                        558 (712)
                      502 ---~R~~aIr~lL~R~~---------------------------e-L~IP~~WI~eAkAl~ar~~gd~~e~~-
 Q Consensus
                                                                                                                        558 (712)
                             T Consensus
                                                                                                                        465 (661)
                      389 TDVELCHEALRELVLETKEFTVLLGKIGRDGARIPGVIEERQPLLHVRDEKEFL--HTITEQA-ARRADEDGRIYDSILL
 T 2qx5_A
                                                                                                                        465 (661)
 T ss dssp
                          НИНИНИНИНИНИНИНИНИССИНИНИСЕССТІЗСЕЕССИНИНІССОСТІЗСЕНИНИН—-ИНИНИНИ-ИНИНИНІТСИНИНИНИ
 T ss pred
                          0 ss pred
                          НННссСНННННННННН
 Q Fri_Mar_04_23:
                     559 LLLGSSYDLAEMAIVTSLGP
                      559 Ll~A~~~eAH~v~v~~laP
                          +--||+|+.|-++.+.|+.
 T Consensus
                      466 Y~La~~~d~vl~lln~~Ls~
                                                   485 (661)
 T 2qx5 A
                      466 YOLAEEYDIVITLVNSLLSD
                                                   485 (661)
                          ннитсининининини
 T ss dssp
 T ss pred
```

```
PDB
                      SCOPe
                                                Pub Med
->103u_A Conserved hypothetical protein TM0613; structural genomics, joint center for structural genomics, J
protein structure initiative, PSI; 1.75A {Thermotoga maritima} SCOP: a.24.16.3
 Probab=37.90 E-value=2.8e+02 Score=25.47 Aligned_cols=93 Identities=22% Similarity=0.199 Sum_probs=0.0
              Q ss pred
Q Fri Mar 04 23: 475 TFAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDTIKRLVMREITLLRASTNDHILNRL----KIPSQLIFNAQALK----
                                                                  545 (712)
            475 t-sfA-QLe--Glw--AvFVllHl-d---R--aIr-lL-R------L-e-L----IP--WI-eAkAl-----
O Consensus
                                                                  545 (712)
            .+.-|.-+..|.||||++ ...+..++.|...-..+..|...+ ...|...+ ...|...+...|.

19 ~L~~A~~~l~~g~y~~a~F~aq~----QA~EkalKAlL~~g~~pktH~l~~Ll~~l~~~~e~~~~L~~yi~
T Consensus
                                                                   93 (135)
            T 1o3u A
                                                                   93 (135)
T ss dssp
              T ss pred
Q ss_pred
              нньссн----ннннннннессинннннн
Q Fri Mar 04 23: 546 DRYEGNY----LSEVQNLLLGSSYDLAEMAI 572 (712)
            546 ar~~qd~----e~~~Ll~A~~~~eAH~v~
O Consensus
                                    572 (712)
            +||.+++ ...+.--...+.|.+++
94 -RYp------P----t-e-ae-ai--Ae-vi 125 (135)
T Consensus
            94 TRYPDALPSGSPRNRYSRIEAERLVNYAEKII 125 (135)
T 103u A
T ss_dssp
              ----CCSCTTHHHHHHHHHHHHHHHHHH
T ss_pred
              hcCCccccCCcccCCHHHHHHHHHHHHH
                     PDB<sup>N</sup>
PROTEIN DATA BANK
NCBI
                                    Pub Med
>2pm7 A Protein WEB1, protein transport protein SEC31; beta propeller, alpha solenoid; 2.35A {Saccharomyces
cerevisiae PDB: 2pm6
               A 3mzl B
Probab=35.36 E-value=3e+02 Score=30.14 Aligned_cols=166 Identities=14% Similarity=0.081 Sum_probs=0.0
              Q Fri_Mar_04_23: 140 MKERRFTASYT-FAKFSTGSMLLTKDIVGKSGVSIKRLPTELQRKFLFDDVYLDKEIEKVTIEARKSNPYPQISESSLLF 218 (712)
            O Consensus
              T Consensus
             7 LQAPTWYGEPSPAAHWAFGGKLVQITPDGKG-VSITNPKISGLESNTTLSEALKT-----KD-----FKPL
T 2pm7 A
                                                                   66 (399)
T ss_dssp
              T ss_pred
              Q ss pred
Q Fri_Mar_04_23: 219 KDALDYMEKTSSDYNLWKLSSILFDPVSYPYKTDNDQVKMALLKKERHCRLTSWI----VSQIGP-----
O Consensus
            219 ~d~~~~~e~~vW~L~saLFd~~~~~~~~Rr~~Ls~WL---~~v~~~~
                                                                  279 (712)
            T Consensus
T 2pm7_A
            67 INQRLVKVIDDVNEEDWNMLEKL-SMDG------TEEFLKEALAFDNDESDAQDDANNEKEDDGEEFF 127 (399)
T ss dssp
              T ss pred
              -----Ссени
Q ss pred
            280 -----EIEEKIRN---SSNEIEQIFLYLLLNDVVRASKLAIESK-----NGHLS 320 (712)
Q Fri_Mar_04_23:
            T Consensus
T 2pm7 A
              ---сссссссссвсссянняннинниттснининниттснининнинттсссинининнинниннинттвснин
T ss_dssp
T ss_pred
              нниннесссенинининининини
Q ss pred
Q Fri Mar 04 23: 321 VLISYLGSNDPRIRDLAELQLQKWST 346 (712)
            321 ~Llsq~gs~~~~r~~~~QL~~W~~ 346 (712)
O Consensus
              +|-+.+++-+.+-.... |..||+
            208 11~~v~~~~v~~~-1~~Wre
                                231 (399)
T Consensus
            208 TLYSTSKREVDDLVENLD--VSOWKF
T 2pm7 A
                                231 (399)
T ss dssp
              НННННТТССНННННВС--GGGHHH
T ss_pred
              нининессининнь ссс--инини
No 21
                                          Pub Med
>3mkq B Coatomer subunit alpha; beta-propeller, alpha-solenoid, transport protein; 2.50A {Saccharomyces
Probab=29.44 E-value=4.4e+02 Score=25.24 Aligned_cols=96 Identities=15% Similarity=0.016 Sum_probs=0.0
              Q ss pred
Q Fri Mar 04 23: 476 FAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDTIKRLVMREITLLRAST-----NDHILNRLKIPSQLIFNAQALKD
                                                                  546 (712)
            Q Consensus
                                                                  546 (712)
              ..|--.|+ .|.|+.|.=++..+..=+..-+..+..=-.+-.-
            T Consensus
                                                                   86 (177)
            10 IRFDLALE-YGNLDAALDEAKKLNDSITWERLIQEALAQGNASLAEMIYQTQHSFDKLSFLYLVTGDVNKL--SKMQNIA
T 3mkq_B
                                                                   86 (177)
              T ss dssp
              T ss pred
              ньсссининининессинининин
Q ss pred
Q Fri_Mar_04_23: 547 RYEGNYLSEVQNLLLGSSYDLAEMAIVT 574 (712)
            547 r--qd---e--Ll-A----eAH-v-v- 574 (712)
O Consensus
```

```
.+. | ++-...+++.+ | ++++ | -++++.
               87 ---g---A----l--g----ai-m--- 114 (177)
 T Consensus
               87 QTREDFGSMLLNTFYNNSTKERSSIFAE 114 (177)
 T 3mka B
                  ннттснининининтснининини
 T ss dssp
 T ss_pred
                  ннсссининининнессинининин
                            PDB"
 No 22
                                    NCBI
                                                  Pub Med
->4bzj_A Protein transport protein SEC31; secretion, trafficking; 40.00A (Saccharomyces cerevisiae) PDB: 4bzk_A
 Probab=27.74 E-value=5.9e+02 Score=32.20 Aligned_cols=173 Identities=12% Similarity=0.112 Sum_probs=0.0
                  0 ss pred
 Q Fri Mar 04 23: 479 AAQLEFAQLHGHSLFVSCFLNDDKAAEDTIKRLVMREIT------P
                                                                                534 (712)
 O Consensus
               479 A~QLe~~Glw~~AvFVllHl~d~~~R~~aIr~lL~R~~~~~~L~e~L~I----------P
                                                                                534 (712)
               T Consensus
                                                                                 606 (1273)
               527 VKNSLENDLLMEAMVIALDSNNERLKESVKNAYFAKYGSKSSLSRILYSISKREVDDLVENLDVSQWKFISKAIQNLYPN
 T 4bzj_A
                                                                                606 (1273)
                  T ss dssp
                  нининессинининине
 T ss pred
 Q ss_pred
                  Q Fri_Mar_04_23: 535 S--QLIFNAQALKDRY--EGNYLSEVQNLLLGSSYDLAEMAIVTSLG--PRLLLSNNPVQNN----ELKTLREILNEF--
                                                                                 602 (712)
               535 ~--~WI~eAkAl~ar~-~qd~~e~~~Ll~A~~~eAH~v~v~la--P~~II~~~~~d~~~L~~Ll~~f--
 Q Consensus
                                                                                 602 (712)
                  + ++-.-.+--|. +|+....+-|+|-||+.++.-.+.++++. -+.+.+
                                                             .+.+ ....|.+|++++
 T Consensus
               607 -----l---lg-rl---g---a-lcyl-a----------------------------l----iEk---
                                                                                 683 (1273)
               607 DIAQRNEMLIKLGDRLKENGHRQDSLTLYLAAGSLDKVASIWLSEFPDLEDKLKK---DNKTIYEAHSECLTEFIERFTV
                                                                                 683 (1273)
 T 4bzj A
 T ss dssp
                  T ss_pred
 Q ss_pred
                  -----ccccCCChhhcchнниннннн---CCccнниннинннннннн
 Q Fri_Mar_04_23: 603 -----PDSERDKWSVSINVFEVYLKLVLD--NVETQETIDSLISGMKIFYDQ-YKHCREVAACC 658 (712)
 O Consensus
               658 (712)
                      T Consensus
                                                                     744 (1273)
               684 FSNFINGSSTIN----NEQLIAKFLEFINLTTSTGNFELATEFLNSLPSDNEEVKTEKARVLIAS 744 (1273)
 T 4bzj_A
 T ss_dssp
                  ННТТSCC---CC----СНИНИНИНИНИНИНИТТТСИНИНИНИНИН SCTTCHHHHHHHHHHHH
                  ннин heccccc---- hининининининин hhcccнининин hccccсининининин
 T ss_pred
                            PDB SMDB NCBI
 No 23
                                                  Pub Med
>3mkq_B Coatomer subunit alpha; beta-propeller, alpha-solenoid, transport protein; 2.50A {Saccharomyces
 cerevisiae}
 Probab=22.81 E-value=2.5e+02 Score=26.96 Aligned cols=61 Identities=8% Similarity=0.062 Sum probs=0.0
                  нниннинесссинининнин
 Q ss_pred
 Q Fri_Mar_04_23: 279 PEIEEKIRNSSNEIEQIFLYLLLNDVVRASKLAIESKNGHLSVLISYLGSNDPRIRDLAEL 339 (712)
               339 (712)
 O Consensus
                                                                  140 (177)
 T Consensus
                80 SKMQNIAQTREDFGSMLLNTFYNNSTKERSSIFAEGGSLPLAYAVAKANGDEAAASAFLEQ 140 (177)
 T 3mkq_B
                  ННИНИННТТСИНИНИННИТСИНИННИННТТСИНИННИННИНТТСИНИННИННИН
 T ss_dssp
 T ss_pred
                  нинининесссининининесснинининесссининин
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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