

```
34 3mkq_B Coatomer subunit alpha; 22.9 5.7E+02 0.016 26.0 10.7 96 793-906
                                                                                          16-115 (177)
35 Scqs_A Elongator complex prote 21.7 2.7E+02 0.0074 32.9 9.0 86 753-847 169-255 (435)
                                     PDB"
                                              NCBI
                                                                    Pub Med
          Nuclear pore complex protein NUP133; transport protein; 23.00A (Homo sapiens)
 Probab=100.00 E-value=1.1e-143 Score=1404.87 Aligned_cols=950 Identities=14% Similarity=0.176 Sum_probs=0.0
                        Q ss pred
 Q Fri_Mar_04_23:
                    42 ISMEQQQLRLHSHFDNSKVFTENNRYIVKTLQ-TDYSSGF-----SNDDELNGYIDMQIGYGLVNDHKKVYIWNIHST 113 (1157)
                     T Consensus
 T 5a9q 3
                     56 SSLSSRGTPTR-MFPHHS-ITESVNYDVKTFGSSLPVKVMEALTLAEVD-DQLTINID-EGWACLVCKEKLIUWKIALS 131 (1156)
 T ss dssp
                        T ss_pred
                        CCC--CCeEEEeCCCccCCCCCceEEE-ecCC---CCccccccccCCCCCCeEEEEECCCCe--eeccchhhhcc
 Q ss_pred
 Q Fri Mar 04 23: 114 QKD--TPYITVPFRSDDNDEIAVAPRCIL-TFPA---TMDESPLALNPNDQDETGGLIIIKGSKAI--YYEDINSINNLN
                                                                                                             185 (1157)
                    T Consensus
                                                                                                             195 (1156)
 T 5a9q 3
                    132 PITKLSVCKELQLP-PSDFHWSADLVALSYSSPSGEAHS-----TQAVAVMVATR-EGSIRYWPSLAGEDT-- 195 (1156)
 T ss dssp
                                           .....
                        CCCCCcceEecCC-CccccccccEEecCCCCcccc------CCCceEEEECC-CceEEEccCcccCCC-
 T ss_pred
 Q ss_pred
                        chhccCcceEEEEecCCCCC-ceEEEEEeecCccEEEEEeecCCCCeeeEehhhhccCccCccchhhcc--
 Q Fri Mar 04 23: 186 FKLSEKFSHELELPINSSGG-EKCDLMLNCEPAGIVLSTNMGRIFFITIRNSMGKPQLKLGKLLNKPFKLGIWSKIFN--
                                                                                                             262 (1157)
                    186 l-l-----l-L----g-E-vt-l-n-epag-IlaTS-gRl--lslrd--Gkp-l-----L-k----g-
 O Consensus
                                                                                                             262 (1157)
                             T 5a9q 3
                    196 -----YTEAFVDSG--GDKTYSFLTAVQGGSFILSSSGSQLIRL---IPESSGKIHQH-IL-PQ-GQGMLSGIGRKV
                                                                                                             259 (1156)
 T ss dssp
                        -----cceEeccC---CceEEEEEecCCCeEEEEe---CCCCCcceEEE-Ec-cC-CCcccchhhhhh
 T ss pred
 Q ss pred
                        -----C--CCCeEEEecCCCCcceEEEEEEECCCeEEEEEeecCCCcceEeeeccHHHHHHHHhhcCCC-----
 Q Fri_Mar_04_23: 263 -----T---NSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQLSATNSHPTKLIDVNIYEAILESLQDLYPF----- 326 (1157)
                    263 ------di-si-g----g-r-i-ilt--g-lq-W-------di---i---l----p------
+ +..|++|+.++ |+|.+||+|+++|++|+++.++++.++|+++.+|++
260 -s-fg--------lyiLts--iq-W------------di---i---l-----s-----
 Q Consensus
                                                                                                             326 (1157)
 T Consensus
                    260 SSLFGILSPSSDLTLSSVLWDR----ERSSFYSLTSS-NISKWELD-DS-SEKHAYSWDINRALKENITDAIWGSESNYE 332 (1156)
 T 5a9q 3
 T ss_dssp
 T ss_pred
                        hhhhcCCCCccceeEEEecC----CceEEEEEccC-ccEEEEec-CC-CceeeehhHHHHHHHHHHHHCcccccccc
                        Q ss pred
                    327 ---AHGTLKIWDSHPLQDESSQLFLSSIYDSSCNE-TYYILSTIIFDSSSNSFTIFSTYR--LNTFMESIT-DTKFKPKI
 Q Fri Mar 04 23:
                    327 ---~~l~iLD~~~~~~lvL~s~~~~~~y~L~~~i~~~~i~~~~i~~~~i~~~~l~~y~~~~~~PrL
 O Consensus
                                                                                                             399 (1157)
                    ----i--y----
 T Consensus
                                                                                                   ~~~~prL
                                                                                                             407 (1156)
                    333 AIKEGVNIRYLDLKQNC-DG-LVILAAAWHSADNPCLIYYSL-ITIEDNG--CQMSDAVTVEVTQYNPPFQSEDLILCQL
 T 5a9q 3
                                                                                                             407 (1156)
 T ss_dssp
                        T ss_pred
                        EecCC-CCccccceEEEEECCEEEEEccccccCCCCCChheEEEec-CCCeEEEEecCCCceEEE
 Q ss pred
 Q Fri_Mar_04_23:
                    400 \hspace{0.1cm} \texttt{FIPQM-ENANDTNEVTSILVMFPNAVVITQVNSKLDSSYSMRRKWEDIVSLR-NDIDIIGSGYDSKSLYVLTKQMGVLQF}
                                                                                                             477 (1157)
                    | . + | | + | + + + + + + | | + + | | | + + + + | | + + + + | + + + | | + + + | + + + | + + + | + + + | + + + | + + + | + + + | + + + + | + + + + + | + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + | + + + + + | + + + + + + | + + + + + + | + + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + + | + + + | + + + | + + + | + + + | + + + | + + + | + + + | + + + | + + + | + + + | + + + | + + + | + + + | + + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + + | + | + + | + | + | + + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | 
 T Consensus
                    408 ~1P~~~
                                                                                                             473 (1156)
                    408 TVPNFSNQ-----TAYLYNESAVYVCSTGTGKF----SLPQEKIVFNAQGDSVLGAGACGGVPIIFSRNSGLVSI
 T 5a9g 3
                                                                                                             473 (1156)
                        _____
 T ss dssp
                        EEECCCCc-----EEEEEECCCEEEEEECCCCC-----CCccceEEeccCCCeEEEeeccCCcEEEE
 T ss pred
 Q ss_pred
                        Q Fri Mar_04 23: 478 FVKENE---ETNSKPEV-------GFVKSHVDQAVYFSKINANPID------FNLPPEISL
                                                                                                             522 (1157)
                    478 ~~~~~~npl~----F-l~~1~
 Q Consensus
                                                                                                             522 (1157)
                    T Consensus
                    474 TSRENVSILAEDLEGSLASSVAGPNSESMIFETTTKNETIAQEDKIKLLKAAFLQYCRKDLGHAQMVVDELFSSHSDLDS
 T 5a9q_3
                                                                                                             553 (1156)
 T ss dssp
                        -----CTTTHHHHTTTTTTTTTTTTTTTTTHHHHHHSCCC
 T ss pred
                        Q ss_pred
                        Q Fri_Mar_04_23: 523 DQESIEHDLKLTSEEIFHSNG------KYIPPMLNTLGQHLSVRKEFFQNFLTFVAKNFN------YK
                                                                                                             578 (1157)
                    O Consensus
 T Consensus
                    554 D-SELDRAVTQISVDLMDDYPASDPRWAESVPEEAPGFSNTSLIILHQLEDKMKAHSFLMDFIHQVGLFGRLGSFPVRG-
 T 5a9q 3
 T ss_dssp
                        T-TTTTTSSHHHHHHTTSSCC-----CCSHHHHHHHHHTTTSSSHHHHTTCCCCCCCCSSCC-
                        с-нинининининининин
 T ss_pred
                        Q ss pred
 Q Fri_Mar_04_23: 579 ISPELKLDLIEKFEILNCCIKFNSIIRQSD-VLNDIWEKTLSNYNLTQNEHLTTKTVVINSPDVFPVIFKQFLNHVVFVL 657 (1157)
                   657 (1157)
```

```
T Consensus
                                                                                                    710 (1156)
                  632 TPMATRLLLCEHAEKLSAAIVLKNHHSRLSDLVNTAILIALNKREYEIPSNLTPADVFFREVSQVDTICECLLEHEEQV-
 T 5a9g 3
                                                                                                    710 (1156)
                      ----CHHHHHHHHHHHTTTTTTSCCCTTHHHHHHHHHHTTSCCCCSSCCSCCCHHHHTTCGGGTSSTTTTSSSSSSS-
 T ss dssp
 T ss_pred
                      ссссссснининин--нинининининин---нругоссссссори---нинининин----
 Q ss pred
                  658 FPSQNQNFKLNVTNLIN--LCFYDGILEEGEKTIRY---ELLELDPMEVD-TSKLPWFINFD---YLNCINQCFFD-FTF
 O Fri Mar 04 23:
                                                                                                    727 (1157)
                      658
                                                                                                    727 (1157)
 O Consensus
                      T Consensus
                                                                                                    788 (1156)
                  711 I.RD-APMDSIEWAEVVINVNNILKDMLQAASH-YRONRNSLYRREESLEKEPEYVPWTATSGPGGIRTVIIRQHEIVLKV
 T 5a9q 3
                                                                                                    788 (1156)
                      T ss dssp
 T ss pred
                      Q ss pred
                      ссс--сhhнининининининининининин
 Q Fri Mar 04 23:
                  728 ACE--EEGSLDSYKEGLLKIVKILYYOFNOFKIWINTQ-PVKSVNANDNFININNLYDDNHLDWNHVLCKVNLKEQCIQI
                                                                                                    804 (1157)
                  728 -----l--qL--L---ll---e---wl------l---y---R---i--L---q--e-A--L
 Q Consensus
                                                                                                    804 (1157)
                      +.+ ++.++.+++||+.|+++|++|.+++.|++.+ ..
                                                                 +++++++|.++|..||++|+++|+++|++|
                  789 ----d--l--qL--L-d-ll---
                                                      T Consensus
                                                                                                    862 (1156)
                  789 AYPQADSNLRNIVTEQLVALIDCFLDGYVSQLKSVDKSSNR-----ERYDNLEMEYLQKRSDLLSPLLSLGQYLWAASL
 T 5a9q 3
                                                                                                    862 (1156)
 T ss_dssp
                      TTTTTSSCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHTTCCSSS-----GGGTTHHHHHHHTTTTTSTTHHHHSCTTTHHHH
                      T ss_pred
                      ниносинининине
 Q ss pred
 Q Fri_Mar_04_23:
                  805 AEFYKOLSGLVQTLQTLDQNDSTTVSLYETFFNEFPK-EFSFTLFEYLIKHKKLNDLIFRFPQQHDVLIQFFQESAPKYG
                                                                                                    883 (1157)
 O Consensus
                  883 (1157)
                  T Consensus
                                                                                                    933 (1156)
                  863 AEKYCDFDILVQMCEQTDNQS----RLQRYMTQFADQNFSDFLFRWYLEKGKRGKLLSQPISQHGQLANFLQAH-E---
 T 5a9q_3
                                                                                                    933 (1156)
                      HHHTSCCHHHHHHHHHSSCT----THHHHHHHHSCSSCHHHHTHHHHCC-----CGGGTHHHHHHTC-S---
 T ss dssp
 T ss_pred
                      ННһhССННИНННННссСснн-----ННННННННСсСһнннннннннhСссһнһhНнннннннhhС-С---
 Q ss pred
                      Сссининнинеснининниннинниннинниннинниннин-СССсссининниннинниннин
 Q Fri_Mar_04_23:
                  884 HVAWIQQILDGSYADAMNTLKNITVDDSKKGESLSECELHLNVAKLSSLLV-EKDNLDINTLRKIQYNLDTIDAEKNISN
                                                                                                    962 (1157)
                  Q Consensus
 T Consensus
                  934 HLSWLHEINSQELEKAHATLLGLANME---TRYFAKKKTLLGLSKLAALASDFSEDMLQEKIEEMAEQERFLLHQETLPE 1010 (1156)
 T 5a9q 3
 T ss dssp
                      T ss_pred
                      НЬЫЬЬЬНЫННЫН НЬИНИНИННЫН НЬИНИННЫН НЬОССОССИНИННЫН НЬССС----СЬИНИННЫН НЬИНИННЫН НЬИНИНН НЬИНИННЫН НЬИНИНН НЬИНИНН НЬИНИНН НЬИНИНН НЬИНИНН НЬИНИНН НЬИНИН НЬИНИН НЬИНИНН НЬИНИН НЬИНИН НЬИНИН НЬИНИНН НЬИНИН НЬИНИ НЬИНИН НЬИНИН НЬИНИН НЬИНИН НЬИНИН НЬИНИН НЬИНИН НЬИНИН НЬИНИН НЬИНИ НЬИНИН НЬИН НЬИНИН НЬИНИН НЬИНИН НЬИНИН НЬИНИН НЬИНИ НЬИНИН НЬИНИ НЬИНИН НЬИНИН НЬИНИН НЬИНИ НЬИНИН НЬИНИН НЬИНИ НЬИНИН НЬИНИН Н
 Q ss pred
 Q Fri Mar 04 23: 963 KLKKGEVQICKRFKNGSIREVFNILVEELKSTTVVNLSDLVELYSMLD----DEESLFIPLRLLSVDGNLLNFEVKKFLN 1038 (1157)
                  963 ~i~~~~
                             ·----a---a------l-----l-----l----ldllTl-d--------F--AL-vl-----e----l- 1038 (1157)
 O Consensus
                                            T Consensus
                 1011 ~il~-----
                 1011 QLLA-----EKQL-----NLSAMPVLTAPQLIGLYICEENRRANEYDFKKALDLLEYIDEEED-ININDLK 1070 (1156)
 T 5a9q 3
                      THHH-----HTTC-----CSSSSCCCCHHHHHHHBSSSTTCTTCCHHHHHHTTTTTTSSCC----CCHHHHH
 T ss_dssp
                      T ss pred
 Q ss pred
                      нинининесссс-----сссининининин рессссссссинин ресссссс рынин---
 O Fri Mar 04 23: 1039 ALVWRRIVLLNAS-----NE----GDKLLOHIVKRVFDEELPKNNDFPLPSVDLLCDKSLLTPEYISE-TYG 1100 (1157)
 Q Consensus
                 1039 ~~IWrR~~l~DdW-----D~----~T~Ly~tL~~~~~~p~~~l~~~~~l~~~~~1100 (1157)
                 T Consensus
 T 5a9q_3
                 1071 LEILCKALQRDNWSSSDGKDDPIEVSKDSIFVKILQKLLKDGIQLSE-YLPEVKDLL---QADQLGSLKSNPYFE 1141 (1156)
 T ss dssp
                      HHHHHHHHHTTCC-----CHHHHHHHHCC-----CTTSCSHH---HHC------C
                      НННННННННҺССНҺНсССсҺҺННННННННННННННННҺССССссс-сСССНННН---СсҺҺҺҺссССсННН
 T ss_pred
->4q9t_A Nucleoporin NUP133; nuclear pore complex, NUP84 complex, ALPS motif structural genomics, PSI-biology;
 3.00A {Vanderwaltozyma polyspora}
 Probab=100.00 E-value=1.7e-83 Score=761.32 Aligned_cols=421 Identities=44% Similarity=0.779 Sum_probs=0.0
 Q ss_pred
                      hhhcccCCCcEEEecCCCEEEEecCCCcchhc-----ccCCceEEEEcCCCCEEEEEcCCCeEEEEecCCCCCCCC
                  48 OLRLHSHFDNSKVFTENNRYIVKTLOTDYSSGF-----SNDDELNGYIDMOIGYGLVNDHKKVYIWNIHSTOKDTPY
 Q Fri Mar 04 23:
                                                                                                    119 (1157)
                            --d---vlt-n--Y-Vs-lp-lP-----q-id--sG-Alv-----
 Q Consensus
                   48 ~
                                                                                     ~~VW~y~s~~~~p~
                                                                                                    119 (1157)
                      ---vlt-n--y-V--l---p--l---al------g-iD--sG-Alvv----l-VW-y-s---s
                                                                                                     81 (459)
 T 4q9t A
                    2 SLTSNNKYGNTKILTETEKYSVTKLSTDLSFLPGSNGNNNTIDTHHFEGLVDTALOKALVNDLDHIYIWNYNSIOKDTPI
                                                                                                     81 (459)
 T ss dssp
                      -----CEEEEECSSEEEEECSCCCCSCC------CCCCEEETTTEEEEECSSEEEEECTTSCSCCCCE
                      cccccCCCcEEEEecCCEEEEECCCCchHHhhhhhhccccccCCceEEEECCCCEEEEEecCCCCCCCcc
 T ss_pred
                      EEEeCCCcccCCCCCcceEEEecC-CCCccccccccCCC-----CCCeEEEEECCCCe--eecccchhhhccchhcc
 Q ss_pred
 Q Fri_Mar_04_23: 120 ITVPFRSDDNDEIAVAPRCILTFP-ATMDESPLALNPNDQD-----ETGGLIIIKGSKAI--YYEDINSINNLNFKLSE
                                                                                                    190 (1157)
 Q Consensus
                  190 (1157)
                        ++|||| ++..++++|+|+|+| +++|+.+++++|+++
                                                                                                    160 (459)
 T Consensus
                   82 CKISLH-DDYSVLSSPPICLFTSSISSTNNDTANYNNNASGNINSGKFNNGICIINKKNSQFLYFEDISTINNLYTKLSK
                                                                                                    160 (459)
 T 4q9t_A
 T ss_dssp
                      T ss pred
```

```
Q ss_pred
               CcceEEEEecCCCCceEEEEeecCccEEEEEeecCccEEEEEeecCcCCceeeEehhhhccCccCccchhhccCCCCeEEE
                                                                      270 (1157)
Q Fri Mar 04 23: 191 KFSHELELPINSSGEKCDLMLNCEPAGIVLSTNMGRIFFITIRNSMGKPQLKLGKLLNKPFKLGIWSKIFNTNSSVVSL
             191 -----I-L----gE-vt-l-n-epag-IlaTS-gRl--lslrd--Gkp-l-----L-k----g---i-----I-si
                                                                      270 (1157)
            T Consensus
                                                                      237 (459)
T 4q9t A
                                                                      237 (459)
               --CEEECCCC--SSCCEEEEEETTTEEEEEETTSCEEEECCSCSSCCSCCEEEEEECCCCCSSSSCC-GGGCEEEE
T ss dssp
               ccceeEEEecC--CCcEEEEEEeCCCEEEEEEeCCcceEEEEEeecCCCCCcccccc-CcCcEEEE
T ss_pred
               ecccccccerrereccccerrerecccccereeccHHHHHHHhbccccccccrrereccccc--crrere
Q ss_pred
Q Fri Mar 04 23: 271 RNGPILGKGTRLVYITTNKGIFQTWQLSATNSHPTKLIDVNIYEAILESLQDLYPFAHGTLKIWDSHPLODE--SSOLFL
                                                                      348 (1157)
             271 ~-g~~~~g~r~i~ilt~~g~lq~W~~~~~g~~~~~di~~~i~~l~~~p~~~~l~iLD~~~~~~--~~lvL
Q Consensus
                                                                      348 (1157)
               238 --g----g-r-v-ilTs-g-lq-W-i------di---l---l------l-iLD------g----l-vL
T Consensus
T 4q9t A
            238 KKGPIVGKGERLLYITTRGGSLQIWQLS-INSKSFKRLEINIYEHVLDSLQDLYPFAHGTLAFLDSHPIYSDTSSAHLTL
                                                                      316 (459)
T ss_dssp
               ERRERCSTTCEREERERTTSEERERERC-SSSCCERERERCHHHHHHHHHTTCGGGTTTCERERERESCSSCSSREERE
               ECCCCCCcceEEEEEeCCCcEEEEEc-CCCceeEEEeechHHHHHHHHHhhhCcCccCcEEEEEE
T ss pred
               EEecCCCCceeEEEEEEECCCCceEEEEEEEeecccCcc-cCCCceEEecC------CCCccccccceEEEEE
Q ss pred
Q Fri_Mar_04_23: 349 SSIYDSSCNETYYLLSTIFFDSSSNSFTIFSTYRLNTFMESIT-DTKFKPKIFIPQ------MENANDTNEVTSILVMF
                                                                      420 (1157)
Q Consensus
             349 ~s~~~~~vy~L~~~i~~~~i~~~~l~~y~~~~~prL~lp~~~~~q~~~~afV~f
                                                                      420 (1157)
               +|||+|
             317 vs-s----y-Lvt-----i----i--y------prL-lp------
T Consensus
                                                                -~afv~f
             317 ASISNG-NEIYYLMITVILDEKTNSFQIFSIYKLNTYFTKSTVDLNHKPQLFIPNALDSIVSPTL-----SVYVLF
T 4q9t A
                                                                      386 (459)
T ss_dssp
               T ss_pred
               Q ss_pred
               CCEEEEEccccccCCCCCChheEEEecCCCeEEEecCCCceEEEEccCCC
Q Fri_Mar_04_23: 421 PNAVVITQVNSKLDSSYSMRRKWEDIVSLRNDIDIIGSGYDSKSLYVLTKQMGVLQFFVKENE
                                                          483 (1157)
Q Consensus
             421 ~~aVv~~s1~~~~s~~~~eD~I~f~~~~ilGsG~~~~~l~t~~~Gvv~i~~~~~
                                                           483 (1157)
             T Consensus
                                                           449 (459)
             387 NNAVVMTQISSKLDSSFPLRRKWEDIIRFNKDVEIIGSGYSTDSIYVICKDMGVLKIASHSNN 449 (459)
T 4q9t A
               SSEEEEEEESCCCCSSCCCCCEEEEECCTTCCEEEEEECSSCEEEETTTEEEEEEC---
T ss_dssp
               T ss pred
                       PDB<sup>IN</sup>
PROTEIN DATA BANK
                             NCBI Pub Med
No 3
>3i4r_B Nuclear pore complex protein NUP133; protein transport, structural protein, kinetochore, mRNA transport,
nucleus, phosphoprotein, translocation; 3.53A {Homo sapiens}
Probab=100.00 E-value=4.7e-83 Score=792.31 Aligned_cols=552 Identities=14% Similarity=0.164 Sum_probs=0.0
               Q ss_pred
Q Fri_Mar_04_23: 491 VGFVKSHVDQAVYF-SKINANPIDFNLPPEISLDQ-----ESIEHDLKLTSEEIFHS-----NGKYIPPM
                                                                      549 (1157)
             491 ~~~KS~leQAvf~~~~~npl~F~l~~~l~~~~i~~a~~~is~eIl~S------s~~ip~~
                                                                      549 (1157)
O Consensus
              +++|+|++
T Consensus
                                                                       81 (644)
              2 SHMDKIKLLKAAFLQYCRKDLGHAQMVVDELFSSHSDLDSDSELDRAVTQISVDLMDDYPASDPRWAESVPEEAPGFSNT
T 3i4r B
                                                                       81 (644)
               T ss_dssp
               T ss_pred
Q ss pred
               Q Fri_Mar_04_23: 550 LNTLGQHLSVRKEFFQNFLTFVAKNFN-----YKISPELKLDLIEKFEILNCCIKFNSIIRQSD-VLNDIWEKTL
                                                                      618 (1157)
             550 ~~sL~~qL~~R~~~l~~Li~fl~~~~~~kls~~tr~~Lle~aEKlaaa~~Lw~~~~~~~l~~i~~vl
                                                                      618 (1157)
             T Consensus
                                                                      160 (644)
T 3i4r B
                                                                      160 (644)
               T ss dssp
               сининининининининининин
T ss pred
               НьсССССССССНИННььсСниннинниннинннын ньессссссинниннин--инининниннин--ин
Q ss_pred
Q Fri Mar 04 23: 619 SNYNLTQNEHLTTKTVVINSPDVFPVIFKQFLNHVVFVLFPSQNQNFKLNVTNLIN--LCFYDGILEEGEKTIRY---EL
                                                                      693 (1157)
            693 (1157)
Q Consensus
             161 ~~~~~~l~~~d~F~~~vs~i~~l~~~l~~~l~~~~~~~~~~~~~ean~i~~vl~~a~~-yR~~~~~
T Consensus
                                                                      237 (644)
             161 NKREYEIPSNLTPADVFFREVSOVDTICECLLEHEEOV-LRD-APMDSIEWAEVVINVNNILKDMLOAASH-YRONRNSL
                                                                      237 (644)
T 3i4r B
               TSCCCCSSCCSCCCHHHHTTCGGGTSSTTTTSSSSSS-SCC----CCTTSSHHHHHHHHHHHHTTHHHHT-TTTCC---
T ss dssp
               T ss pred
Q ss_pred
               Q Fri_Mar_04_23:
             694 LELDPMEVD-TSKLPWFINFD---YLNCINQCFFD-FTFACE--EEGSLDSYKEGLLKIVKILYYQFNQFKIWINTQPVK
                                                                      766 (1157)
             694 ~-1~-~-1~-~--PW~t~~--i~~1~~1~~-~-~--1~~1~~qL~-L~~11~~~e~~wl~~-e~~wl~~-~-
O Consensus
                                                                      766 (1157)
             T Consensus
                                                                      316 (644)
             238 YRREESLEKEPEYVPWTATSGPGGIRTVIIRQHEIVLKVAYPQADSNLRNIVTEQLVALIDCFLDGYVSQLKSVDKSSN-
T 3i4r B
                                                                      316 (644)
T ss_dssp
               T ss_pred
               сссиннининининининининининин
Q ss pred
Q Fri_Mar_04_23: 767 SVNANDNFININNLYDDNHLDWNHVLCKVNLKEQCIQIAEFYKDLSGLVQTLQTLQTLDQNDSTTVSLYETFFNEFPK-EFSF
                                                                      845 (1157)
            845 (1157)
O Consensus
```

```
|++.||++||+ +||+
 T Consensus
                          317 ----rl--y--R---i--L--g--e-A--LAEky-Df--Lv-lce------rl--y---f----Fa-
                                                                                                                                               387 (644)
                          317 ----RERYDNLEMEYLQKRSDLLSPLLSLGQYLWAASLAEKYCDFDILVQMCEQTDNQS-----RLQRYMTQFADQNFSD
 T 3i4r B
                                                                                                                                              387 (644)
                               T ss dssp
 T ss_pred
                               нинининессинины
 Q ss pred
 Q Fri_Mar_04_23:
                          846\ {\tt TLFEYLIKHKKLNDLIFRFPQQHDVLIQFFQESAPKYGHVAWIQQILDGSYADAMNTLKNITVDDSKKGESLSECELHLN}
                                                                                                                                               925 (1157)
                          846 ~lf~~yi~~g~~~~LL~~~~~~FL~~~p~~~~lsWI~dI~~~~y~~As~tL~~lA~~~~~~~l~~kk~~LS
                                                                                                                                               925 (1157)
 Q Consensus
                               388 -lp-rwylekgkrgkllsQpisQhgQlanflQah-e---hLSwlheinsQelekahatllglanme---tryfakkktllg
 T Consensus
 T 3i4r B
                                                                                                                                               460 (644)
                               T ss dssp
                               T ss pred
 Q ss pred
                               Q Fri Mar 04 23:
                          926 VAKLSSLLV-EKDNLDINTLRKIOYNLDTIDAEKNISNKLKKGEVOICKRFKNGSIREVFNILVEELKSTTVVNLSDLVE 1004 (1157)
                          926 LaKLa-LA-----l--i~-L-li-iQe-L---i----a---a----a-----l------L---eLid 1004 (1157)
 Q Consensus
                                                                                                                        ++++++|+|++||
                                |||||+||+ ++....++.++|+++|++++|+.|++.+++
                          461 lAKLa~lA~~~~~l~~i~~L~~i~iQ~~l~~i~~i~~i~
 T Consensus
                                                                                                                                     ~eLi
 T 3i4r_B
                          \bf 461\ LSKLAALASDFSEDMLQEKIEEMAEQERFLLHQETLPEQLLA------EKQL------NLSAMPVLTAPQLIG
                                                                                                                                               521 (644)
                               T ss_dssp
                               T ss_pred
                               нносс----сынинининныныныныннынниннининессСс------сс-----ссСнинининнынынын
 Q ss pred
 Q Fri_Mar_04_23: 1005 LYSMLD----DEESLFIPLRLLSVDGNLLNFEVKKFLNALVWRRIVLLNAS-----NE-----GDKLLQHIVKRVFDEE 1069 (1157)
                     1005 llTl~d----~-F-~AL~vl~--~-~e~~~l~~lWrR~~l~DdW-----D~----T-Ly~tL~-~-~~ 1069 (1157)
 O Consensus
                         T Consensus
                                                                                                                                               600 (644)
                          522 LYICEENRRANEYDFKKALDLLEYIDEEED-ININDLKLEILCKALQRDNWSSSDGKDDPIEVSKDSIFVKILQKLLKDG
 T 3i4r B
                                                                                                                                              600 (644)
                               T ss dssp
 T ss_pred
                               ННСССсссСНИННИННИНННИННЕСССС - АНИНИНИННИННИНННИН В НЕСТАТИВНИТЕТ В НЕВИЗИВНИТЕТ В НЕВИЗИВИТЕТ В НЕВИЗИВНИТЕТ В НЕВИЗИВНИТЕТ В НЕВИЗИВНИТЕТ В НЕВИЗИВНИТЕТ В НЕВИЗИВИТЕТ В НЕВИЗИВИТЕТ В НЕВИЗИВИТЕТ В НЕВИЗИВИТЕТ В НЕВ
 Q ss pred
                               cccccCCCCCHHHh
 Q Fri_Mar_04_23: 1070 LPKNNDFPLPSVDLL 1084 (1157)
                        1070 ~~~~p~~~1 1084 (1157)
 Q Consensus
                          .... +.||..+++
601 ~~~~~Lp~~~~ll 614 (644)
 T Consensus
                          601 IQLSE-YLPEVKDLL 614 (644)
 T 3i4r B
 T ss dssp
                                ----CTTSCSHH
                               Cchhh-cCCCHHHhc
 T ss_pred
 No 4
                                                PDB'
                                                               NCBI
                                                                                         Pub Med
🗌 >3kfo_A Nucleoporin NUP133; nuclear pore complex, yeast, proteolysis, structural genomics, PSI2, protein
  structure initiative; HET: MSE; 1.90A {Saccharomyces cerevisiae}
 Probab=100.00 E-value=1.4e-63 Score=554.95 Aligned_cols=279 Identities=100% Similarity=1.381 Sum_probs=0.0
                               СССссСссАннинннесСниннинннинннн
 Q ss pred
 Q Fri_Mar_04_23: 878 SAPKYGHVAWIQQILDGSYADAMNTLKNITVDDSKKGESLSECELHLNVAKLSSLLVEKDNLDINTLRKIQYNLDTIDAE
                                                                                                                                               957 (1157)
                          878 ~~p~~~lsWI~dI~~~y~~As~tL~~lA~~~~~~l~~kk~~LSLaKLa~LA~~~~~~~l~~i~~~L~li~iQ
 Q Consensus
                                                                                                                                               957 (1157)
                              T Consensus
                                                                                                                                                80 (288)
                            2 S-LKYGHVAWIQQILDGSYADAMNTLKNITVDDSKKGESLSECELHLNVAKLSSLLVEKDNLDINTLRKIQYNLDTIDAE
 T 3kfo A
                                                                                                                                                80 (288)
 T ss dssp
 T ss_pred
                               Q ss pred
 O Fri Mar 04 23:
                          958 KNISNKLKKGEVQICKRFKNGSIREVFNILVEELKSTTVVNLSDLVELYSMLDDEESLFIPLRLLSVDGNLLNFEVKKFL 1037 (1157)
                          958 e-L---i-----eLidlTl-d----F--AL-vl-----e----1 1037 (1157)
 O Consensus
                           T Consensus
 T 3kfo A
                               T ss dssp
                               нинининарурунинин
 T ss pred
                               нинининасссосссининининный сосссосссосссининый сосссостининий сосстаний сосстаний сосстаний сосстаний сосссостиний сосссостиний сосстаний сосстании сосстаний сосстаний
 Q ss_pred
 Q Fri Mar 04 23: 1038 NALVWRRIVLLNASNEGDKLLQHIVKRVFDEELPKNNDFPLPSVDLLCDKSLLTPEYISETYGRFPIDQNAIREEIYEEI 1117 (1157)
                        1038 ~~~IWrR~~l~DdWD~~~T~Ly~tL~~~
                                                                                   ---p----1--
                                                                                                                              -~i~~d~~~E~ 1117 (1157)
 Q Consensus
                               ---IWrR--1-DdWD---T-Lf-tL-----1P----11------1
                          161 NALVWRRIVLLNASNEGDKLLQHIVKRVFDEELPKNNDFPLPSVDLLCDKSLLTPEYISETYGRFPIDQNAIREEIYEEI 240 (288)
 T 3kfo A
 T ss dssp
                               T ss_pred
                               Q ss pred
 Q Fri_Mar_04_23: 1118 SQVETLNSDNSLEIKLHSTIGSVAKEKNYTINYETNTVEY 1157 (1157)
 Q Consensus
                        1118 ~-1~~~~~157 (1157)
                          280 (288)
 T Consensus
                          241 SQVETLNSDNSLEIKLHSTIGSVAKEKNYTINYETNTVEY
 T 3kfo A
                                                                                        280 (288)
 T ss_dssp
                               HHHHHHTGGGHHHHHHHHHHHHHHHTTSSEEEETTTTEEEE
 T ss pred
                               нининрироссининининнин
```

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PDB"
No 5
                           SCOPe
                                             NCBI
                                                     S
                                                            Pub Med
🗌 >1xks_A Nuclear pore complex protein NUP133; beta-propeller, helical insertions, protein transport; 2.35A {Homo
 sapiens | SCOP: b.69.14.1
Probab=100.00 E-value=1.1e-60 Score=565.24 Aligned cols=367 Identities=16% Similarity=0.211 Sum probs=0.0
                  Q ss pred
               59\ \text{KVFTENNRYIVKTLQ-TDYSSGFS-----N-DDELNGYIDMQIGYGLVNDHKKVYIWNIHSTQKDT--PYITVPFRSDDN}
Q Fri_Mar_04_23:
               59 ~vlt~n~Y~Vs~lp~~lP~~~~~g~id~~sG~Alv~~~~~VW-y~s~~~p-~~~~pLp~~
                T Consensus
                                                                                  84 (450)
T 1xks_A
                7 HSITESVNYDVKTFGSSLPVKVMEALTLAEVDDQLTINIDE-GGWACLVCKEKLIIWKIALSPITKLSVCKELQLP-PSD
                                                                                  84 (450)
 T ss_dssp
                  ----CCSSEEEEECSSCCCHHHHHHHHCCTTSCEEEEECT-TSEEEEEETTEEEEEECCSSCCGGGCCEEEEECC-CCS
T ss_pred
                  CCCCCceEEEecCCCCcccccccccCCCCCeEEEEECCCCe--eecccchhhhccChhccCcceEEEEecCCCCCce
Q ss pred
Q Fri Mar 04 23: 130 DEIAVAPRCILTFPATMDESPLALNPNDQDETGGLIIIKGSKAI--YYEDINSINNLNFKLSEKFSHELELPINSSGGEK
                                                                                  207 (1157)
               207 (1157)
 Q Consensus
               ..+...|++++++.++ ++.+++||||+|+| +|+ ||||+| +++++|..++|. ++|+
85 ----a-v-l----psg-------s---pGlliVsp--G-VryWesI-------ve--i-L---g-E-
T Consensus
                                                                                  144 (450)
               85 FHWSADLVALSYSSPSG-----EAHSTQAVAVMVATR-EGSIRYWPSLAG-----EDTYTEAFVDSG--GDKT
T 1xks A
                                                                                  144 (450)
                  SCCCGGGEEEECC-----TTCCEEEECCT-TCEEEEESCTTC-----TTCCEEEECC-----CC
T ss dssp
                  cccCCceEEEeecCCC------CccCCCCceEEEEcC-CccEEEccccc-------CCCceEEEEecC--CCce
T ss_pred
Q ss_pred
                  EEEEEeeCCceEEEEeecccEEEEEeeCCCCCeeeEehhhhccCccCccchhhccC----CCCeEEE-----ecCCCCCc
Q Fri Mar 04 23: 208 CDLMLNCEPAGIVLSTNMGRIFFITIRNSMGKPQLKLGKLLNKPFKLGIWSKIFNT----NSSVVSL-----RNGPILGK
                                                                                 278 (1157)
               208 vt~l~n~epag~IlaTS~gRl~~lslrd~~Gkp~l~~~~L~k~~~~g~~
                                                         ---i----g--
O Consensus
                                                                                  278 (1157)
               T 1xks A
               145\ \mathtt{YSFLTAVQGGSFILSSSGSQLIRLIPESS-GK--IHQH-IL-PQ-GQGMLSGIGRKVSSLFG-ILSPSSDLTLSSVLWDR}
                                                                                  217 (450)
T ss dssp
                  EEEEEETTTEEEEEETTCCEEEEEECTT-SC-EEEE-EC-TT-CCCC------CCCCEEEEEEET
                  eEEEEEcCCCcEEEEecCC-Ce--EEEE-Ee-cC-CCccccccchhhhhhcc-ccccccceeeeeccC
T ss pred
Q ss pred
                  cceeeeeeccCcceeeeccHHHHHHHHHhhccccc----------CCEEEEEeeEccCccceeeee
 Q Fri_Mar_04_23: 279 GTRLVYITTNKGIFQTWQLSATNSHPTKLIDVNIYEAILESLQDLYPFAH------GTLKIWDSHPLQDESSQLFLS
                                                                                 349 (1157)
Q Consensus
               279 g~r~i~ilt~~g~lq~W~~~~~g~~~~~di~~i~~l~~~p~~~~-~-----l~iLD~~~~~~~lvL~
                                                                                  349 (1157)
               T Consensus
               218 ERSSFYSLTSS-NISKWELD--DSSEKHAYSWDINRALKENITDAIWGSESNYEAIKEGVNIRYLDLKQNC-DG-LVILA
T 1xks A
                                                                                  292 (450)
T ss_dssp
                  T ss_pred
                  CCEEEEEECCC-CEEEEEEcc--CCCceeeeecchHHHHHHHHHHHHHHCCCcccccccCccCccCccEEEEEEECC-CC-EEEEE
                  EecCCCCC----ceeEEEEE----EEeCCCCceEEEEEEeecccCCcc-cCCCCceEEecC-CCCccccccceEEEEE
Q ss pred
               350 SIYDSSCN----ETYYILSTI----IFDSSSNSFTIFSTYRLNTFMESIT-DTKFKPKIFIPQ-MENANDTNEVTSILVM
Q Fri Mar 04 23:
                                                                                  419 (1157)
               419 (1157)
O Consensus
                  +..+. . .++1+1+++
                                    .+..++ ++|.
                                                 +..|..+.+ ....+|||++|+ ||.
                                                                           +|||+
                                                           ~~~prL~vP~~pg~----afv~
               293 s~~~~
T Consensus
                           -~~Y~Lvt~~
                                      ----v-----
                                                                                  356 (450)
               293 AAWHS--ADNPCLIYYSLITIEDNGCQMSDA--VTVE----VTQYNPPFQSEDLILCQLTVPNFSNQ------TAYLY
T 1xks A
                                                                                  356 (450)
                  EEECT--TSSSCBEEEEEEECCBTTBCCSC--EEEE----ECSCCCBCCCGGGCCCEEECCCSSSS------EEEEE
 T ss_dssp
                  EEecC--CCCccEEEEEEEEcCceeCCCc--eEEE----EEecCCCCCccccceEEEeecCCCC------EEEEE
T ss_pred
                  ECCEEEEEccccccCCCCCChheEEEec-CCCeEEEecCCCceEEEEecC
Q ss pred
Q Fri_Mar_04_23:
               420 FPNAVVITQVNSKLDSSYSMRRKWEDIVSLR-NDIDIIGSGYDSKSLYVLTKQMGVLQFFVKE
                                                                    481 (1157)
               420 f~~aVv~~sl~~~~s~~~~eD~I~f~~~~~ilGsG~~~~~l~t~~~Gvv~i~~~~
                                                                    481 (1157)
               T Consensus
                                                                    413 (450)
               357 NESAVYVCSTGTGKFS-----LPQEKIVFNAQGDSVLGAGACGGVPIIFSRNSGLVSITSRE
T 1xks A
                                                                    413 (450)
T ss_dssp
                  CSSEEEEECTTCTTC-----CCCEEEECCGGGCCEEEEEETTEEEEEEECC
T ss_pred
                  ECCEEEEEcCCCCC-----CcceEEEEecCCCEEEEEecCCCeEEEEecCCC
No 6
                           PDB™
PROTEIN DATA BANK
                                    NCBI
                                                  Pub Med
□ >3cqc_B Nuclear pore complex protein NUP133; nucleoporin, mRNA transport, nucleus, phosphoprotein, protein
 transport, translocation; 2.53A {Homo sapiens} PDB: 3cqg _B
Probab=100.00 E-value=5.5e-35 Score=316.80 Aligned_cols=190 Identities=13% Similarity=0.174 Sum_probs=0.0
                  сссСссНининненнининниннниннинн
0 ss pred
Q Fri_Mar_04_23: 881 KYGHVAWIQQILDGSYADAMNTLKNITVDDSKKGESLSECELHLNVAKLSSLLV-EKDNLDINTLRKIQYNLDTIDAEKN
                                                                                  959 (1157)
               881 ~~~lsWI~dI~~~y~~As~tL~~lA~~~~~~l~~kk~~LSLaKLa~LA~~~~~~~~l~~i~~L~li~iQe~
                                                                                  959 (1157)
                T Consensus
                                                                                   78 (227)
                2 ASHMLSWLHEINSOELEKAHATLIGLANME---TRYFAKKKTLIGLSKLAALASDFSEDMLOEKIEEMAEOERFLLHOET
T 3cqc_B
                                                                                  78 (227)
T ss dssp
                  T ss_pred
                  СССсссиннинньссинниннинниннын---ссиннинниннинныннын оссссиннинныннынныннын
Q ss_pred
                  Q Fri_Mar_04_23: 960 ISNKLKKGEVQICKRFKNGSIREVFNILVEELKSTTVVNLSDLVELYSMLD----DEESLFIPLRLLSVDGNLLNFEVKK 1035 (1157)
                               Q Consensus
               960 L~~~i~~~
                                     ++++|++||+|++++.+.++ ..++
 T Consensus
                79 1~~~i~~----
               79 LPEOLLA-----EKQL-----NLSAMPVLTAPQLIGLYICEENRRANEYDFKKALDLLEYIDEEED-ININ 138 (227)
T 3cqc_B
T ss dssp
                  CCTTHHH-----HTTC-----CSSSSCCCCHHHHHHHHTSCTTCTTCCHHHHHHHHTTTTTTCC----CCSH
```

```
T ss_pred
                  ННННННННННОСССС-----CC-----CCHHHHHHHHHHhhhcccccccCCCCCHHHhcCCCcCchhHHHH
0 ss pred
 Q Fri_Mar_04_23: 1036 FLNALVWRRIVLLNAS-----NE-----GDKLLQHIVKRVFDEELPKNNDFPLPSVDLLCDKSLLTPEYISE 1097 (1157)
              1036 ~1~~~IWrR~~l~DdW~~----D~~----T-Ly~tL~~~~~~p~~~l~~1~~1~~1097 (1157)
.++++||||++||| ++ ++|+||+|++......+.||..+++ +.+.+.|+.
139 ~1~~~IWrR~~l~DdW~~i~~~~~~l~~T~lf~~l~~~~~~~LP~~~ll~~~~~l~~l~~~207 (227)
T Consensus
               139 DLKLEILCKALQRDNWSSSDGKDDPIEVSKDSIFVKILQKLLKDGIQLSE-YLPEVKDLL---QADQLGSLKS 207 (227)
T 3cqc B
                  HHHHHHHHHHHTTCC-----CHHHHHHHHTTC-----CTTSCSHH---HHC----
T ss_dssp
                  T ss_pred
                            PDB PROTEIN DATA BANK
PROTEIN DATA BANK
PROTEIN DATA BANK
PROTEIN DATA BANK
No 7
>5a9q A Nuclear pore complex protein NUP155; transport protein; 23.00A (Homo sapiens)
 Probab=99.25 E-value=7.4e-06
                         Score=109.45 Aligned_cols=823 Identities=12% Similarity=0.114 Sum_probs=0.0
                  Q ss_pred
O Fri Mar 04 23:
               67 YIVKTLQTDYSSGFSN----DDELNGYIDMQIGYGLVNDHKKVYIWNIHSTQKDTPYITVPFRSDDNDEIAVAPRCILTF 142 (1157)
                Q Consensus
T Consensus
                81 TSSTRRVPLPPELVEOFGHMOCNCMMGVFPPTSRAWLTIDSDTFMWNYEDGGD---LAYFDGI,----SETTLAVGI,-VK
T 5a9q A
                                                                                   151 (1391)
                  EEEEEEECCHHHHHTTSCCSSCEEEEEETTTEEEEEETTEEEEEESSCSSC---EEEECCC-----CSCCCEEEE-EC
T ss dssp
                  ceecccCCCHHHHHHHhhcccccccccHhhCceEEEECCEEEEEECCCCC---ceeecCC----CceEEEEEE-ec
T ss pred
Q ss_pred
                  CCCCccccccccCCCCCCEEEEECCC----Ce-eeccchh------hhccchhccCcceE-EEEEcCCCCCceE
Q Fri Mar 04 23: 143 PATMDESPLALNPNDQDETGGLIIIKGSK---AI-YYEDINSI-----NNLNFKLSEKFSHE-LELPINSSGGEKC
                                                                                   208 (1157)
               O Consensus
               T 5a9q A
               152 PKAG----IFQP---HVRHLLVLATPVDIVILGLSYANLQTGSGVLNDSLSGGMQL----LPDPLYSLPTD---NTYL
                                                                                   215 (1391)
T ss dssp
                  CCSS----SSCS---SSSEEEEEECSSEEEEEEECCC-------CCCEEE----EECCC-CEECT---TTCE
                  CCCC----cchh---cCcEEEEEeccceEEEEEecCCCCCcccccCCCcceEE----ecCCceEEecC---CeEE
T ss pred
Q ss pred
                  EEEEeeCCceEEEEeecCcCCeeeEehhhhccCccCcchhhc-----cCCCCeEEEecCCCCCcc
 Q Fri_Mar_04_23: 209 DLMLNCEPAGIVLSTNMGRIFFITIRNSMGKPQLKLGKLLNKPFKLGIWSKIF-----NTNSSVVSLRNGPILGKGT 280 (1157)
               209 t-l-n-epag~IlaTS-gRl--lslrd--Gkp~l-----L-k----g----i----------I-si--g-----g-
+.++-...-|-++...|.|+-|.=...|=-.=.|+.+ + ...+|.++++...+...|+.|.....
216 --I--t--GRIF-gg-dg-lyEl-Y------Wf--rc-ki-n---T----s-llPs--------I-qi-vD-sR----
Q Consensus
                                                                                   280 (1157)
T Consensus
                                                                                   288 (1391)
               216 LTITSTDNGRIFLAGKDGCLYEVAYQAEAGWFSQRCRKI-NH--SKSSLSFLVPSLLQFTFSEDDPILQIAIDNSR----
T 5a9q A
T ss_dssp
                  T ss_pred
                  EEEEEcCCCCEEEeecCCCceccCccccCcceE-eC--CccchhHhcchhhhhccCCCCceEEEEEcCCC----
                  EEEEEEECCCeEEEEEeecCCC-CceEeeeccHHHHHHHHHHhhhcCCCCcCCEE-EEEeEEcc-CCCCCEEEEEEE
Q ss pred
Q Fri Mar 04 23:
               281 RLVYITTNKGIFQTWQLSATNS-HPTKLIDVNIYEAILESLQDLYPFAHGTLK-IWDSHPLQ-DESSQLFLSSIYDSSCN
                                                                                   357 (1157)
               281 r-i-ilt--g-lq-W------g------di---i--p----l--iLD------lvL-s------
..+|++++|.++|++..+|+-.++.--....+.|..+|+..+|+..+|+..+|
289 -lLYtLs--s-I-vy-l---g-----v-----i---a-----l---f--IvsI-pI---ES----LvAvT-----
O Consensus
                                                                                    357 (1157)
T Consensus
                                                                                    364 (1391)
               289 NILYTRSEKGVIQVYDLG-QDGQGMSRVASVSQNAIVSAAGNIARTIDRSVFKPIVQIAVIENSESLDCQLLAVTH---A
T 5a9q A
                                                                                    364 (1391)
                  TEEEEEETTSCEEEEEE-TTEEECC-CEECHHHHHHHHHSSCCSTTCTTTCC-CCEEEECCTTTCSSEEEEEECS---S
 T ss_dssp
                  CEEEEecCCCeeeEEEEccHHHHHHHHHHHHHHhhhhcchhcCCCeEEEEEcChHhCcceEEEEECC---C
T ss_pred
                  ceeEEEEE----EEeCCCCeEEEEEEeeccCCcc-cCCCCceEeecCCCcccccceEEEEE
Q ss pred
Q Fri_Mar_04_23: 358 ETYYILSTI----IFDSSSNSFTIFSTYRLNTFMESIT-DTKFKPKIFIPQMENANDTNEVTSILVMF----PNAVVIT 427 (1157)
               .++++.+-
               365 G-RlYfs-----p---L-l-hvR-PP-------v--a-ys-G------d-L---
T Consensus
                                                                                    434 (1391)
               365 GVRLYFSTCPFRQPLARPNT--LTLVHVRLPPGFSASSTVEKPSKVHRALYSKGI------LLMAASENEDNDILWCV
T 5a9g A
                                                                                    434 (1391)
                  CCEEEEECCCBC---CBCCC--CEEEEEECCCSSSTTCCSSCSBCTTCEEETTTE------EEEEEECC-CCEEEEEE
T ss dssp
                  eEEEEEecCCCCCCCCC--eEEEEEecCCCCCccccCCCCceeEEEEEcCCE-----EEEEEECCCCCCCEEEEE
T ss pred
Q ss pred
                  428 QVNSKLDSSYSMRRKWEDIVSL------RNDIDIIGSGYD-----SKSLYVLTKQMGVL
Q Fri Mar 04 23:
                                                                                   475 (1157)
               428 sl----s--s--eD-I-f------lGsG------l-t---Gvv
Q Consensus
                                                                                    475 (1157)
                      ++..++-+...+
                                       435 s-d-____l-E-----i-g---i-v-----p----p-----p----nel--Q---ppr-f-vLTn-Gi-
T Consensus
                                                                                    509 (1391)
               435 NHDT----FPFQKPMMETQMTAGVDGHSWALSAIDELKVDKIITPLNKDHIPITDSPVVVQQHMLPPKKFVLLSAQGSL
T 5a9q_A
                                                                                    509 (1391)
                  EECT----TTTSSSCCEEEEEESCCSCCCEEECC------CCCCCCSSSTTSSCTTTTTTTSCCCEEEEECSSEEE
T ss dssp
                  cCCC----cccCCCcceeEEeccCceeEEEeccccccCCCCccchhheeccCCCcceEEEEeCCeeE
T ss pred
Q ss_pred
                  EE-EecCcc---------hHHHHHHHHHHHhhh-cCCC------
Q Fri_Mar_04_23: 476 QF-FVKENE-----ETNSKPE------UGFVKSHVDQAVYF-SKIN-----
                                                                                   508 (1157)
               476 ~i~~~~KS~leOAvf~~~~~KS~leOAvf~~~~~
O Consensus
                                                                                   508 (1157)
               T Consensus
                                                                                    589 (1391)
               510 MFHKLRPVDQLRHLLVSNVGGDGEEIERFFKLHQEDQACATCLILACSTAACDREVSAWATRAFFRYGGEAQMRFPTTLP
T 5a9q A
T ss_dssp
                  ЕЕЕеCChнининин
T ss_pred
                     ннинн--ноооооо-------ОоооооО
Q ss pred
 Q Fri_Mar_04_23: 509 ------PPEISLDQ--ESIEHD 530 (1157)
               509 -----1~~i~~a 530 (1157)
```

T Consensus T 5a9q_A T ss_dssp T ss_pred		+. +.++++.++. +-+t		(1391) (1391)
Q ss_pred Q Fri_Mar_04_23: Q Consensus		HHHHHHHHHCCccCCCchhHHHHHHHHHH		(1157) (1157)
T Consensus T 5a9q_A T ss_dssp T ss_pred		1SRllrpiWvs-il-iLLFlgg		(1391) (1391)
Q ss_pred Q Fri_Mar_04_23: Q Consensus				(1157) (1157)
T Consensus T 5a9q_A T ss_dssp T ss_pred		RPENGNPQQMQQELQRKFHEAQLSEKISLQATQQLVRKSYQALALWKLLCEHQFTITVAELQKELQEQLKIT		(1391) (1391)
Q ss_pred Q Fri_Mar_04_23: Q Consensus	630	CHHHHhhcCHHHHHHHHHHHHHHHHHHhhccccccccHHHHHHHH	709	(1157) (1157)
T Consensus T 5a9q_A T ss_dssp T ss_pred		tF-dLglaLi-alInisvd-isLr		(1391) (1391)
Q ss_pred Q Fri_Mar_04_23: Q Consensus		cchHHHHHHHHHHHhhcccchhHHHHHHHHHHHHHH		(1157) (1157)
T Consensus T 5a9q_A T ss_dssp T ss_pred		-s-dDvkA-E-LA-k		(1391) (1391)
Q ss_pred Q Fri_Mar_04_23: Q Consensus	787	HHHHHHHHCCChhHHHHHHHH	825	(1157) (1157)
T Consensus T 5a9q_A T ss_dssp T ss_pred		-icl-y-GaVeL-LADpAlgD		(1391) (1391)
Q ss_pred Q Fri_Mar_04_23: Q Consensus			877 877	(1157) (1157)
T Consensus T 5a9q_A T ss_dssp T ss_pred		VPKKPGPPVLSSDPNMLSNEEAGHHFEQMLKLSQRSKDELFSIALYNWLIQVDLADKLLQVASPFLEPHLVRMAKVD		
Q ss_pred Q Fri_Mar_04_23: Q Consensus		CCCcccCcchHHHHHhhcCHHHHHHHHHHHhhh-c-ccccCCHHHHHHHHHH		(1157) (1157)
T Consensus T 5a9q_A T ss_dssp T ss_pred		~~~~dLWryy-k~~~~AA-vL-LA-s~~~i-L-RieyLsrA~~aks~~~~11-eleek QNRVRYMDLLWRYYEKNRSFSNAARVLSRLADMHSTEISLQQRLEYIARAILSAKSSTAISSIAADGEFLHELEEK Сининининининининининининининининин		
Q ss_pred Q Fri_Mar_04_23: Q Consensus	951	HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH	1024	(1157)
T Consensus T 5a9q_A T ss_dssp T ss_pred		L-VA-iQ-il-1		
Q ss_pred Q Fri_Mar_04_23: Q Consensus	1025	hccCCCHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH		

```
T 5a9q_A
             1211 YSD-----PILVQTLWQDII 1225 (1391)
                 ССС-----НИНИНИНИНИ
T ss_dssp
                 ССС-----ННННННННН
T ss pred
                           PDB
                                   NCBI
                                           Pub Med
>3i5p_A Nucleoporin NUP170; helical stack, membrane, mRNA transport, nuclear pore complex, nucleus,
phosphoprotein, protein transport; 3.20A {Saccharomyces cerevisiae}
 Probab=98.13 E-value=1.3e-05 Score=97.29 Aligned_cols=179 Identities=11% Similarity=0.157 Sum_probs=0.0
                 Q Fri Mar_04_23: 843 FSFTLFEYLIKHKKLNDLIFRFPQQHDVLIQFFQESAP----KYGHVAWIQQILDGSYADAMNTLKNITVDDSKKGESLS
                                                                               918 (1157)
              Q Consensus
                                                                               918 (1157)
T 3i5p_A
              180 FHYHMYDWLVSONREEKILDIET---PFILPYLMEK-AGSSLKISNILWVYYSRRSKFFESAEILYRLATSN--FDITLF
                                                                               253 (525)
T ss_dssp
                 HHHHHHHHHHTTCGGGGGGCCC---TTHHHHHHHT-CC---CHHHHHHTHHHHCCSHHHHHHHHHSSS--SCCCHH
                 T ss_pred
                 Q ss pred
 Q Fri_Mar_04_23: 919 ECELHLNVAKLSSLLV-EKDN--LDINTLRKIQYNLDTIDAEKNISNKLKKGEVQICKRFKN--GSIREVFNILVEELKS
                                                                               993 (1157)
Q Consensus
              993 (1157)
              .-.. ....+.++
                                                           ---~r~~~~~~
T Consensus
                                                                           --L~
T 3i5p_A
              254 ERIEFLSRANGFCNSVSPLSQKQRIVQLASRIQDACEVAGIQGDILSLVYT-----DARIDSAIKDELIKT----LD
                                                                               321 (525)
T ss dssp
                 T ss_pred
                 нининининироссСссонинининининининининин
Q ss pred
                 Q Fri Mar 04 23:
              994 TTVVNLSDLVELYSMLDDEESLFIPLRLLSVDGNLLNFEVKKFLNALVWRRIV 1046 (1157)
O Consensus
              994 ~~~L~~~eLIdllTl~d~~~F~~AL~vl~~~~~e~~~l~~~IWrR~~ 1046 (1157)
              T Consensus
              322 GKILSTSELFNDFAVPLSYHEIALFIFKIADFRD-----HEVIMAKWDELF
T 3i5p A
                 нссссиннисссстттсининниннитссс-----ининининни
T ss_dssp
T ss_pred
                 сссССННИННИНННЫМ сснининниннесСССС------
                          PDB"
PROTEIN DATA BANK
                                  NCBI
No 9
                                           Pub Med
->4mhc_A Nucleoporin NUP157; nuclear pore complex, adaptor nucleoporin, DNA binding prote binding protein,
nucleocytoplasmic transport; 2.40A {Saccharomyces cerevisiae}
Probab=96.40 E-value=0.54 Score=60.00 Aligned cols=257 Identities=14% Similarity=0.210 Sum probs=0.0
                 EEEEecCCCcchhccc----CCceEEEEcCCCCEEEEEcCCceEEEecCCCCCCCCCEEEEec
Q ss_pred
Q Fri_Mar_04_23:
               67 \ \texttt{YIVKTLQTDYSSGFSN----DDELNGYIDMQIGYGLVNDHKK} \texttt{VYIWNIHSTQKDTPYITVPFRSDDNDEIAVAPRCILTF}
                                                                               142 (1157)
               O Consensus
                                                                               142 (1157)
               T Consensus
                                                                               141 (826)
               71 FQRQQVTNIPDEVLSQVSNTEIKSDMGIFLELNYCWITSDNKLILWNINNSSE--YHCIDEI----EHTILKVK-LVK
                                                                               141 (826)
T 4mhc A
 T ss_dssp
                 EEEEEEECCHHHHTTTSCCSSCEEEEETTTTEEEEEETTBEEEEETTTSSC---EEEECCC-----CSCEEEEE-EEC
                 eeecccCCCHHHHHHHhhhccccceeccHhHCeEEEEECCCEEEEEECCCCc---ceeeCCC----CceeEEEE-Eec
T ss_pred
                 CCCCcccccccCCCCCCeEEEEECCCCe---eeccchhhhccchhccCcceEEEEEecCCCCceEEEEEeeCCce
Q ss pred
Q Fri_Mar_04_23:
              143 PATMDESPLALNPNDQDETGGLIIIKGSKAI----YYEDINSINNLNFKLSEKFSHELELPINSSGGEKCDLMLNCEPAG
                                                                               218 (1157)
              143 \ p -----s --p GlviV - p - t G -----y Wes I --a --lg l -l ------- gE -v t -l -n -epag
                                                                               218 (1157)
              T Consensus
                                                                               203 (826)
              142 PSPN----TFVS--SVENLLIVATLFDIYILTISFN-DRTHELNI----FNTGLKVNVT---GFNVSNIISYERTG
T 4mhc A
                                                                               203 (826)
T ss_dssp
                 CCCC----cchh--cceEEEEEeecCeEEEEEEec--CCCCceEe----EccceEeecC--CeEEEEEEECCCC
T ss pred
Q ss_pred
                 EEEEecc---ccEEEEEeeCCCCCeeeEehhhhccCccCccchhhcc------CCCCeEEEec
Q Fri_Mar_04_23: 219 IVLSTNM---GRIFFITIRNSMGKPQLKLGKLLNKPFKLGIWSKIFN------TNSSVVSLRN
                                                                               272 (1157)
              219 ~IlaTS~--gRl~-lslrd~-Gkp~l~~~L~k~~~~g~~~i~~----------------I~si~~
Q Consensus
                                                                               272 (1157)
              T Consensus
                                                                               280 (826)
T 4mhc_A
              {\tt 204~QIFFTGATDGVNVWELQYNCSENLFNSKSNKI-CL--TKSNLANLLPTKLIPSIPGGKLIQKVLEGDAGTEEETISQLEV}
                                                                               280 (826)
T ss_dssp
                 EEEEEETTSTTCCEEECCC-----CC-EE-ESSCC------CCSEEEEEE
T ss pred
                 CEEEeecCCCCceEEEEEcccCccccCcceE-EC--CcchhhcCCcccccccchhhhhhhhhccccccCCCCceEEEEE
Q ss pred
                 CCCCCcccEEEEEECCCeEEEEEeecCCCCceEeeeccHHHHHHHHHhhcCc-----CccCEEEEEeEEcC-CCCcEE
Q Fri Mar 04 23: 273 GPILGKGTRLVYITTNKGIFQTWQLSATNSHPTKLIDVNIYEAILESLQDLYP----FAHGTLKIWDSHPLQ-DESSQL
                                                                               346 (1157)
              273 g~~~~g~r~i~ilt~~g~lg~W~~~~~g~~~~~di~~~i~~~l~~~p----~~~l~iLD~~~~~~~1
O Consensus
                                                                               346 (1157)
              .....+|+++++|+.+++|++...+|....|.....+|...+|+|+..++|+...++|
281 D-SR-----iLYtLs--s-I-vy-1-----l-vy-----i-vy-1-----IvsI-pI---ES--1
T Consensus
T 4mhc A
              281 DQSR----GVLHTLSTKSIVRSYLIT--SNGLVGPVLIDA-AHIRRGMNALGVKNSPLLSNRAFKIAKIVSISMCENNDL
T ss_dssp
                 ETTT----TEEEEEETTSCEEEEEE--TTEEEEEEEECH-HHHHHHHHHTCCCCGGGSTTTCCEEEEEECCTTTCSSE
T ss_pred
                 Q ss pred
                 EEEEecCCCCceeEE
 Q Fri Mar 04 23: 347 FLSSIYDSSCNETYYI 362 (1157)
 O Consensus
              347 vL~s~~~~~y~ 362 (1157)
                 -|++++.. ..+-|+
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T Consensus
                  354 ~LvAvT~~--G~RlYf 367 (826)
 T 4mhc A
                  354 FLAVITTT--GVRLYF 367 (826)
                      EEEEETT--CCEEEE
 T ss dssp
 T ss pred
                      EEEEECCC--eeEEEE
 No 10
                                                              Pub Med
>3noO A DNA gyrase subunit A; DNA topology, topoisomerase, C-terminal DO gyrase, DNA binding protein, isomerase;
 HET: DNA GOL; 1.30A {Aquifex aeolicus}
 Probab=77.05 E-value=26 Score=38.78 Aligned_cols=111 Identities=12% Similarity=0.057 Sum probs=0.0
                      EEEEECCCCe-eeccchhhhccchhccCcceEEEEEecCCCCceEEEEEeeCCce-EEEEeeccccEEEEEeeCCCCCee
 0 ss pred
 Q Fri Mar 04 23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELELPINSSGGEKCDLMLNCEPAG-IVLSTNMGRIFFITIRNSMGKPQ 241 (1157)
                  164 lviV-p-tG--yWesI--a--lgl-l------l-L----gE-vt-l-n-epag--IlaTS-gRl--lslrd--Gkp- 241 (1157)
                  T Consensus
                  130 ILLFTK-KGRVARFSVREVPPST---PGARGVQG-IKLE--KNDETSGLRIWNGEPYLLVITAKGRVKKISHE----- 195 (276)
 T 3no0 A
                      EEEEET-TSEEEEEEGGGSCBCC---TTCCCEEC-CCCC--TTCCEEEEEEESSCSEEEEEETTSCEEEEEGG------
 T ss dssp
                      EEEEEC-CCEEEEEccccccc---CCCCceEe-EccC--CCCEEEEEEEecCCceEEEeEHH------
 T ss pred
 Q ss_pred
                      eEehhhhccC-ccCcchhhccCCCCeEEEecCCCCcccEEEEEECCCeEEEEee
 Q Fri_Mar_04_23: 242 LKLGKLLNKP-FKLGIWSKIFNTNSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQLS 298 (1157)
                  242 l----L-k----q---i-----I-si--q----q-r-i-ilt--q-lq-W---
 Q Consensus
                                                                               298 (1157)
                     T Consensus
                  196 ----EIPKTNRGVKGTEVS--GTKDTLVDLIPIK----EEVELLITTKNGKAFYDKIN 243 (276)
 T 3no0 A
 T ss dssp
                      ----GSCCCCTTCCCEECC--CSSSCEEEEEEES----SEEEEEEETTSCEEEEEE
                      ----HccccCCCccEEEe--CCCCEEEEEEeC----CCCEEEEECCCCcEEEEECC
 T ss pred
 No 11
                                 SCOPe PROTEIN DATA BANK
                                                       NCBI
>> zio_A DNA gyrase subunit A; beta pinwheel, topoisomerase, spiralling beta pinwheel, DNA wrapping, isomerase, DNA bindng protein; HET: DNA; 2.60A {Escherichia coli} SCOP: b.68.10.0
Probab=70.79 E-value=34 Score=38.57 Aligned_cols=111 Identities=12% Similarity=0.176 Sum_probs=0.0
                      EEEEECCCCe-eecccchhhhccchhccCcceEEE----EecCCCCceEEEEEee----CCceEEEEEeccccEEEEEee
 Q Fri_Mar_04_23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELE----LPINSSGGEKCDLMLNC----EPAGIVLSTNMGRIFFITIR 234 (1157)
                  164 lviV-p-tG--yWesI--a--lql-l-------l-L----qE-vt-l-n----epaq-IlaTS-qRl--lslr 234 (1157)
 Q Consensus
                   T Consensus
 T 1zi0 A
                   56 ILCFSS-RGRVYSMKVYQLPEATR----GARGRPIVNLLPLE--QDERITAILPVTEFEEGVKVFMATANGTVKKTVLT
                      EEEEET-TSEEEEEEGGGSCCCCS----SSCCEEGGGTSCCC--TTCCEEEEEEESCCCTTCEEEEEETTSEEEEEGG
 T ss dssp
                      EEEEeC-CCeEEEEEHhHcCCCCC-----cCcCeEHhhccCCC--CCCEEEEEEeccCCCcceEEEECCCCeEEEeEHH
 T ss_pred
                      \tt CCCCCeeeEehhhhccCccCccchhhccCCCCCeEEEecCCCCcccEEEEEEECCCeEEEEEee
 Q ss_pred
 Q Fri_Mar_04_23: 235 NSMGKPQLKLGKLLNKPFKLGIWSKIFNTNSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQLS 298 (1157)
                  235 d--Gkp-l----L-k----g----i-si--g-----g-r-i-ilt--g-lq-W--- 298 (1157)
+|-.++..|+-.-+...+++++.... +..+|++.|+..|+...+..+
 O Consensus
                  128 -----
                                  -----i-l-T--G--irf--
                                                                                    175 (307)
 T Consensus
                  128 -----EFN-RLRTAGKVAIKLVDGDELIGVDLTS----GEDEVMLFSAEGKVVRFKES 175 (307)
 T 1zi0_A
                      -----GGT-TCCTTCEESSCCCTTCCEEEEEEC----TTCEEEEEETTSEEEEEEGG
 T ss_dssp
                      -----Hhh-cccCCceEEEEeCCCCEEEEEEeC----CCCEEEEEEEHH
 T ss_pred
 No 12
                                  PDB
                                                             Pub Med
🗌 >316v_A GYRA, DNA gyrase subunit A; gyrase A C-terminal domain, GYRA C-terminal domain, DNA wrapping,
 beta-strand-bearing proline, ATP-binding; HET: DNA; 2.19A {Xanthomonas campestris PV}
 Probab=68.37 E-value=29 Score=40.25 Aligned cols=112 Identities=11% Similarity=0.144 Sum probs=0.0
 Q ss_pred
                      EEEEECCCCe-eecccchhhhcc-chhccCcceEEEEecCCCCceEEEEee----CCceEEEEEeecccEEEEEeeCCC
 Q Fri_Mar_04_23: 164 LIIIKGSKAI-YYEDINSINNLN-FKLSEKFSHELELPINSSGGEKCDLMLNC----EPAGIVLSTNMGRIFFITIRNSM 237 (1157)
                  O Consensus
 T Consensus
                   60 LLTFTS-SGKVFWLPVHQLPEAGSN--ARGRPIINWIPLE--SGERVQAVLPVREYADNRYVFMATRNGTVKKTPLS--- 131 (370)
 T 316v_A
 T ss dssp
                      EEEEET-TSEEEEEEGGGSCBCCTT--SCCEEGGGSCCCC--TTCCEEEEEEESCCCTTCEEEEEETTSEEEEEEGG---
                      EEEEeC-CCeEEEEEHHHCcCCCcc--CCCcChhhccCCC--CCCEEEEEeecCCCCcEEEEEehH---
 T ss pred
                      {\tt CCeeeEehhhhccCccccchhhccCCCCeEEEecCCCCcccEEEEEEECCCeEEEEE}
 Q ss pred
                  238 GKPQLKLGKLLNKPFKLGIWSKIFNTNSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQ
 Q Fri Mar 04 23:
                  238~Gkp{\sim}1{\sim}\cdots{\sim}L{\sim}k{\sim}\cdots{\sim}g{\sim}\cdots{\sim}1{\sim}si{\sim}g{\sim}\cdots{\sim}g{\sim}r{\sim}i{\sim}ilt{\sim}\neg g{\sim}lq{\sim}W{\sim}
 O Consensus
                                                                                296 (1157)
                             +|-...|+..--+...+.++++.....
                                                              .+|+++|+.|.+-...
                  132 -----d-i-l-T--G--irf-
 T Consensus
                                                                                177 (370)
                  132 -----EFAFRL-ARGKIAINLDEGDALVGVALTDGD----RDVLLFASNGKTVRFG
 T 316v A
                                                                               177 (370)
                      -----GGCSCC-TTCEESSCCCTTCCEEEEEECSC----CEEEEEETTSEEEEEE
 T ss dssp
                      -----HhhccC-CCceEEEEeCCCCEEEEEEcCCC----CEEEEEcCCCEEEEEC
 T ss_pred
                                  PDB Pub NCBI Pub Med
 No 13
🗌 >1zvt_A Topoisomerase IV subunit A; beta-pinwheel, ATPase, supercoiling, decatenation, DNA bindi topology; 1.70A
 {Escherichia coli} PDB: 4mn4 _A*
 Probab=68.21 E-value=18 Score=39.77 Aligned cols=112 Identities=12% Similarity=0.174 Sum probs=0.0
```

```
Q ss pred
                           EEEEECCCCe-eecccchhhhccChccCcceEEEEecCCCCCceEEEEEeeCCc-eEEEEeecCccEEEEEeeCCCCCee
 Q Fri Mar 04 23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELELPINSSGGEKCDLMLNCEPA-GIVLSTNMGRIFFITIRNSMGKPQ 241 (1157)
 O Consensus
                      164\ lviV-p-tG--yWesI--a--lgl-l-----lL----gE-vt-l-n-epa-g-IlaTS-gRl--lslrd--Gkp- \\ 241\ (1157)
                       +++++. |+ ||=++..+-, | -++..+-++|. ||-++..+++|. ||-++++|..|+.++++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+.+++|..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+..|+...|+..|+..|+...|+..|+..|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|+...|
                        47 VVFVDS-TGRSYAIDPITLPSAR---GQGEPLTGKLTLP--PGATVDHMLMESDDQKLLMASDAGYGFVCTFN-----
 T 1zvt_A
 T ss_dssp
                           EEEEET-TSEEEEECGGGSCCSS---SCCEEGGGTCCCC--TTCCEEEEEECCCTTCEEEEEBTTSEEEEEGG-----
                           EEEEeC-CCeEEEEEhhhCCCCC---CCceeeeeEECCC--CCCEEEEEEeCCCCEEEEEEHH-----
 T ss_pred
                           eEehhhhccC-ccCcchhhccCCCCeEEEecCCCCcccEEEEEEE
 Q ss_pred
                                                                                                297 (1157)
 Q Fri_Mar_04_23: 242 LKLGKLLNKP-FKLGIWSKIFNTNSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQL
 O Consensus
                      242 l-----L-k-----g----i------I-si--g----g-r-i-ilt--g-lq-W---
                                                                                                297 (1157)
                      T Consensus
                                                                                                161 (256)
                      114 ----DLVARNRAGKALI-TLPENAHVMPPVVIED----ASDMLLAITQAGRMLMFPV 161 (256)
 T 1zvt A
                         ----GGCCCSTTCEECB-CCCTTCCBCCCEECCC----TTCEEEEEEETTSEEEEEEG
 T ss dssp
 T ss pred
                           ----HCCCCCCCEEEE-EeCCCCEEEEEEECC----CCCEEEEEEECCCEEEEE
                                       PDB<sup>N</sup>
PROTEIN DATA BANK
 No 14
                                                    NCBI Pub Med
🗌 >4100_A Protein ELys; beta propeller, structural protein, nuclear pore complex, WD repeat, mRNA transport; 1.90A
 {Mus musculus}
 Probab=67.89 E-value=94 Score=37.42 Aligned cols=116 Identities=12% Similarity=0.113 Sum probs=0.0
                           CCceEEEcCC-CCEEEEEcCCeEEEEecCCCCCCCCeEEEeCCCCCCCCceEEEec-CCCCccccccccCCCCC
 Q ss pred
 Q Fri Mar 04 23:
                       83 DDELNGYIDMQ-IGYGLVNDHKKVYIWNIHSTQKDTPYITVPFRSDDNDEIAVAPRCILTF-PATMDESPLALNPNDQDE
                                                                                                                            160 (1157)
                       O Consensus
                                                                                                                            160 (1157)
 T Consensus
                                                                                                                             93 (497)
                        34 ESVLRGKFAAGKNGLACLACGPQLEVVNSLTG---ERLSAYRFS-GV--NEQPPVVLAVKEFSWHK------
 T 4i0o A
                                                                                                                             93 (497)
 T ss_dssp
                           SCCCEEEECSSSSCEEEEEETTEEEEEETTTC---CEEEEEECC-CT--TSSCCEEEEEEEETT------
 T ss pred
                           hhhccceEeCCceeEEEEeeCCeEEEEEccCC---CEEEEEEcc-CC--CCcCceEEEeecCCcc-------
 Q ss pred
                           CCeEEE-EECCCCe---eecccchhhhccchhccCcceEEEEEecCCCCceEEEEEeeCC-----
 Q Fri_Mar_04_23: 161 TGGLII-IKGSKAI---YYEDINSINNLNFKLSEKFSHELELPINSSGGEKCDLMLNCEP-------A 217 (1157)
 Q Consensus
                      161 ~pGlvi-V~p~tG~---yWesI~~a~~lgl~l~~~~~~l~L~~~~gE~vt~l~n~ep------a
                                                                                                                           217 (1157)
                       T Consensus
                       94 RTGLLIGLEEADGSVLCLY-DLGI-----SRVVKAVVLP---GRVTAIEPIINHGGASASTOHLHPSLRWLFG 157 (497)
 T 4i0o A
                           EEEEEEEECSSSEEEEE-ETTT----TEEEEEEEES---SCEEEEEEESCSSCGGGTTSCHHHHTSSS
 T ss_dssp
                           ccceeeeecccccececcccchhhHhhcccc
 T ss_pred
 Q ss pred
                           eEEEEecccEEEEee
 Q Fri Mar 04 23: 218 GIVLSTNMGRIFFITIR 234 (1157)
                      218 g~IlaTS~gRl~~lslr 234 (1157)
 O Consensus
                           -+-|+|..|+++++.+.
 T Consensus
                      158 vlavGt~~G~vlLiDL~ 174 (497)
                      158 VAAVVTDVGQILLIDLC 174 (497)
 T 4i0o A
                           EEEEETTCCEEEECC
 T ss dssp
                           eEEEEeCCCEEEEEcc
 T ss pred
                                          PDB"
 No 15
                                                       NCBI Pub Med
>4kmo B Putative vacuolar protein sorting-associated PROT; membrane trafficking, SM protein, HOPS complex,
 thermophIle, transport protein; 2.60A {Chaetomium thermophilum}
 Probab=63.26 E-value=2e+02 Score=32.61 Aligned_cols=134 Identities=10% Similarity=0.112 Sum_probs=0.0
                           Q ss pred
 O Fri Mar 04 23: 789 NHVLCKVNLKEOCIOIAEFYKDLSGLVOTLOTLDONDSTTVSLYETFFNEFPKEFSFTLFEYLIKH-----KKLNDLIF 862 (1157)
                      789 i~L~~g~~e~A~~LAEky~Df~sLVel~~~~~~rl~~Yf~kfg~~FA~~lf~~yi~~~-----g~~~LL~ 862 (1157)
 O Consensus
                       T Consensus
                                                                                                                            104 (333)
 T 4kmo B
 T ss dssp
                           НИНИНТТСТТИНИНИНИТСНИНИНИНИНИНИНИНИН -- ВИНИНИНИНИТС-----С----
                           T ss pred
                           Q ss_pred
 Q Fri_Mar_04_23: 863 RFPQQHDVLIQFFQESAPKYGHVAWIQQILDGSYADAMNTLKNITVDDSKKGESLSECELHLNVAKLSSLLV-E-KDNLD 940 (1157)
                      O Consensus
                                                                                                                            940 (1157)
                      105 -----à-y-q------d---e-a----à----à
 T Consensus
                                                                                                                            156 (333)
 T 4kmo B
                      105 ----TALLKDLYYQ------DDRRLDGASVFIREALQQ---PETRTASDKLDLAA---NLLQGNQKEH 156 (333)
 T ss_dssp
                           ----HHHHHHHHH-----HHSSSCTTC
                           T ss_pred
 Q ss_pred
                           НИНИНИНИНИНИНИНИНИ
 Q Fri_Mar_04_23: 941 INTLRKIQYNLDTIDAEKNI 960 (1157)
 O Consensus
                      941 ~~~l~~i~~~L~li~iQe~L 960 (1157)
                      .-..+.+++..++..|+..|
157 -----Ll--Q--L 176 (333)
 T Consensus
                      157 VFELGALKEAKMLLRMOETF 176 (333)
 T 4kmo_B
 T ss dssp
                           нинининининининин
 T ss_pred
                           нинининининининини
```

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No 16
                                               SCOPe
                                                               PDB"
                                                                                            Pub Med
                                                                               NCBI
> > 1 xp5_A Topoisomerase IV; broken beta-propeller, hairpin-invaded beta-propeller, six- bladed beta-propeller;
  1.79A {Geobacillus stearothermophilus} SCOP: b.68.10.1
 Probab=63.16 E-value=49 Score=37.60 Aligned_cols=113 Identities=12% Similarity=0.215 Sum_probs=0.0
                               EEEEECCCCe-eeccchhhhccchhccCcceEEE--EecCCCCceEEEEEeeCC----ceEEEEEeecCC
 Q ss pred
 Q Fri Mar 04 23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELE--LPINSSGGEKCDLMLNCEP----AGIVLSTNMGRIFFITIRNS 236 (1157)
 Q Consensus
                          164 \  \, lviV-p-tG--yWesI--a--lgl-l-------l-L----gE-vt-l-n-ep----ag-IlaTS-gRl--lslrd- \\  \, 236 \  \, (1157)
                           124 (323)
 T Consensus
 T 1wp5_A
                                                                                                                                               124 (323)
 T ss_dssp
                               EEEEET-TSEEEEEEGGGSCBCC---TTSCCEEGGGTSCCC--TTCCEEEEEEESCTTSSCEEEEEETTSEEEEEEGG--
 T ss_pred
                               EEEEcC-CCEEEEEhhhCcCCC---CccCcCHhhccCCC--CCEEEEEEEecccCCceEEEECCCCEEEEeEHH--
 Q ss_pred
                               CCCeeeEehhhhacCc-cCacchhhacCCCCeEEEeacCCCCCacEEEEEEECCCeEEEEEE
 Q Fri_Mar_04_23: 237 MGKPQLKLGKLLNKPF-KLGIWSKIFNTNSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQLS 298 (1157)
                          237 ~Gkp~l~~~~L~k~~~~q~~~i~~~~~I~si~~q~~~~q~r~i~ilt~~q~lq~W~~~
                                                                                                                        298 (1157)
 O Consensus
                          T 1wp5_A
                          125 -----HYK-AQRYSKPLTGINLKNDDQVVDVHLT----DGMNELFLVTHNGYALWFDES 173 (323)
                               -----GGC-CSCCSSCEECSCCCTTCCEEEEEEE----CSCSEEEEEETTSEEEEEEGG
 T ss_dssp
                               -----Hhc-ccccCCceEEEEeCCCCEEEEEEe----CCCCeEEEEEEChh
 T ss pred
 No 17
                                               SCOPe PROTEIN DATA BANK
                                                                                                         Pub Med
>4g3n_A DNA gyrase subunit A; DNA gyrase C-terminal domain, beta-propeller, topoisomerase isomerase; HET: DNA;
 1.40A {Mycobacterium tuberculosis} SCOP: b.68.10.0 PDB: 3ucl _A*
 Probab=57.75 E-value=63 Score=36.71 Aligned_cols=110 Identities=9% Similarity=0.045 Sum_probs=0.0
                               EEEEECCCCe-eecc--cchhhhccChccCcceEEE--EecCCCCcceEEEEEeeCCce-EEEEEeecCcC
 Q ss_pred
 Q Fri Mar 04 23: 164 LIIIKGSKAI-YYED--INSINNLNFKLSEKFSHELE--LPINSSGGEKCDLMLNCEPAG-IVLSTNMGRIFFITIRNSM 237 (1157)
                          164 lviV-p-tG--vWes--I--a--lgl-l------l-L----gE-vt-l-n-epag--IlaTS-gRl--lslrd-- 237 (1157)
 O Consensus
                          T Consensus
                          160 LLLVSA-NGQSIRFSATDEALRPMG-----RATSGVQGMRFN--IDDRLLSLNVVREGTYLLVATSGGYAKRTAIE---
                                                                                                                                               227 (327)
 T 4g3n A
                               EEEEET-TSEEEEEECCTTTSCBCC----SSSCCEESCCCC-TTCCEEEEEECCTTCEEEEEEETTSEEEEEEGG---
 T ss_dssp
                               EEEEeC-CCEEEEEcccccCCCC-----ccccceeeEEcC--CCCEEEEEEEcCCCEEEEEEHH---
 T ss pred
 Q ss_pred
                               CCeeeEehhhhccC-ccCccchhhccC-CCCeEEEecCCCCccEEEEEEE
 Q Fri Mar 04 23: 238 GKPQLKLGKLLNKP-FKLGIWSKIFNT-NSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQL 297 (1157)
                          238 Gkp-l----L-k----q----i----I-si--q--r-i-ilt--q-lq-W-- 297 (1157)
 O Consensus
                                         ++-... +. | +..-+... +..+++++.... +..+ | ++++ | +. | .+-...+
                          228 ----e~~~R~gkG~~~~~~lv~~~v~---~i~l~t~~G~~ir~~~ 277 (327)
 T Consensus
                          228 -----EYPVQGRGGKGVLTVMYDRRRGRLVGALIVD----DDSELYAVTSGGGVIRTAA 277 (327)
 T 4g3n A
                               -----GSCBCCTTSCCEESSCCCTTTCCEEEEEEC----TTCEEEEEESSSCEEEEG
 T ss dssp
                               -----HhhcccCCcceeeeeccCCcceeeeee
 T ss_pred
 No 18
                                             SCOPe PROTEIN DATA BANK
                                                                               NCBI
                                                                                                         Pub Med
🗌 >1suu_A DNA gyrase subunit A; topoisomerase,DNA gyrase, beta-propeller, beta-pinwheel, ISO; HET: DNA; 1.75A
  {Borrelia burgdorferi} SCOP: b.68.10.1
 Probab=57.34 E-value=57 Score=36.82 Aligned cols=111 Identities=17% Similarity=0.129 Sum probs=0.0
                               EEEEECCCCe-eeccchhhhccChhccCcceEEEE----ecCCCCCceEEEEEee----CCceEEEEEeccccEEEEEee
 Q ss_pred
 Q Fri_Mar_04_23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELEL----PINSSGGEKCDLMLNC----EPAGIVLSTNMGRIFFITIR 234 (1157)
                          164 lviV-p-tG--yWesI--a--lgl-l------l----gE-vt-l-n----epag-IlaTS-gRl--lslr 234 (1157)
 O Consensus
                           T Consensus
                           61 LFMISN-EGKLYLINAYEIKDSSR----ASKGQNISELINLG-DQEEILTIKNSKDLTDDAYLLLTTASGKIARFEST 132 (312)
 T 1suu A
                               EEEEET-TSEEEEEEGGGSCC------CBGGGTSCCC--TTCCEEEEEEESCCCTTCEEEEEEETTSEEEEEEGG
 T ss dssp
 T ss_pred
                               EEEEcc-cceeeeeeHHHCCCCcc----cCCCeehhhccCcc--CCCEeeeeeeeHH
                               \tt CCCCCeeeEehhhhccCccCccchhhccCCCCeEEEecCCCCccEEEEEEECCCeEEEEEeee
 Q ss pred
 Q Fri_Mar_04_23: 235 NSMGKPQLKLGKLLNKPFKLGIWSKIFNTNSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQLS
                                                                                                                         298 (1157)
                          235 \ d \sim Gkp \sim 1 \sim \sim \sim L \sim k \sim \sim \sim g \sim \sim \sim i \sim \sim \sim \sim I \sim si \sim g \sim \sim \sim g \sim r \sim i \sim ilt \sim g \sim lq \sim W \sim \sim 10^{-10} \, cm^{-1} \sim 10^{-10}
 Q Consensus
                          +|..++..|+-+++++... ++..|+++|+|-...+
133 ------G~~i~l~~D~lv~~~~~i~l~T~~G~~r~~~
                                                                                                                         180 (312)
 T Consensus
                          133 -----DFK-AVKSRGVIVIKLNDKDFVTSAEIVF----KDEKVICLSKKGSAFIFNSR
 T 1suu A
                                                                                                                        180 (312)
                               -----GGC-C----CEECBCCCTTCCEEEEEEC----TTCEEEEEEETTSEEEEEEGG
 T ss_dssp
                               -----Hcc-hhccCceEEEEcCCCCEEEEEEeC----CCCEEEEEeCCCcEEEEEhh
 T ss pred
                                                POE NCBI Pub Med
 No 19
             Topoisomerase IV subunit A; beta-pinwheel, ATPase, supercoiling, decatenation, DNA bindi topology; 3.00A
  {Escherichia coli}
 Probab=53.41 E-value=34 Score=42.95 Aligned cols=113 Identities=14% Similarity=0.192 Sum probs=0.0
                               Q ss pred
 O Fri Mar 04 23:
                          164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELELPINSSGGEKCDLMLNCEPA-GIVLSTNMGRIFFITIRNSMGKPQ 241 (1157)
                          164 lviV-p-tG--yWesI--a--lgl-l------l-L----gE-vt-l-n-epa-g-IlaTS-gRl--lslrd--Gkp- 241 (1157)
+++++. .|+ ||-+...|.-. .++..+-++|. .||.|+..+++. -++++|..|.+.++...
517 ll-ft---G--y-----iP---------G--i---l-l----e-i----------l--aT--G-vKrt-l------ 583 (716)
 T Consensus
```

```
T 1zvu A
                 517 VVFVDS-TGRSYAIDPITLPSAR---GQGEPLTGKLTLP--PGATVDHMLMESDDQKLLMASDAGYGFVCTFN----- 583 (716)
 T ss_dssp
                     EERERT-TSEERERCTTTSCCCC-----CBSTTTSCCC--TTCCEEREECCCTTCEERERRTSEEREEGG-----
 T ss_pred
                     EEEEeC-CCCEEEEEeeeCCCcC---CCCCCHHCCCCC--CCCeEEEEEecCCCeEEEEeEHH------
                    Q ss pred
 Q Fri_Mar_04_23: 242 LKLGKLLNKPFKLGIWSKIFNTNSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQL
                                                                         297 (1157)
 Q Consensus
                 242 l----L-k----g----i------I-si--g--r-i-ilt--g-lq-W--
                                                                         297 (1157)
                 631 (716)
 T Consensus
                 584 ----DLVARN-RAGKALITLPENAHVMPPVVI---EDASDMLLAITQAGRMLMFPV
 T 1zvu A
                                                                         631 (716)
                    ----GGCCCS-TTCEECBCCCTTCCBCCCEEC---CCTTCEEEEEETTSEEEEEES
 T ss_dssp
                     ----HhcccC-cccEEEEECCCCEEEEEEe---cCCCCEEEEEech
 T ss_pred
                              SCOPe PODEN PROTEIN DATA BANK
 No 20
                                                    NCBI
                                                                     Pub Med
->4g3n_A DNA gyrase subunit A; DNA gyrase C-terminal domain, beta-propeller, topoisomerase isomerase; HET: DNA;
1.40A (Mycobacterium tuberculosis) SCOP: b.68.10.0 PDB: 3ucl _A*
Probab=48.22 E-value=1.2e+02 Score=34.46 Aligned cols=112 Identities=10% Similarity=0.097 Sum probs=0.0
                    EEEEECCCCe-eecccchhhhccCccceEEEEecCCCCcceEEEEEee----CCceEEEEEeccccEEEEEeeCCCC
 Q Fri_Mar_04_23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELELPINSSGGEKCDLMLNC----EPAGIVLSTNMGRIFFITIRNSMG 238 (1157)
                 164\ lviV-p-tG--yWesI--a--lgl-l-----ler-gE-vt-l-n----epag-IlaTS-gRl--lslrd--G \\ 238\ (1157)
 Q Consensus
                  T Consensus
 T 4g3n_A
                  56 ILFFTT-QGRVYRAKAYDLPEAS---RTARGQHVANLLAFQPEERIAQVIQIRGYTDAPYLVLATRNGLVKKSKLT---- 127 (327)
 T ss dssp
                     EEEEET-TSEEEEEEGGSCBCC---TTCCCEEHHHHTTCCTTCCEEEEEEESSTTSSSEEEEEETTSEEEEEEGG----
 T ss_pred
                    EEEEeC-CCEEEEEHHHCCCCC---CCCCCEHHHHCCCCCCCCEEEEEEccCCCCCCEEEEE
 Q ss pred
                    Q Fri_Mar_04_23: 239 KPQLKLGKLLNKP-FKLGIWSKIFNTNSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQ
                                                                           296 (1157)
                 239 kp-l----L-k-----g---i------I-si--g---g-r-i-ilt--g-lq-W-

.+ ++.+|+-+-+...+.++++..........|++.|+.|.+-....

128 ------r-G---i-lke-D-l--------d-l-l-T--G---r--
 O Consensus
                                                                           296 (1157)
 T Consensus
                                                                           173 (327)
                 128 -----DF--DSNRSGGIVAVNLRDNDELVGAVLCSAG----DDLLLVSANGQSIRFS
 T 4q3n A
                    -----GG--CCCCSEEESCCCCTTCCEEEEEECTT----CEEEEEETTSEEEEEE
 T ss_dssp
 T ss_pred
                     -----Hh--hccccCceEEEEECCCCEEEEEEecCC----CEEEEEEeCCCEEEEEc
                                PDB"
                                         NCBI
 No 21
                                                    Pub Med
>3f7f_A Nucleoporin NUP120; nuclear pore complex, macromolecular assembly, membrane coat, nucleocytoplasmic transport, beta-propeller; 2.60A {Saccharomyces cerevisiae} PDB: 3h7n_A 3hxr_A
 Probab=47.03 E-value=49 Score=42.02 Aligned_cols=89 Identities=17% Similarity=0.207 Sum_probs=0.0
                    EEEeeCCceEEEEeccccEEEEEeeCCCCCeeeEehhhhccC-ccCccchhhccC-----CCCeEEEecCCCCcccEEE
 Q ss_pred
 Q Fri_Mar_04_23: 210 LMLNCEPAGIVLSTNMGRIFFITIRNSMGKPQLKLLNKP-FKLGIWSKIFNT----NSSVVSLRNGPILGKGTRLV
                                                                                              283 (1157)
                 O Consensus
                                                                                              283 (1157)
                 T Consensus
                 165 FLFYVSPQFSVVFLEDGGLLGLKKVDGVH----YEPLLFNDNSYLKCLTRFFSRSSKSDYDSVISCKLF----HERYL 234 (729)
 T 3f7f A
                     EEEECSSSBEEEEETTSCEECCEESSSSC----EECCCCCCGGGGGGGSTTCCTTCSSCCCCEEEEEE-----TTTEE
 T ss_dssp
                     EEEecCCCEEEEEcCCCCC----cceeeeccccHHhhHHHHhCCCCCCCcccEEEEEc----CCcEE
 T ss_pred
                    EEEECCCeEEEEEeecCCCCceEeeec
 Q ss pred
 Q Fri_Mar_04_23: 284 YITTNKGIFQTWQLSATNSHPTKLIDV
                                              310 (1157)
                 284 ~ilt~~g~lq~W~~~~~g~~~~~
                                               310 (1157)
                    ++++..++.+|++. +|....+.
                 235 ftL~~D~~LRiWsl~--t~~~l~~~dL 259 (729)
 T Consensus
                 235 IVLTQNCHLKIWDLT--SFTLIQDYDM 259 (729)
 T 3f7f A
 T ss_dssp
                    EEEETTCEEEEEETT--TTEEEEEEET
                     EEEEcCCeEEEEcc--CcceEeecc
 T ss pred
 No 22
                                PDB
                                                           PubMed
📄 >3noO_A DNA gyrase subunit A; DNA topology, topoisomerase, C-terminal DO gyrase, DNA binding protein, isomerase;
 HET: DNA GOL; 1.30A {Aquifex aeolicus}
 Probab=46.40 E-value=1.7e+02 Score=32.24 Aligned_cols=104 Identities=16% Similarity=0.153 Sum_probs=0.0
                    EEEEECCCCe-eecccchhhhccchhccCcceEEEEecc-CCCCceEEEEEeeCC--ceEEEEEeccccEEEEEeeCCCCC
 Q ss pred
 Q Fri_Mar_04_23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELELPIN-SSGGEKCDLMLNCEP--AGIVLSTNMGRIFFITIRNSMGK
                                                                                              239 (1157)
                 164 lvV-p-tg--yWesI--a--lgl-l-------l-L-----ge--tl-ln-ep--ag-1laTs--gRl--lslrd--Gk +++++...|+ ||=.+...|.
                  T Consensus
                                                                                               98 (276)
                  38 LFLVSN-RGRVYWIAGSOALOG-----SKVSLKSREEKIVGAFIREKFGNRLLLATKKGYVKKIPLA----
 T 3no0 A
                                                                                               98 (276)
                    EEEEET-TSEEEEECSHHHHTS-----EECCCSSTTCCEEEEEEGGGSCSEEEEEETTSEEEEEGG----
 T ss dssp
                     EEEECC-CCEEEEEEHHHCCCC-----chhhhcCCCCeEEEEEEccCCEEEEeEHH----
 T ss pred
 Q ss pred
                    eeeEehhhhccCccCccchhhccCCCCEEEEecCCCCCccEEEEEEECCCeEEEEEee
 Q Fri_Mar_04_23: 240 PQLKLGKLLNKPFKLGIWSKIFNTNSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQLS
                                                                           298 (1157)
                 240 p-l-----L-k----g----i-----I-si--g----g-r-i-ilt--g-lq-W---
                                                                           298 (1157)
 Q Consensus
                  T Consensus
                                                                           145 (276)
                  99 -----EFEY-K-AQGMPIIKLTEGDEVVSIASSVDE----THILLFTKKGRVARFSVR
 T 3no0_A
 T ss_dssp
                    ----GTTT-C-STTEECSCCCTTCCEEEEEECCSS----CEEEEEETTSEEEEEEGG
                     -----Hhhc-c-CCCeEeeecCCCCEEEEEEEcCC----CEEEEEECCCEEEEEEcc
 T ss_pred
```

```
PDB"
 No 23
                                                    Pub Med
      M_E Nucleoporin NUP120; structural protein, immune system, transport protein-immune complex; 7.38A
 {Saccharomyces cerevisiae S288C} PDB: 4xmn _E
 Probab=40.40 E-value=92 Score=41.31 Aligned_cols=87 Identities=15% Similarity=0.178 Sum probs=0.0
                     EEEeeCCceEEEEeccccEEEEEecCCCCeeeEehhhhccCccCcc--hhhccC----CCCeEEEecCCCCcccE
 Q ss pred
 Q Fri_Mar_04_23: 210 LMLNCEPAGIVLSTNMGRIFFITIRNSMGKPQLKLGKLLNKPFKLGIW---SKIFNT----NSSVVSLRNGPILGKGTR
                                                                                               281 (1157)
                 T Consensus
                                                                                               240 (1045)
 T 4xmm E
                 173 FLFYVSPQFSVVFLEDGGLLGLKKVDG-VHYEPLL-FN---DNSYLKSLTRFFSRSSKSDYDSVISCKLF----HER
                                                                                               240 (1045)
 T ss dssp
                     EEEECSSSEEEEETTSCEEEEEESSS-SCEEECC--CC----CCGGGGGGGSTTCCSSCSCCCCEEEEEE-----TTT
 T ss_pred
                     EEEecCCCEEEEEecCC-CCeeEEE--ec----CccHHHHHHHHhcCCCCCCccceEEEEe-----CCc
                     EEEEECCCeEEEEEeecCCCCceEeeec
 Q ss pred
 Q Fri Mar 04 23: 282 LVYITTNKGIFQTWQLSATNSHPTKLIDV
                                                 310 (1157)
                 282 ~i~ilt~~g~lq~W~~~~~g~~~
                                                 310 (1157)
 Q Consensus
                     .++++..++.+|++. +|....+.
 T Consensus
                 241 ~lftL~~D~~LRiWsl~--t~~~l~~~dL
                                                267 (1045)
                 241 YLIVLTQNCHLKIWDLT--SFTLIQDYDM
 T 4xmm E
                                                 267 (1045)
                     EEEEETTCEEEEEETT--TTEEEEEEG
 T ss dssp
 T ss pred
                     EEEEEEcCCeEEEEEcC--CCceEEeecc
 No 24
                               SCOPe PROTEIN DATA BANK
                                                                      Pub Med
> > 1 xp5_A Topoisomerase IV; broken beta-propeller, hairpin-invaded beta-propeller, six- bladed beta-propeller;
 1.79A {Geobacillus stearothermophilus} SCOP: b.68.10.1
 Probab=40.04 E-value=2.4e+02 Score=31.97 Aligned_cols=113 Identities=12% Similarity=0.172 Sum_probs=0.0
                     EEEEECCCCe-eeccchhhhccChccCcceEEEE-ecCCCCcceEEEEEeeCCc--eEEEEeecccEEEEEeeCCCCC
 Q ss pred
 O Fri Mar 04 23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELEL-PINSSGGEKCDLMLNCEPA--GIVLSTNMGRIFFITIRNSMGK
                                                                                               239 (1157)
                 164\ lviV-p-tG-yWesI-a-lgl-l-a-c-l-L-a-gE-vt-l-n-epa-g-IlaTS-gRl--lslrd--Gk \\ 239\ (1157)
                 ++++++. .|+ ++=.++..|- ...+..+ .|. .||.||...+++ ...+++. ..|- ...+++...+++...|

158 i-1-T--G--irf--ei--gR-----a-Gv--i-L----d-Vv-------l--vt--G--Kr--l-e---
 T Consensus
                                                                                               228 (323)
                 158 LFLVTH-NGYALWFDESEVSIVGV-----RAAGVKGMNLK--EGDYIVSGQLITSKDESIVVATQRGAVKKMKLTEFEK-
 T 1wp5 A
                                                                                               228 (323)
                     EEEEET-TSEEEEEEGGGSCBCCS----SCCCEECCCCC-TTCCEEEEEECCTTCEEEEEEETTSEEEEEEGGGSCC-
 T ss_dssp
                     EEEEEC-CCeEEEEEhhhcCccC-----CCCCeEeEeec--CCCEEEEEEEccCCceEEEccHHHccc-
 T ss_pred
 Q ss pred
                     eeeEehhhhacCacCacchh-hacC-CCCeEEEecCCCCaccEEEEEEECCCeEEEEEee
 Q Fri Mar 04 23: 240 PQLKLGKLLNKPFKLGIWSK-IFNT-NSSVVSLRNGPILGKGTRLVYITTNKGIFOTWOLS 298 (1157)
                 240 p-l----L-k----g----i----I-si--g----g-r-i-ilt--g-lq-W---
 O Consensus
                                                                              298 (1157)
                          . .|. +.|... -+.. .+.++++... .++.+|.+.|++|.+..+.
                 229 -----i--kg--kGv-----lv-----v----i-l-t--G--ir----
 T Consensus
                                                                              276 (323)
                 229 -----A-TRA-KRGVVILRELKANPHRISGFVVA----QDSDTIYLQTEKSFIETIKVG 276 (323)
 T 1wp5 A
 T ss_dssp
                     ----C-CTT-SCCEECSCCCSSCCCEEEEEE---CTTCEEEEEETTSCEEEEEGG
                     -----C-CCC-CCceECeecccCCCCeEEEEEe----CCCCeEEEEEcCCCeEEEEeHh
 T ss pred
                                PDB"
PROTEIN DATA BANK
                                          NCBI
                                                   Pub Med
🗆 >4uuy_A Vacuolar membrane protein PEP3; transport protein, HOPS, membrane fusion, vacuole, endosome; 2.14A
 {Saccharomyces cerevisiae}
 Probab=38.45 E-value=3.6e+02 Score=30.95 Aligned cols=105 Identities=8% Similarity=0.073 Sum probs=0.0
 Q ss pred
                     Q Fri Mar 04 23:
                  89 YIDMOIGYGLVNDHKKVYIWNIHSTOKDTPYI-TVPFRSDDNDEIAVAPRCILTFPATMDESPLALNPNDODETGGLIII
                                                                                               167 (1157)
                  89 ~id~~sG~Alv~~~~~VW~y~s~~~p-~~-pLp~~~~~plp~~l~p~~~~~s~~pGlviV
 O Consensus
                                                                                               167 (1157)
                     .+..+++-++..+++..
                                              |..+ ++++| .. ..+.-+..+|+.|...
                  23 ~1~V~nn~1~1~1~~~11RidL~~-
                                             --p~~v~~i~lp-~~--i~~vflDPtG~-
                  23 HLKVSNDQLIVTTQRTIYRINLQD----PAIVNHFDCP-LS--KELETIMNVHVSPMGS------VILIR
 T 4uuy A
                                                                                                79 (349)
 T ss_dssp
                     EEEEETTEEEECSSEEEEETTS----TTCEEEEECC-CC--SSSCCEEEEECTTSS------CEEEE
                     T ss pred
 Q ss pred
                     ECCCCe-eecccchhhhccchhccCcceEEEEecCCCCcceEEEEEeecCcceEEEEeecc-cEEEEEe
 Q Fri_Mar_04_23:
                 168\ \texttt{KGSKAI-YYEDINSINNLNFKLSEKFS} \\ \texttt{HELELPINSSGGEKCDLMLNCEPAGIVLSTNMG-RIFFITI}
                                                                                    233 (1157)
 Q Consensus
                 233 (1157)
                  T Consensus
                                                                                    130 (349)
                  80 TN-FGRYMLLKDGEFTQLNK-----IK---NLDLSSLHWINETTFLMGIKKTPKLYRVEL
 T 4uuy_A
 T ss_dssp
                     ET-TSCEEEEETTEEEECGG-----GT---TCCEEEEEESSSSEEEEEETTSCEEEEEE
 T ss_pred
                     ec-CCcEEEeCccceechh------cc---CceEEEEEECCCCCEEEEEEE
                                PDB<sup>™</sup>
PROTEIN DATA BANK
                                          NCBI
                                                    Pub Med
🗌 >4bzj_A Protein transport protein SEC31; secretion, trafficking; 40.00A {Saccharomyces cerevisiae} PDB: 4bzk_A
 Probab=35.65 E-value=8.1e+02 Score=33.17 Aligned cols=209 Identities=11% Similarity=0.077 Sum probs=0.0
                     нинининесссиринининининессинининин
 Q ss pred
 Q Fri Mar 04 23:
                 786 LDWNHVLCKVNLKEQCIQIAEFYKDLSGLVQTLQTLD-QNDSTTVSLYETFFNEFPK--EFSFTLFEYLIKHKKLNDLIF
                 786 ---i--L---g--e-A--LAEky-Df-sLVel-------rl--Yf-kfg---FA--lf--yi--g----LL- 862 (1157)
...|.++..|.++.|+.+|=++.+|.=+.|......-+. -...||.+... .++..|+ +|-.+..++.
511 e--i---l--G--e-Av--cl-------Al-lA---g--l-----y------p--rll----i---d--dvv- 586 (1273)
 T Consensus
```

```
T 4bzj_A
               511 EQTISKNLVSGNIKSAVKNSLENDLLMEAMVIALDSNNERLKES--VKNAYFAKYGSKSSLSRILY--SISKREVDDLVE 586 (1273)
T ss dssp
                  НИНИНИНИТСКИНИНИНИНИТТСКИНИНИНИТТСССТТИНИН -- ТИНИНИТТТТСКИНИНИН-- НИНТТССИНИНИ
T ss_pred
                  Q ss pred
Q Fri_Mar_04_23:
               863 RF--POOHDVLIOFFOESAPKYGHVAWIQOILDG--SYADAMNTLKNITVDDSKKGESLSECELHLNVAKLSSLLV-EKD
                                                                                  937 (1157)
Q Consensus
               863 ~~-~~~L~FL~~~p~~~lsWI~dI~~~-~y~As~tL~~lA~~~~~l~kk~~LSLaKLa~LA~~~~
                                                                                  937 (1157)
                 ---~a~lcyl~a~~-
               587 ~~~l~~wke~l~~~t~~~----
                                                                                  640 (1273)
T Consensus
               587 NLDVSQWKFISKAIQNLY-P------NDIAQRNEMLIKLGDRLKEN---G------HRQDSLTLYLAAGS--
T 4bzj_A
                                                                                  640 (1273)
                  НВСGGGHHHHHHHHHC-Т------ТСНИНИНИННННННТТ--Т------СНИНИНИННННТС--
T ss dssp
                  ссСининининин
T ss_pred
Q ss_pred
                  Q Fri_Mar_04_23:
               938 NLDINTLRKIQYNLDTID------AEKNISNKLKKGEVQICKRFKNGSIREVFNILVEELKSTTVVNLSDLVE 1004 (1157)
               O Consensus
                                                            --+|+..++ ....+.|.+
                   .++.+.-.++|.-.. +-+.|.+.|..
                                          ----iEk----
T Consensus
               641 --LDKVASIWLSEFPDLEDKLKKDNKTIYEAHSECLTEFIER------FTVFSNFIN--GSSTINNEQLIA 701 (1273)
T 4bzj A
                  T ss_dssp
                  T ss pred
                  ННСсс---сhнннннннннннннннннннннннннн
Q ss pred
Q Fri_Mar_04_23: 1005 LYSMLD----DEESLFIPLRLLSVDGNLLNFEVKKFLNALVWRRI 1045 (1157)
 Q Consensus
              1005 llTl~d----F-~AL~vl~~~~~e~~~l~~~IWrR~ 1045 (1157)
                  .|.---
                         +...|..|++.|....+ +.....++...|.+-+
                   ---eya--la--G----A---l-------r-r-r---a- 744 (1273)
T Consensus
               702 KFLEFINLTTSTGNFELATEFLNSLPS--DNEEVKTEKARVLIAS 744 (1273)
T 4bzi A
T ss_dssp
                  ННИНИННИТТТСИНИННИННЫ SCT--ТСИНИННИННИННИ
T ss_pred
                  нининининининининин
                            PDB"
                                             Pub Med
No 27
                                    NCBI
34gq2 Mucleoporin NUP120; beta propeller alpha helical, component of nuclear pore COMP transport protein; 2.40A
 {Schizosaccharomyces pombe} PDB: 4fhm B
Probab=32.16 E-value=1.8e+02 Score=38.17 Aligned_cols=90 Identities=13% Similarity=0.094 Sum_probs=0.0
Q ss pred
                  EEEEeeCCcceEEEEeccccEEEEEecCCCCeeeEehhhhccCccCcc---chhhc--cCCC------CeEEEecCCCC
Q Fri_Mar_04_23: 209 DLMLNCEPAGIVLSTNMGRIFFITIRNSMGKPQLKLGKLLNKPFKLGI---WSKIF--NTNS-----SVVSLRNGPIL 276 (1157)
               Q Consensus
                                                                                  276 (1157)
               T Consensus
                                                                                  244 (950)
               174 DLMAAISTSEICVSFFNGGLTKIILNPKDASHYEOH--I----DDSSYLFSLKKYLSLOAFKADYRSPNTIISMIFL---
T 4gq2 M
                                                                                  244 (950)
T ss_dssp
                  EEEEECSSSEEEEETTSCEEEEEEETTTTEEEEEE--E----CCCCCCCBCC-------CCSSCCCTTCEEEEEEE---
                  eEEEEeCCCeEEEEEecCCCceeEEEe-----cCCcHHHHHhhhccccCCCCCccceEEEEEe---
T ss pred
                  CcccEEEEEECCCeEEEEEeecCCCCceEeeec
Q ss_pred
Q Fri_Mar_04_23: 277 GKGTRLVYITTNKGIFQTWQLSATNSHPTKLIDV 310 (1157)
               277 --g-r-i-ilt--g-lq-W-----g-----
                                              310 (1157)
Q Consensus
               .++..+++++.++|.+|++..+|
245 -----lftL-D--LRiWsl---t---dl
                                              275 (950)
T Consensus
               245 -STYNVLVMLSLDYKLKVLDLS--TNQCVETIEL 275 (950)
T 4gq2 M
                  -TTTTEEEEEETTCEEEEEETT--TTEEEEEEC
T ss_dssp
                  -CCccEEEEECCC--CCCEEEeecc
T ss pred
                                                    Pub Med
>5a9g 1 Nucleoporin SEH1: transport protein: 23.00A (Homo sapiens)
 Probab=30.63 E-value=61 Score=44.54 Aligned_cols=95 Identities=12% Similarity=0.146 Sum_probs=0.0
                  EEeeCCceEEEEeccccEEEEEeeCCCCCeeeEehhhhccC-ccCcchhhccC------CCCeEEEecCCCCcccE
Q Fri Mar_04_23: 211 MLNCEPAGIVLSTNMGRIFFITIRNSMGKPQLKLGKLLNKP-FKLGIWSKIFNT-----NSSVVSLRNGPILGKGTR 281 (1157)
Q Consensus 211 l-n-epag-IlaTS-gRl--lslrd--Gkp-l----L-k-----g----i------I-si--g----g-r 281 (1157)
               T Consensus
               {\tt 221~LSSDGEALFALPCASGGIFVLKLPPYDIPGMVSVVEL-KQSSVMQRLLTGWMPTAIRGDQSPSDRPLSLAVHCVEHD--A}
T 5a9q 1
T ss_dssp
                  T ss_pred
                  ecCCCceEEEEEcCCccCCCcceeee-ccccchhhhhhhccCccccCCCCcceeEEEEecCCc--e
Q ss pred
                  EEEEECCCeEEEEEeecCCCcceEeeeccH
Q Fri_Mar_04_23: 282 LVYITTNKGIFQTWQLSATNSHPTKLIDVNI
                                           312 (1157)
O Consensus
               282 ~i~ilt~~g~lq~W~~~~~g~~~~~di 312 (1157)
                  .+++++.++++.+|++. .++ .+...|+
               298 ~LftL~~D~~LRiWsl~~~~~dl
T Consensus
                                           324 (1436)
T 5a9q_1
               298 FIFALCQDHKLRMWSYK-EQM---CLMVADM
                                           324 (1436)
T ss dssp
                  EEEEETTSEEEEEETT-TTE---EEEEEEC
T ss_pred
                  EEEEEecCCeeEeeecc-cCc---EEEEech
                            PDB"
No 29
                                    NCBI
                                                  Pub Med
🗌 >1zvt_A Topoisomerase IV subunit A; beta-pinwheel, ATPase, supercoiling, decatenation, DNA bindi topology; 1.70A
 {Escherichia coli} PDB: 4mn4 _A*
 Probab=29.30 E-value=3.5e+02 Score=29.43 Aligned cols=109 Identities=11% Similarity=0.070 Sum probs=0.0
```

```
Q ss_pred
                            CCCeEEEECCCCe-eecccchhhhccchhccCcceEEEEecCCCCCceEEEEEeeCCce-EEEEeccccEEEEEeeC--
 Q Fri Mar 04 23: 160 ETGGLIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELELPINSSGGEKCDLMLNCEPAG-IVLSTNMGRIFFITIRN--
                                                                                                                                235 (1157)
                       160 ~~pGlviV~p~tG~-yWesI~~a~lql~l~~~~~l~L~~~qE~vt~l~n~epaq~~IlaTS~qRl~~lslrd--
 O Consensus
                                                                                                                                235 (1157)
                            1 ~E~~~V~~T~~~G~IKr~~~~~
                                                            -----t-d-ll--T--G-----eip
 T Consensus
                                                                                                                                  65 (256)
                         1 SEPVTIVLSQ-MGWVRSAKGHD-----IDAP---GLNYK-AGDSFKAAVKGKSNQPVVFVDSTGRSYAIDPITLP
 T 1zvt_A
                                                                                                                                  65 (256)
                            CCEEEEEET-TSEEEEESSC-----CCST---TSCCC-TTCCEEEEEEETTSCEEEEETTSEEEEECGGGSC
 T ss_dssp
                            CCCEEEECC-CCEEEEeEhhH------hhhh----hcCCC--CCCEEEEEEecCCCeEEEEEhhhCC
 T ss pred
                            \verb|CCCCeeeEehhhhccCccCcchhhccCCCCeEEEecCCCCcceEEEEEECCCeEEEEEeee| \\
 Q ss_pred
 Q Fri Mar 04 23: 236 SMGKPQLKLGKLLNKPFKLGIWSKIFNTNSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQLS 298 (1157)
                       236 ~~Gkp~l~~~~L~k~~~q~~~i~~~~~I~si~~q~~~~q~r~i~ilt~~q~lq~W~~~
 O Consensus
                                                                                                           298 (1157)
                            ..|+-...+..++ +- ....|+++-+.+. ...+++|..|.+.+..+.
                         66 ~~r~g~~v~~li~~L-----e~iv~~~~~~ll~~f~~G~~Krt~l~
 T Consensus
                        66 SARGQGEPLTGKL-TL-----PPGATVDHMLMESD----DQKLLMASDAGYGFVCTFN 113 (256)
 T 1zvt A
 T ss_dssp
                            CSSSCCEEGGGTC-CC-----CTTCCEEEEECCCT---TCEEEEEBTTSEEEEEEGG
 T ss_pred
                            CCCCceeeeeEE-CC-----CCCEEEEEEECC----CCEEEEEEHH
                                          SCOPe PDB PROTEIN DATA BANK
 No 30
                                                                       NCBI
                                                                                            Pub Med
>\textsime > \textsime 1 DNA gyrase subunit A; beta pinwheel, topoisomerase, spiralling beta pinwheel, DNA wrapping, isomerase, DNA bindng protein; HET: DNA; 2.60A {Escherichia coli} SCOP: b.68.10.0
 Probab=26.55 E-value=3.3e+02 Score=30.46 Aligned cols=110 Identities=11% Similarity=0.104 Sum probs=0.0
                            EEEEECCCCe-eecccchhhhccCcceEEEEEecCCCcceEEEEEeeCCc-eEEEEeecccEEEEEeeCCC----
 Q Fri Mar 04 23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELELPINSSGGEKCDLMLNCEPA-GIVLSTNMGRIFFITIRNSM---- 237 (1157)
                       164\ lviV-p-tG--yWesI--a--lgl-l-----l----l-----gE-vt-l-n-epa-g-IlaTS-gRl--lslrd------ 237\ (1157)
 O Consensus
                       T Consensus
 T 1zi0 A
                       160 VMLFSA-EGKVVRFKESSVRAMG---CNTTGVRG-IRLG--EGDKVVSLIVPRGDGAILTATQNGYGKRTAVAEYPTKSR 232 (307)
 T ss dssp
                            EEEEET-TSEEEEEEGGGSCBCC---TTCCCEEC-CCCC--TTCCEEEEECCCSSCEEEEEETTSEEEEECGGGSCCCCT
 T ss_pred
                            EEEEeC-CCeEEEEEHHHccccC---CCCCeEe-eccC--CCCEEEEEEEecCCCeEEEEeeHHHcccCCC
                            -CCeeeEehhhhccCccCccchhhccCCCCeEEEecCCCCcccEEEEEEECCCeEEEEEee
 Q ss_pred
 Q Fri Mar 04 23: 238 -GKPQLKLGKLNKPFKLGIWSKIFNTNSSVVSLRNGPILGKGTRLVYITTNKGIFQTWQLS 298 (1157)
 Q Consensus
                       238 -Gkp-l----L-k----g----i-----I-si--g-r-i-ilt--g-lq-W--- 298 (1157)
                             T Consensus
                       233 ~
                                                                                                         276 (307)
                       233 ATKGVISIK-VTERN-----GLVVGAVQVD----DCDQIMMITDAGTLVRTRVS 276 (307)
 T 1zi0 A
                            TSCCEESSC-CCTTT-----CSEEEEEEC---TTCEEEEEESSCCEEEEEGG
 T ss_dssp
 T ss pred
                            CCcCeEEE-EcCCC-----CeEEEEEEeC----CCCEEEEEEEHH
                                            PDB<sup>™</sup>
PROTEIN DATA BANK
 No 31
                                                                                Pub Med
            Coatomer subunit alpha; beta-propeller, alpha-solenoid, transport protein; 2.50A {Saccharomyces
3mkq B
 cerevisiae}
 Probab=24.66 E-value=97 Score=31.84 Aligned cols=41 Identities=10% Similarity=0.150 Sum probs=0.0
                            ннинининининин
 Q ss pred
                       780 LYDDNHLDWNHVLCKVNLKEQCIQIAEFYKDLSGLVQTLQT
 Q Fri Mar 04 23:
                       780 ~y~~~R~~~i~~L~~~g~~e~A~~LAEky~Df~sLVel~~~
 Q Consensus
                                                                                820 (1157)
                       . | . . + - . . + + + . | + + + | + . + | + + | . + - . . . + | + . + | + + | . + | . + | . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + | + . + 
 T Consensus
                                                                                 140 (177)
                       100 FYNNSTKERSSIFAEGGSLPLAYAVAKANGDEAAASAFLEQ
 T 3mkq_B
                                                                                140 (177)
                            ннитсининининиттсининининиттсинининин
 T ss dssp
 T ss pred
                            ннсссининининнсссинининнин
                                           PDB<sup>N</sup>
                                                         NCBI
 No 32
                                                                       Pub Med
□ >5cqs_A Elongator complex protein 1; familial dysautonomia, ELP1 subunit, DIME protein binding; 2.70A
 {Saccharomyces cerevisiae}
 Probab=23.98 E-value=7.4e+02 Score=29.10 Aligned_cols=126 Identities=5% Similarity=-0.084 Sum probs=0.0
                            нининисссирининининин
 Q ss pred
 Q Fri Mar 04 23:
                       789 NHVLCKVNLKEQCIQIAEFYKDLSGLVQTLQTLDQNDSTTV-SLYETFFNEFPK-EFSFTLFEYLIKHKKLNDLIFR--F
                                                                                                                                864 (1157)
                       789 i~-L~~g~e-A~-LAEky~Df~sLVel~~~~~~rl~~Yf~kfg~-~FA~~lf~~yi~~g~~~~LL~~-~
 Q Consensus
                                                                                                                                864 (1157)
                       205 (435)
 T Consensus
                       128 AVAYEMLGKLKEAMGAYQSAKRWREAMSIAVQKFPEEVESVAEELISSLTFEHRYVDAADIQLEYL--DNVKEAVALYCK
 T 5cgs A
                                                                                                                                205 (435)
                            T ss_dssp
                            T ss pred
                            0 ss pred
 Q Fri_Mar_04_23:
                       865 PQQHDVLIQFFQESAPKYGHVAWIQQILD-GSYADAMNTLKNITVDDSKKGESLSECELHL
                                                                                                         924 (1157)
                            \hbox{\tt ------L--FL----p----lsWI-dI-----y--As-tL--lA------l---kk---L}
                       T Consensus
                                                                                                         258 (435)
                       206 AYRYDIASLVAIKA----KKDELLEEVVDPGLGEGFGIIAELLADCK----GQINSQLRRL
 T 5cqs A
                                                                                                         258 (435)
                            ТТСНИНИНИННТ---ТСТТИНИНТИНИНИНИНИНИНИНИН----НИНИНИНИС-
 T ss_dssp
                            T ss_pred
```

```
PDB"
                                                           SCOPe
                                                                                                                                  Pub Med
>1suu A DNA qyrase subunit A; topoisomerase, DNA qyrase, beta-propeller, beta-pinwheel, ISO; HET: DNA; 1.75A
   {Borrelia burgdorferi} SCOP: b.68.10.1
   Probab=23.47 E-value=6.7e+02 Score=27.95 Aligned cols=112 Identities=11% Similarity=0.025 Sum probs=0.0
                                       Q ss pred
  Q Fri Mar 04 23: 164 LIIIKGSKAI-YYEDINSINNLNFKLSEKFSHELELPINSSGGEKCDLMLNCEPA-GIVLSTNMGRIFFITIRNSMGKPQ 241 (1157)
                                 164 lviV-p-tG--yWesI--a--lgl-l-----l-L----gE-vt-l-n-epa-g-IlaTS-gRl--lslrd--Gkp- 241 (1157)
  Q Consensus
                                T Consensus
                                                                                                                                                                               230 (312)
                                 165 VICLSK-KGSAFIFNSRDVRLTN---RGTQGVCG-MKLK--EGDLFVKVLSVKENPYLLIVSENGYGKRLNMS-----
  T 1suu A
                                                                                                                                                                               230 (312)
                                       EEEEET-TSEEEEEEGGGSCBCC---TTBCCEEC-CCCC--TTCCEEEEEECTTCSEEEEEEETTSEEEEEEGG-----
  T ss dssp
                                       EEEEeC-CCCEEEEEhhHCCccC---CCCCCeEE-EEeC--CCCEEEEEEEECCCCeEEEEEHH------
  T ss pred
  Q ss_pred
                                       eEehhhhccC-ccCcchhhccCC--CCeEEEecCCCCcceEEEEEECCCeEEEE
  Q Fri Mar 04 23: 242 LKLGKLLNKP-FKLGIWSKIFNTN--SSVVSLRNGPILGKGTRLVYITTNKGIFQTWQL
                                                                                                                                            297 (1157)
  O Consensus
                                 242 \ l ---- L - k ---- g ---- i --- I - si -- g ---- g - r - i - ilt -- g - lq - W --- I - si --- g --- I - si --- I - si
                                                                                                                                             297 (1157)
                                T Consensus
                                                                                                                                             281 (312)
                                 231 ----KISELKRGATGYTSYKKSDKKAGSVVDAIAV----SEDDEILLVSKRSKALRTVA
  T 1suu A
                                                                                                                                            281 (312)
  T ss_dssp
                                       ----GSCBCCTTCCCEECSCTTCTTTCSEEEEEEE----CTTCEEEEEEETTCEEEEEEG
  T ss_pred
                                       ----HCCCCCCCCEEEEEccCCCCCeEEEEEH
                                                             PDB"
                                                                              NCBI
                                                                                                               Pub Med
>3mkq_B Coatomer subunit alpha; beta-propeller, alpha-solenoid, transport protein; 2.50A {Saccharomyces
  cerevisiae}
  Probab=22.85 E-value=5.7e+02 Score=25.99 Aligned_cols=96 Identities=13% Similarity=0.096 Sum_probs=0.0
                                       ННССС/hhнниннинhcc---ннинниннниннесс-рининниннниннесс-рининниннесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-рининнесс-
  Q ss pred
  Q Fri_Mar_04_23: 793 CKVNLKEQCIQIAEFYKD---LSGLVQTLQTLDQNDSTTVSLYETFFNEFPK-EFSFTLFEYLIKHKKLNDLIFRFPQQH
                                                                                                                                                                                868 (1157)
  O Consensus
                                 793 ~~~g~~e~A~~LAEky~D---f~sLVel~~~~~~rl~~Yf~kfg~-~FA~~lf~~yi~~g~~~~LL~~~~~
                                                                                                                                                                                868 (1157)
                                  T Consensus
                                  16 LEYGNLDAALDEAKKLNDSITWERLIQEALAQGN----ASLAEMIYQTQHSFDKLSFLYLVT---GDVNKL----SKM
  T 3mkq B
                                                                                                                                                                                  82 (177)
                                       ННТТСИНИНИНИНИССИИНИНИНИНИНИНИТС----ИНИНИНИНТТСНИНИНИНИНИ---ТСИНИН-----ИНИ
  T ss_dssp
                                       T ss_pred
                                       нниннинн
  Q ss pred
   Q Fri_Mar_04_23:
                                869 DVLIQFFQESAPKYGHVAWIQQILDGSYADAMNTLKNI
                                                                                                          906 (1157)
  O Consensus
                                 869 ~~L~~FL~~~p~~~~lsWI~dI~~~~y~~As~tL~~l
                                                                                                         906 (1157)
                                  ..+..+... +.+...|+++.|-+.++
83 a~a~~g~-----A----l~g~--ai~m~---
  T Consensus
                                                                                                         115 (177)
  T 3mkq_B
                                  83 QNIAQTREDF----GSMLLNTFYNNSTKERSSIFAEG 115 (177)
  T ss dssp
                                       НИНИНТТСН----НИНИНИНННТСИНИНННИНН
                                       нининссси----нинининнессинининин
  T ss pred
                                                             PDB"
                                                                              NCBI
  No 35
                                                                                                               Pub Med
□ >5cqs_A Elongator complex protein 1; familial dysautonomia, ELP1 subunit, DIME protein binding; 2.70A
   {Saccharomyces cerevisiae}
  Probab=21.68 E-value=2.7e+02 Score=32.91 Aligned_cols=86 Identities=12% Similarity=0.008 Sum_probs=0.0
  Q ss pred
                                       Q Fri_Mar_04_23: 753 FNQFKIWINTQPVKSVNANDNFININNLYDDNHLDWNHVLCKVNLKEQCIQIAEFYKDLSGLVQTLQTLDQNDSTTV-SL
                                                                                                                                                                                831 (1157)
  O Consensus
                                 831 (1157)
                                       T Consensus
                                                                                                                                                                               239 (435)
                                 169 AEELISSLTFEHR----YVDAADIQLEYLDNVKEAVALYCKAYRYDIASLVAIKAKKDELLEEVVDPGLG---EGFGI
  T 5cqs A
                                                                                                                                                                               239 (435)
  T ss dssp
                                       НИНИНИНИТС----НИНИНИНИНИССИИНИНИНИНТТСИИНИНИНИТСТИИНИТИНИНИНИ----ИНИНИ
                                       T ss pred
                                       ннинннн
  Q ss pred
  Q Fri_Mar_04_23:
                                 832 YETFFNEFPKEFSFTL 847 (1157)
   Q Consensus
                                 832 l~~Yf~kfq~~FA~~l
                                                                    847 (1157)
                                       +..|++..+..|-..+
  T Consensus
                                 240 ~~e~l~d~~~~
                                                                    255 (435)
                                 240 TAELLADCKGOTNSOL
  T 5cgs A
                                                                    255 (435)
                                       нинининининин
   T ss_dssp
   T ss_pred
                                        нинининининини
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.
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PDB: Bourne, PE. et al. (2004) The distribution and query systems of the RCSB Protein Data Bank. NAR 32: D223.

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