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Bioinformatics Toolkit

Max-Planck Institute for Developmental Biology

Quickfinder

Search **Alignment** **Sequence Analysis** **2ary Structure** **3ary Structure** **Classification** **Utils**

CS-BLAST HHblits HHpred HHsenser HMMER3 PatternSearch ProtBLAST PSI-BLAST SimShiftDB

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HHpred - Results

Job-ID: 4234647 Date: 14:24 on Mar 21 2014

Help

Results **Histogram** **Reduced alignment** **Representative alignment** **Full alignment**

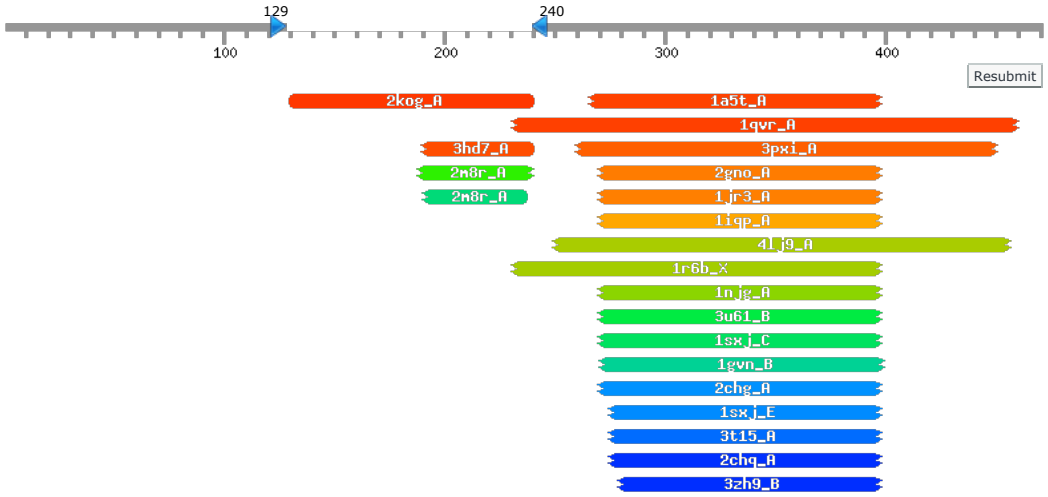
Create model Merge Q/T alignments Forward to PCoils Forward HMM Save Export

Color alignments

color only SS color alignments color alignments

View alignment

Note: click **PDBalert** to upload your query sequence and get alerted by email as soon as better PDB templates get available.



HHpred has detected hits to coiled coil-containing proteins.
You may consider running a PCOILS prediction on your query.

Query lull1 (seq=MADSGLREPQ...SSIEEQGCLF Len=470 Neff=3.6 Nseqs=81)
Parameters score SS:yes search:local realign with MAP:no

No	Hit		Prob	E-value	P-value	Score	SS	Cols	Query HMM	Template HMM
1	2kog_A	Vesicle-associated memb	95.3	0.015	4.6E-07	50.7	4.2	112	129-240	1-119 (119)
2	1qvr_A	CLPB protein; coiled co	94.6	0.55	1.7E-05	52.2	15.0	206	231-459	526-756 (854)
3	1a5t_A	Delta prime, HOLB; zinc	94.4	0.2	6.2E-06	48.2	9.7	122	266-397	4-144 (334)
4	3hd7_A	Vesicle-associated memb	93.5	0.2	6.2E-06	41.5	6.8	51	190-240	39-91 (91)
5	3pxi_A	Negative regulator of g	92.0	2.9	9E-05	46.3	15.4	174	260-449	487-673 (758)
6	2gno_A	DNA polymerase III, gam	89.5	1	3.2E-05	42.7	7.9	116	270-397	2-118 (305)
7	1jr3_A	DNA polymerase III subu	89.3	2.3	7.1E-05	41.2	10.2	115	270-397	21-155 (373)
8	1iqp_A	RFCS; clamp loader, ext	85.9	2.9	9.1E-05	39.7	8.6	116	270-397	30-146 (327)
9	4lj9_A	Chaperone protein CLPB;	80.0	11	0.00036	37.1	10.4	186	250-455	29-238 (339)
10	1r6b_X	CLPA protein; AAA+, N-t	79.7	38	0.0012	37.8	15.4	157	231-397	426-604 (758)
11	1njg_A	DNA polymerase III subu	78.2	13	0.00041	34.4	9.7	117	270-397	28-162 (250)
12	2m8r_A	Syntaxin-1A; snare, pre	72.7	10	0.00032	31.6	6.7	52	188-239	46-108 (109)
13	3u61_B	DNA polymerase accessor	66.1	27	0.00084	32.8	8.9	104	270-397	31-142 (324)
14	1sxj_C	Activator 1 40 kDa subu	64.4	15	0.00047	35.3	7.0	116	270-397	30-146 (340)
15	2m8r_A	Syntaxin-1A; snare, pre	62.9	3.3	0.0001	34.6	1.8	47	191-237	63-109 (109)
16	1gvn_B	Zeta; postsegregational	61.2	1.1E+02	0.0034	28.2	12.5	118	271-398	10-146 (287)
17	2chg_A	Replication factor C sm	52.3	62	0.0019	28.6	8.3	116	270-397	22-138 (226)
18	1sxj_E	Activator 1 40 kDa subu	51.7	1.3E+02	0.004	28.3	10.8	119	275-397	20-170 (354)
19	3t15_A	Ribulose bisphosphate c	49.1	1.5E+02	0.0047	28.1	10.9	117	275-397	18-161 (293)
20	2chq_A	Replication factor C sm	44.1	54	0.0017	30.4	6.9	115	275-397	23-138 (319)
21	3zh9_B	Delta; hydrolase, repli	43.9	42	0.0013	32.3	6.2	106	279-397	3-118 (347)
22	1sxj_B	Activator 1 37 kDa subu	39.6	1.3E+02	0.0042	28.2	8.9	110	270-397	26-143 (323)
23	3pe5_A	Uncharacterized protein	38.6	7.2	0.00022	39.9	0.0	53	187-239	5-57 (403)
24	2yhs_A	FTSY, cell division pro	34.5	2.5E+02	0.0078	28.7	10.6	130	250-395	243-381 (503)
25	1shu_X	Anthrax toxin receptor	32.3	1E+02	0.0031	26.5	6.3	121	249-382	60-182 (182)
26	2bjv_A	PSP operon transcriptio	31.9	3.4E+02	0.011	25.4	10.5	127	259-397	1-147 (265)
27	1jql_B	DNA polymerase III, del	28.9	1.4E+02	0.0045	25.1	6.6	104	281-397	9-113 (140)
28	3arc_L	Photosystem II reaction	28.0	53	0.0017	23.8	3.0	20	220-239	16-35 (37)
29	1v7p_C	Integrin alpha-2; snake	27.7	1.3E+02	0.0039	26.5	6.2	128	252-385	66-199 (200)
30	3te6_A	Regulatory protein SIR3	21.4	4.7E+02	0.015	25.8	9.6	118	274-397	29-169 (318)
31	4i9w_A	Potassium channel subfa	21.2	4E+02	0.012	25.6	8.8	96	186-287	2-97 (309)
32	2og2_A	Putative signal recogni	20.1	4.5E+02	0.014	26.6	9.2	66	252-317	107-183 (359)

No 1 PDB PROTEIN DATA BANK MMDB NCBI PubMed

>2kog_A Vesicle-associated membrane protein 2; synaptobrevin, VAMP2, DPC micelle, snare, coiled coil, membrane

```
fusion, transmembrane; NMR {Rattus norvegicus}
Probab=95.31  E-value=0.015  Score=50.70  Aligned_cols=112  Identities=14%  Similarity=0.283  Sum_probs=0.0

Q ss_pred               ccccccccccCchhhccCcccCCCCCCCccccCCCCcccccCccchhhHHhcc-----CCCccccchHhhhhhhhhhHHH
Q lull1          129 DAHLGSSSVALPKEASDGTGASQEPPTTDSQEAQSPGHSSAGQEGEDTLRRRL-----LAPEAGSHPQQTQKLEEIKENA  203 (470)
Q Consensus      129 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-----~~~~~~~~~~~~~~~~~~~~~~  203 (470)
                       ++|..++++..|.....+.+++..++...+....--.--...-.+-++.++.-+     ----.+.=++.|+.|...-..-
T Consensus        1 ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~kl~~iq~~v~evk~iM~~Ni~kil~RgekLe~L~~KS~~L~~~S~~F   80 (119)
T 2kog_A          1 GSHMSATAATVPPAAPAGEGGPPAPPPNLTSNRRLQQTQAQVDEVVDIMRVNVDKVLERDQKLSELDDRADALQAGASQF   80 (119)
T ss_dssp             ---CCCCCCCCCCCCCCCCCCCCCCCCSSSSCSHHHHSSHHHHHHHHHHHHHHHHHHCCCCSSCCCCSCCSCCCSSSHHH
T ss_pred             CCCCCCCCCCCCCCCCCCCCCCCCCCCCCcccHHHHHHHHHHHHHHHHHHHHHHHHHHcccHHHHHHHHHhHHHHHHHH


Q ss_pred               HHHHHHHHHHHHHHHHH--HHHHHHHHHHHHHHHHhhhhc
Q lull1          204 QDTMRQINKKGFWSYG--PVILVVLVVAVVASSVNSYYS  240 (470)
Q Consensus      204 ~~~~~~~~~~k~~~~y~--~~~i~~li~iv~l~~i~~~~s  240 (470)
                       +..-|+.+++-||+..  .++||++++++++++++|++|++
T Consensus       81 ~k~a~~lkrkm~w~~~K~~ii~~~v~~i~l~~ii~~f~t  119 (119)
T 2kog_A         81 ETSAAKLKRKYWWKNLKMMIILGVICAIILIIIIVYFST  119 (119)
T ss_dssp             HHHHHHHHHHHSCHHHHHHHHHHHHHHHHHHHHHHHHHHC
T ss_pred             HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHhhhheeC
```

No 2

\>1qvr_A CLPB protein; coiled coil, AAA ATPase, chaperone; HET: ANP; 3.00A {Thermus thermophilus} SCOP: a.174.1.1 c.37.1.20 c.37.1.20

```
Probab=94.58  E-value=0.55  Score=52.22  Aligned_cols=206  Identities=16%  Similarity=0.209  Sum_probs=0.0

Q ss_pred               HHHHHhhhhcCccccccccchhHHHHHHHHHHHHHHhcCCCCHHHHHHHHHHHHHHHhcCCCCCCCeEEEEecCCCh---HHH
Q lull1          231 VASSVNSYYSSPAQQVPKNPALEAFLAQFSQLEDKFPGQSSFLWQRGRKFLQKHLNASNPTEPATIIFTAAREG---RET  307 (470)
Q Consensus      231 ~l~~i~~~~~ssPa~~~~~~~~a~e~f~~qf~~LK~kFPsQse~LWk~lr~~LekhLn~s~p~ePaViLfta~~~A---e~T  307 (470)
                       |..++....+.|-..+.+.++ +.+..--+.|+.+.++|++-+=.+.+.....-...-.+++.|..-+|+.|.++   +++
T Consensus      526 v~~v~s~~tgip~~~~~~~~e~~~~l~~L~~~L~~~V~gQ~eAi~~Ia~ai~~~rsGl~~~~kP~~~fLF~GptGvGKtel  604 (854)
T 1qvr_A         526 IAEIVSRWTGIPVSKLLEGER-EKLLRLEEELHKRVVGQDEAIRAVADAIRRARAGLKDPNRPIGSFLFLGPTGVGKTEL  604 (854)
T ss_dssp             HHHHHHTTSSCHHHHTTCCHH-HHHHSHHHHHHHHHSCSCHHHHHHHHHHHHHHHHGGGCSCSSSCSEEEEEBSCSSSSHHHH
T ss_pred             HHHHHHHHHCCChHhhChhHH-HHHHHHHHHHHhCcccCChHHHHHHHHHHHHHHHhcCCCCCCCCCeEEEEECCCCCCHHHH


Q ss_pred               HHHHHHHHHHHhccccCCcceeeChHHhccCCc---------hHHHHHHHHHHHHHHhhcC-CcEEEEeehhhCChHHHHH
Q lull1          308 LKCLSHHVADAYTSSQKVSPIQIDGAGRTWQDS---------DTVKLLVDLELSYGFENG-QKAAVVHHFESFPAGSTLI  377 (470)
Q Consensus      308 l~CLa~~LA~aySs~~~~s~I~IdG~~~a~~DS---------D~vKl~lDe~L~s~Fe~g-~kaAVV~~LE~LPP~AaLI  377 (470)
                       ++.||+.+=...+.+      |.||--.|..-.+          .|+...---+|-++..+. ..|+++-++|.-.|..-.+
T Consensus      605 AkaLA~~lFGs~~~l-----iridMSey~e~~svsrLiG~ppGYvGy~~~g~LteaVr~~P~sVil~d~ieka~~~~~~~~  679 (854)
T 1qvr_A         605 AKTLAATLFDTEEAM-----IRIDMTEYMEKHAVSRLIGAPPGYVGYEEGGQLTEAVRRRPYSVILFDEIEKAHPDVFNI  679 (854)
T ss_dssp             HHHHHHHHHHSSGGGE-----EEECTTTCCSSGGGGGC-------------CHHHHHHHCSSEEEEESSGGGSCHHHHHH
T ss_pred             HHHHHHHHcCCCcce-----EeccccccchhhHHHhcCCCCCCCcCcCCCChhhHHHHHhCCCEEEEehhhhhcCHHHHHH


Q ss_pred               HHHhcCCC--------CcccccEEEEEEEeccccc----ccccCChHHHHHHHHHHHHHHHHhccccCcccccccCChhhcch
Q lull1          378 FYKYCDHE--------NAAFKDVALVLTVLLEEET----LEASVGPRETEEKVRDLLWAKFTNSDTPTSFNHMDSDKLSG  445 (470)
Q Consensus      378 FH~YCDhE--------NA~fKdvaL~LTV~leeet----L~~~s~s~kevEEkV~d~Lw~k~~~~s~~~~s~n~Md~DkL~p  445 (470)
                       |-...|..        ..-|+|++||||=-+.+.     .........+.+.+++.|...|.                   ..
T Consensus      680 ~~~~~~~g~~~d~~g~~~~~~~~~iii~tsn~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~f~----------------pe  743 (854)
T 1qvr_A         680 LLQILDDGRLTDSHGRTVDFRNTVIILTSNLGSPLILEGLQKGWPYERIRDEVFKVLQQHFR----------------PE  743 (854)
T ss_dssp             HHHHHTTTEECCSSSCCEECTTEEEEEEECCTTHHHHHHHHHTTCCHHHHHHHHHHHHHTTSC----------------HH
T ss_pred             HHHhhccCCceeCCCCCEEcceeeeEeecCcccCcCHHHHhhcccCCHHHHHHHHHHHHHhhCC----------------HH


Q ss_pred               HHHHhhcceEEeec
Q lull1          446 LWSRISHLVLPVQP  459 (470)
Q Consensus      446 L~SRIS~~VL~VqP  459 (470)
                       |+.|| +.|++..|
T Consensus      744 fl~r~~d~iv~F~~  756 (854)
T 1qvr_A         744 FLNRL-DEIVVFRP  756 (854)
T ss_dssp             HHHTC-SBCCBCCC
T ss_pred             HHhhC-CeEEEcCC
```

No 3

\>1a5t_A Delta prime, HOLB; zinc finger, DNA replication; 2.20A {Escherichia coli K12} SCOP: a.80.1.1 c.37.1.20

PDB: 1jr3 _E* 1xxh _E* 1xxi _E* 3glf _E* 3glg _E* 3glh _E* 3gli _E*

```
Probab=94.38  E-value=0.2  Score=48.19  Aligned_cols=122  Identities=11%  Similarity=0.068  Sum_probs=0.0

Q ss_pred               cCCCCHHHHHHHHHHHHHHHhcCCCCCCCeEEEEecCCCc-hHHHH-HHHHHHHH----------------HHhccccCCcc
Q lull1          266 FPGQSSFLWQRGRKFLQKHLNASNPTEPATIIFTAARE-GRETL-KCLSHHVA----------------DAYTSSQKVSP  327 (470)
Q Consensus      266 FPsQse~LWk~lr~~LekhLn~s~p~ePaViLfta~~~-Ae~Tl-~CLa~~LA----------------~aySs~~~~s~  327 (470)
                       ||=|.+ +|+.++..+++      .+=|-.+||....+ ++.++ +.+|..|-                ..+....++..
T Consensus        4 ypw~~~-~~~~L~~~~~~~~~~~~~~l~ha~L~~G~~G~GK~~lA~~~A~~l~c~~~~~~~~~~c~~c~sC~~i~~~~hpD~   76 (334)
T 1a5t_A          4 YPWLRP-DFEKLVASYQA------GRGHHALLIQALPGMGDDALIYALSRYLLCQQPQGHKSCGHCRGCQLMQAGTHPDY   76 (334)
T ss_dssp             CGGGHH-HHHHHHHHHHT------TCCCSEEEEECCTTSCHHHHHHHHHHHHTCSSCBTTBCCSCSHHHHHHHHTCCTTE
T ss_pred             CcccHH-HHHHHHHHHc------CCccceeeeCCCCCcHHHHHHHHHHHHHhCCCCCCCCCCCCCHHHHHHHHcCCCCCe


Q ss_pred               eeeChHHhcc-CCchHHHHHHHHHHHHHHhhcCCCcEEEEeehhhCChHHHHHHHHhcCCCCcccccceEEEEE
Q lull1          328 IQIDGAGRTW-QDSDTVKLLVDLELSYGFENGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALVLT  397 (470)
Q Consensus      328 I~IdG~~~a~~DSD~vKl~lDe~L~s~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~LT  397 (470)
                       +.+.+...++ +.-|+++-.++.-....+++++|++|.+.|.+...|+-+|=++-+-   +-+++++||+
T Consensus       77 ~~~~~~~~~~~I~id~IR~l~~~~~~~~~~~~~~~Kv~II~~ad~m~~~~~AaNaLLK~LEE---Pp~~~~fIL~  144 (334)
T 1a5t_A         77 YTLAPEKGKNTLGVDAVREVTEKLNEHARLGGAKVVWVTDAALLTDAAANALLKTLEE---PPAETWFFLA  144 (334)
T ss_dssp             EEECCCTTCSSBCHHHHHHHHHHTTSCCTTSSCEEEEESCGGGBCHHHHHHHHHHTS---CCTTEEEEEE
T ss_pred             eccchhhccCCCCHHHHHHHHHHHHhhHHhCCCEEEEEeCchhhHHHHHHHHHHhcC---CCCCceeEee
```

No 4

\>3hd7_A Vesicle-associated membrane protein 2; membrane protein, coiled-coil, 4-helical bundle, cell juncti

cytoplasmic vesicle, membrane, phosphoprotein; HET: GGG; 3.40A {Rattus norvegicus} PDB: 3ipd _A
Probab=93.50 E-value=0.2 Score=41.49 Aligned_cols=51 Identities=12% Similarity=0.258 Sum_probs=0.0

```
Q ss_pred              Hhhhhhhhhh HHHHHHHHHHHHHHHHHH--HHHHHHHHHHHHHHHHHhhhhc
Q lull1         190  PQQTQKLEEIKENAQDTMRQINKKGFWSY--GPVILVVLVVAVVASSVNSYYS  240 (470)
Q Consensus     190  ~~~~~~~~~~~~~~~~~~~~~~~k~~~~~y--~~~~~i~~li~iv~l~~i~~~~~s  240 (470)
                    ++.|+.|.+.-..-..+-|+...+-||+.  ..+++|+++++++++++++.+||+
T Consensus      39  ~~ks~~L~~~s~~F~~~a~~l~r~m~w~~~k~~~ii~~~~~~~l~~ii~~f~~   91 (91)
T 3hd7_A        39  DDRADALQAGASQFETSAAKLKRKYWWKNLKMMIILGVICAIILIIIIVYFST   91 (91)
T ss_dssp            HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHTTCC
T ss_pred            HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHhcC
```

No 5

>3pxi_A Negative regulator of genetic competence CLPC/MEC; CLPB, proteolysis, CLPX, HSP100/CLP, AAA+ proteins, PR binding; 6.93A {Bacillus subtilis} PDB: 3j3r _A 3j3u _A 3j3s _A 3j3t _A
Probab=92.02 E-value=2.9 Score=46.30 Aligned_cols=174 Identities=13% Similarity=0.179 Sum_probs=0.0

```
Q ss_pred              HHHHHhcCCCCHHHHHHHHHHHHHHHhcCCCCCCCeEEEEecCCCh---HHHHHHHHHHHHHHhccccCC-cceeeChHHh
Q lull1         260  SQLEDKFPGQSSFLWQRGRKFLQKHLNASNPTEPATIIFTAAREG---RETLKCLSHHVADAYTSSQKV-SPIQIDGAGR  335 (470)
Q Consensus     260  ~~LK~kFPsQse~LWk~lr~~LekhLn~s~p~ePaViLfta~~~A---e~Tl~CLa~~LA~aySs~~~~-s~I~IdG~~~  335 (470)
                    +.|+.+..+|++-+=...+........-..+..|.-.+|+.|.++   .++++.||..+      +.+. ..+.+|...|
T Consensus     487  ~~L~~~v~GQ~~ai~~i~~~i~~~~~gl~~~~~p~~~~lf~GptGvGKtelak~la~~l------~~~~~~~~~i~~dmse~  560 (758)
T 3pxi_A       487  NILHSRVIGQDEAVVAVAKAVRRARAGLKDPKRPIGSFIFLGPTGVGKTELARALAESI------FGDEESMIRIDMSEY  560 (758)
T ss_dssp            HHHHTTSCSCHHHHHHHHHHHHHHHTTTCSCTTSCSEEEEEESCTTSSHHHHHHHHHHH------HSCTTCEEEEEGGGG
T ss_pred            hcchheeeccHHHHHHHHHHHHHHHHcCCCCCCCCCCcceEeecCCCccHHHHHHHHHHHh------cCcchhhhccccccc
```

```
Q ss_pred              ccCCCchHHHHHHHHHHHHHHhhcCCCcEEEEeehhhCChHHHHHHHHHhcCC--------CCccccceEEEEEEecccccccc
Q lull1         336  TWQDSDTVKLLVDLELSYGFENGQKAAVVHHFESFPAGSTLIFYKYCDH--------ENAAFKDVALVLTVLLEEETLEA  407 (470)
Q Consensus     336  a~~DSD~vKl~lDe~L~s~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDh--------ENA~fKdvaL~LTV~leeetL~~  407 (470)
                    ..-.+-...  .|-+.++   ++...+.++=++|...|....+|..+.|.        ...-|+|++||||=-+-.+.
T Consensus     561  ~~~~s~~~g-~L~~~vr---~~p~sVvl~DeieKah~~v~~~llq~ld~G~l~d~~g~~vd~~n~iiI~TSN~g~~~---  633 (758)
T 3pxi_A       561  MEKHSTSGG-QLTEKVR---RKPYSVVLLDAIEKAHPDVFNILLQVLEDGRLTDSKGRTVDFRNTILIMTSNVGASE---  633 (758)
T ss_dssp            CSSCCCC----CHHHHH---HCSSSEEEEECGGGSCHHHHHHHHHHHHHSBCC-----CCBCTTCEEEEEESSSTTC---
T ss_pred            cccCccccc-chHHHHH---hCCCeEEEehhhhhcCHHHHHHHHHHhhcCCeeECCCCCCEEecCceEEEECCCCCchh---
```

```
Q ss_pred              ccChHHHHHHHHHHHHHHHhccccC-ccccccCChhhcchHHHH
Q lull1         408  SVGPRETEEKVRDLLWAKFTNSDT-PTSFNHMDSDKLSGLWSR  449 (470)
Q Consensus     408  s~s~kevEEkV~d~Lw~k~~~s~~-~~s~n~Md~DkL~pL~SR  449 (470)
                       ...+...+.+++.--|.+.-. ---|+.++.+.+..++.+
T Consensus     634  ---~~~~~~~~l~~~f~pefl~Rid~ii~f~pl~~~~~~~I~~~  673 (758)
T 3pxi_A       634  ---KDKVMGELKRAFRPEFINRIDEIIVFHSLEKKHLTEIVSL  673 (758)
T ss_dssp            ---CHHHHHHHHHHSCHHHHTTSSEEEECC--CHHHHHHHHHH
T ss_pred            ---HHHHHHHHHHhhCCHHHHhhCCEEEEeCCCCHHHHHHHHHH
```

No 6

>2gno_A DNA polymerase III, gamma subunit-related protein; structural genomics, joint center for structural genomics, J protein structure initiative; HET: DNA; 2.00A {Thermotoga maritima} SCOP: a.80.1.1 c.37.1.20
Probab=89.54 E-value=1 Score=42.67 Aligned_cols=116 Identities=15% Similarity=0.113 Sum_probs=0.0

```
Q ss_pred              CHHHHHHHHHHHHHHHhcCCCCCCCeEEEEecCCChHHHH-HHHHHHHHHHhccccCCcceeeChHHhccCCChHHHHHHHH
Q lull1         270  SSFLWQRGRKFLQKHLNASNPTEPATIIFTAAREGRETL-KCLSHHVADAYTSSQKVSPIQIDGAGRTWQDSDTVKLLVD  348 (470)
Q Consensus     270  se~LWk~lr~~LekhLn~s~p~ePaViLfta~~~Ae~Tl-~CLa~~LA~aySs~~~~s~I~IdG~~~a~~DSD~vKl~lD  348 (470)
                    .++.=+.++..|.+       ..-|+.++-+....++.++ .+++..|  ...+..++..+.|+++...  +..|+++-+.
T Consensus       2  ~~~~~~~~l~~~~~~~~-------~~~~~~~~l~~g~~g~gk~~~~a~~~~~~~i~~~~~~~~~~HpD~~~i~~~~~~~-I~Id~IR~l~~   72 (305)
T 2gno_A         2  AKDQLETLKRIIEK------SEGISILINGEDLSYPREVSLELPEYV--EKFPPKASDVLEIDPEGEN-IGIDDIRTIKD   72 (305)
T ss_dssp            --CHHHHHHHHHHT------CSSEEEEEECSSSSHHHHHHHHHHHHH--HTSCCCTTTEEEECCSSSC-BCHHHHHHHHH
T ss_pred            cHHHHHHHHHHHHC------CCCCeEEEECCCCCCHHHHHHHHHHHH--hccccCCCCEEEEeCCCCCC-CCHHHHHHHHH
```

```
Q ss_pred              HHHHHHhhcCCCcEEEEeehhhCChHHHHHHHHHhcCCCCCccccceEEEEE
Q lull1         349  LELSYGFENGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALVLT  397 (470)
Q Consensus     349  e~L~s~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~LT  397 (470)
                    .--...++++.|++||.+.|.+...|+.+|=+   .-.-+-+++++||+
T Consensus      73  ~~~~~p~~g~~KVvIId~ad~m~~~AaNALLK---tLEEPp~~t~fIL~  118 (305)
T 2gno_A        73  FLNYSPELYTRKYVIVHDCERMTQQAANAFLK---ALEEPPEYAVIVLN  118 (305)
T ss_dssp            HHTSCCSSSSSEEEEETTGGGBCHHHHHHTHH---HHHSCCTTEEEEEE
T ss_pred            HHhhccccCCCCeEEEEEeChhhcCHHHHHHHHH---HhhcCCCCCCCcccceec
```

No 7

>1jr3_A DNA polymerase III subunit gamma; processivity, processivity clamp, clamp loader, AAA+ ATPase, transferase; HET: DNA; 2.70A {Escherichia coli} SCOP: a.80.1.1 c.37.1.20 PDB: 1xxh _B* 3glh _B* 3glf _B* 3gli _B* 3glg 1xxi _B*
Probab=89.27 E-value=2.3 Score=41.23 Aligned_cols=115 Identities=16% Similarity=0.127 Sum_probs=0.0

```
Q ss_pred              CHHHHHHHHHHHHHHHhcCCCCCCCeEEEEecCCChHHHHHHHHHHHHHHHH--------------------hccccCCccee
Q lull1         270  SSFLWQRGRKFLQKHLNASNPTEPATIIFTAAREGRETLKCLSHHVADA--------------------YTSSQKVSPIQ  329 (470)
Q Consensus     270  se~LWk~lr~~LekhLn~s~p~ePaViLfta~~~Ae~Tl~CLa~~LA~a--------------------ySs~~~~s~I~  329 (470)
                    .+.+++.++..+.+       .+-|-.+||....+.-.+  .+|..+|..                    +.+..++..+.
T Consensus      21  ~~~~~~~~l~~~~~~~~------~~~~ha~L~~G~~G~GK~~~~~a~~~a~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~d~~~   92 (373)
T 1jr3_A        21  QEHVLTALANGLSL------GRIHHAYLFSGTRGVGKT--SIARLLAKGLNCETGITATPCGVCDNCREIEQGRFVDLIE   92 (373)
T ss_dssp            CHHHHHHHHHHHHH------TCCCSEEEEESCTTSSHH--HHHHHHHHHHSCTTCSCSSCCSSSHHHHHHHTSCCSSCEE
T ss_pred            cHHHHHHHHHHHHc------CCCCeeeeECCCCCCHH--HHHHHHHHHHhCCCCCCCcCCCCcccchHHHHHHHcCCCCcEEE
```

```
Q ss_pred              eChHHhccCCChHHHHHHHHHHHHHHhhcCCCcEEEEeehhhCChHHHHHHHHHhcCCCCCccccceEEEEE
Q lull1         330  IDGAGRTWQDSDTVKLLVDLELSYGFENGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALVLT  397 (470)
Q Consensus     330  IdG~~~a~~DSD~vKl~lDe~L~s~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~LT  397 (470)
                    +++...  ...|+++-.+..--...++++.|++||.+.|.+...|+.+|=+   --+-++++++||+
T Consensus      93  ~~~~~~~~~~i~~ir~l~~~~~~~~~~~~~~~ki~ii~~~~~~~l~~~~~~~n~llk~lE---ep~~~~~~~il~  155 (373)
T 1jr3_A        93  IDAASR--TKVEDTRDLLDNVQYAPARGRFKVYLIDEVHMLSRHSFNALLKTLE---EPPEHVKFLLA  155 (373)
```

```
T ss_dssp             EETTCS--CCSSCHHHHHHHTTSCCSSSSSSEEEEEECGGGSCHHHHHHHHHHHH---SCCSSEEEEEE
T ss_pred             eccccc--CCHHHHHHHHHHHhhcccCCCCeEEEEECcCccCHHHHHHHHHHHh---CCCcCeEEEEe
```

No 8 SCOP PDB NCBI PubMed

```
>1iqp_A RFCS; clamp loader, extended AAA-ATPase domain, complex with ADP, replication; HET: ADP; 2.80A
{Pyrococcus furiosus} SCOP: a.80.1.1 c.37.1.20
Probab=85.87  E-value=2.9  Score=39.69  Aligned_cols=116  Identities=8%  Similarity=0.051  Sum_probs=0.0

Q ss_pred             CHHHHHHHHHHHHHHcCCCCCCCeEEEEecCCchHHHHHHHHHHHHHhccccCC-cceeeCHHHhccCCchHHHHHH
Q lull1           270 SSFLWQRGRKFLQKHLNASNPTEPATIIFTAAREGRETLKCLSHHVADAYTSSQKV-SPIQIDGAGRTWQDSDTVKLLVD  348 (470)
Q Consensus       270 se~LWk~lr~~LekhLn~s~p~ePaViLfta~~~Ae~Tl~CLa~~LA~aySs~~~~s~I~IdG~~~a~~DSD~vKl~lD  348 (470)
                      ++++.+.++..+..      .+-|.+||.+..-.++.+   ||..||......... ....+++.+....+.........
T Consensus        30 ~~~~~~~l~~~l~~------~~~~~lLl~Gp~G~GKtt---la~~la~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  100 (327)
T 1iqp_A           30 QEHIVKRLKHYVKT------GSMPHLLFAGPPGVGKTT---AALALARELFGENWRHNFLELNASDERGINVIREKVKEF  100 (327)
T ss_dssp             CHHHHHHHHHHHH------TCCCEEEEESCTTSSHHH---HHHHHHHHHHGGGHHHHEEEEETTCHHHHTTHHHHHHH
T ss_pred             cHHHHHHHHHHHc------CCCCeEEEECcCCCCHHH---HHHHHHHHhhhhcccccceeeeeccCCCCChHHHHHHHHH


Q ss_pred             HHHHHHHhcCCcEEEEeehhhCChHHHHHHHHhcCCCCcccccceEEEEE
Q lull1           349 LELSYGFENGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALVLT  397 (470)
Q Consensus       349 e~L~s~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~LT  397 (470)
                      ......+....++.||-++|.++.++..+|-++.+.   ..+++.+||+
T Consensus       101 ~~~~~~~~~~kviiide~d~l~~~~~~Ll~~lE~~~~~~~~~Il~  146 (327)
T 1iqp_A          101 ARTKPIGGASFKIIFLDEADALTQDAQQALRRTMEM---FSSNVRFILS  146 (327)
T ss_dssp             HHSCCGGGCSCEEEEEETGGGSCHHHHHHHHHHHH---TTTTEEEEEE
T ss_pred             HHhhhccCCCceEEEEechhhCCHHHHHHHHHHHc---CCCCeEEEEe
```

No 9 PDB NCBI PubMed

```
>4lj9_A Chaperone protein CLPB; AAA+ protein, nucleotide binding domain, molecular chaperone disaggregase; HET:
ACP; 1.70A {Thermus thermophilus} PDB:  4lj8 _A*  4lja _A*  4lj6 _A*  4lj4 _A*  4lj5 _A*  4lj7 _A*  4fd2 _A*  4fct _A*  4fc
 4fcv _A*
Probab=79.96  E-value=11  Score=37.06  Aligned_cols=186  Identities=15%  Similarity=0.174  Sum_probs=0.0

Q ss_pred             hhHHHHHHHHHHHHHhCCCCHHHHHHHHHHHHHhCCCCCCCCeEEEEecCCch---HHHHHHHHHHHHHhccccCCc
Q lull1           250 PALEAFLAQFSQLEDKFPGQSSFLWQRGRKFLQKHLNASNPTEPATIIFTAAREG---RETLKCLSHHVADAYTSSQKVS  326 (470)
Q Consensus       250 ~a~e~f~~qf~~LK~kFPsQse~LWk~lr~~LekhLn~s~p~ePaViLfta~~~A---e~Tl~CLa~~LA~aySs~~~~s  326 (470)
                      ...+.+.+~~+.|+++.=+|+.-+=+.....-.....-.++..|.-.+|+++.++   ..++++|+..|-..-..+.
T Consensus        29 ~~~~~l~~l~~~L~~~IiGQ~~ai~~i~~~l~~~~~~l~~~~~p~~~~l~~GpsG~GKT~la~~la~~L~~~~~~~~~~  105 (339)
T 4lj9_A           29 GEREKLLRLEEELHKRVVGQDEAIRAVADAIRRARAGLKDPNRPIGSFLFLGPTGVGKTELAKTLAATLFDTEEAMI---  105 (339)
T ss_dssp             HHHHHHSCHHHHHHTTCCSCHHHHHHHHHHHHHHTTCSCTTSCSEEEEEESCTTSSHHHHHHHHHHHHSSGGGEE---
T ss_pred             HHHHHHHHHHHHhCCeeeCHHHHHHHHHHHHHHHhCCCCCCCCCceEEEEcCCCCCHHHHHHHHHHHHcCCcchhc---


Q ss_pred             ceeeChHHhccCCchHHHH-------------HHHHHHHHHhcCCcCEEEEeehhhCChHHHHHHHHhcCC--------C
Q lull1           327 PIQIDGAGRTWQDSDTVKL-------------LVDLELSYGFENGQKAAVVHHFESFPAGSTLIFYKYCDH--------E  385 (470)
Q Consensus       327 ~I~IdG~~~a~~DSD~vKl-------------~lDe~L~s~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDh--------E  385 (470)
                        .+|...+....+...-.                .|-+.++.   +...+.++=+||..++.....|..+.|.        .
T Consensus       106 ~~~id~s~~~~~~~~~l~Gs~~GYvG~~~~~L~~~l~~~~~~~VIllDEieK~~~~v~~~Ll~il~~G~~~d~~g~  180 (339)
T 4lj9_A          106 ~~QIDMTEYMEKHAVSRLIGAPPGYVGYEEGGQLTEAVRR---RPYSVILFDEIEKAHPDVFNILLQILDDGRLTDSHGR  180 (339)
T ss_dssp             --EEEGGGCCSTTHHHHHCCCTTSTTTTTCCHHHHHHHH---CSSCEEEEESGGGSCHHHHHHHHHHHSEEECTTSC
T ss_pred             --eeccccccchHHHHhCCCCCCCcCcCcCCHHHHHHHh---CCCeEEEEechhCCHHHHHHHHHHcCcEEECCCCC


Q ss_pred             CccccceEEEEEEecccccccccccHHHHHHHHHHHHHHHhccccCccccccCChhhcchHHHHHhcceE
Q lull1           386 NAAFKDVALVLTVLLEEETLEASVGPRETEEKVRDLLWAKFTNSDTPTSFNHMDSDKLSGLWSRISHLVL  455 (470)
Q Consensus       386 NA~fKdvaL~LTV~leeetL~~s~s~kevEEkV~d~Lw~k~~~s~~~~s~n~Md~DkL~pL~SRIS~~VL  455 (470)
                      .--+.++++|+|--+-.+.+.............+...            ..+...-=..|+.||...|.
T Consensus       181 ~i~~~n~iii~tsn~g~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~f~~e~l~R~~~ii~  238 (339)
T 4lj9_A          181 TVDFRNTVIILTSNLGSPLILEGLQKGWPYERIRDEVF-------------KVLQQHFRPEFLNRLDEIVV  238 (339)
T ss_dssp             EEECTTCEEEEECCTTHHHHHHHHHTCCHHHHHHHH-------------HHHHHCCHHHHTTSSEEEE
T ss_pred             EecCcccEEeccccccHHHHHhhcccchhhHHHHH-------------HHHHHCCHHHHccCCEEEE
```

No 10 SCOP PDB NCBI PubMed

```
>1r6b_X CLPA protein; AAA+, N-terminal domain, CLPS, crystal, binding mechanism, hydrolase; HET: ADP; 2.25A
{Escherichia coli} SCOP: a.174.1.1 c.37.1.20 c.37.1.20 PDB:  1ksf _X*
Probab=79.68  E-value=38  Score=37.81  Aligned_cols=157  Identities=17%  Similarity=0.169  Sum_probs=0.0

Q ss_pred             HHHHHHHhhhCCccccccccchhHHHHHHHHHHHHHhcCCCCHHHHHHHHHHHHHcCCCCCCCe-EEEEecCCch---HH
Q lull1           231 VASSVNSYYSSPAQQVPKNPALEAFLAQFSQLEDKFPGQSSFLWQRGRKFLQKHLNASNPTEPA-TIIFTAAREG---RE  306 (470)
Q Consensus       231 ~l~~i~~~~ssPa~~~~~~~a~e~f~~qf~~LK~kFPsQse~LWk~lr~~LekhLn~s~p~ePa~ViLfta~~~A---e~  306 (470)
                      +.-.|...-..|...+. ....+.+.+~~+.|+.+.-+|++-+=...+.....-..=.++..|. +|||+ ++++   .+
T Consensus       426 i~~vv~~~tgip~~~~~~~~~~l~~L~~~l~~rviGQ~~Av~~v~~al~~~~gl~~~~rP~gsfLf~-GPtGvGKTe  503 (758)
T 1r6b_X          426 IESVVARIARIPEKSVS-QSDRDTLKNLGDRLKMLVFGQDKAIEALTEAIKMARAGLGHEHKPVGSFLFA-GPTGVGKTE  503 (758)
T ss_dssp             HHHHHHHSCCCCCCSS-SSHHHHHHHHHHHTTTSCSCHHHHHHHHHHHHHTTCSCTTSCSEEEEEE-CSTTSSHHH
T ss_pred             HHHHHHHHhCCCccccc-ccHHHHHHHHHHHHhhhhcCcHHHHHHHHHHHHHHhcCCCCCCCCceEEEEE-eCCcccHHH


Q ss_pred             HHHHHHHHHHHHhcccCCcceeeeChHHh---------ccCCchHHHHHHHHHHHHhcCCcEEE-EeehhhCChHHHH
Q lull1           307 TLKCLSHHVADAYTSSQKVSPIQIDGAGR---------TWQDSDTVKLLVDLELSYGFENGQKAAV-VHHFESFPAGSTL  376 (470)
Q Consensus       307 Tl~CLa~~LA~aySs~~~~s~I~IdG~~~~~~~~~~~a~~DSD~vKl~lDe~L~s~Fe~g~kaAV~V~~LE~LPP~AaL  376 (470)
                      +++.||+.+-        ...|.+|-..|          ..-.+.++...=--+|-+.......+.| +=.+|.--|..-.
T Consensus       504 lAk~LA~~lf---------~~liriDMsEy~e~~svsrLiGsppGyvG~~e~g~Lte~Vr~~P~sVvLlDEIEKAhp~V~~  575 (758)
T 1r6b_X          504 VTVQLSKALG--------IELLRFDMSEYMERHTVSRLIGAPPGYVGFDQGGLLTDAVIKHPHAVLLLDEIEKAHPDVFN  575 (758)
T ss_dssp             HHHHHHHHHT--------CEEEEEEGGGCSSSSCCSSSCCCCSCSHHHHHTTHHHHHHHHCSSEEEEEETGGGSCHHHHH
T ss_pred             HHHHHHHHh--------hhhEEEecccccccchhhHHHHcCCCCCCCCCCCCCCcchhhhcCCCeEEEEecchhhcCHHHHH


Q ss_pred             HHHHhcCC--------CCccccccEEEEE
Q lull1           377 IFYKYCDH--------ENAAFKDVALVLT  397 (470)
Q Consensus       377 IFH~YCDh--------ENA~fKdvaL~LT  397 (470)
                      +|..+.|.        ...-|+|++||+|
T Consensus       576 lllqildeG~ltD~~Gr~vdF~ntIiImT  604 (758)
```

```
T 1r6b_X            576 ILLQVMDNGTLTDNNGRKADFRNVVLVMT  604 (758)
T ss_dssp               HHHHHHHHSEEEETTTEEEECTTEEEEEE
T ss_pred               HHHHHhccCeEECCCCCEEeccccEEEec
```

No 11

>1njg_A DNA polymerase III subunit gamma; rossman-like fold, AAA+ ATPase domains, sensor 1, sensor 2, transferase; HET: DNA; 2.20A {Escherichia coli} SCOP: c.37.1.20 PDB: 1njf _A*
Probab=78.23 E-value=13 Score=34.39 Aligned_cols=117 Identities=15% Similarity=0.162 Sum_probs=0.0

```
Q ss_pred               CHHHHHHHHHHHHHHhcCCCCCCCeEEEEecCCc-hHHHH-HHHHHHHH----------------HHhccccCCcceeeC
Q lull1             270 SSFLWQRGRKFLQKHLNASNPTEPATIIFTAARE-GRETL-KCLSHHVA----------------DAYTSSQKVSPIQID  331 (470)
Q Consensus         270 se~LWk~lr~~LekhLn~s~p~ePaViLfta~~~-Ae~Tl-~CLa~~LA----------------~aySs~~~~s~I~Id  331 (470)
                        ++++=+.++..+..      .+-|-.+||....+ ++.++ ++++..+.                ...........+.++
T Consensus          28 ~~~~~~~L~~~~~~------~~~~~~lLl~Gp~G~GKttla~~~~~~l~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~e~~  101 (250)
T 1njg_A            28 QEHVLTALANGLSL------GRIHHAYLFSGTRGVGKTSIARLLAKGLNCETGITATPCGVCDNCREIEQGRFVDLIEID  101 (250)
T ss_dssp               CHHHHHHHHHHHHH------TCCCSEEEEECSTTSCHHHHHHHHHHHHHCTTCSCSSCCSCSHHHHHHHTTCCSSEEEEE
T ss_pred               cHHHHHHHHHHHHc------CCCCceEEEECCCCCcHHHHHHHHHHHhCCccccCCcccccHHHHHHHcCCCCceEEec


Q ss_pred               hHHhccCCchHHHHHHHHHHHHHHhhcCCcEEEEeehhhCChHHHHHHHHHhcCCCCccccceEEEEE
Q lull1             332 GAGRTWQDSDTVKLLVDLELSYGFENGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALVLT  397 (470)
Q Consensus         332 G~~~a~~DSD~vKl~lDe~L~s~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~LT  397 (470)
                        +...   ...|.++-.+..-....+.++.++.||-+++.++.++..+|.++++   -..+++.+||+
T Consensus         102 ~~~~--~~~~~ir~li~~~~~~~~~~~~~~kviIdeid~l~~~a~~~Ll~~le---~~~~~~~~~~Il~  162 (250)
T 1njg_A           102 AASR--TKVEDTRDLLDNVQYAPARGRFKVYLIDEVHMLSRHSFNALLKTLE---EPPEHVKFLLA  162 (250)
T ss_dssp               TTCG--GGHHHHHHHHHSCCCSCSSSSSEEEEEETGGGSCHHHHHHHHHHHH---SCCTTEEEEEE
T ss_pred               chhc--CCHHHHHHHHHHHhhccccCCCEEEEEeCcCcCCHHHHHHHHHHHH---hCCCCEEEEEe
```

No 12

>2m8r_A Syntaxin-1A; snare, prefusion, membrane protein; NMR {Rattus norvegicus} PDB: 3hd7 _B* 3ipd _B
Probab=72.72 E-value=10 Score=31.62 Aligned_cols=52 Identities=17% Similarity=0.194 Sum_probs=0.0

```
Q ss_pred               chHhhhhhhhhhHHHHHHHHHHHHHHHH-----------HHHHHHHHHHHHHHHHHHHHHHhhhh
Q lull1             188 SHPQQTQKLEEIKENAQDTMRQINKKG-----------FWSYGPVILVVLVVAVVASSVNSYY  239 (470)
Q Consensus         188 ~~~~~~~~~~~~~~~~~~~~~~~~~~k~-----------~~~y~~~~i~~li~iv~l~~i~~~~~  239 (470)
                        .+..-....+.|-+.|.+-+.+-++..           +|.|+.++++++++++++++.++|
T Consensus          46 ~Qge~id~Ie~nv~~a~~~v~~g~~eL~kA~~~qk~~rk~~~~~~~~~~~~i~~l~l~~~i~~~f  108 (109)
T 2m8r_A            46 SQGEMIDRIEYNVEHAVDYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIIIASTIGGIF  108 (109)
T ss_dssp               TTHHHHHHHHHHHHHHHHHHHHHHHHHHHHTCSCCSSTTHHHHHHHHHHHHHHHHHHHHHHHHHHHHTSC
T ss_pred               HhhHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHhHHHHHHHHHHHHHHHHHHHHHHHHHc
```

No 13

>3u61_B DNA polymerase accessory protein 44; AAA+, ATP hydrolase, clamp loader, sliding clamp, primer-TEM DNA, DNA binding protein-DNA complex; HET: DNA ADP 08T; 3.20A {Enterobacteria phage T4} PDB: 3u5z _B* 3u60 _B*
Probab=66.09 E-value=27 Score=32.82 Aligned_cols=104 Identities=18% Similarity=0.249 Sum_probs=0.0

```
Q ss_pred               CHHHHHHHHHHHHHHhcCCCCCCCeEEEEec-CCchHHHH-HHHHHHHHHhccccCCcceeeChHHhccCCchHHHHHHH
Q lull1             270 SSFLWQRGRKFLQKHLNASNPTEPATIIFTA-AREGRETL-KCLSHHVADAYTSSQKVSPIQIDGAGRTWQDSDTVKLLV  347 (470)
Q Consensus         270 se~LWk~lr~~LekhLn~s~p~ePaViLfta-~~~Ae~Tl-~CLa~~LA~aySs~~~~s~I~IdG~~~a~~DSD~vKl~l  347 (470)
                        .+.+++.++..+.      ..+-|.++||..  .-.++.++ ++|+..+        +...+.+++.+..         .-.+
T Consensus          31 ~~~~~~~l~~~l~------~~~~~~~~~~L~~G~~G~GKT~la~~la~~l--------~~~~~~~~i~~~~~~~~~~~~~~~i   89 (324)
T 3u61_B            31 PAFDKETFKSITS------KGKIPHIILHSPSPGTGKTTVAKALCHDV--------NADMMFVNGSDCK-------IDFV   89 (324)
T ss_dssp               CHHHHHHHHHHHH------TTCCCSEEEECSSTTSSHHHHHHHHHHHHT--------TEEEEEEETTTCC-------HHHH
T ss_pred               cHHHHHHHHHHHH------cCCCCeEEEeeCcCCCCHHHHHHHHHHHHh--------CCCEEEEcccccC-------HHHH


Q ss_pred               HHHHHHHhhc-----CCcEEEEeehhhCC-hHHHHHHHHhcCCCCccccceEEEEE
Q lull1             348 DLELSYGFEN-----GQKAAVVHHFESFP-AGSTLIFYKYCDHENAAFKDVALVLT  397 (470)
Q Consensus         348 De~L~s~Fe~-----g~kaAVV~~LE~LP-P~AaLIFH~YCDhENA~fKdvaL~LT  397 (470)
                        .+.+......     +.++.+|-+++.++  ..+...|+++-+...   .++.+|+|
T Consensus          90 ~~~~~~~~~~~~~~~~~~~~vliiDEi~~l~~~~~~~~~L~~~le~~~~~~~~~~~iI~~  142 (324)
T 3u61_B            90 RGPLTNFASAASFDGRQKVIVIDEFDRSGLAESQRHLRSFMEAYS---SNCSIIIT  142 (324)
T ss_dssp               HTHHHHHHBCCCSSCEEEEEEESCCCGGGHHHHHHHHHHHHHHHG---GGCEEEEE
T ss_pred               HHHHHHHHhhcccCCCCeEEEEECCccccCHHHHHHHHHHHHHhCC---CCcEEEEE
```

No 14

>1sxj_C Activator 1 40 kDa subunit; clamp loader, processivity clamp, DNA sliding clamp, AAA+ at polymerase, DNA-binding protein; HET: AGS ADP; 2.85A {Saccharomyces cerevisiae} SCOP: a.80.1.1 c.37.1.20
Probab=64.43 E-value=15 Score=35.30 Aligned_cols=116 Identities=10% Similarity=0.158 Sum_probs=0.0

```
Q ss_pred               CHHHHHHHHHHHHHHhcCCCCCCCeEEEEecCCchHHHH-HHHHHHHHHhccccCCcceeeChHHhccCCchHHHHHHHH
Q lull1             270 SSFLWQRGRKFLQKHLNASNPTEPATIIFTAAREGRETL-KCLSHHVADAYTSSQKVSPIQIDGAGRTWQDSDTVKLLVD  348 (470)
Q Consensus         270 se~LWk~lr~~LekhLn~s~p~ePaViLfta~~~Ae~Tl-~CLa~~LA~aySs~~~~s~I~IdG~~~a~~DSD~vKl~lD  348 (470)
                        ++++.+.++..+.+      .+-|..||.+..-.++.|+ ++|+..+   +........+..++.+....+........-
T Consensus          30 ~~~~~~~L~~~i~~------~~~~~~lLl~Gp~G~GKTtla~~la~~~~~---~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  100 (340)
T 1sxj_C            30 QNEVITTVRKFVDE------GKLPHLLFYGPPGTGKTSTIVALAREI---YGKNYSNMVLELNASDDRGIDVVRNQIKDF  100 (340)
T ss_dssp               CHHHHHHHHHHHHT------TCCCCEEEECSSSSHHHHHHHHHHH---HTTSHHHHEEECTTSCCSHHHHHTHHHHH
T ss_pred               CHHHHHHHHHHHHC------CCCCEEEEECcCCCCHHHHHHHHHHhh---ccCCccccceeeecccCCCChhHHHHHHHHHHH


Q ss_pred               HHHHHHhhcCCcEEEEeehhhCChHHHHHHHHhcCCCCccccceEEEEE
Q lull1             349 LELSYGFENGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALVLT  397 (470)
Q Consensus         349 e~L~s~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~LT  397 (470)
                        ........++.++.+|..++.+.+.+..+|.++-+..   -+.+.++||
T Consensus         101 ~~~~~~~~~~~~kiiiDe~d~l~~~~q~aLl~~le~~~---~~~~~~~il~  146 (340)
T 1sxj_C           101 ASTRQIFSKGFKLIILDEADAMTNAAQNALRRVIERY---TKNTRFCVL  146 (340)
T ss_dssp               HHBCCSSSCSCEEEEETTGGGSCHHHHHHHHHHHHHT---TTTEEEEEE
T ss_pred               HHhhhccCCCeEEEEEeccccCCHHHHHHHHHHHHhcC---CCCeEEEee
```

No 15

>2m8r_A Syntaxin-1A; snare, prefusion, membrane protein; NMR {Rattus norvegicus} PDB: 3hd7 _B* 3ipd _B
Probab=62.95 E-value=3.3 Score=34.58 Aligned_cols=47 Identities=6% Similarity=0.061 Sum_probs=0.0

```
Q ss_pred               hhhhhhhhhhHHHHHHHHHHHHHHHHHHHHHHHHHHHHHhh
Q lull1           191 QQTQKLEEIKENAQDTMRQINKKGFWSYGPVILVVLVVAVVASSVNS  237 (470)
Q Consensus       191 ~~~~~~~~~~~~~~~~~~~~~~k~~~~~y~~~~~i~~li~iv~l~~i~~  237 (470)
                        ..+++-.+.-+.|...-|+..|+.||.++.+++.++++++++.+++|
T Consensus        63 ~~v~~g~~eL~kA~~~qk~~rk~~~~~~~~~~~~i~~l~l~~~i~~~fg  109 (109)
T 2m8r_A           63 DYVERAVSDTKKAVKYQSKARRKKIMIIICCVILGIIIASTIGGIFG  109 (109)
T ss_dssp              HHHHHHHHHHTCSCCSSTTHHHHHHHHHHHHHHHHHHHHHHHHHHTSCC
T ss_pred              HHHHHHHHHHHHHHHHHHHHHhhHHHHHHHHHHHHHHHHHHHHHHHHcC
```

No 16

>1gvn_B Zeta; postsegregational killing system, plasmid; 1.95A {Streptococcus pyogenes} SCOP: c.37.1.21 PDB: 3q8x _B*
Probab=61.15 E-value=1.1e+02 Score=28.23 Aligned_cols=118 Identities=12% Similarity=0.078 Sum_probs=0.0

```
Q ss_pred               HHHHHHHHHHHHHHhcCCCCC-CCeEEEEecCCChHHHHHHHHHHHHHHHhccccCCcceeeChHHhccCCch--------
Q lull1           271 SFLWQRGRKFLQKHLNASNPT-EPATIIFTAAREGRETLKCLSHHVADAYTSSQKVSPIQIDGAGRTWQDSD--------  341 (470)
Q Consensus       271 e~LWk~lr~~LekhLn~s~p~-ePaViLfta~~~Ae~Tl~CLa~~LA~aySs~~~~s~I~IdG~~~a~~DSD--------  341 (470)
                        +++=+++...+...+..+.+. .|-.|||....++=.|+  |+..||+.+    +...+.||+.++......
T Consensus        10 ~e~~~~~~~~~~~~~~~~~~~~~~P~~ill~GppGsGKT~--la~~la~~~----~~~~v~i~~d~~~~~~~~~~~~~~~~~   83 (287)
T 1gvn_B          10 KQFENRLNDNLEELIQGKKAVESPTAFLLGGQPGSGKTS--LRSAIFEET----QGNVIVIDNDTFKQQHPNFDELVKLY   83 (287)
T ss_dssp              HHHHHHHHHHHHHHHTTCCCCSSCEEEEEECCTTSCTHH--HHHHHHHHT----TTCCEEECTHHHHTTSTTHHHHHHHH
T ss_pred              HHHHHHHHHHHHHHhcCCCCCCCCEEEEEeCCCCcCHHH--HHHHHHHhc----CCCceeecHHHHHHhccchhHHHHhh

Q ss_pred               ----------HHHHHHHHHHHHHhcCCcEEEEeehhhCChHHHHHHHHHhcCCCCccccceEEEEEE
Q lull1           342 ----------TVKLLVDLELSYGFENGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALVLTV  398 (470)
Q Consensus       342 ----------~vKl~lDe~L~s~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~LTV  398 (470)
                                  .....++..+...+.++..  ++.+-..--+...+-+-..+...+..+  +++++++
T Consensus        84 ~~~~~~~~~~~~~~~~~~~~~a~~~~~~~--~~~~~~~~~~~~~~~~~~~~~~~~~~~gy~v--~~v~~~a~  146 (287)
T 1gvn_B          84 EKDVVKHVTPYSNRMTEAIISRLSDQGYN--LVIEGTGRTTDVPIQTATMLQAKGYET--KMYVMAV  146 (287)
T ss_dssp              GGGCHHHHHHHHHHHHHHHHHHHHHHHTCC--EEECCCCCCSHHHHHHHHHHHTTTCEE--EEEEECC
T ss_pred              hHHHHHHhhhcccchhHHHHHHHHHHhCCCC--CCCCCcccHHHHHHHHHHHHHHhCCCeE--EEEEEEC
```

No 17

>2chg_A Replication factor C small subunit; DNA-binding protein, DNA replication, clamp loader, AAA+ ATPase, ATP-binding, nucleotide-binding; HET: ANP; 2.1A {Archaeoglobus fulgidus}
Probab=52.32 E-value=62 Score=28.59 Aligned_cols=116 Identities=10% Similarity=0.073 Sum_probs=0.0

```
Q ss_pred               CHHHHHHHHHHHHHHhcCCCCCCCeEEEEecCCChHHHHHHHHHHHHHHHhcc-ccCCcceeeChHHhccCCchHHHHHHH
Q lull1           270 SSFLWQRGRKFLQKHLNASNPTEPATIIFTAAREGRETLKCLSHHVADAYTS-SQKVSPIQIDGAGRTWQDSDTVKLLVD  348 (470)
Q Consensus       270 se~LWk~lr~~LekhLn~s~p~ePaViLfta~~~Ae~Tl~CLa~~LA~aySs-~~~~~s~I~IdG~~~a~~DSD~vKl~lD  348 (470)
                        ++++=+.++..+++       .+-|.+||.+..-.++.|+  +..++.....  ..+...+.++..+....+.-......-.
T Consensus        22 ~~~~~~~~l~~~i~~------~~~~~~lll~Gp~G~GKTt~---a~~i~k~l~~~~~~~~~~~~~~~~s~~~~~~~~~~~~~~   92 (226)
T 2chg_A          22 QDEVIQRLKGYVER------KNIPHLLFSGPPGTGKTAT---AIALARDLFGENWRDNFIEMNASDERGIDVVRHKIKEF   92 (226)
T ss_dssp              CHHHHHHHHHHHHT------TCCCCEEEECSTTSSHHHH---HHHHHHHHHGGGGGGEEEEETTCTTCHHHHHHHHHHHH
T ss_pred              hHHHHHHHHHHHHHC------CCCCeEEEECCCCCCHHHH---HHHHHHHHhccccccccceeecccCCcHHHHHHHHHHHH

Q ss_pred               HHHHHHhhcCCcEEEEeehhhCChHHHHHHHHHhcCCCCcccccceEEEEE
Q lull1           349 LELSYGFENGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALVLT   397 (470)
Q Consensus       349 e~L~s~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~LT   397 (470)
                        ........+..++.+|.+++.++.++...|.++-+..+   +...+|++
T Consensus        93 ~~~~~~~~~~~~~~~~iiide~d~l~~~~~~~~~~ll~~le~~~~~~~~~~~~i~~  138 (226)
T 2chg_A          93 ARTAPIGGAPFKIIFLDEADALTADAQAALRRTMEMYS---KSCRFILS  138 (226)
T ss_dssp              HTSCCSTTCSCEEEEEETGGGSCHHHHHHHHHHHHHTT---TTEEEEEE
T ss_pred              HhhhhhcCCCceeEeehhhhhcCHHHHHHHHhhhhccCC---cceEEEec
```

No 18

>1sxj_E Activator 1 40 kDa subunit; clamp loader, processivity clamp, DNA sliding clamp, AAA+ at polymerase, DNA-binding protein; HET: AGS ADP; 2.85A {Saccharomyces cerevisiae} SCOP: a.80.1.1 c.37.1.20
Probab=51.68 E-value=1.3e+02 Score=28.29 Aligned_cols=119 Identities=12% Similarity=0.188 Sum_probs=0.0

```
Q ss_pred               HHHHHHHHHHhcCCCCCCCeEEEEecCCChHHHH-HHHHHHH---------------------HHHhccccCCcceeeCh
Q lull1           275 QRGRKFLQKHLNASNPTEPATIIFTAAREGRETL-KCLSHHV---------------------ADAYTSSQKVSPIQIDG  332 (470)
Q Consensus       275 k~lr~~LekhLn~s~p~ePaViLfta~~~Ae~Tl~-~CLa~~L---------------------A~aySs~~~~s~I~IdG  332 (470)
                        +.....|++.+..... -|+.||.+..-.++.|+ ++||..+                     -.......+...+.++.
T Consensus        20 ~~~~~~~L~~~~~~~~~~~~~~p~lLl~Gp~G~GKTt~a~~la~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   98 (354)
T 1sxj_E          20 EELTNFLKSLSDQPRD-LPHLLLYGPNGTGKKTRCMALLESIFGPGVYRLKIDVRQFVTASNRKLELNVVSSPYHLEITP   98 (354)
T ss_dssp              HHHHHHHHTTTTCTTC-CCCEEEECSTTSSHHHHHHTHHHHHSCTTCCC-----------------CCEECSSEEECC
T ss_pred              HHHHHHHHHHhCCCC-CCeEEEECCCCcCHHHHHHHHHHHHhcCCccccccccccccccccchhhhccccCCCceeeec

Q ss_pred               HHhccCCchHHHHHHHHHH----------HHHHHhcCCcEEEEeehhhCChHHHHHHHHHhcCCCCcccccceEEEEE
Q lull1           333 AGRTWQDSDTVKLLVDLE----------LSYGFENGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALVLT   397 (470)
Q Consensus       333 ~~~a~~DSD~vKl~lDe~----------L~s~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~LT   397 (470)
                        .+....+...++-.+...            ....+....++.|+.+++.+...+....|.+.-+...   +++.++||
T Consensus        99 ~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~kiiide~d~l~~~~~~~~l~~~le~~~~~~~~~~~~~il~  170 (354)
T 1sxj_E          99 SDMGNNDRIVIQELLKEVAQMEQVDFQDSKDGLAHRYKCVIINEANSLTKDAQAALRRTMEKYS---KNIRLIMV  170 (354)
T ss_dssp              C----CCHHHHHHHHHHTTTTC------------CCEEEEEECTTSSCHHHHHHHHHHHHHST---TTEEEEEE
T ss_pred              cccccCCCccceeehhhhhhHHhhhhhhcccccCCCCceEEEeecccccchHhhHHHHHHHHHhcc---cceEEEeec
```

No 19

>3t15_A Ribulose bisphosphate carboxylase/oxygenase activ chloroplastic; photosynthesis, rubisco activase, AAA+ protein; 2.95A {Nicotiana tabacum} PDB: 3zw6 _A
Probab=49.14 E-value=1.5e+02 Score=28.05 Aligned_cols=117 Identities=9% Similarity=0.090 Sum_probs=0.0

```
Q ss_pred            HHHHHHHHHHHcCCCCCCCCeEEEEecCCchHHHHHHHHHHHHHHhcccccCCcceeeChHHhccCCchHHHHHHHHHHHH
Q lull1          275 QRGRKFLQKHLNASNPTEPATIIFTAAREGRETLKCLSHHVADAYTSSQKVSPIQIDGAGRTWQDSDTVKLLVDLELSYG  354 (470)
Q Consensus      275 k~lr~~LekhLn~s~p~ePaViLfta~~~Ae~Tl~CLa~~LA~aySs~~~~s~I~IdG~~~a~~DSD~vKl~lDe~L~s~  354 (470)
                     +.....+...+.....+.|..+||....+.=.|+  |+..||...    +...+.+++.++...-.......+.+.++.+
T Consensus       18 ~~~~~~~k~~l~~~~~~~p~~lLl~GppGtGKT~~~la~aiA~~l~~~~~~~~i~v~~~~l~~~~~g~~~~~i~~~f~~a   91 (293)
T 3t15_A          18 KLVVHITKNFLKLPNIKVPLILGIWGGKGQGKSF~~QCELVFRKM~~~~GINPIMMSAGELESGNAGEPAKLIRQRYREA   91 (293)
T ss_dssp            HHHHHHHHTTSCCTTCCCCSEEEEEEECTTSCHHH~~HHHHHHHHH~~~~TCCCEEEEEHHHHHCC~~~HHHHHHHHHHHH
T ss_pred            HHHHHHHHHHHcCCCCCCCeEEEEECCCCCCHHH~~HHHHHHHHh~~~~CCCEEEEeHHHhhhccCchhHHHHHHHHHHH


Q ss_pred            h~~~~hcCCcEEEEeehhhCChHHH~~~~~~~~~~~~~HHHHHhCCCC~~~~~~~~~~cccccEEEEE
Q lull1          355 F~~~~ENGQKAAVVHHFESFPAGST~~~~~~~~~~~~~LIFYKYCDHEN~~~~~~~~~~AAFKDVALVLT  397 (470)
Q Consensus      355 F~~~~e~g~kaAVV~~LE~LPP~Aa~~~~~~~~~~~~~LIFH~YCDhEN~~~~~~~~~~A~fKdvaL~LT  397 (470)
                     .    .....+.++=++|.+-+...              -.|..+.|...          ....++++|.|
T Consensus       92 ~~~~~~~~~~vl~iDEiD~~~~~~~~~~~~~~~~~~v~~~Ll~~ld~~~~~~~~~~~~~~~~~~v~vI~t  161 (293)
T 3t15_A          92 AEIIRKGNMCCLFINDLDAGAGRMGGTTQYTVNNQMVNATLMNIADNPTNVQLPGMYNKQENARVPIIVT  161 (293)
T ss_dssp            HHHHTTSSCCCEEEECCC~~~~~~~~~~~~~~CHHHHHHHHHHHHCCC~~~~~~~~~~~~CCCCCCEEEE
T ss_pred            HHHHhCCCeEEEEehhhhCCCCCCCccccchHHHHHHHHHHHhcccccccccccccccCCCCEEEEe
```

No 20

>2chq_A Replication factor C small subunit; DNA-binding protein, DNA replication, clamp loader, AAA+ ATP ATP-binding, nucleotide-binding; HET: ANP; 3.5A {Archaeoglobus fulgidus} PDB: 2chv _A
Probab=44.11 E-value=54 Score=30.42 Aligned_cols=115 Identities=10% Similarity=0.047 Sum_probs=0.0

```
Q ss_pred            HHHHHHHHHHHcCCCCCCCeEEEEecCCchHHHHHHHHHHHHHHhcc-ccCCcceeeChHHhccCCchHHHHHHHHHHHH
Q lull1          275 QRGRKFLQKHLNASNPTEPATIIFTAAREGRETLKCLSHHVADAYTS-SQKVSPIQIDGAGRTWQDSDTVKLLVDLELSY  353 (470)
Q Consensus      275 k~lr~~LekhLn~s~p~ePaViLfta~~~Ae~Tl~CLa~~LA~aySs-~~~~s~I~IdG~~~a~~DSD~vKl~lDe~L~s  353 (470)
                     +.....|...+.......   +||....+-=.|  .||..||+..-. ........+++.+....+.-......-.....
T Consensus       23 ~~~~~L~~~~~~~~~~~~lL~~Gp~G~GKt~~tla~~lak~l~~~~~~~~~~~~~~s~~~~~~~~~~~~~~~~~~~~~  97 (319)
T 2chq_A          23 DEVIQRLKGYVERKNIPH~~~LLFSGPPGTGKT~~ATAIALARDLFGENWRDNFIEMNASDERGIDVVRHKIKEFARTAP  97 (319)
T ss_dssp            HHHHHHHHTTTTTTCCCC~~~EEEESSSSSSHH~~HHHHHHHHHHTTCHHHHCEEEETTSTTCTTTSSHHHHHHHSCC
T ss_pred            HHHHHHHHHHHCCCCCE~~~EEEECCCCCCHH~~HHHHHHHHHcccccccccceeeccccCCcHHHHHHHHHHHHHhh


Q ss_pred            HhhcCCcEEEEeehhhCChHHHHHHHHHcCCCCcccccceEEEEE
Q lull1          354 GFENGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALVLT  397 (470)
Q Consensus      354 ~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~LT  397 (470)
                     ...++.++.+|.+++.+...+..+|.++++...   +.+.+||+
T Consensus       98 ~~~~~~~viiide~d~l~~~~~~l~~~~e~~~~~~~~~~il~  138 (319)
T 2chq_A          98 IGGAPFKIIFLDEADALTADAQAALRRTMEMYS~~~KSCRFILS  138 (319)
T ss_dssp            SSSCCCEEEEEETGGGSCHHHHHTTGGGTSSSS~~~SSEEEEEE
T ss_pred            ccCCceEEEEEecccccccHHHHHHHHHHHhCC~~~cccccecc
```

No 21

>3zh9_B Delta; hydrolase, replication; 2.10A {Bacillus subtilis}
Probab=43.89 E-value=42 Score=32.27 Aligned_cols=106 Identities=9% Similarity=0.013 Sum_probs=0.0

```
Q ss_pred            HHHHHHHcCCCCCCCCeEEEEecCCchHHHHHHHHHHHH-HHhcccccC-cceeeChHHhccCCchHHHHHHHHHHHHHh
Q lull1          279 KFLQKHLNASNPTEPATIIFTAAREGRETLKCLSHHVA-DAYTSSQKV-SPIQIDGAGRTWQDSDTVKLLVDLELSYGFE  356 (470)
Q Consensus      279 ~~LekhLn~s~p~ePaViLfta~~~Ae~Tl~CLa~~LA~aySs~~~~s~I~IdG~~~a~~DSD~vKl~lDe~L~s~Fe  356 (470)
                     .-|.+++++  .+-+-++||.....  -..+-.+..|+ .+..... ..+.++|.+..      +.-.++.--..-|-
T Consensus        3 ~~l~~~i~~~~~~l~~~yll~G~e~~~l~~~~~~l~~~~~~~~~~~~~~d~~~~~~~~~~~l~~~~~~plf   72 (347)
T 3zh9_B           3 FDVWKSLKK~~GEVHPVYCLYGKET~~YLLQETVSRIRQTVVDQETKDFNLSVFDLEEDP~~~~~~LDQAIADAETFPFM   72 (347)
T ss_dssp            HHHHHHHHT~~TCCCSEEEEESSCH~~HHHHHHHHHHHHHCCGGGHHHHEEEEETTTSC~~~~~~HHHHHHHHTSCCSS
T ss_pred            HHHHHHHHc~~CCCCceEEEEcCcH~~HHHHHHHHHHHHcCCCcccccCCeEEEeCCCCC~~~~~~HHHHHHHHcCCCCC


Q ss_pred            cCCcEEEEeehhhCCh--------HHHHHHHHHcCCCCcccccceEEEEE
Q lull1          357 NGQKAAVVHHFESFPA--------GSTLIFYKYCDHENAAFKDVALVLT  397 (470)
Q Consensus      357 ~g~kaAVV~~LE~LPP---------AaLIFH~YCDhENA~fKdvaL~LT  397 (470)
                     .++|+.+|.+.+.+..        .+.-+|-+|+.+   +-+++++||+
T Consensus       73 ~~~kvvii~~~~~l~~~~~~~~~~~~~~aLl~~le~~~p~~~~~lIl~  118 (347)
T 3zh9_B          73 GERRLVIVKNPYFLTGEKKKEKIEHNVSALESYIQS~~~PAPYTVFVLL  118 (347)
T ss_dssp            SSCEEEEEECCGGGSCSCTTSSCCCCHHHHHHHHHS~~~CCTTEEEEEE
T ss_pred            CCceEEEEEChhhhhcccccccccccHHHHHHHHhC~~~CCCCeEEEEE
```

No 22

>1sxj_B Activator 1 37 kDa subunit; clamp loader, processivity clamp, DNA sliding clamp, AAA+ at polymerase, DNA-binding protein; HET: AGS ADP; 2.85A {Saccharomyces cerevisiae} SCOP: a.80.1.1 c.37.1.20
Probab=39.57 E-value=1.3e+02 Score=28.20 Aligned_cols=110 Identities=14% Similarity=0.163 Sum_probs=0.0

```
Q ss_pred            CHHHHHHHHHHHHHHcCCCCCCCeEEEEecCCchHHHH-HHHHHHHHHHcccccCCcceeeChHHhccCCchHHHHHHH
Q lull1          270 SSFLWQRGRKFLQKHLNASNPTEPATIIFTAAREGRETL-KCLSHHVADAYTSSQKVSPIQIDGAGRTWQDSDTVKLLVD  348 (470)
Q Consensus      270 se~LWk~lr~~LekhLn~s~p~ePaViLfta~~~Ae~Tl~~CLa~~LA~aySs~~~~s~I~IdG~~~a~~DSD~vKl~lD  348 (470)
                     ++++.+.++..+.+       .+-|..||.+..-.++.|+ ++||..+    +-.....++.++..+...       +..+.
T Consensus       26 ~~~~~~L~~~l~~~~~~~~~~Ll~Gp~G~GKttla~~la~e~~~~~~~~~~~~~~~s~~~~~~~~~~~~~   90 (323)
T 1sxj_B          26 NKETIDRLQQIAKD------GNMPHMIISGMPGIGKTTSVHCLAHEL~~~LGRSYADGVLELNASDDRG------IDVVR  90 (323)
T ss_dssp            CTHHHHHHHHHHS------CCCCCEEEECSTTSSHHHHHHHHHHH~~~HGGGHHHHEEEECTTSCCS------HHHHH
T ss_pred            cHHHHHHHHHHHC------CCCCEEEEECcCCCCHHHHHHHHHHHh~~~CCCCCCCeeeecccccccc------hHHHH


Q ss_pred            HHHHHH-------hhcCCcEEEEeehhhCChHHHHHHHHHcCCCCcccccceEEEEE
Q lull1          349 LELSYG-------FENGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALVLT  397 (470)
Q Consensus      349 e~L~s~-------Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~LT  397 (470)
                     ......       .....+++++-.++.+..++..+|.+..+...   +.+.++|+
T Consensus       91 ~~~~~~~~~~~~~~~~kviiide~d~l~~~~~~l~~~~e~~~~~~~~~~il~  143 (323)
T 1sxj_B          91 NQIKHFAQKKLHLPPGKHKIVILDEADSMTAGAQQALRRTMELYS~~~NSTRFAFA  143 (323)
T ss_dssp            THHHHHHHBCCCCCTTCCEEEEEESGGGSCHHHHHTTHHHHHHTT~~~TTEEEEEE
T ss_pred            HHHHHHhhhcccccccCCcEEEEEeCcccCCHHHHHHHHHHhhhhcc~~~cceeEeec
```

No 23

>3pe5_A Uncharacterized protein; structural genomics, PSI-biology, protein structure initiati northeast structural genomics consortium, NESG; 2.38A {Clostridium leptum}
Probab=38.59 E-value=7.2 Score=39.91 Aligned_cols=53 Identities=9% Similarity=0.050 Sum_probs=0.0

```
Q ss_pred             cchHhhhhhhhhhHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHhhhh
Q lull1         187 GSHPQQTQKLEEIKENAQDTMRQINKKGFWSYGPVILVVLVVAVVASSVNSYY  239 (470)
Q Consensus     187 ~~~~~~~~~~~~~~~~~~~~~~~~~~k~~~~~y~~~~~i~~li~iv~l~~i~~~~~  239 (470)
                      ..+++.+.+.-..+.+.+.-.|+..++.++.++.++++++|++++.+.+|.++
T Consensus       5 rr~~~p~~r~~~~~r~~~~~~~~~rr~~~~r~~~~~~i~~~l~v~~v~~~~~~~~~~~~~~  57 (403)
T 3pe5_A          5 RRYQEPQNRDISSRSNGKNPFKRSTGRKVSNVIIIILCVVFSGLGGVIVYAHG   57 (403)
T ss_dssp            -----------------------------------------------------
T ss_pred             ccccCCCCCCccccCCCCCCCCCCCcccHhHHHHHHHHHHHHHHHHHHHHHHH
```

No 24

>2yhs_A FTSY, cell division protein FTSY; cell cycle, protein targeting, simibi class GTPase, GTP-BIND membrane, nucleotide-binding; 1.60A {Escherichia coli} PDB: 2qy9 _A 2xxa _B* 1fts _A 3zn8 _D
Probab=34.47 E-value=2.5e+02 Score=28.71 Aligned_cols=130 Identities=13% Similarity=0.105 Sum_probs=0.0

```
Q ss_pred             hhHHHHHHHHH-HHHHhcCCCCHHHHHHHHHHHHHHHh------cCCCCCCCeEEEEe--cCCchHHHHHHHHHHHHHHHhc
Q lull1         250 PALEAFLAQFS-QLEDKFPGQSSFLWQRGRKFLQKHL------NASNPTEPATIIFT--AAREGRETLKCLSHHVADAYT  320 (470)
Q Consensus     250 ~a~e~f~~qf~~~LK~kFPsQse~LWk~lr~~LekhL------n~s~p~ePaViLft--a~~~Ae~Tl~CLa~~LA~ayS  320 (470)
                      ...+.+++.++ .++.+-=.-.+.+++.++..|.+.|      .....+.|.||+|+  .|-+=.-|+-+||..+.....
T Consensus     243 ~~a~~iie~l~~~~~~~~~~~~~~~~e~~~~~~l~~~~l~~~~l~~~~~~~~~~~~~~~~~~~~~~i~~vG~~G~GKTTt~aKla~~~~~~~~~~~  322 (503)
T 2yhs_A        243 ETTRKIITNLTEGASRKQLRDAEALYGLLKEEMGEILAKVDEPLNVEGKAPFVILMVGVNGVGKTTTIGKLARQFEQQGK  322 (503)
T ss_dssp            HHHHHHHHHHHHHHHHHHTCCBGGGHHHHHHHHHHHHHHHTTBCCCCCCSCTTEEEEEECCTTSSHHHHHHHHHHHHHHTTC
T ss_pred             HHHHHHHHHHHHHHHhcccCCCHHHHHHHHHHHHHHHHhhcccccccccCCCCEEEEEeCCCCCCccccchHHHHHHHhcccc


Q ss_pred             cccCCcceeeChHHhccCCchHHHHHHHHHHHHHHhhcCCcEEEEeehhhCChHHHHHHHHhcCCCCcccccceEEE
Q lull1         321 SSQKVSPIQIDGAGRTWQDSDTVKLLVDLELSYGFENGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALV  395 (470)
Q Consensus     321 s~~~~s~I~IdG~~~a~~DSD~vKl~lDe~L~s~Fe~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~  395 (470)
                      +.               .-+..|+++..-.++|+..-+.=.--++++.-    +.+.+-+++..++.-.....|++||
T Consensus     323 ~v--------------~l~~~Dt~R~~A~eQL~~~~~~~l~v~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~d~~~~~~~~~~~~~~~~~~~~~~~~~~~~~d~vli  381 (503)
T 2yhs_A        323 SV--------------MLAAGDTFRAAAVEQLQVWGQRNNIPVIAQHT---GADSASVIFDAIQAAKARNIDVLIA  381 (503)
T ss_dssp            CE--------------EEECCCTTCHHHHHHHHHHHHHHHTCCEECCST---TCCHHHHHHHHHHHHHHHHTTCSEEEE
T ss_pred             ee--------------eEEeecccccHHHHHHHHHHHhcCCceeeeccc---CCCHHHHHHHHHHHHHHHHcCCCEEEe
```

No 25

>1shu_X Anthrax toxin receptor 2; alpha/beta rossmann fold, membrane protein; 1.50A {Homo sapiens} SCOP: c.62.1.1
PDB: 1tzn _a 1sht _X 1t6b _Y*
Probab=32.27 E-value=1e+02 Score=26.47 Aligned_cols=121 Identities=9% Similarity=0.039 Sum_probs=0.0

```
Q ss_pred             chhHHHHHHHHHHHHHHhcCCCCHHHHHHHHHHHHHHHHhcCCCCCCCe-EEEEecCCchHHHHHHHHHHHHHHHHhccccCCcc
Q lull1         249 NPALEAFLAQFSQLEDKFPGQSSFLWQRGRKFLQKHLNASNPTEPA-TIIFTAAREGRETLKCLSHHVADAYTSSQKVSP  327 (470)
Q Consensus     249 ~~a~e~f~~qf~~~LK~kFPsQse~LWk~lr~~LekhLn~s~p~ePa-ViLfta~~~Ae~Tl~CLa~~LA~aySs~~~~s~  327 (470)
                      ..........++.|+..+|+-...+++.++...+...+...++.|. +|||+-+.........+......+...--..-+
T Consensus      60 ~~~~~~~~~~~~~i~~~~~~~~~~~~~G~T~~~~al~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~iilltDG~~~~~~~~~~~~~~~~~~~~~~a~~~~~~~~i~v~~  139 (182)
T 1shu_X        60 TGDRGKISKGLEDLKRVSPVGETYIHEGLKLANEQIQKAGGLKTSSIIIALTDGKLDGLVPSYAEKEAKISRSLGASVYC  139 (182)
T ss_dssp            ECCHHHHHHHHHHHHHTCCCCSCCCHHHHHHHHHHHHHHHHHTGGGSCEEEEEEECCCCCTTHHHHHHHHHHHHHHHTTCEEEE
T ss_pred             ccchHHHHHHHHhhhcccCCCCCCchHHHHHHHHHHHHHHHhcccCCCCceEEEEecCCCCCCCccHHHHHHHHHHHHCCCEEEE


Q ss_pred             eeeChHHhccCCchHHHHHHHHHHHHHHhhcCCcEEEE-eehhhCChHHHHHHHHhc
Q lull1         328 IQIDGAGRTWQDSDTVKLLVDLELSYGFENGQKAAVV-HHFESFPAGSTLIFYKYC  382 (470)
Q Consensus     328 I~IdG~~~a~~DSD~vKl~lDe~L~s~Fe~g~kaAVV-~~LE~LPP~AaLIFH~YC  382 (470)
                      |-+...+.                .+|+..-....+.+ .+++.|+-=.-.+.-++|
T Consensus     140 vgig~~~~-------------~~L~~ia~~~~~~~f~~~~~~~~~~~L~~i~~~~i~~~iC  182 (182)
T 1shu_X        140 VGVLDFEQ-------------AQLERIADSKEQVFPVKGGFQALKGIINSILAQSC  182 (182)
T ss_dssp            EECSSCCH-------------HHHHHHSSSGGGEEESSSTTHHHHHHHHHHHHTBC
T ss_pred             EECCcccH-------------HHHHHHhCCCCCeEEecCCHHHHHHHHHHHHHHhhC
```

No 26

>2bjv_A PSP operon transcriptional activator; AAA, transcription activation, gene regulation, sigma54 activator, enhancer binding protein, PSPF; 1.7A {Escherichia coli} PDB: 2bjw _A 2c96 _A* 2c98 _A* 2c99 _A* 2c9c _A* 2vii _A*
Probab=31.92 E-value=3.4e+02 Score=25.35 Aligned_cols=127 Identities=13% Similarity=0.140 Sum_probs=0.0

```
Q ss_pred             HHHHHHhcCCCCHHHHHHHHHHHHHHHHhcCCCCCCCeEEEEecCCchHHHHHHHHHHHHHHHHhccccCCcceeeChHHhccC
Q lull1         259 FSQLEDKFPGQSSFLWQRGRKFLQKHLNASNPTEPATIIFTAAREGRETLKCLSHHVADAYTSSQKVSPIQIDGAGRTWQ  338 (470)
Q Consensus     259 f~~LK~kFPsQse~LWk~lr~~LekhLn~s~p~ePaViLfta~~~Ae~Tl~CLa~~LA~aySs~~~~s~I~IdG~~~a~~  338 (470)
                      |.++++..=+++ ..|+.++..+.+.-....|     |+|.+-.-.++.++=.+++.    +|.......+.++....
T Consensus       1 ~~~~~~~liG~S-~~~~~~~~~~~~~i~~~a~~~~~p----vlI~GE~GtGK~~lA~~ih-----~s~~~~~~~~~~~~~~~~~~~~~~---  68 (265)
T 2bjv_A          1 MAEYKDNLLGEA-NSFLEVLEQVSHLAPLDKP----VLIIGERGTGKELIASRLHY----LSSRWQGPFISLNCAAL---  68 (265)
T ss_dssp            ---------CCC-HHHHHHHHHHHHHTTSCSC----EEEECCTTSCHHHHHHHHHH----TSTTTTSCEEEEEGGGS---
T ss_pred             CCccccCCeEEcC-HHHHHHHHHHHHHhCCCCC----EEEECCCCcCHHHHHHHHHH----hccccCCCCceEEecccc---


Q ss_pred             CchHHHHHHHHHHHHHHhhcCCCc------------EEEEeehhhCChHHHHHHHHhcCC--------CCcccccceEEEEE
Q lull1         339 DSDTVKLLVDLELSYGFENGQK------------AAVVHHFESFPAGSTLIFYKYCDH--------ENAAFKDVALVLT  397 (470)
Q Consensus     339 DSD~vKl~lDe~L~s~Fe~g~k------------aAVV~~LE~LPP~AaLIFH~YCDh--------ENA~fKdvaL~LT  397 (470)
                      +.+.....+.......|....+            +.++.+++.||+.--..|..|.++        .++.-.++-||++
T Consensus      69 ~~~~~~~~~~~l~g~~~~~~~~~~~~~~~~~~~~~~~g~le~a~~~GtL~l~~i~~L~~~~~Q~~L~~~~L~~~~~~~~~~~~~~~~~~~~~riI~s  147 (265)
T 2bjv_A         69 NENLLDSELFGHEAGAFTGAQKRHPGRFERADGGTLFLDELATAPMMVQEKLLRVIEYGELERVGGSQPLQVNVRLVCA  147 (265)
T ss_dssp            CHHHHHHHHHHCCC---------CCCCHHHHTTTSEEEEESGGGSCHHHHHHHHHHHHHCEECCCCC--CEECCCEEEEE
T ss_pred             ccchHHHHHhCCccCCCcccCCCCChhheecCCcEEEEecccccCHHHHHHHHHHHHHhCcEEeCCCCceeeeeeEEEec
```

No 27

>1jql_B DNA polymerase III, delta subunit; processivity clamp, clamp loader, DNA replication, AAA+ ATPase, transferase; HET: DNA; 2.50A {Escherichia coli} SCOP: c.37.1.20

```
Probab=28.90  E-value=1.4e+02  Score=25.11  Aligned_cols=104  Identities=10%  Similarity=-0.006  Sum_probs=0.0

Q ss_pred            HHHHhcCCCCCCCeEEEEecCCchHHHHHHHHHHHHHhcccCCCcceeeChHHhccCCchHHHHHHHHHHHHhhcCCc
Q lull1          281 LQKHLNASNPTEPATIIFTAAREGRETLKCLSHHVADAYTSSQKVSPIQIDGAGRTWQDSDTVKLLVDLELSYGFENGQK  360 (470)
Q Consensus      281 LekhLn~s~p~ePaViLfta~~~Ae~Tl~CLa~~LA~aySs~~~~s~I~IdG~~~a~~DSD~vKl~lDe~L~s~Fe~g~k  360 (470)
                     |.++|+++   -|.++||. |.+.--.-+++..-...+.........+...+.+..      ..-.++.--.--|=++++
T Consensus        9 L~~~L~~~~~l~~vYll~-G~E~~l~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~t~plF~~~k   78 (140)
T 1jql_B           9 LRAQLNEG---LRAAYLLL-GNDPLLLQESQDAVRQVAAAQGFEEHHTFSIDPNTD------WNAIFSLCQAMSLFASRQ   78 (140)
T ss_dssp            HHHHHHHC---CCSEEEEE-SSCHHHHHHHHHHHHHHTTCCEEECCCCSTTCC------HHHHHHHHCCCTTCCCE
T ss_pred            HHHHHHcc---CCcEEEEE-eCcHHHHHHHHHHHHHHhcCCchhhhhhccCCCCC------HHHHHHHHhcCCCCcCcE


Q ss_pred            EEEEeehh-hCChHHHHHHHHHcCCCCcccccceEEEEE
Q lull1          361 AAVVHHFE-SFPAGSTLIFYKYCDHENAAFKDVALVLT  397 (470)
Q Consensus      361 aAVV~~LE~~LPP~AaLIFH~YCDhENA~fKdvaL~LT  397 (470)
                     +.+|++.. .++....-+|..||.+-++   +++|||+
T Consensus       79 lv~i~~~~~~~~~~~~~L~~y~~~~~~~---~~ili~~  113 (140)
T 1jql_B          79 TLLLLLPENGPNAAINEQLLTLTGLLHD---DLLLIVR  113 (140)
T ss_dssp            EEEEECCTTCSCTTHHHHHHHHHHCCS---SCCEEEE
T ss_pred            eeeccccccCCCCHHHHHHHHHHcCCCC---CEEEEEE
```

No 28

>3arc_L Photosystem II reaction center protein L; PSII, membrane-protein complex, transmembrane alpha-helix, E transport, photosynthesis; HET: OEX CLA PHO BCR PL9 SQD LMG UNL LMT HTG DGD LHG HEM; 1.90A {Thermosynechococcus vulcanus} PDB: 1s5l _L* 3a0b _L* 3a0h _L* 2axt _L* 3bz1 _L* 3bz2 _L* 3kzi _L* 3prq _L* 3prr _L* 4fby _L* 4il6 _L 4ixr _L*

```
Probab=28.05  E-value=53  Score=23.76  Aligned_cols=20  Identities=30%  Similarity=0.521  Sum_probs=0.0

Q ss_pred            HHHHHHHHHHHHHHHHHHH
Q lull1          220 PVILVVLVVAVVASSVNSYY  239 (470)
Q Consensus      220 ~~~i~~li~iv~l~~i~~~~  239 (470)
                     .+.||+|++.|+.+++.+||
T Consensus       16 sLy~Glllifvl~vlfssyf   35 (37)
T 3arc_L          16 SLYLGLLLILVLALLFSSYF   35 (37)
T ss_dssp            HHHHHHHHHHHHHHHHHHH
T ss_pred            hHHHHHHHHHHHHHHHHHh
```

No 29

>1v7p_C Integrin alpha-2; snake venom, C-type lectin, antagonist, cell adhes glycoprotein, toxin-cell adhesion complex; HET: NAG; 1.90A {Homo sapiens} SCOP: c.62.1.1 PDB: 1aox _A 1dzi _A

```
Probab=27.69  E-value=1.3e+02  Score=26.47  Aligned_cols=128  Identities=9%  Similarity=-0.066  Sum_probs=0.0

Q ss_pred            HHHHHHHHHHHHHcCCCCHHHHHHHHHHHHHcCCCCCCC----eEEEEecCCchHHHHHHHHHHHHHcccccCCcc
Q lull1          252 LEAFLAQFSQLEDKFPGQSSFLWQRGRKFLQKHLNASNPTEP----ATIIFTAAREGRETLKCLSHHVADAYTSSQKVSP  327 (470)
Q Consensus      252 ~e~f~~qf~~LK~kFPsQse~LWk~lr~~LekhLn~s~p~eP----aViLfta~~~Ae~Tl~CLa~~LA~aySs~~~~s~  327 (470)
                     ...+...+..++. +.+-...+..+++.....++.....|    .+|||+.+..  .--.-+...+..+...--..-.
T Consensus       66 ~~~~~~~i~~~~~~~g~~~~~~~Al~~~~~~~f~~~~~~R~~~~~~viliTdg~s~~~d~~~~~~~~~~~~~~gi~i~~  142 (200)
T 1v7p_C          66 KEEMIVATSQTSQ-YGGDLTNTFGAIQYARKYAYSAASGGRRSATKVMVVVTDGES--HDGSMLKAVIDQCNHDNILRFG  142 (200)
T ss_dssp            HHHHHHHHHCCC-CCCSCCCHHHHHHHHHHHTTSGGGTCCTTSEEEEEEEESSCC--SCGGGHHHHHHHHHTTEEEEE
T ss_pred            HHHHHHHHHccc-cCCCCccHHHHHHHHHHHccccccCCCCCCCEEEEEEeCCCC--CCchhHHHHHHHHHhCCCEEEE


Q ss_pred            eeeCHHHhccCCCchHHHHHHHHHHHHHHhc--CCcEEEEeehhhCCchHHHHHHHHHcCCC
Q lull1          328 IQIDGAGRTWQDSDTVKLLVDLELSYGFEN--GQKAAVVHHFESFPAGSTLIFYKYCDHE  385 (470)
Q Consensus      328 I~IdG~~~a~~DSD~vKl~lDe~L~s~Fe~--g~kaAVV~~LE~LPP~AaLIFH~YCDhE  385 (470)
                     +-+.+.............   .++|+..-..  ...++.+.++..|+--.-.+..++|.-|
T Consensus      143 v~v~~~~~~~~~~~~~~---~~eL~~iAs~p~~~~~f~~~~~~L~~i~~~l~~~Ic~ie  199 (200)
T 1v7p_C         143 IAVLGYLNRNALDTKNL---IKEIKAIASIPTERYFFNVSDEAALLEKAGTLGEQIFSIE  199 (200)
T ss_dssp            EEECHHHHHTTCCCHHH---HHHHHHHSCSSHHHHEEEESSSGGGHHHHHHHHHHHTC-
T ss_pred            EEeccccccccccchhh---HHHHHHHhCCCHHHeEEEeCCHHHHHHHHHHHHHhhcCC
```

No 30

>3te6_A Regulatory protein SIR3; heterochromatin, gene silencing, SIR complex, HMR, HML, TELO AAA+ domain, structural, nucleus, gene RE; 2.80A {Saccharomyces cerevisiae}

```
Probab=21.39  E-value=4.7e+02  Score=25.80  Aligned_cols=118  Identities=10%  Similarity=0.080  Sum_probs=0.0

Q ss_pred            HHHHHHHHHHHHcCCCCCCCeEEEEecCCchHHHH-HHHHHHHHHHhcccc--CCcceeeChHHhccCCchHHHHHHHH
Q lull1          274 WQRGRKFLQKHLNASNPTEPATIIFTAAREGRETL-KCLSHHVADAYTSSQ--KVSPIQIDGAGRTWQDSDTVKLLVDLE  350 (470)
Q Consensus      274 Wk~lr~~LekhLn~s~p~ePaViLfta~~~Ae~Tl~CLa~~LA~aySs~~~~s~I~IdG~~~a~~DSD~vKl~lDe~  350 (470)
                     +..+..+|+..+..  .+.+.++|.+..-.++-++ +.++..+........  ....+.|||...  .++..+--.|-++
T Consensus       29 ~~~i~~~L~~~i~~~~~~~~lli~GpPGTGKT~~v~~v~~~L~~~~~~~~~~~~~v~INc~~~~~~t~~~~~~~I~~~  104 (318)
T 3te6_A          29 FTRIFLPIYDSLMS--SQNKLFYITNADDSTKFQLVNDVMDELITSSARKELPIFDYIHIDALEL--AGMDALYEKIWFA  104 (318)
T ss_dssp            HHHHHHHHHHHHT--TCCCEEEEECCCSHHHHHHHHHHHHHHTTTTTSSCCEEEEEEETTCC--C--HHHHHHHHH
T ss_pred            HHHHHHHHHHHcC--CCCCeEEEECCCCCCHHHHHHHHHHHHHHHhcCCCceEEEEEeccc--CCHHHHHHHHHH


Q ss_pred            H--------------HHHHh------cCCcEEEEeehhhCChHHHHHHHHcCCCCcccccceEEEEE
Q lull1          351 L--------------SYGFE------NGQKAAVVHHFESFPAGSTLIFYKYCDHENAAFKDVALVLT  397 (470)
Q Consensus      351 L--------------~s~Fe------~g~kaAVV~~LE~LPP~AaLIFH~YCDhENA~fKdvaL~LT  397 (470)
                     |              +..|.      +...++++-.++.|.  .-.+||.|-+.....-.++++|++
T Consensus      105 L~g~~~~~~~~~~L~~~f~~~~~~~~~~ii~lDE~d~l~~~q~~L~~l~~~~~~~~s~~~vI~i  169 (318)
T 3te6_A         105 ISKENLCGDISLEALNFYITNVPKAKKRKTLILIQNPENLL--SEKILQYFEKWISSKNSKLSIICV  169 (318)
T ss_dssp            HSCCC--CCCCHHHHHHHHHHSCGGGSCEEEEEEECCSSSC--CTHHHHHHHHHHCSSCCEEEEEE
T ss_pred            hcCCCCCchHHHHHHHHHHHHHhcCCCceEEEEecHHHhh--cchHHHHHHHhcccccCCcEEEEEE
```

No 31

>4i9w_A Potassium channel subfamily K member 4; potassium ION channel, metal transport; 2.75A {Homo sapiens} PDB: 3um7 _A

```
Probab=21.23  E-value=4e+02  Score=25.62  Aligned_cols=96  Identities=13%  Similarity=0.012  Sum_probs=0.0
```

```
Q ss_pred              ccchHhhhhhhhhhHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHhhhhcCccccccccchhHHHHHHHHHHHHHHh
Q lull1            186 AGSHPQQTQKLEEIKENAQDTMRQINKKGFWSYGPVILVVLVVAVVASSVNSYYSSPAQQVPKNPALEAFLAQFSQLEDK  265 (470)
Q Consensus        186 ~~~~~~~~~~~~~~~~~~~~~~~~~~~k~~~~~y~~~~~i~~li~iv~l~~i~~~~ssPa~~~~~~~~~a~e~f~~qf~~LK~k  265 (470)
                       +.+.||++-+..+....+.-..++.-+  +.....+++.+++=++++++|....-.|+..    ..-+.+.+..+.+-+.
T Consensus        2 ~~~~~~~~~~~~~~~~~~~~~~~~~~~--~~~~~l~L~~l~i~Y~llGA~IF~~iE~~~e~----~~~~~~~~~~~~~~~~   75 (309)
T 4i9w_A           2 TTAPQEPPARPLQAGSGAGPAPGRAMR--STTLLALLALVLLYLVSGALVFRALEQPHEQ----QAQRELGEVREKFLRA   75 (309)
T ss_dssp              --------------------------C--HHHHHHHHHHHHHHHHHHHHHHHHHHHHHGGGTT----HHHHHHHHHHHHHHHH
T ss_pred              CCCCCCCCCCCCCCCCCCCCchhhcc--hHHHHHHHHHHHHHHHHHHHHHHHHHHHCCcHHH----HHHHHHHHHHHHHHHh


Q ss_pred              cCCCCHHHHHHHHHHHHHHHhcC
Q lull1            266 FPGQSSFLWQRGRKFLQKHLNA  287 (470)
Q Consensus        266 FPsQse~LWk~lr~~LekhLn~  287 (470)
                       +..-+.+-+......+.+.+..
T Consensus       76 ~~~~~~~~l~~~~~~~~~~~~~   97 (309)
T 4i9w_A          76 HPCVSDQELGLLIKEVADALGG   97 (309)
T ss_dssp              CTTCCHHHHHHHHHHHHHHHHHT
T ss_pred              cccCCHHHHHHHHHHHHHHHHHc
```

No 32

>**2og2_A** Putative signal recognition particle receptor; nucleotide-binding, protein transport; 2.00A {Arabidopsis thaliana}

Probab=20.10 E-value=4.5e+02 Score=26.58 Aligned_cols=66 Identities=14% Similarity=0.149 Sum_probs=0.0

```
Q ss_pred              HHHHHHHHH-HHHHhcCCCCHHHHHHHHHHHHHHHh--------cCCCCCCCeEEEEecCCCh--HHHHHHHHHHHHH
Q lull1            252 LEAFLAQFS-QLEDKFPGQSSFLWQRGRKFLQKHL--------NASNPTEPATIIFTAAREG--RETLKCLSHHVAD  317 (470)
Q Consensus        252 ~e~f~~qf~~~LK~kFPsQse~LWk~lr~~LekhL--------n~s~p~ePaViLfta~~~A--e~Tl~CLa~~LA~  317 (470)
                       .+.+++.++ .+..+-......+++.++..|.+.|        .......|.||+|+.-.++  .-|+-+||.++..
T Consensus      107 ~~~i~~~l~~~~~~~~~~~~~~~~~~~l~~~l~~~L~~~~~~~~~~~l~~~~~~p~vi~~vG~~GvGKTTTiaKLA~~~~~  183 (359)
T 2og2_A         107 TVRIVERLREDIMSGKLKSGSEIKDALKESVLEMLAKKNSKTELQLGFRKPAVIMIVGVNGGGKTTSLGKLAHRLKN  183 (359)
T ss_dssp              HHHHHHHHHHHHHTTSCCSHHHHHHHHHHHHHHHHHCCC---CSCCCCSSSSEEEEEECCTTSCHHHHHHHHHHHHH
T ss_pred              HHHHHHHHHHHHhhcCCCCHHHHHHHHHHHHHHHhccccCcccccccCCCCeEEEEECCCCCCcccchHHHHHHHHH
```

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-

PDB: Bourne, PE. *et al.* (2004) The distribution and query systems of the RCSB Protein Data Bank. NAR 32: D223.

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