

W-L1LR	+ ~ 2
rwrllaslyrdriqsaleeesvfavtavnasektvvealfqrdslvrqsqlvvdwlesiakdeigefsdniefyaksv	
ИННИНИВНИНИНИНЕСС-ССССС-СССТТSCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHSCCCCCC	
ИНИНИНИНИНННИН НесссссссећћессССССС ИНИНИНИНН НЕСЕННИНИНИНННИННННННОСССССССССЬЋЪћЪћссСС	3
cccccCCccccCCCcccCCCccce <mark>ннининниннинн</mark> нСССнининниннноссни .NSITSGGLKSCDLDFPLRENTNVLDVKDKEEDHIFFKYIYELILAGAIDEALEEAKLSDNISI	
Tf-llR-GeAlcgq-wr	A 2
+ +++ +.	
ENTLHTLKQRQLTSYVGSVRPLVTELDPDAPIRQK-MPLDDLDREDEVRLLKYLFTLIRAGMTEEAQRLCKRCGQAWR	
ИНИНИСCCCSCCSTHUHHHHSS-SCSCHHHHHHHHHHHHHHHHHHHHHHHHHHH	
НесСссссСссссссссссссссСсhhнннннннннннннсСССснннннннн	H
CLCGIQEYLNPVIDTQIANEFNTQQGIKKHSLWRRTVYSLSQQAGLDPYERAIYSYLSGAIPNQEVLQYSDWESDLHI	
sL~G~~~~dp~~d~~~~~~~G~~~r~LWk~~c~~la~~~~yErAiY~~LsG~l~~~~~v~c~sWeD~Lwa + .+ + +++++.++++ ++ + + +	
L-GldpGnr-LWKclayERAIYg-LsGdll-v-c-sWeD-LwA	
LEGWKLYHDPNVNGGTELEPVEGNPYRRIWKISCWRMAEDELFNRYERAIYAALSGNLKQLLPV-CDTWEDTVWA	
ИНИТТЯВСВСТТТССТТССЯЯСВЯВЯСНИНИНИНИННИНОЯЯЯСИНИНИНИНИТСССЯНИН-ТССИНИНИНИ HeCchhhcCceccCccccccChhнинининининининининининининининининосснининини	
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IQILQTEIENYLLENNQVGTDELILPLPSHALTVQEVLNRVASRHPSESEHPIRVLMASVILDSLPSVIH 1-11vd1	
+++++ +++.+.+.+ +.++ + .+.+++ ++ +++ ++. ++ + + + + ++ +	+
nldvel	
ИНИНИНИНИНИНИТТСSCGGGCCSCCСССССИНИНИНИНИНССИНИНСИНИНИНИНИНИ	H
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ИНННИНННОССССесесесесь ИННИНИНИННИННИНОССЕССЫ В НЕНИНИННИННИННЕННЕН В СССЕСЬ В НИНИНИНЕССЕННИН В ТОГО В НЕГО В VEMILDVV KGTEASNDIID KPYLLRIVTHLAICLDIIN POGSVEBV DKSKLITTY ISLLKL QGLYEN IP I YATFINESD	
/EMLLDVVKGTEASNDIIDKPYLLKIVTHLAICLDIINPGSVEEVDKSKLITTYISLLKLQGLYENIPIYATFLNESD LiIYILEliply-S-L	
٠٠- +	+
····lIIYILeLIplyas-Lp KWLSKSRNNLPGHLLRFMTHLJLFFRTLG-LQTKEEVSIEVLKTYIQLLIREKHTNLJAFYTCHLPQDL	
HHCCC-SSCHНИНИНИНИНИНИНИНЫS-SCSCНИНИНИНИНИНИНИНИТССGGGHHUHTTCGGGG ИННbcCCCCchhнининининининин C-CCchhинининининининисСсесенининосСни	Т
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EACSFILSSLEDPQVRKKQIETINFLRLPASNILRRTTQRVFDETEQEYSPS-NEISISFDVNNIDMHLIYGVEWLIE	- !
2-ys~-Li-d~-eRL-la~gldv~-i-k~-ve-i~vs~-D~-lI~sleWL ++ + + ++ ++ ++ ++ ++ +.+ + +	- !
e-YsLi-deRL-laglDvi-kve-ivsDlIrslEWL	
AQYALFLESVTEFEQRHHCLELAKEADLDVATITKTVVENIRKKDNGEFSHHDLAPALDTGTTEEDRLKIDVIDWLVF	
CCHHHHHHHHHHHHHHHCCCHHHHHHHHHCCCHHHHHHH	
<pre>KLYVDAVHSIIALSRRFLLNGRVKALEQFMERNNIGEICKN-YELEKIADNISKDENEDQFLEEITQYEHLIKGIREYeAln-l-R-FLgkl-AAr-lpl</pre>	
.~~~eAl~~n~L~R~FL~~gkl~AAr~l~~rlp~d~i~~~~~~~~~~~~~~~i~E~l~~~yl~ale~f \QRAEALKQGNAIMRKFLASKKHEAAKEVFVKIPQDSIAEIYNQCEEQGMESPLPAEDDNAI <mark>R</mark> EHLCIRAYLEAHETF	
SGНИНИЕЙНИНИНИНТТСКИНИНИНИНИНОСТВИНИСССИНИИНИНИНИНИНИНИНИНИНИНИ SCHИНИНИНИНИНИНИНСССИНИНИНИНИНССИНИНИНИНЫНЫНЫСССССССОНЫНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИНИН	H
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VQKSVSLLSSESNIPTTFLVDLTSSNF	
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IFKHMNSVPQKPALIPQPTFTEKVAHEHKEKKYEMDFGIWKGHLDALTADVKEKMYNVLLFVDGGWMVD <mark>VREDAK</mark> IННННТCCCCCCCCSSCCHНННННННННННННННННННННННН	
иннисССССсссссоннининнинниннинниннинниннинниннинниннин	
CCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	
&ADYEILYEIRALYTPFLLMELHKKLVEAAKLLKIPKFISEALAFTSLVANENDKIYLLFQSSGKLKEYLDLVARTAT liRyiP-lil-LhLalalaVA-elyFrl-e-l	
++ + + ++ + + ++ + + + + +	
~r~~ql~~IR~~YIPelil~Lh~~L~~s~~~cl~LA~~VA~e~~~ly~~F~~~rL~elL~~vaesSl IERTHQMVLLRKLCLPMLCFLLHTILHSTGQYQECLQLADMVSSERHKLYLVF-SKEELRKLLQKLRESSL	
	H

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Siko_C Nucleoporin NUP84; NPC, transport, WD repeat, autocatalytic cleavage, mRNA transport, nuclear pore
 complex, nucleus, phosphoprotein; 3.20A {Saccharomyces cerevisiae} PDB: 4xmm _F 4xmm _F 3jro _C
 Probab=100.00 E-value=1.7e-94 Score=813.15 Aligned_cols=459 Identities=99% Similarity=1.436 Sum probs=0.0
                              Q ss pred
 Q Fri_Mar_04_23:
                            1\ \texttt{MELSPTYQTERFTKFSDTLKEFK1EQNNEQNPIDPFN11} \\ \textbf{REFRSAAGQLALDLANSGDESNV1SSKDWELEARFWHLVEL}
                                                                                                                                           80 (726)
 O Consensus
                           1 ~~~~~~Fa~I,~~~~~E~tW~I,l~~
                                                                                                                                           80 (726)
                              --lv--f--ic-----
 T Consensus
                                              ~~Fa~~l~~~
                                                                                                                         ~E~~tW~Ll~~
                                                                                                                                           80 (460)
                              {\tt MELSPTYQTERFTKFSDTLKEFKIEQNNEQNPIDPFNIIREFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLALDLANSGDESNVISSKDWELEARFWHLVELDERFRSAAGQLAUDTHANGGDESNVISSKDWELEARFWHLVELDERFRSAAGQLAUDTHANGGDESNVISSKDWELEARFWHLVELDERFRSAAGQLAUDTHANGGDESNVISSKDWELEARFWHLVELDERFRSAAGQLAUDTHANGGDESNVISSKDWELEARFWHLVELDERFRSAAGQLAUDTHANGGDESNVISSKDWELEARFWHLVELDERFRSAAGQLAUDTHANGGDESNVISSTUDTHANGG
 T 3iko C
                                                                                                                                           80 (460)
 T ss_dssp
                                  T ss pred
                              Q ss pred
 O Fri Mar 04 23:
                          81 LLVFRNADLDLDEMELHPYNSRGLFEKKLMODNKOLYOIWIVMVWLKENTYVMERPKNVPTSKWLNSITSGGLKSCDLDF
                                                                                                                                          160 (726)
                                                                       -d----e---I--WLe--a------l----W--T-----v--LDPDA
                                                                                                                                          160 (726)
                              ----d----e---v--WLe--a------------W--T---g-v--LDpDA
 T Consensus
                                                                                                                                          160 (460)
                          81 LLVFRNADLDLDEMELHPYNSRGLFEKKLMQDNKQLYQIWIVMVWLKENTYVMERPKNVPTSKWLNSITSGGLKSCDLDF
 T 3iko C
                                                                                                                                          160 (460)
                              T ss dssp
 T ss_pred
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 Q ss pred
                         161 PLRENTNVLDVKDKEEDHIFFKYIYELILAGAIDEALEEAKLSDNISICMILCGIQEYLNPVIDTQIANEFNTQQGIKKH
 Q Fri Mar 04 23:
                                                                                                                                          240 (726)
                         161 p-R----L---D---e--l----f-llR-G---eA--lc---gq-wrAasL-G-----dp--d-----
                                                                                                                                          240 (726)
 Q Consensus
                              T Consensus
                                                                                                                                          240 (460)
                         161 PLRENTNVLDVKDKEEDHIEFKYLYELTLAGAIDEALEEAKLSDNISICMILCGIOEYLNPVIDTOTANEENTOOGIKKH
 T 3iko C
                                                                                                                                          240 (460)
                              T ss dssp
                              сссСССССссьнинининининининининин
 T ss pred
                              Q ss_pred
 Q Fri_Mar_04_23:
                         241 SLWRRTVYSLSQQAGLDPYERAIYSYLSGAI-PNQEVLQYSDWESDLHIHLNQILQTEIENYLLENNQVGTDELILPLPS
                                                                                                                                          319 (726)
                         241 ~LWk~~c~~la~~~~vErAiY~~LsG~l~~~~v~c~sWeD~Lwa~~n~ll~~~vd~~l~~~~
 Q Consensus
                                                                                                                                 ~~lp~
                                                                                                                                          319 (726)
                              T Consensus
                         241 SLWRRTVYSLSQQAGLDPYERAIYSYLSGAIPNQEVLQ-YSDWESDLHIHLNQILQTEIENYLLENNQVGTDELILPLPS
 T 3iko C
                                                                                                                                          319 (460)
 T ss_dssp
                              T ss_pred
                              Q ss pred
 Q Fri_Mar_04_23: 320 HALTVQEVLNRVASRHPSESEHPIRVLMASVILDSLPSVIHSSVEMLLDVVKGTEASNDIIDKPYLLRIVTHLAICLDII
                                                                                                                                          399 (726)
 O Consensus
                         320 ---s---i---L-----ea--p-r-iQ--iI-----ll-----L------LRf-aHL-L-1--1
                                                                                                                                          399 (726)
                              T Consensus
                                                                                                                                          399 (460)
 T 3iko C
                         320 HALTVQEVLNRVASRHPSESEHPIRVLMASVILDSLPSVIHSSVEMLLDVVKGTEASNDIIDKPYLLRIVTHLAICLDII
                                                                                                                                          399 (460)
                              T ss_dssp
 T ss_pred
                              Сессининининесссининенинининин
 Q ss pred
                              Q Fri_Mar_04_23:
                         400 NPGSVEEVDKSKLITTYISLLKLQGLYENIPIYATFLNESDCLEACSFILSSLEDPQVRKK
                                                                                                                 460 (726)
                         460 (726)
 T Consensus
                                                                                                                 460 (460)
 T 3iko C
                         400 NPGSVEEVDKSKLITTYISLLKLQGLYENIPIYATFLNESDCLEACSFILSSLEDPQVRKK
                                                                                                                 460 (460)
 T ss_dssp
                              STTSSCHHHHHHHHHHHHHHHHTTCGGGHHHHHTTCGGGGGC----
 T ss_pred
                              PDB"
 No 3
                                                                                      Pub Med
📄 >3cqc_A Nuclear pore complex protein NUP107; nucleoporin, mRNA transport, nucleus, phosphoprotein, protein
  transport, translocation; 2.53A {Homo sapiens} PDB: 3i4r A 3cqg A
 Probab=100.00 E-value=1.4e-43 Score=371.22 Aligned_cols=216 Identities=21% Similarity=0.335 Sum_probs=0.0
                              ссССССНИНИНИНИНННОС-СССНИНИНИНИНИНИНИНИНИНИНИНИНИНИНННННН- heccecccCCCc
 Q ss pred
 Q Fri_Mar_04_23:
                         498 \ \mathtt{SISFDVNNIDMHLIYGVEWLIE-GKLYVDAVHSIIALSRRFLLNGRVKALEQFMERNNIGEICKN-YELEKIADNISKDE}
                                                                                                                                          575 (726)
                         Q Consensus
                                                                                                                                          575 (726)
 T Consensus
                                                                                                                                           83 (270)
                           4 ALDTGTTEEDRLKIDVIDWLVFDPAQRAEALKQGNAIMRKFLASKKHEAAKEVFVKIPQDSIAEIYNQCEEQGMESPLPA
 T 3cqc A
                                                                                                                                           83 (270)
 T ss dssp
                              -----CHHHHHHHHHHHHHSGGGHHHHHHHHHHHHHHHHTTCHHHHHHHHHSCTTHHHHHC------
                              T ss_pred
                              ссининнийнинниннинниннинниннинниннин
 Q ss pred
 Q Fri Mar 04 23:
                         576 NEDQFLEEITQYEHLIKGIREYEEWQKSVSLLSSESNIPT-----LIEK------LQGFSKDTFE
                                                                                                                                          629 (726)
 Q Consensus
                                                                                                                                          629 (726)
                                                                                          ++|+
                              +.++.++||+||++|++.|++|++++
 T Consensus
                              ----i-E-1----l-al--f--W-----p--p---
                                                                                       ~~~f~e~~a~e~
                                                                                                                                          160 (270)
                          84 EDDNATREHLCTRAYLEAHETFNEWFKHMN---SVPOKPALTPOPTFTEKVAHEHKEKKYEMDFGTWKGHLDALTADVKE
 T 3cqc A
                                                                                                                                          160 (270)
                              T ss dssp
                              hhнниннинниннинниннинниннин---cCCCccccchhнинниннинниннинниннинниннинниннин
 T ss pred
 Q ss_pred
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Q Fri_Mar_04_23: 630 LIK-----TFLVDLTSSNFADSADYEILYEIRALYTPFLLMELHKKLVEAAKLLKIPKFISEALAFTSLVANENDKI 701 (726)
                              O Consensus
                              T Consensus
                                                                                                                                                                             233 (270)
T 3cqc_A
                                     T ss_dssp
                                     T ss pred
                                    ннинньссиннинниннинн
Q ss pred
Q Fri_Mar_04_23:
                              702 YLLFQSSGKLKEYLDLVARTATL 724 (726)
                              702 y~~F~~~rl~e~1~~~~~~
|+|| .++||+|||+++|+||+.
                              234 v~~F-~~rL~elL~~~a~sS~~
                                                                              255 (270)
T Consensus
T 3cqc_A
                              234 YLVF-SKEELRKLLQKLRESSLM 255 (270)
T ss_dssp
                                    GGGS-СНИНИНИНИНИНИНИНИН
                                     ннин-рининининининини
T ss_pred
                                                         PDB"
No 4
                                                                                                          Pub Med
               Nuclear pore complex protein NUP85; transport protein; 23.00A {Homo sapiens}
Probab=97.91 E-value=0.003 Score=74.30 Aligned_cols=418 Identities=14% Similarity=0.129 Sum_probs=0.0
                                    hнинининининин
Q ss pred
Q Fri_Mar_04_23:
                                 9 TERFTKFSDTLKEFKIEQ---NNEQNPIDPFNIIREFRSAAGQLALDLANSGDE-----SNVISSKDWELEARFWHL
                                                                                                                                                                               77 (726)
                                 9 ~~~~Fa~L~~~~~~~lv~f~~ic~~~~~~
                                                                                                                                                                               77 (726)
Q Consensus
                               T Consensus
                                                                                                                                                                             148 (656)
T 5a9g 8
                                                                                                                                                                             148 (656)
T ss_dssp
                                    T ss_pred
                                     Q ss_pred
                                    нинни ресссерственный и пользываний в польз
Q Fri_Mar_04_23:
                               78 VELLLVFRNADLDLDEMELHPYNSRGLFEKKLMODNKOLYQIWIVMVWLKENTYVMERPKNVPTSKWLNSITSGGLKSCD
                                                                                                                                                                             157 (726)
Q Consensus
                               157 (726)
                                    ++.||-+..+..
                                                                                              .-...+++|+....+.++....
T Consensus
                              182 (656)
                              149 CEILFIEVAPAG------PLLLHLLDWVRLHVCEVDSLSA-----
T 5a9q_8
                                                                                                                                                                             182 (656)
T ss_dssp
                                    T ss pred
                                     Q ss_pred
                                    Q Fri Mar 04 23: 158 LDFPLRENTNVLDVKDKEEDHIFFKYIYELILAGAIDEALEEAKLSDN-----ISICMILCGIQEYLNPVIDTQIAN 229 (726)
                              158 \ \mathtt{PDAp-R----L---D---e-l----f-llR-G---eA--lc---gq--------wrAasL-G-----dp--d------}
O Consensus
                                                                                                                                                                             229 (726)
                              ..+....+..||.+++|.+|++++++++.....+..|
183 ------FW--v-lvlrG---A--lL--h-------------LL---P-----
T Consensus
                              183 -----DVLGSENPSKHDSFWNLVTILVLQGRLDEARQMLSKEADASPASAGICRIMGDLMRTMPILSP-----GN
T 5a9q 8
T ss_dssp
                                    T ss_pred
                                     Q ss_pred
                                    Q Fri Mar 04 23: 230 EFNTQQGIKKHSLWRRTVYSLSQQAGLDPYERA--IYSYLSGAIPNQ---EVLQYSDWESDLHIHLNQILQTEIENYLLE
                                                                                                                                                                             304 (726)
                              O Consensus
                                                                                                                                                                             304 (726)
                              +...+...+.-||.-|....+...+|...||.+|||...+...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-..||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-...+|...||.+|-..||.+|-...+|...||.+|-...+|...||.+|-...||.+|-...||.+|-...||.+|-..||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-..||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.+|-...||.
T Consensus
                                                                                                                                                                             310 (656)
                              248 TOTLTELELKWOHWHEECERYLQDSTFATSPHLESLLKIMLGDEAALLEQKEL-LSNWYHF------LVT
T 5a9g 8
                                     T ss_dssp
T ss pred
                                     сССЬНИНИНИНИНИНИНИННЫН МССССЬНИНИНИННЫН СССИНИН ССИНИН ССОИН ССИНИН СССИНИН ССИНИН СССИНИН ССОИНИ ССИНИН ССИНИН ССИНИ ССИНИН ССОИН СОИНИ ССИНИ
                                    0 ss pred
Q Fri_Mar_04_23:
                              \textbf{305} \ \texttt{NNQVGTDELILPLPSHALTVQEVLNRVASRHPS} -- \textbf{ESEHPIRVLMASVILDSLPSVIHSSVEMLLDVVKGTEASNDIIDK}
                                                                                                                                                                             382 (726)
                              T Consensus
                                                                                                                                                                             372 (656)
                              311 RLL-----YSNPTVKPIDLHYYAQSSLDLFLGGESSPEPLDNILLAAFEFDIHQVIKECSIALSNWW------
T 5a9q 8
                                                                                                                                                                             372 (656)
                                    T ss dssp
                                     ННН------hcccccchhhнининининнининнесссссссьнининининнесснининининнесссс-------
T ss pred
                                    ссьянинининининос----СсСсьянинининининын-СССссьянининын
Q ss pred
Q Fri Mar 04 23: 383 PYLLRIVTHLAICLDIINP----GSVEEVDKSKLITTYISLLKL-QGLYENIPIYATFLNESDCLEACSFILSSLE--D
                                                                                                                                                                             454 (726)
                              \texttt{383} \quad \texttt{---LRf-aHL-L-l--l----e-ys--L--i---d}
                                                                                                                                                                             454 (726)
                              T Consensus
                                                                                                                                                                             446 (656)
                              373 ----FVAHLTDLLDHCKLLOSHNLYFGSNMREFLLLEYASGLFAHPSLWQLGVDYFDYCP-ELGRVSLELHIERIPLNT
T 5a9q 8
                                                                                                                                                                             446 (656)
                                    T ss dssp
T ss_pred
                                     Q ss_pred
                                    Q Fri_Mar_04_23: 455 PQVRKKQIETINFLRLP--ASNILRRTTQRVFDETEQEYSPSNEISISFDVNNIDMHLIYGVEWLIEGKLYVDAVHSIIA
                                                                                                                                                                             532 (726)
Q Consensus
                              455 ~~eR~~L~la~~qld--v~i~k~ve~i~~~~~vs~~D~~lI~sleWL~~~~~eAl~~~n~
                                                                                                                                                                             532 (726)
                              .+.=.+.++++++||....|.+...+.+.+.
447 ~~~~k~l~iC~~~L~~~a~~I~~~~g~~~~~g~~~~
                                                                                                   +...|+-|+.-.+...-.=..++.
                                                                                                                                 ---G-AL-w--rA-d---v--i-d-
T Consensus
                                                                                                                                                                             505 (656)
T 5a9q 8
                              447 EQKALKVLRICEQROMTEQVRSICKILAMKAVRNN-------RLGSALSWSIRAKDAAFATLVSDR
T ss dssp
                                     STTHEHHHHHHHHTTCHHHHHHHHHHHC------
```

```
T ss_pred
               0 ss pred
               нининнессининни
Q Fri_Mar_04_23: 533 LSRRFLLNGRVKALEQF
                            549 (726)
             533 l~R~FL~~gkl~AAr~l
                            549 (726)
             ++..+..+|.+....+
506 11~~y~~~g~1~~~~11 522 (656)
T Consensus
             506 FLRDYCERGCFSDLDLI
T 5a9q 8
                            522 (656)
T ss_dssp
T ss_pred
               нинннесссссенин
                        PDB'
No 5
                                            Pub Med
                               NCBI
>4xmm_B Nucleoporin NUP145; structural protein, immune system, transport protein-immune complex; 7.38A
 {Saccharomyces cerevisiae S288C} PDB: 4xmn _B
Probab=97.76 E-value=0.023 Score=66.57 Aligned cols=355 Identities=14% Similarity=0.148 Sum probs=0.0
               нининининин
0 ss pred
Q Fri_Mar_04_23:
             71 \ \ EARFWHLVELLLVFRNADLDLDEMELHPYNSRGLFEKKLMQDNKQLYQIWIVMVWLKENTYVMERPKNVPTSKWLNSITS
             71 E--tW-Ll--L---R-----y-s-----y-s-----d----e---I----WLe--a------l------W--T---
Q Consensus
                                                                       150 (726)
               |...|+|...|+....
                                  +.+..+...+.
                                             ..++...+-+||++..
T Consensus
             171 e~~vW~L~saLfd~~~~~---
                                 217 (652)
             171 DYNLWKLSSILFDPVSYPYK------TDNDQVKMALL---KKERHCRLTSWIVSQI-----
T 4xmm B
                                                                       217 (652)
T ss_dssp
               НЫННИНИННЫСССесесс-----сСеньниннын----нининнинниннин-----
T ss pred
               Q ss pred
Q Fri Mar 04 23: 151 GGLKSCDLDFPLRENTNVLDVKDKEEDHIFFKYIYELILAGAIDEALEEAKLSDNISICMILCGIQEYLNPVIDTQIANE
                                                                       230 (726)
O Consensus
             151 ~~v~~LDPDAp~R~~~~L~~~D~~~e~~l~~~~f~llR~G~~~eA~~lc~~~gq~wrAasL~G~~
                                                            ~~~dp~~d~
                                                                       230 (726)
               ++.++.+....++.+|.+|++|++++|.+|+...|-=.
-----v---v----e-if--L---I-eA---Ai--gd-rLA-Llsq---
T Consensus
                                                                       266 (652)
             218 ------GPEIEEKIRNSSNEIEQIFLYLLLNDVVRASKLAIESKNGHLSVLISYL-----
T 4xmm B
                                                                       266 (652)
               -------ннинининсссининининтсинининитсининин
T ss dssp
T ss pred
                  ------ннинининносссинининнинсссининининнин
Q ss_pred
               Q Fri_Mar_04_23: 231 FNTQQGIK-KHSL------WRRTVYSLSQQAGLDPYERAIYSYLSGAI------PNQEVLQYSDWESDLHIHLNQILQ
                                                                       295 (726)
                ----G----r-L------Wk--c--la-----yErAiY--LsG-l-------v-c-sWeD-Lwa--n-ll-
Q Consensus
             231
                                                                       295 (726)
                          .+|.+ .|.+
                       ~~~~QL~~W
T Consensus
T 4xmm B
             267 ---GSNDPRIRDLAELOLOKWSTGGC-----SIDKNISKIYKLLSGSPFEGLFSLKELES--EFSW------
                                                                       322 (652)
               T ss dssp
T ss_pred
               Q ss_pred
Q Fri_Mar_04_23:
             296 TEIENYLLENNOVGTDELILPLPSHALTVOEVLNRVASRHP-SESEHPIRVLMASVILDSLPSVIHSSVEMLLDVVKGTE
                                                                       374 (726)
             Q Consensus
                                                                       374 (726)
               T Consensus
                                                                       383 (652)
               LCLLNLTLCYGQIDEY-----SLESLVQSHLDKFSLPYDDPIGVIFQLYAANENTEKLYKEVRQRT-----
T 4xmm_B
                                                                       383 (652)
               T ss_dssp
               T ss pred
               Q ss pred
             375 ASNDIIDKPYLLRIVTHLAICLDIINPGSVEEVDKSKLITTYISLLKLQGLYENIPIYATFLN----ESDCLEACSFIL
Q Fri Mar 04 23:
                                                                       449 (726)
O Consensus
             449 (726)
                    +|.=-|+-=||+-+|+.+|.....+...+...|+.-|...|+.+.--+=+.+|+
                                                            + . . . . ++ . . ++-
             384 ------lD-rLsW-L--vL-a-g---s---d-l---fA-QLe--Glw-wAiFVllHl-d---R--air-lL-R--
T Consensus
                                                                       456 (652)
             384 -----NALDVQFCWYLIQTLRFNGTRVFSKETSDEATFAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDTIKRLVMREI
T 4xmm B
                                                                       456 (652)
               T ss dssp
               T ss pred
               Q ss pred
Q Fri Mar 04 23:
             450 SSLEDPQVRKKQIETINFLRLPASNILRRTTQRVFDETEQEYSPSNEISISFDVNNIDMHLIYGVEWLIEGKLYVDAV-H
                                                                       528 (726)
               ~~i~d~~eR~~~L~la~~~gldv~~i~k~~ve~i~~~~~~~~~vs~~D~~lI~sleWL~~~~~eAl-~
Q Consensus
                                                                       528 (726)
             ..+.+++ --.+.+|++..=|-...+-+...+..- .++.|+-.+|.+|= .
457 ------L-e-L-IP--WI-eAkAl-a---gd-------e---Ll-A----eAH-v
T Consensus
                                                                       511 (652)
             457 TLLRAST---NDHILNRLKIPSQLIFNAQALKDRYEGNYLS-----EVQNLLLGSSYDLAEMA
T 4xmm B
                                                                       511 (652)
               T ss dssp
T ss_pred
               ссссьн----нинининсссининининининини
               нинининине---С---Сининининин
Q ss_pred
Q Fri Mar 04 23:
             529 SIIALSRRFLLN---G---RVKALEOFMERNNIGEICKNYELE
                                             565 (726)
Q Consensus
             529 ~~n~l~R~FL~~--g---kl~AAr~l~~~~p~~~l~~~
                                              565 (726)
             .+.|-..++ + +++..+.++.|...+.|...+|..+
512 -v-vaP-II------d---L--11--fp---I--W--g
T Consensus
                                             553 (652)
T 4xmm_B
             512 IVTSLGPRLLLSNNPVQNNELKTLREILNEFPDSE-RDKWSVS
                                              553 (652)
               ннинс-----Синининининин
T ss_dssp
               НННhhhHHHHhcccCccccHHHHHHHHHhCcccc-CCChhhC
T ss pred
                        PDB"
```

```
>2qx5_A Nucleoporin NIC96; mRNA transport, nuclear pore complex, nucleus, protein transport, translocation,
 transport, transport protein; 2.50A {Saccharomyces cerevisiae} PDB: 2rfo _A
 Probab=97.73 E-value=0.00021 Score=83.77 Aligned_cols=237 Identities=17% Similarity=0.137 Sum probs=0.0
                             Q ss pred
 T 2qx5_A
                             IWALIFYLLRAGLIKEALQVLVENKANIKKVEQSFLTYFKAYASSKDHGLPVEYSTK-----LHTEYNQHIKSS-- 223 (661)
                              ННИНИНИНТТТСНИНИНИННТGGGC-----СНИНИНИНС------
 T ss_dssp
                              сниннинненнинниннинниннинниннинниннин
 T ss pred
                             СССеннининненнессерирования с на составляющий положения в на составляющим положения в на составляющий положения в на составления 
 Q ss pred
 Q Fri_Mar_04_23: 254 AGLDPYERAIYSYLSGAIPNQEVL--QYSDWESDLHIHLNQILQTEIENYLLENNQVGTDELILPLPSHALTVQEVLNRV
                        254 ~~~~yErAiY~~LsG~1~~~~~v-~-c~sWeD~Lwa~~n~11~~~vd~~1~~~~~~1p~~~~s~~i~~~L 331 (726)
                        ..-++++-+.+
 T Consensus
                                                                                                                                       288 (661)
 T 2gx5 A
                                                                                                                                       288 (661)
 T ss dssp
                               T ss_pred
                             ньыьынынынниннинниннинниннинниннинныннын
 Q ss pred
 Q Fri_Mar_04_23: 332 ASRHPSESEHPIRVLMASVILDSLPSVIHSSVEMLLDVVKGTEASNDIIDKPYLLRIVTHLAICLDIINPGSVEEVDKSK
                                                                                                                                       411 (726)
                        332 -----ea--p-r-iQ--iI------ll------L------LRf-aHL-L-l--l-----
 Q Consensus
                                                                                                                                       411 (726)
                              . ..++.--+ --- --- --- ---
                                                                                                     .+|++|.|...|.-.+++
 T Consensus
                        289 ~-~Ge~F~p-~yf~vLlLsgqFE~AI~~L~~~~vd------AVH~AIaL~~~gLL~~~---
                                                                                                                                      343 (661)
                        289 T-SYGPSRFSN-YYLOTLLLSGLYGLAIDYTYTF-SEMD-------AVHLAIGLASLKLFKIDS---S 343 (661)
 T 2qx5 A
                             T ss dssp
 T ss pred
                             Q ss_pred
                             ННИНИНННННСССесьниннннне--нининннессининннннн
 Q Fri_Mar_04_23: 412 LITTYISLLKLQGLYENIPIYATFLNESDCLEA--CSFILSSLEDPQVRKKQIETINFL
                                                                                                            468 (726)
                        412 iI--YI--L-----eLIplY-S-L-----e---ys--L--i-d--eR---L-la---
 Q Consensus
                                                                                                            468 (726)
                        ++...---+...||..|++....+.||-.++...++++
344 lls------lnfarLI--Yt--F---d---Al-Y--li----d-----l----l-eL
 T Consensus
                        344 TRLT-KKPKRDIRFANILANYTKSFRYSDPRVAVEYLVLITLNEGPTDVELCHEALREL
 T 2qx5 A
                                                                                                            401 (661)
 T ss_dssp
                              ссс-ССсссснинининниннин
 T ss_pred
                                             PDB<sup>N</sup>
PROTEIN DATA BANK
                                                         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
 Probab=97.50 E-value=0.0083 Score=69.32 Aligned_cols=246 Identities=13% Similarity=0.082 Sum_probs=0.0
                             Q ss pred
 Q Fri_Mar_04_23: 180 FFKYIYELILAGAIDEALEEAKLSD-----NISICMILCGIQEYLNPVIDTQIANEFNTQQGIKKHSLWR
                                                                                                                                       244 (726)
                        Q Consensus
                                                                                                                                       244 (726)
                        T Consensus
                                                                                                                                       307 (570)
                        245 FWKLLNQLVLRGLLSQAIGCIERSDLLPYLSDTCAVSFDAVSDSIELLKQYPKDSSS-----TFREWK
 T 3f3f_C
                                                                                                                                       307 (570)
 T ss_dssp
                             T ss_pred
                              ННН----НННННСССССНИН-----НННННННСССсhhheeceCCCHHHHHHHHHHHHHHHHHHHHHCCCchhhhhh
 Q ss pred
 Q Fri_Mar_04_23: 245 RTV----YSLSQQAGLDPYE----RAIYSYLSGAIPNQEVLQYSDWESDLHIHLNQILQTEIENYLLENNQVGTDELIL
                                                                                                                                      315 (726)
 O Consensus
                        315 (726)
                             T Consensus
                                                                                                                                       368 (570)
                        308 NLVLKLSQAFGSSATDISGELRDYIEDFLLVIGGNQRKILQY-SRTWYES------FCGFLLYYIPSL-
 T 3f3f C
                                                                                                                                       368 (570)
                              HHHHHHHHHTSCCCSCHHHHHHHHHHHHHHT-CHHHHHHT-CSSHHHH------HHHCCCCCCCCG-
 T ss_dssp
                              НИНИНИНННЫ ССССССИВНИНИННИННИН В НЕСТИТИТЕТ В НЕСТИТИТЕТ
 T ss_pred
                             cCCCCCCHHHHHHHHhhhhhhhhhhh
 Q ss pred
 Q Fri_Mar_04_23:
                        {\tt 316~PLPSHALTVQEVLNRVASRHPSESEHPIRVLMASVILDSLPSVIHSSVEMLLDVVKGTEASNDIIDKPYLLRIVTHLAIC}
                                                                                                                                       395 (726)
                        316 ~lp~~~s~~i~~L~~~~ea~~p~r~iQ~~iI~~~~~ll~~~~~L~~~~
 Q Consensus
                                                                                                      -----LRf-aHL-L-
                                                                                                                                       395 (726)
                        T Consensus
                                                                                                                                       423 (570)
                        369 -----ELSAEYLQMSLEANVVDITNDWEQPCVDIISGKIHSILPVMESL-DSC------TAAFTAMI
 T 3f3f C
                                                                                                                                       423 (570)
 T ss dssp
                             -----GGHHHHHHHHHHSCCCTTSSSHHHHHHHHTTCCGGGHHHHHHH-CHH--------HHHHHHHH
                              T ss_pred
                             Q ss pred
                        396 LDIINP-GS-----VEEV------DKSKLITTYISLLK---LQGLYENIPIYATFLN---ESDCLEA
 Q Fri Mar 04 23:
                                                                                                                                       444 (726)
 Q Consensus
                        396 l--l----e---e--
                                                                                                                                       444 (726)
                        +...|. .+..+...|- .+.++..-|.+..+ .+.+...
424 l---g-L------dl-dl-s---ire-lll-YA--l-l-s---lW-vai-yL--c------g---
 T Consensus
                                                                                                                                       503 (570)
                        T 3f3f C
                                                                                                                                       503 (570)
 T ss dssp
                             T ss pred
 Q ss pred
                             нининьсс--сининининининсссс--инининининин
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Q Fri_Mar_04_23: 445 CSFILSSLE--DPQVRKKQIETINFLRLP--ASNILRRTTQRVFDE 486 (726)
                                    445 ys--L--i--d--eR---L-la---gld--v--i-k--ve-i---
                                    -+.+|..+. ..+.-.+.|+++++||. ...|.+...+.+.+
504 i-elL-riPl-t----k-l-iC----L---a--I----q-----
  T Consensus
                                                                                                                                       549 (570)
                                    504 IAELLPHYPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSA
  T 3f3f C
                                            T ss_dssp
  T ss_pred
                                            ниннресссссрининининининессининининининин
  No 8
                                                                                                                              Pub Med
>4xmm_D Nucleoporin NUP85; structural protein, immune system, transport protein-immune complex; 7.38A
  {Saccharomyces cerevisiae S288C} PDB: 4xmn D
Probab=97.46 E-value=0.0078 Score=71.37 Aligned_cols=285 Identities=14% Similarity=0.100 Sum_probs=0.0
  Q ss_pred
                                            Q Fri_Mar_04_23: 180 FFKYIYELILAGAIDEALEEAKLSD-----NISICMILCGIQEYLNPVIDTQIANEFNTQQGIKKHSLWRRTVY
                                                                                                                                                                                                       248 (726)
  O Consensus
                                    180 l----f-llR-G---eA--lc---q-wrAasL-G----dp--d-------G---r-LWk--c-
                                                                                                                                                                                                       248 (726)
                                    ..-...-||..|-
  T Consensus
                                                                                                                                                                                                        282 (715)
  T 4xmm D
                                           282 (715)
                                            T ss_dssp
                                            T ss pred
                                            Q ss pred
  Q Fri_Mar_04_23:
                                    249 SLSQ----QAGLDPYE-----RAIYSYLSGAIPNQEVLQYSDWESDLHIHLNQILQTEIENYLLENNQVGTDELILPLPS
                                                                                                                                                                                                        319 (726)
                                    T Consensus
                                                                                                                                                                                                        339 (715)
                                    283 KLSQAFGSSATDISGELRDYIEDFLLVIGGNQRKILQY-SRTWYES------FCGFLLYYIPSL----
  T 4xmm_D
                                                                                                                                                                                                        339 (715)
  T ss dssp
                                            HHHHHHHTSCCCSCHHHHHHHHHHHHHHHTCHHHHHHT-CSSHHHH-------HHHCCCCCCCCG-----
  T ss_pred
                                            Q ss pred
                                                                                                                                                                                                        399 (726)
  Q Fri Mar 04 23:
                                    320 HALTVQEVLNRVASRHPSESEHPIRVLMASVILDSLPSVIHSSVEMLLDVVKGTEASNDIIDKPYLLRIVTHLAICLDII
                                            Q Consensus
                                                                                                                                                                                                        399 (726)
                                                ..+...+...+
                                                                                                                                                                ++- |+||++=++...
  T Consensus
                                    340 ---1~-y-----d-----d-----e----i-egd---vL--1---1---------d-w----aAhladLl---
                                                                                                                                                                                                        398 (715)
                                    340 -- FLSARYLOMSLEANVVDTTNDWEOPCVDTTSGKTHSTLPVMES-L------DSC--TAAFTAMTCEAK
  T 4xmm D
                                                                                                                                                                                                        398 (715)
                                            T ss dssp
                                            T ss_pred
                                            СС-СсС-----Срыннининнин---рССсссыннинь---
  Q ss_pred
  Q Fri Mar 04 23: 400 NP-GSV------EEVDKSKLITTYISLLK--LQGLYENIPIYATFLN--ESDCLEACSFI
                                                                                                                                                                                                        448 (726)
                                            ~~~~~eLIplY~S~L~~~~evys~~
  O Consensus
                                    400
                                                                                                                                                                                                        448 (726)
                                            T Consensus
  T 4xmm D
                                    399 GLIENIFEGEKNSDDYSNEDNEMLEDLFSYRNGMASYMLNSFAFELCSLGDKELWPVAIGLIALSATGTRSAKKMVIAEL
                                                                                                                                                                                                        478 (715)
                                            T ss_dssp
  T ss pred
                                            Ссссссссссссссссссьный на положений положении положении положений положении положений положений положении положении положении положении п
                                            Q ss pred
  Q Fri_Mar_04_23:
                                    449 LSSLE--DPQVRKKQIETINFLRLP--ASNILRRTTQRVFDETEQEYSPSNEISISFDVNNIDMHLIYGVEWLIEGKLYV
                                                                                                                                                                                                        524 (726)
                                    Q Consensus
                                                                                                                                                                                                        524 (726)
                                    +...||-|+.-.+.+.
                                                                                                                                                          -----g~AL~~~rA~d~~
  T Consensus
                                    479 LPHYPFVTNDDIEWMLSICVEWRLPEIAKEIYTTLGNQMLSAH-----NIIESIANFSRAGKYE
  T 4xmm D
  T ss_dssp
                                            T ss_pred
                                            ресссссениянияния нессияния и на выпуска в предоставления в предоставления
                                            нинининининиссс
  Q ss pred
  Q Fri_Mar_04_23:
                                    525 DAVHSIIALSRRFLLNGR
                                                                                 542 (726)
  O Consensus
                                    525 eAl~~~n~l~R~FL~~qk
                                                                                 542 (726)
                                    -.=..++.|+...+.+|+
538 ~V~~i~~~l~~~g~
  T Consensus
                                                                                  555 (715)
                                    538 LVKSYSWLLFEASCMEGQ
  T 4xmm D
                                                                                 555 (715)
  T ss_dssp
                                            СИНИНИНИНИНИНИНИНИ
                                            нниннинниннин
  T ss_pred
                                                                    PDB<sup>™</sup>
PROTEIN DATA BANK
                                                                                         NCBI
  No 9
                                                                                                                             Pub Med
33bg1_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=97.22 E-value=0.037 Score=61.88 Aligned_cols=276 Identities=14% Similarity=-.149 Sum_probs=0.0
                                            Q ss pred
  Q Fri_Mar_04_23:
                                     71 EARFWHLVELLLVFRNADLDLDEMELHPYNSRGLFEKKLMQDNKQLYQIWIVMVWLKENTYVMERPKNVPTSKWLNSITS 150 (726)
  Q Consensus
                                      71 \ \ E \sim t \ W \sim L1 \sim L2 \sim R2 \sim 2000 \sim 2
                                                                                                                                                                                                       150 (726)
                                    |...|+|...|+....+ ...++...++||++...

120 e~~vW_L~saLfd~~~~~~ 166 (442)
  T Consensus
                                    120 DYNLWKLSSILFDPVSYPYK------TDNDQVKMAL---LKKERHCRLTSWIVSQI------
  T 3bq1 B
                                                                                                                                                                                                       166 (442)
  T ss_dssp
                                            НИНИНИНИНТSCCCSSC-----CSCHHHHHHH----НИНИНИНИНИН ------------
  T ss_pred
```

```
Q ss pred
                             Q Fri Mar 04 23: 151 GGLKSCDLDFPLRENTNVLDVKDKEEDHIFFKYIYELILAGAIDEALEEAKLSDNISICMILCGIQEYLNPVIDTQIANE
                                                                                                                                      230 (726)
                        151 \hspace{0.1cm} \text{--v--LDPDAp-R-----L---D---e--l----f-llR-G----eA--lc---gq-wrAasL-G-----dp--d-------} \\
 O Consensus
                                                                                                                                      230 (726)
                        167 -----GPEIEEKIRNSSNEIEQIFLYLLLNDVVRASKLAIESKNGHLSVLISYLG-SNDPRIRDLAELQ
 T 3bg1_B
                                                                                                                                      229 (442)
 T ss_dssp
                             T ss_pred
                             ------нининининосссинининин
                             ссссСсhhннннннннhccccеннннннннссс-----hhccccCcннннннннннннннн
 Q ss_pred
 Q Fri_Mar_04_23: 231 FNTQQGIKKHSLWRRTVYSLSQQAGLDPYERAIYSYLSGAI------PNQEVLQYSDWESDLHIHLNQILQTEIENYLL
                                                                                                                                      303 (726)
                        O Consensus
 T Consensus
                        230 LQKWSTGGC-----SIDKNISKIYKLLSGSPFEGLFSLKELES-EFSW-----LCLLNLTL
 T 3bg1_B
                                                                                                                                      279 (442)
                             HHHTTSSCC-----CSCHHHHHHHHHHHSCSTTSTTCSGGGGG-TSCH-----HHHHHHHH
 T ss dssp
 T ss pred
                             HHHHHHCCC-----HHHHHHHHHHCCCcccccchhccC--CCCH------HHHHHHHH
 Q ss pred
                             Q Fri_Mar_04_23:
                        304 ENNOVGTDELILPLPSHALTVOEVLNRVASRHPSESEHPIRVLMASVILDSLPSVIHSSVEMLLDVVKGTEASNDIIDKP
                                                                                                                                     383 (726)
                        Q Consensus
                                                                                                                                      383 (726)
 T Consensus
                                                                                                                                      336 (442)
 T 3bq1 B
                                                                                                                                     336 (442)
                             T ss_dssp
                             HCCCCCCC-----CHHHHHHHHHHHhhCCCccCHHHHHHHHHhCCCc-----CHHHHhCccccCCCccc-----
 T ss_pred
                             сhинининининн
 Q ss pred
 Q Fri Mar 04 23: 384 YLLRIVTHLAICLDIINPGSVEEVDKSKLITTYISLLKLQGLYENIPIYATFLNESDCLEACSFILSS 451 (726)
                        384 ~~LRf~aHL~L~l~~l~~~~~~iI~~YI~~L~~~~~eLIplY~S~L~~~~e~ys~~L~~
 O Consensus
                        -|+-=||++|+.+|....+..+.-.|+.-|...|+.+.--+=+.+|+.+...+-|...
337 ---rLsw-l---vL-a-g----s----d-lt--fA-QLe--Glw-wAiFVllHl-d---R--aIr-lL-
337 --VQFCWYLIQTLRFNGTRVFSKETSDEATFAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDTIKRLVM
 T Consensus
                                                                                                                      402 (442)
 T 3bg1_B
                                                                                                                      402 (442)
                            T ss_dssp
                              T ss_pred
                                           PDB NCBI PublMed
 No 10
>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=96.91 E-value=0.015 Score=69.29 Aligned_cols=267 Identities=13% Similarity=0.162 Sum_probs=0.0
 Q ss pred
                             Q Fri Mar 04 23:
                         71 EARFWHLVELLLVFRNADLDLDEMELHPYNSRGLFEKKLMQDNKQLYQIWIVMVWLKENTYVMERPKNVPTSKWLNSITS 150 (726)
                         71 E--tW-Ll--L---R------y-s-----d----e---I--WLe--a------W--T---
 O Consensus
                             T Consensus
                        429 DYNLWKLSSILFDPVSYPYK------TDNDQVKMALLKKERHCR---LTSWIVSQI------ 475 (753)
 T 3jro A
                             T ss_dssp
                             T ss pred
 Q ss_pred
                             Q Fri_Mar_04_23: 151 GGLKSCDLDFPLRENTNVLDVKDKEEDHIFFKYIYELILAGAIDEALEEAKLSDNISICMILCGIQEYLNPVIDTQIANE
                                                                                                                                      230 (726)
                        151 ~v~~LDPDAp~R~~~~L~~D~~e~~l~~~f~llR~G~~eA~~lc~~~qq~wrAasL~G~~~~dp~~d~~~~~
 Q Consensus
                                                                                                                                      230 (726)
                               .+...+......+..+|.+|-.+|+|.+|.+|.+|.+|.+|.-..-|.-...
                        476 ------GPEIEEKIRNSSNEIEOIFLYLLINDVVRASKLAIESKNGHLSVLISYLG-----
 T 3jro A
                                                                                                                                      525 (753)
 T ss dssp
                             -----HHHHHTTTTSCSCTTHHHHHHTTTTCHHHHHHHHTTCCHHHHHGGGCS-----
 T ss_pred
                             Q ss_pred
 Q Fri_Mar_04_23: 231 FNTQQGIK------KHSLWRRTVYSLSQQAGLDPYERAIYSYLSGAI------PNQEVLQYSDWESDLHIHLNQIL
                                                                                                                                     294 (726)
                        231 \hspace{0.1cm} \hbox{$\sim\sim\sim\sim$G$} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim$r$} \hspace{0.1cm} \hbox{$LWk$} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim\sim$yErAiY$} \hspace{0.1cm} \hbox{$\sim\simLsG$} \hspace{0.1cm} \hbox{$1-\sim\sim\sim\sim$v$} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim$v$} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim$v$} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim\sim$v$} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim\sim\sim$v$} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim\sim\sim$v$} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim\sim\sim$v$} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim\sim\sim v$} \hspace{0.1cm} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim\sim\sim v$} \hspace{0.1cm} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim\sim\sim v$} \hspace{0.1cm} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim\sim\sim\sim v$} \hspace{0.1cm} \hspace{0.1cm} \hbox{$\sim\sim\sim\sim\sim\sim\sim v$} \hspace{0.1cm} \hspace{0.1cm
 Q Consensus
                                                                                                                                     294 (726)
                                   T Consensus
                                                                                                                                      592 (753)
                        526 ----SNDPRIRDLAELQLQKWSTGG-----CSIDKNISKIYKLLSGSPFEGLFSLKELES--EFSWLCLLNLTLCYGQ
 T 3jro_A
                                                                                                                                      592 (753)
                             ----SCCHHHHHHHHHHHHHTTT-----CCCCHHHHHHHHHTSSSCCSSSTTCCGGGGT--TSCHHHHHHHHHHTSC
 T ss dssp
                             ----СССИНИНИННИНННОС-----СССИНИНИНННЫСССссссссорьссс--СССИНИНИННЫССС
 T ss pred
                             Q ss pred
                        295 QTEIENYLLENNQVGTDELILPLPSHALTVQEVLNRVASRHPSESEHPIRVLMASVILDSLPSVIHSSVEMLLDVVKGTE
 Q Fri Mar 04 23:
                                                                                                                                      374 (726)
 O Consensus
                        295 ---vd--l------lp----s--i---L-----ea--p-r-iQ--iI------ll------L------
                                                                                                                                      374 (726)
                                                           T Consensus
                                                                                                                                      638 (753)
                        593 -----IDEYSLESLVQSHLDKFSLPYDDPIGVIFQLYAANE----NTEKLYKEVR---
 T 3jro A
                                                                                                                                      638 (753)
  T ss_dssp
                              T ss pred
                             Сесесесениянинининненнин
 Q ss pred
 Q Fri Mar 04 23: 375 ASNDIJDKPYLLRIVTHLAICLDIINPGSVEEVDKSKLITTYISLLKLQGLYENIPIYATFLNESDCLEACSFILSS 451 (726)
                        Q Consensus
 T Consensus
```

```
T 3jro A
                          639 ----QRTNALDVQFCWYLIQTLRFNGTRVFSKETSDEATFAFAAQLEFAQLHGHSLFVSCFLNDDKAAEDTIKRLVM 711 (753)
 T ss_dssp
                                T ss pred
                                ----ССССССссриннининне
                                                                                           Pub Med
                                                                NCBI
🗌 >4ycz_B NUP85; structural protein complex, nuclear pore complex, macromolec assemblies, structural protein; 4.10A
  {Thielavia heterothallica}
  Probab=96.25 E-value=0.096 Score=63.12 Aligned_cols=321 Identities=12% Similarity=0.101 Sum_probs=0.0
                                НИНИНИНННИСССИНИНИНИНННОС--сИНИНИННССССССС---СССССССССССССССССС
 Q Fri_Mar_04_23: 180 FFKYIYELILAGAIDEALEEAKLSD-NISICMILCGIQEYL---NPVIDTQIANEFNTQQGIKK-------HSLW
                                                                                                                                                 243 (726)
                          180 1~~~f~11R~G~~~eA~~1c~~~g~-q~wrAasL~G~~~~-dp~~d~~~~~~G~~~-----r~LW 243 (726)
 Q Consensus
                          T 4ycz B
                          {\tt 223} \ \ {\tt FWQAVFIALLRGKVGDAARLLDQAGWGHVRRG--QRGEYAYVGQALENVQRAVDETIAVLESCPGFDGNWEIWSSDWTLF}
                                                                                                                                                 300 (933)
 T ss dssp
                                T ss_pred
                                HHHHHHH------HhCCCCc------HHHHHHHHHHCCCchhhccccCCC
 Q ss pred
 Q Fri_Mar_04_23: 244 RRTVYSL-----SQQAGLD-------PYERAIYSYLSGAIPNQEVLQYSD
                                                                                                                                                 281 (726)
 Q Consensus
                          244 k~~c~~l------a~~~vErAiy~~LsG~l~~~~v~c~s
                                                                                                                                                 281 (726)
                          T Consensus
 T 4ycz_B
                          {\tt 301\ RVRARGLLEHLRRFAEGKDSAFGASAFSASAASAQSRQSMAGLARRAESQVPWEIYENLNIVFDIVLGQQGAILEA-AQD}
                                                                                                                                                 379 (933)
 T ss dssp
                                                                           -----CHHHHHHHHHHHHHHHHHHHHH
                                НННННННННННННС-----
 T ss_pred
                                Q ss pred
                                Q Fri Mar 04 23: 282 WESDLHIHLNQILQT------EIENYLLENNQVGTDELILPLPSHALTVQEVLNRVAS-----RHPSESEHPIRV
                                                                                                                                                 345 (726)
                          O Consensus
                                                                                                                                                 345 (726)
 T Consensus
                                                                                                                                                 452 (933)
                          380 WLEATVGLFGWWDERASRTEKPLSTSQSLSRSQ------ALVLASAPANSESYLDRLARAFHTAVESDFHFNSQNAVEI
 T 4ycz B
                                                                                                                                                 452 (933)
 T ss_dssp
                                                 -----CCHHHHHHHHTTTTSSCCCCC----
 T ss_pred
                                Q ss pred
                                Q Fri_Mar_04_23: 346 LMASVILDSLPSVIHSS-----VEMLLDVVKGTEASNDIIDKPYLLRIVTHLA-ICLDIINPGSVE-----
                                                                                                                                                 405 (726)
                          +..+|+..+|+..+| +..+.+..+ | |..+|+...+..+ | |..+|+...+|+...+| | |..+|+...+|+...+| | |..+|+...+|+...+| | |..+|+...+|+...+| | |..+|+...+|+...+| | |..+|+...+|+...+|+...+| | |..+|+...+|+...+|+...+| | |..+|+...+|+...+|+...+| | |..+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+...+|+
 T Consensus
                                                                                                                                                 520 (933)
                          453 GMACVFEDNIKGVIGLLRGWSLPIAAAVAEIASLGKW-----LPPHRPSGVYGLEDLDMDDLEVLGMDPGAPD 520 (933)
 T 4ycz B
 T ss_dssp
                                HHHHHHSSCCHHHHHHHHHSSCTHHHHHHHHHTTTSC------C------C-----
                                T ss pred
                               Q ss_pred
                          406 --EVDKSKLITTYISLLKL-----QGL------YENIPIYATFLN-----ESDCLEACSFILSSLE--DPQVRKKQI
                                                                                                                                                 462 (726)
 Q Fri Mar 04 23:
                          406 -----eLiply-S-L-----e-ys--L-i--d--eR---L
 Q Consensus
                                                                                                                                                 462 (726)
                          +...+.+|..|++..| +... ++...|+..+|..+...+|..+...+|..+..+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+....+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|..+...+|...+|...+...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...+|...
 T Consensus
                                                                                                                                                 600 (933)
 T 4ycz B
                                                                                                                                                 600 (933)
 T ss_dssp
                                chhhнининининининин
 T ss pred
 Q ss_pred
                                Q Fri Mar 04 23: 463 ETINFLRLP--ASNILRRTTQRVFDETEQEYSPSNEISISFDVNNIDMHLIYGVEWLIEGKLYVDAVHSIIALSRRFLLN
                                                                                                                                                 540 (726)
                          463 ~la~~~qld--v~i~k~~ve~i~~~~~~vs~~D~~lI~sleWL~~~~eAl~~n~l~R~FL~~
 O Consensus
                                                                                                                                                 540 (726)
                          T Consensus
                          601 FLLNELGMIEFAEDTTETYGDILARDSH------RYGEAMWYYALAHRPNKVREVMNLLTSYSLIQ
 T 4ycz B
                                                                                                                                                 660 (933)
 T ss_dssp
                                T ss_pred
 Q ss_pred
 Q Fri_Mar_04_23: 541 GR 542 (726)
                          541 gk 542 (726)
 O Consensus
                                +.
 T Consensus
                          661 s~
                                    662 (933)
 T 4ycz_B
                          661 ST 662 (933)
 T ss_dssp
 T ss pred
                                CC
 No 12
                                                                                         Pub Med
🗌 >4bzj_A Protein transport protein SEC31; secretion, trafficking; 40.00A (Saccharomyces cerevisiae) PDB: 4bzk_A
 Probab=95.89 E-value=0.11 Score=65.82 Aligned_cols=209 Identities=15% Similarity=0.160 Sum_probs=0.0
                                Q ss pred
 Q Fri_Mar_04_23: 182 KYIYELILAGAIDEALEEAKLSDNISICMILCGIQEYLNPVIDTQIANEFNTQQGIKKHSLWRRTVYSL-SQQAGLDPYE 260 (726)
                          182 ---f-llr-G---eA--lc---gq-wrAasL-G-----dp--d-------------------yE 260 (726) +.+-+.|..|++++|+++|...|.+-.|.|--. |+...+|+++|+++|--.|
```

512 ~-i~~l~~G~e~Av~~cl~~~~~Al~lA~~------g~~~l~~x~~y~~~~y~~~~p~~ 570 (1273)

T Consensus

```
T 4bzj_A
                   512 OTISKNIJVSGNIKSAVKNSLENDLLMEAMVIALD------SNNER-LKESVKNAYFAKYGSKSSLS 570 (1273)
 T ss_dssp
                       T ss_pred
                       Q ss pred
 Q Fri_Mar_04_23: 261 RAIYSYLSGAIPNQEVLQY--SDWESDLHIHLNQILQT--EIENYLLENNQVGTDELILPLPSHALTVQEVLNRVASRHP
                                                                                                           336 (726)
 Q Consensus
                   261 rAiY~~LsG~l~~~~v~c-~sWeD~Lwa~~n~ll~~-~vd~~l~~~~~~~lp~~~s~~i~~L~~~~i~~L~~~~
                                                                                                           336 (726)
                   T Consensus
                                                                                                           622 (1273)
                   571 RILYSISKREVDDLVEN-LDVSQWKFISKAIQNLYPNDIAQRNEMLIKLG---DRL-----
 T 4bzj_A
                                                                                                           622 (1273)
                       T ss_dssp
 T ss_pred
                       нинининьссинининьс-ссининининины
 Q ss_pred
                       НЬЫЬНИНИНИНИНИССИНИНИНИНИНИНИНИНИНИНИНИ
 Q Fri_Mar_04_23: 337 SESEHPIRVLMASVILDSLPSVIHSSVEMLLDVVKG---TEASNDIIDKPYLLRIVTHLAICLDIINP-GSVEEVDKSKL
                                                                                                           412 (726)
 O Consensus
                   337 ~ea~~p~r~iQ~~iI~~~~~L~~~~L~~~~~~LRf~aHL~L~l~~l~~l~~l~~~~~~i
                                                                                                           412 (726)
                       --- this time is in the second second
                                                                                                           702 (1273)
 T Consensus
                   623 KENGHRODSLTLYLAAGSLDKVASIWLSEFPDLEDKLKKDNKTIYEAHSECLTEFIERFTVFSNFINGSSTINNEQLIAK 702 (1273)
 T 4bzj A
                       T ss_dssp
                       T ss pred
                       НННННННННСССссhНННННhcCCHH
 Q ss pred
 Q Fri_Mar_04_23: 413 ITTYISLLKLQGLYENIPIYATFLNES
                                                     439 (726)
 Q Consensus
                   413 I~~YI~~L~~~~eLIplY~S~L~~~
                   +..|..|..|+.++==-|+..||.+
703 ~-eya~-la~-G~-~-A~--l~-~~~ 729 (1273)
 T Consensus
                   703 FLEFINLTTSTGNFELATEFLNSLPSD 729 (1273)
 T 4bzj A
 T ss_dssp
                       нинининитттснинининин
 T ss_pred
                       нинининнноссининниннноссо
                                    PDB"
 No 13
                 Pub Med
>5a9q 5 Nuclear pore complex protein NUP96; transport protein; 23.00A (Homo sapiens)
 Probab=95.26 E-value=1.3 Score=53.95 Aligned cols=266 Identities=20% Similarity=0.221 Sum probs=0.0
 Q ss pred
                       Q Fri Mar_04 23: 181 FKYIYELILAGAIDEALEEAKLSDNISICMILC--GIQEYLNPVIDTQIANEFNTQQGIKKHSL------WRRTVYSLS
                                                                                                           251 (726)
                   Q Consensus
                                                                                                           251 (726)
                       ++.+|.+|-+|++++|.+++...|++.+|..|. |+
                                                                                                11...
                   451 ~e~if~~L~g~~I~eAc~~Ai~~gd~rLAtLLsq~gg-------s~~~R~~~~QL~~W~~~----
 T Consensus
                                                                                                           506 (937)
 T 5a9q 5
                   451 VEAVFSYLTGKRISEACSLAOOSGDHRLALLLSOFVG------SOSVRELLTMOLVDWHOL----O
                                                                                                           506 (937)
 T ss dssp
                       T ss_pred
 Q ss_pred
                       Q Fri_Mar_04_23: 252 QQAGLDPYERAIYSYLSGAIPNQEVLQYS------DWESDLHIHLNQI-----LQTEIENYLLENNQVGT-DEL
                                                                                                           313 (726)
                   Q Consensus
                                                                                                           313 (726)
                   T Consensus
                                                                                                           583 (937)
                   507 ADSFIQDERLRIFALLAGKP--VWQL-SEKKQINVCSQLDWKRSLAIHLWYLLPPTASISRALSMYEEAFQNTSDSDRYA
 T 5a9q 5
                                                                                                           583 (937)
 T ss_dssp
                       T ss_pred
                       Q ss_pred
 Q Fri_Mar_04_23: 314 ILPLPSHALTVQEVLNRVASRHPSESEHPIRVLMASVILD-SLPSVIHSSVEMLLDVVKGTEASNDIIDKPYLLRIVTHL
                                                                                                           392 (726)
 O Consensus
                   \tt 314 \  \, \sim \sim lp \sim \sim s \sim \sim i \sim \sim L \sim \sim \sim ea \sim p \sim r \sim iQ \sim iI \sim \sim \sim \sim ll \sim \sim \sim L \sim \sim \sim \sim \sim \sim \sim LRf \sim aHL
                                                                                                           392 (726)
                   T Consensus
                                                                                                           648 (937)
                   584 CSPLPSYLEGSGCVIAEEQNSQTPLRDVCFHLLKLYSDRHYDLNQLLE-----PRSITADPLDYRLSWHL
                                                                                                           648 (937)
 T 5a9q 5
 T ss_dssp
                            -----HHHTTCCCSCHHHHHHHHHHHTCC-CHHHHHH------HHHTTCCCSCHHHHHHHH
                       CCCCCcccccccccccccCCCCCHHHHHHHHHhcCCCCCCHHHHhhC------hhccCCCccCCccHHHH
 T ss_pred
                       Q ss pred
                   \textbf{393} \  \, \textbf{AICLDIINPGSVEEVDKSKLITTYISLLKLQGLYENIPIYATFLN} ---- \textbf{ESDCLEACSFILSSLEDPQVRKKQIETINF}
 Q Fri_Mar_04_23:
                                                                                                           467 (726)
                   Q Consensus
                                                                                                           467 (726)
 T Consensus
                                                                                                           728 (937)
                   649 WEVLRALNYTHLSAQCEGVLQASYAGQLESEGLWEWAIFVLLHIDNSGIREKAVRELLTRHCQLLETPESWAKETFLTQK
 T 5a9q 5
                                                                                                           728 (937)
 T ss dssp
                       ниннинесссессининининининининининин
 T ss_pred
                       сСССНИННИННИННИННН
 Q ss_pred
 Q Fri_Mar_04_23: 468 LRLPASNILRRTTQRVFDETE 488 (726)
 Q Consensus
                   468 ~gldv~~i~k~~ve~i~~~~
                                               488 (726)
                       + | ++..= | -...+-+...+
 T Consensus
                   729 L~IP~~WI~eAkAl~ar~~gd 749 (937)
                   729 LRVPAKWIHEAKAVRAHMESD 749 (937)
 T 5a9q 5
 T ss dssp
                       ТТССНИННИННИННИННИТС
                       сСССНИНИНИНИНИНИНИН
 T ss pred
```

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PDB™
PROTEIN DATA BANK
                                                                                                                                                                        PubMed
>2pm7_A Protein WEB1, protein transport protein SEC31; beta propeller, alpha solenoid; 2.35A {Saccharomyces
   cerevisiae PDB: 2pm6 A 3mzl B
   Probab=94.68 E-value=1.2 Score=49.12 Aligned_cols=215 Identities=13% Similarity=0.113 Sum_probs=0.0
                                                           нининининининСССининининина Ссинининин СССиссос Ссиссос Ссиссос Ссиссос Ссий - нининининин - нh CC
   Q ss pred
   Q Fri_Mar_04_23: 177 DHIFFKYIYELILAGAIDEALEEAKLSDNISICMILCGIQEYLNPVIDTQIANEFNTQQGIKK-HSLWRRTVYSL-SQQA
                                                                                                                                                                                                                                                                                254 (726)
                                                  177 e--l----f-llR-G---eA--lc---gq-wrAasL-G-----dp--d-------G----r-LWk--c--l-a---
   O Consensus
                                                                                                                                                                                                                                                                                254 (726)
                                                  . ..+|+++.-+. .+..
                                                                                                                                                                                                                                                                                200 (399)
   T Consensus
                                                  143 SGNIEQTISKNLVSGNIKSAVKNSLENDLMMEAMVIALDS-----NNERLKESVKNAYFAKYG
   T 2pm7 A
                                                                                                                                                                                                                                                                               200 (399)
   T ss dssp
                                                           T ss pred
   Q ss_pred
                                                           Q Fri Mar 04 23: 255 GLDPYERAIYSYLSGAIPNQEVLQY--SDWESDLHIHLNQILQTEIENYLLENNQVGTDELILPLPSHALTVQEVLNRVA
                                                                                                                                                                                                                                                                               332 (726)
                                                  O Consensus
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                                                           yhtini lase i ver sines interest in it ver i to the interest in the interest i
   T Consensus
                                                                                                                                                                                                                                                                               255 (399)
                                                  201 SKSSLSRILYSISKREVDDLVEN-LDVSQWKFI-----SKA-----IQNLYPNDIAQRNEMMIKLG
   T 2pm7 A
                                                                                                                                                                                                                                                                                255 (399)
   T ss_dssp
                                                           T ss_pred
                                                            СССЬНИНИНИНСССИНИНИНЬ СССИНИНИНИ СССИНИНИНИ ССССОВЬНИНИНИНИНИ СССОВЬНИНИНИНИНИ СССОВЬНИКИ СОВЬНИКИ СССОВЬНИКИ СССОВЬНИКИ СССОВЬНИКИ СТОВЬНИКИ СОВЬНИКИ СТОВЬНИКИ СТОВЬНИКИ СТОВЬНИКИ СТОВЬНИКИ СТОВЬНИКИ СТОВЬНИКИ СТОВЬНИКИ
   Q ss_pred
                                                           hhhhhhhhнниннинсснининнинниннниннесс--ссссссссснинниннинннин-hcc-ccchhи
   Q Fri Mar_04 23: 333 SRHPSESEHPIRVLMASVILDSLPSVIHSSVEMLLDVVKGT--EASNDIIDKPYLLRIVTHLAICLDI-INP-GSVEEVD
                                                                                                                                                                                                                                                                                408 (726)
   O Consensus
                                                  408 (726)
                                                  T Consensus
                                                                                                                                                                                                                                                                                334 (399)
   T 2pm7_A
                                                  {\tt 256~DRMKENG-HRQDSLTLYLAAGSLDKVASIWLSEFPDLEDKLKKDNKTIYEAHSECMTEFIERFTVFSNFINGSSTINNEQ}
                                                                                                                                                                                                                                                                               334 (399)
   T ss_dssp
                                                            НИНИТТ-СИНИНИНИНТСИИНИНИНИНЫНИНЫНИНИНИТТССИИНИНИНИНИНИНИНИТТSCC---CCCHH
   T ss pred
                                                           Q ss pred
                                                           нинининининносссеринининосссии
   Q Fri_Mar_04_23: 409 KSKLITTYISLLKLQGLYENIPIYATFLNES
                                                                                                                                                 439 (726)
   Q Consensus
                                                  409 ~~~iI~~YI~~L~~~~eLIplY~S~L~~~
                                                                                                                                                  439 (726)
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335 l~~~l~yA~~LA~~G~~~A~Yl~~i~~~
   T Consensus
                                                                                                                                                 365 (399)
                                                  335 LIAKFLEFINLTTSTGNFELATEFLNSLPSD 365 (399)
   T 2pm7 A
                                                           нининининнитттснинининны
   T ss_dssp
                                                            нинининининин
   T ss pred
                                                                                        PDB<sup>IN</sup>
PROTEIN DATA BANK

NCBI
   No 15
                                                                                                                                                                          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=90.29 E-value=1.6 Score=52.95 Aligned_cols=250 Identities=13% Similarity=0.089 Sum_probs=0.0
                                                           Q ss pred
   Q Fri_Mar_04_23:
                                                 182 KYIYELILAGAIDEALEEAKLSDNISICMILCGIQEYLNPVIDTQIANEFNTQQGIKKHSLWRRTVYSLSQQAGLDPY-- 259 (726)
                                                  259 (726)
                                                  T Consensus
                                                                                                                                                                                                                                                                                522 (876)
                                                  465 EKAIICLAGNRVADACGYLLAAGNFRLATLVSGIGMODGDMKA------OLKDWR-----ESNVLAEFS
   T 4ycz A
                                                                                                                                                                                                                                                                                522 (876)
                                                           HHHHHHHSSSCCHHHHHHHHHHSSGGGHHHHHHHHTTC-----
   T ss_dssp
                                                            T ss_pred
                                                           --HHHHHHHHCCCchhhccccCCСHHHHHHHHHHH-----HHHHHHHHHHCCCChhhhhhhcCCCCCCCHHHHHHHHH
   Q ss pred
   Q Fri Mar 04 23: 260 --ERAIYSYLSGAIPNQEVLQYSDWESDLHIHLNQI-----LQTEIENYLLENNQVGTDELILPLPSHALTVQEVLNRVA
                                                                                                                                                                                                                                                                               332 (726)
                                                  260\ -- \text{ErAiY} \sim LsG - 1 \sim - \sim v - c - s \text{WeD-Lwa--} n - 1 - - \sim - 1 \sim - v d \sim 1 - \sim - \sim - \sim - 1 p \sim - s \sim - i \sim - L \sim 1 - c \sim - 1 \sim - v d \sim 1 - c \sim - c \sim - 1 p \sim - c \sim - i \sim - 1 \sim - v d \sim 1 - c \sim - c \sim - 1 p \sim - c \sim - i \sim - 1 \sim - v d \sim 1 - c \sim - c \sim - 1 p \sim - c \sim - i \sim - 1 \sim - v d \sim 1 - c \sim - c \sim - 1 p \sim - c \sim - i \sim - 1 \sim - v d \sim 1 - c \sim - v 
   O Consensus
                                                                                                                                                                                                                                                                                332 (726)
                                                                 ....+=-+| -++..+..
   T Consensus
                                                                                                                                                                                                                                                                                590 (876)
                                                  523 QPVRAIYELLAGNAGVCAGVKNVPIENRVDSFTISQRFGLDWMRSFGLRL-FYTTGATA-----NVAEAVRSFQ
   T 4ycz A
                                                                                                                                                                                                                                                                                590 (876)
   T ss dssp
                                                           T ss pred
   Q ss_pred
                                                           {\tt 333~SRHPSE-SEHPIR} \\ {\tt VLMASVILDSLPSVIHSSVEMLLDVVKGTEASNDIIDKPYLLRIVTHLAICLDIINP---GSVEEVD} \\ {\tt 133} \\ {\tt CRHPSE-SEHPIR} \\ {\tt VLMASVILDSLPSVIHSSVEMLLDVVKGTEASNDIIDKPYLLRIVTHLAICLDIINP---GSVEEVD} \\ {\tt CRHPSE-SEHPIR} \\ {\tt
   Q Fri_Mar_04_23:
                                                                                                                                                                                                                                                                                408 (726)
                                                  408 (726)
   O Consensus
                                                                                                         +..+.++...
                                                                                                                                                            ....++.=-|+-=||.-+|+.+|.
   T Consensus
                                                                                                   -----d--l-w-l---l--
                                                                                                                                                                                                                                                                                 647 (876)
   T 4ycz A
                                                  591 ADIEODKEPEP-----DSALWSLLKAF-----ANOEFDWSDTRLGWLLTKAIYATGKVSFGODAAEK
                                                                                                                                                                                                                                                                                647 (876)
   T ss dssp
                                                           HHHHTSSSCSC-----SCHHHHHHHTT-----SCSCCCCC--CCHHHHHHHHSCC---CCSTHHH
   T ss_pred
                                                           HHhhcCCCCCC-----ccHHHHHHHh------cCCCCChhhcccHHHHHHHHhccccccchhhH
   Q ss_pred
                                                           Q Fri_Mar_04_23:
                                                  409 KSKLITTYISLLKLQGLYENIPIYATFLN----ESDCLEACSFILSSLEDPQVRKKQIETINFLRLPASNILRRTTQRV
                                                                                                                                                                                                                                                                                483 (726)
                                                  O Consensus
                                                                                                                                                                                                                                                                                483 (726)
                                                                                                                                                                                                                                                                                727 (876)
   T Consensus
                                                  648 LDKASLAYASALTAQSQWVPATFVLLQLSDAASREAAVRDHLGRHARRIGSPRNPNSAFSSLRKFGVPETWIWEAKALDF
                                                                                                                                                                                                                                                                                727 (876)
   T 4ycz_A
   T ss dssp
                                                            НИНИНИНИННЯSSCSHHHHHHHTCCSSHHHHHHHHHHHHHHHHC---CCSSHHHHHHHHTTTCCTTHHHHHHHHH
   T ss_pred
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Q ss_pred
                           HHhcc
 Q Fri Mar 04 23: 484 FDETE
                                   488 (726)
 O Consensus
                      484 ~~~
                                   488 (726)
                      728 ~~~~
 T Consensus
                                   732 (876)
                      728 RARGD 732 (876)
 T 4ycz A
 T ss_dssp
                           HHC--
                           hhccc
 T ss pred
 No 16
                                                                            Pub Med
🗎 >3mzk_B Protein transport protein SEC16; alpha-helical-stack, beta-propeller; 2.69A {Saccharomyces cerevisiae}
 Probab=89.43 E-value=0.87
                                  Score=50.96 Aligned_cols=87 Identities=15% Similarity=0.230 Sum_probs=0.0
                           Q Fri Mar 04 23: 177 DHIFFKYIYELILAGAIDEALEEAKLSDNISICMILCGIQEYLNPVIDTQIANEFNTQQGIKKHSLWRRTVYSLSQQAGL
                                                                                                                           256 (726)
                      177 \ e^{-1} - r^{-1} - r^{-
 O Consensus
                                                                                                                           256 (726)
                      ...+|+++.-+..++...
 T Consensus
                                                                                                   -q~e~-~v~~~v~~~~
                                                                                                                           207 (441)
                      150 DINCOMRVLAFLQTGNHDEALRLALSKRDYAIALLVGSLM-----GKDRWSEVIQKYLYEGFT
 T 3mzk B
                                                                                                                           207 (441)
 T ss_dssp
                           СИНИНИНИНИТСИНИНИНИНИТСИНИНИНИТЬ....СИНИНИНИНИНИТС.
 T ss_pred
                           Q ss_pred
                           c-----CCHHHHH
 Q Fri Mar 04 23:
                      257 D------SDWESDL
                                                                                       286 (726)
 O Consensus
                      257 ~-----yErAiY~~LsG~l~~~~v~c-----sWeD~L
                                                                                       286 (726)
                          T Consensus
                      208 AGPNDQKELAHFLLLIFQVFVGNSKMAIKS-FYTNNETSQWASENWKSIV 256 (441)
 T 3mzk B
 T ss dssp
                           ----СТИНИНИНИНИНИНТТТСИНИНИН-ИНИСИНИНИНИНИНЫНИН
 T ss pred
                           cCCCcccchнинининисСhнинин-hcCcccchhнининин
                                          PDB
 No 17
                                                                             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
 Probab=33.62 E-value=79 Score=36.50 Aligned cols=96 Identities=13% Similarity=0.158 Sum probs=0.0
                           нинининСССинининин
 Q ss pred
 Q Fri_Mar_04_23: 181 FKY1YELILAGAIDEALEEAKLSDNISICMILCGIQEYLNPVIDTQIANEFNTQQGIKKHSLWRRTVYSLSQQAGLDPYE
                                                                                                                          260 (726)
                      O Consensus
                                                                                                                           260 (726)
 T Consensus
                                                                                                                           391 (570)
 T 3f3f C
                      332 IEDFLL-VIGGNORK---ILQYSRTWY--ESFCGFLLYYIP------SLELSAEYLOMSLEANVVDITNDWE
                                                                                                                           391 (570)
                           T ss dssp
                           ННИНИ-НhCCCHHH---НИНИhhhHH--НИНИНhheeCC------CchhHHHHHHHHHHHCCCCcCcHH
 T ss pred
                           НННННННСССеhhheeccCCСННННННННННН
 Q ss pred
                      261 RAIYSYLSGAIPNQEVLQYSDWESDLHIHLNQILQTE 297 (726)
 Q Fri_Mar_04_23:
                      261 rAiY~~LsG~l~~~~v~c~sWeD~Lwa~~n~ll~~~
                                                                        297 (726)
                      T Consensus
 T 3f3f C
                           НИНИННТТССGGGHHH-НИНИСНИННИННИННИН
 T ss_dssp
 T ss_pred
                           НИНИННЕССИНИННИН-НИНИСИНИННИННИНН
                                         PDB"
 No 18
                                                                            Pub Med
->2kw0_A CCMH protein; oxidoreductase, cytochrome C maturation; NMR {Escherichia coli}
 Probab=25.99 E-value=74 Score=27.34 Aligned_cols=45 Identities=20% Similarity=0.234 Sum_probs=0.0
                           Q ss pred
 Q Fri Mar 04 23: 161 PLRENTNVLDVKDKEEDHIFFKYIYELILAGAI-DEALEEA-KLSDNI
                                                                                     206 (726)
                      161 p~R~~~~L~~~D~~~e~~l~~~~f~llR~G~~~eA~~lc~~~~gq~
 Q Consensus
                           |.-++ ..|.+.+..=..+=..|+++|..|+. ++++++- .|.|.+
                                                                                       73 (90)
                       27 p~Cqn-qsIadSna~iA~dlR~~I~e~l~~G~Sd~eI~~~mv~RYGdf
 T Consensus
 T 2kw0 A
                       27 PKCON-NSIADSNSMIATDLROKVYELMOEGKSKKEIVDYMVARYGNF
                                                                                       73 (90)
                           T ss dssp
                           T ss pred
 No 19
                                          PDB<sup>®</sup>
                                                                    Pub Med
>4xmm_D Nucleoporin NUP85; structural protein, immune system, transport protein-immune complex; 7.38A
 {Saccharomyces cerevisiae S288C} PDB: 4xmn _D
 Probab=23.78 E-value=1.2e+02 Score=36.09 Aligned_cols=96 Identities=13% Similarity=0.158 Sum_probs=0.0
 Q ss pred
                           Q Fri Mar 04 23: 181 FKYIYELILAGAIDEALEEAKLSDNISICMILCGIQEYLNPVIDTQIANEFNTQQGIKKHSLWRRTVYSLSQQAGLDPYE
                                                                                                                           260 (726)
 Q Consensus
                      181 ~~~f~11R~G~~~eA~~1c~~~gq~wrAasL~G~~~~dp~~d~~~~~~~G~~~r~LWk~~c~~la~~~~~yE
                                                                                                                           260 (726)
                      ..+.-.-.|...-.-..++.|
                                                                                                                           362 (715)
 T Consensus
                      303 IEDFLL-VIGGNORK---ILOYSRTWY--ESFCGFLLYYIP------SLELSAEYLOMSLEANVVDITNDWE
 T 4xmm D
                                                                                                                           362 (715)
                           T ss_dssp
```

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T ss_pred
                     ННННН-HhCCCHHH---НННННhhHH--НННННhheeCC------CchhHHHHHHHHHHCCCCCCcHHH
                     НННННННСССсhhhccccСССHHHHHHHHHHHHH
 0 ss pred
 Q Fri_Mar_04_23: 261 RAIYSYLSGAIPNQEVLQYSDWESDLHIHLNQILQTE
                                                         297 (726)
                  261 rAiY~~LsG~l~~~~v~c~sWeD~Lwa~~n~ll~~~
 Q Consensus
                                                         297 (726)
                  .++-+++.||+..++..|.+|+-.+=||+--++...
363 ~~~~i-egd~~~vL~~-l~~ld~w~aAhladLl~~~
 T Consensus
                                                         398 (715)
                  363 QPCVDIISGKIHSILPV-MESLDSCTAAFTAMICEAK
 T 4xmm D
                                                         398 (715)
                     T ss dssp
                     ННННННСССИННННН-ННСССИННННННННН
 T ss_pred
                                 PDB'
 No 20
                                           NCBI
                                                             Pub Med
□ >5cqs_A Elongator complex protein 1; familial dysautonomia, ELP1 subunit, DIME protein binding; 2.70A
 {Saccharomyces cerevisiae}
 Probab=22.92 E-value=2.6e+02 Score=30.88 Aligned_cols=84 Identities=14% Similarity=0.076 Sum_probs=0.0
                     0 ss pred
 Q Fri_Mar_04_23: 182 KYIYELILAGAIDEALEEAKLSDNISICMILCGIQEYLNPVIDTQIANEFNTQQGIKKHSLWRRTVYSLSQQAGLDPYER
                  182 ~~~f~llR~G~~~eA~~lc~~~gq~wrAasL~G~~~~dp~~d~~~
                                                                      ~G~~~r~LWk~~c~~la~~
 Q Consensus
                                                                                                 261 (726)
                     +.+-.+++|.+++|++.|.++|+|-.|..+...
                                                                        ....+...+-.+.+
                  126 eA---Y-kag---kAie-y--a--w--al-la----l---
 T Consensus
                                                                       -----la--la-----q----
                                                                                                 184 (435)
                  126 DAAVAYEMLGKLKEAMGAYQSAKRWREAMSIAVQ---KFP------EEVESVAEELISSLTF--EHRYVD 184 (435)
 T 5cqs A
 T ss_dssp
                     НИНИНИНТТСИИНИНИНИТТСИИНИНИНИН -- TCT------TTHHHHHHHHHHHHHHHH---TTCHH
 T ss_pred
                     нинин--cCCchhhccc--cCCCнини
 Q ss pred
 Q Fri Mar 04 23: 262 AIYSYL--SGAIPNQEVL--QYSDWESDL 286 (726)
                                                 286 (726)
 O Consensus
                  262 AiY~~L--sG~l~~~~v--~c~sWeD~L
                  T Consensus
                  185 AADIQLEYLDNVKEAVALYCKAYRYDIAS 213 (435)
 T 5cqs_A
                     нинининиссининининттсинин
 T ss dssp
 T ss pred
                     нниннныессининнинннессининн
                                 PDB'
 No 21
                                                             Pub Med
>2kel A SVTR protein, uncharacterized protein 56B; homodimer, ribbon-helix-helix, transcription repres; NMR
 {Sulfolobus islandicus rod-shaped virus}
 Probab=20.86 E-value=1.7e+02 Score=21.89 Aligned_cols=36 Identities=6% Similarity=0.091 Sum_probs=0.0
                     СНИНИНИНИНИНИНССССИНИНИНИНИНИНИНИНИНИН
 Q ss pred
 Q Fri Mar 04 23: 454 DPQVRKKQIETINFLRLPASNILRRTTQRVFDETEQ 489 (726)
                  454 d~~eR~~~L~la~~~gldv~~i~k~~ve~i~~~
                                                        489 (726)
 Q Consensus
                     +++....-.+|++.|++..++++..+..+..+.++
                  21 --e---l---a---g-s-Se-ir-ai---l----g
 T Consensus
                                                         56 (56)
                  21 DKDLKTRLKVYCAKNNLOLTOAIEEAIKEYLOKRNG
 T 2kel A
                                                         56 (56)
                     ЕННИНИННИННЫ
 T ss_dssp
                     СНИНИНИНИНННЕСССИНИННИНННИНННИН
 T ss_pred
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