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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

New job | Resubmit | Resubmit_HMM | Resubmit/HHsenser | Realign | Log | Input-params | Delete

HHpred - Results

Job-ID: 8752049 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

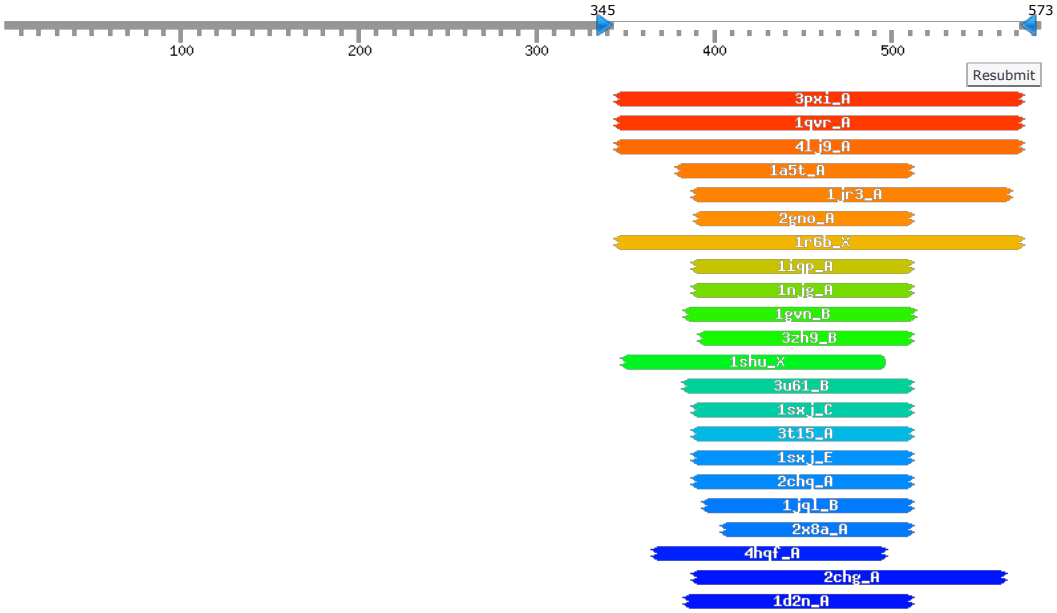
Color alignments

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.

Note: Corrupted alignments are the most common source of high-scoring false positives. Check the query alignment by clicking Show Query Alignment above. To check the template alignments use the logos.



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

Query lap1 (seq=MAGDGRRAEA...ENALKRGICL Len=583 Neff=3.3 Nseqs=77)
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	3pxi_A	Negative regulator of g	95.6	0.14	4.4E-06	57.7	14.2	193	345-573	459-661 (758)
2	1qvr_A	CLPB protein; coiled co	95.2	0.28	8.7E-06	55.7	15.0	206	345-573	526-756 (854)
3	4lj9_A	Chaperone protein CLPB;	91.0	2.3	7.3E-05	42.9	12.3	208	345-573	11-241 (339)
4	1a5t_A	Delta prime, HOLB; zinc	89.5	2	6.3E-05	42.1	10.2	123	379-511	4-144 (334)
5	1jr3_A	DNA polymerase III subu	89.0	5.9	0.00019	39.1	13.2	158	388-566	22-211 (373)
6	2gno_A	DNA polymerase III, gam	88.0	2.4	7.6E-05	41.0	9.5	113	390-511	5-118 (305)
7	1r6b_X	CLPA protein; AAA+, N-t	84.2	20	0.00064	40.8	15.6	206	345-573	426-652 (758)
8	1iqp_A	RFCS; clamp loader, ext	81.7	4.7	0.00015	39.1	8.3	115	388-511	31-146 (327)
9	1njg_A	DNA polymerase III subu	76.9	15	0.00048	34.7	9.9	117	388-511	29-162 (250)
10	1gvn_B	Zeta; postsegregational	72.5	37	0.0012	32.1	11.4	119	384-512	10-146 (287)
11	3zh9_B	Delta; hydrolase, repli	71.3	9.6	0.0003	37.6	7.2	106	392-511	3-118 (347)
12	1shu_X	Anthrax toxin receptor	68.1	9.8	0.00031	33.7	6.0	135	349-496	44-182 (182)
13	3u61_B	DNA polymerase accessor	61.0	41	0.0013	32.3	9.3	104	383-511	31-142 (324)
14	1sxj_C	Activator 1 40 kDa subu	60.2	28	0.00088	34.2	8.1	115	388-511	31-146 (340)
15	3t15_A	Ribulose bisphosphate c	56.5	56	0.0017	31.8	9.4	117	388-511	18-161 (293)
16	1sxj_E	Activator 1 40 kDa subu	52.4	1.4E+02	0.0045	28.6	11.5	119	388-511	20-170 (354)
17	2chq_A	Replication factor C sm	51.6	42	0.0013	31.9	7.5	115	388-511	23-138 (319)
18	1jql_B	DNA polymerase III, del	50.3	59	0.0018	28.2	7.7	99	394-511	9-113 (140)
19	2x8a_A	Nuclear valosin-contain	50.2	1.3E+02	0.0041	28.9	10.8	100	405-511	42-152 (274)
20	4hqf_A	Thrombospondin-related	42.8	1.7E+02	0.0053	27.9	10.3	117	366-496	87-210 (281)
21	2chg_A	Replication factor C sm	41.8	2.1E+02	0.0065	25.8	13.0	158	388-563	23-192 (226)
22	1d2n_A	N-ethylmaleimide-sensit	41.7	2.7E+02	0.0084	27.0	14.3	120	384-511	43-173 (272)
23	2bjv_A	PSP operon transcriptio	37.3	2.5E+02	0.0079	26.9	10.6	127	372-511	1-147 (265)
24	4b4t_H	26S protease regulatory	35.9	1.5E+02	0.0047	31.5	9.5	101	405-511	241-354 (467)
25	2lco_A	WALP19-P8 peptide; prol	35.2	27	0.00086	24.0	2.4	17	337-353	3-19 (26)
26	1jr3_D	DNA polymerase III, del	33.6	3.7E+02	0.011	26.3	12.1	105	394-512	9-114 (343)
27	2lcn_A	WALP19-P10 peptide; pro	33.5	30	0.00095	23.8	2.4	17	337-353	3-19 (26)

```
28 3lp5_A Putative cell surface h  32.2 1.1E+02  0.0035   27.2   6.8   73  403-478     2-103 (250)
29 3syl_A Protein CBBX; photosynt  32.1 3.5E+02    0.011   25.5  15.6  138  368-511    22-175 (309)
30 4b4t_K 26S protease regulatory  30.2 2.3E+02  0.0071   29.6   9.5  101  405-511   204-317 (428)
31 2kog_A Vesicle-associated memb  29.9       30 0.00093  30.7   2.5   21  334-354    95-115 (119)
32 1sxj_B Activator 1 37 kDa subu  29.8 1.3E+02    0.004   29.0   7.2  116  383-511    26-143 (323)
33 4ko8_A Transitional endoplasmi  26.7 3.1E+02  0.0096   29.1   9.9  135  358-511   199-346 (489)
34 3lfh_A Manxa, phosphotransfera  25.9 2.5E+02  0.0079   25.2   7.9   65  409-481     6-70  (144)
35 3j01_B Preprotein translocase   25.9       32    0.001   30.9   2.0   26  333-358     4-29  (116)
36 4b4t_M 26S protease regulatory  25.8 3.1E+02  0.0097   28.6   9.7  101  405-511   213-326 (434)
37 1v54_I STA, cytochrome C oxida  25.2       24 0.00075  29.7   1.0   43  335-377    17-59  (73)
38 4b4t_I 26S protease regulatory  25.1 3.5E+02    0.011   28.3   9.9  101  405-511   214-327 (437)
39 4hqo_A Sporozoite surface prot  24.2   3E+02  0.0094   26.2   8.6  118  365-496    83-207 (266)
40 4mdf_A Metallophosphoesterase;  24.1       87  0.0027   27.4   4.4  104  405-515     7-112 (171)
41 2qz4_A Paraplegin; AAA+, SPG7,  23.8   5E+02    0.016   24.6  11.2  100  405-511    37-151 (262)
42 2qp9_X Vacuolar protein sortin  23.4 2.4E+02  0.0074   28.5   8.0  100  406-511    83-193 (355)
43 4b4t_L 26S protease subunit RP  22.4 3.4E+02    0.011   28.3   9.1  101  405-511   213-326 (437)
44 3lay_A Zinc resistance-associa  22.3 1.3E+02    0.004   28.3   5.4   90  327-432    19-125 (175)
45 3arc_L Photosystem II reaction  21.8       69  0.0022   23.9   2.7   19  337-355    19-37  (37)
46 4cn9_A Proximal thread matrix   21.7 4.1E+02    0.013   26.9   9.4  161  361-537   118-285 (454)
```

No 1

```
>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=95.59  E-value=0.14  Score=57.70  Aligned_cols=193  Identities=17%  Similarity=0.218  Sum_probs=0.0

Q ss_pred            HHHHHHHHHhcCCcccCcchHHHHHHHHHHHHHhcCCCCHHHHHHHHHHHHHhcCCCCCCCCeEEEEecCcc--cHHHH
Q lap1           345 AALASGSFWFFSTPEVETTAVQEFQNQMNQLKNKYQGQDEKLWKRSQTFLEKHLNSSHPRSQPAILLLTAARD--AEEAL  422 (583)
Q Consensus      345 lai~vg~~~~~~~Pqv~~tave~f~~~~~qLKskFPsQse~LWkrlr~~LekhLNts~Pr~ePAVLLLtA~~~~Ae~TL  422 (583)
                     |+-++..+..-+...+.....+.+.+.-+.|+.+..+|++-+=.............-..|+..+.+|||++..+  =.+++
T Consensus      459 v~~vvs~~tgiP~~~l~~~e~~~l~~le~~L~~~v~GQ~~ai~~i~~~i~~~~~gl~~~~~p~~~~lf~GptGvGKtela  538 (758)
T 3pxi_A         459 IAMVVSSWTGVPVSKIAQTETDKLLNMENILHSRVIGQDEAVVAVAKAVRRARAGLKDPKRPIGSFIFLGPTGVGKTELA  538 (758)
T ss_dssp            HHHHHHTTC-------CHHHHSCC-CHHHHHHTTSCSCHHHHHHHHHHHHHTTTCSCTTSCSEEEEEESCTTSSHHHHH
T ss_pred            HHHHHHHHhCCCCcccchhHHHHHHhhhhccchheeeccHHHHHHHHHHHHHHcCCCCCCCCCCceEeecCCCccHHHHH


Q ss_pred            HHHHHHHHHHhcccccCceeEecCcccccccChhHHHHHHHHHHHHHHhcCCcEEEEeehhhCCHHHHHHHHHcCC----
Q lap1           423 RCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESFPAGSTLIFYKYCDH----  498 (583)
Q Consensus      423 qCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~LPP~AaLIFH~YCDh----  498 (583)
                     +.||+.+     .......+.+|...+..-.+...+...+ .++.   +...+.++-++|...|....+|..+.|.
T Consensus      539 k~la~~l-----~~~~~~~i~~dmse~~~~s~~g~L~~~vr~~~~p~sVvl~DeieKah~~v~~~llq~ld~G~l~  609 (758)
T 3pxi_A         539 RALAESI-----FGDEESMIRIDMSEYMEKHSTSGGQLTE-KVRR---KPYSVVLLDAIEKAHPDVFNILLQVLEDGRLT  609 (758)
T ss_dssp            HHHHHHH-----HSCTTCEEEEEGGGGCSSCCCC---CHH-HHHH---CSSSEEEEECGGGSCHHHHHHHHHHHSBCC
T ss_pred            HHHHHHH-----cCcchhhhcccccccccCcccccchHH-HHHh---CCCeEEEehhhhhcCHHHHHHHHHhcCCeeE


Q ss_pred            ----CCcCcccceEEEEEEecccccccCCcCHHHHHHHHHHHHHHhcccccccccccCChhcchHHHHhcceEEeec
Q lap1           499 ----ENAAFKDVALVLTVLLEEETLGTSLGLKEVEEKVRDFLKVKFTNSNTPNSYNHMDPDKLNGLWSRISHLVLPVQP  573 (583)
Q Consensus      499 ----ENA~fKdVaLfLTV~Leeetl~~s~slkEvEEkV~dfL~~k~~~s~~~~swn~Md~DkLdpLISRISh~VLpVqP  573 (583)
                         ...-|+|++||||=.+-.+.          .+.+.+.|+..|.                ..|+.|| +.|+++.|
T Consensus      610 d~~g~~vd~~n~iiI~TSN~g~~~~~~~~~~~~~~~~~l~~~f~----------------pefl~Ri-d~ii~f~p  661 (758)
T 3pxi_A         610 DSKGRTVDFRNTILIMTSNVGASE----------KDKVMGELKRAFR----------------PEFINRI-DEIIVFHS  661 (758)
T ss_dssp            -----CCBCTTCEEEEEESSSTTC----------CHHHHHHHHHSC----------------HHHHTTS-SEEEECC-
T ss_pred            CCCCCEEecCceEEEECCCCCchh----------HHHHHHHHHhCC----------------HHHHhC-CEEEEeCC
```

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=95.18  E-value=0.28  Score=55.67  Aligned_cols=206  Identities=16%  Similarity=0.228  Sum_probs=0.0

Q ss_pred            HHHHHHHHHhcCCcccCcchHHHHHHHHHHHHHhcCCCCHHHHHHHHHHHHHhcCCCCCCCCeEEEEecCcccH---HH
Q lap1           345 AALASGSFWFFSTPEVETTAVQEFQNQMNQLKNKYQGQDEKLWKRSQTFLEKHLNSSHPRSQPAILLLTAARDAE---EA  421 (583)
Q Consensus      345 lai~vg~~~~~~~Pqv~~tave~f~~~~~qLKskFPsQse~LWkrlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae---~T  421 (583)
                     |+-+++.+..-+.-.+.....+.+...-+.|..+.++|++-+=...+..+.--..-.+++ .|..-+|+.|+++.   ++
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 IAEIVSRWTGIPVSKLLEGEREKLLRLEEELHKRVVGQDEAIRAVADAIRRARAGLKDPN-RPIGSFLFLGPTGVGKTEL  604 (854)
T ss_dssp            HHHHHHTTSSCHHHHTTCCHHHHHHSHHHHHHHHSCSCHHHHHHHHHHHHHGGGCSCSS-SCSEEEEEBSCSSSSSHHHH
T ss_pred            HHHHHHHHHCCCChhhCHhhHHHHHHHHHHHHCcccCCHHHHHHHHHHHHHHHcCCCCCC-CCceEEEEECCCCCCCHHHH


Q ss_pred            HHHHHHHHHHHhcccccCceeEecCcccccccCChhH---------HHHHHHHHHHHHhcC-CcEEEEeehhhCCHHHHHH
Q lap1           422 LRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDT---------VKLEVDQELSNGFKNG-QNAAVVHRFESFPAGSTLI  491 (583)
Q Consensus      422 LqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~---------vKleIDeqLks~F~~g~~kaAVVh~LE~LPP~AaLI  491 (583)
                     ++.||+.+=.....      |.||-..|..-++..          ++..-.-+|-++.+.. ..|+++-+||.-.|..-.+
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            HHHHHHHHHSSGGGE-----EEECTTTCCSSGGGGGC--------------CHHHHHHCSSEEEEESSGGGSCHHHHHH
T ss_pred            HHHHHHHHcCCCcce-----EecccccccchhhhhhhcccccccccccccchhhhhhhhcCCCEEEEehhhhhcCHHHHHH


Q ss_pred            HHHhcCCC--------CcCcccceEEEEEEecccc----ccCCcCHHHHHHHHHHHHHHhcccccccccccCChhhcch
Q lap1           492 FYKYCDHE--------NAAFKDVALVLTVLLEEET----LGTSLGLKEVEEKVRDFLKVKFTNSNTPNSYNHMDPDKLNG  559 (583)
Q Consensus      492 FH~YCDhE--------NA~fKdVaLfLTV~Leeet----l~~s~slkEvEEkV~dfL~~k~~s~~~~swn~Md~DkLdp  559 (583)
                     |-.+.|..         ..-|+|++||||=.+-.+.    ...........+.|.+-|+..|.                ..
T Consensus      680 ~~~~~~~g~~~d~~g~~~~~~~~iii~tsn~g~~~~~~~~~~~~~~~~~~~~~~~~~~~f~----------------pe  743 (854)
T 1qvr_A         680 LLQILDDGRLTDSHGRTVDFRNTVIILTSNLGSPLILEGLQKGWPYERIRDEVFKVLQQHFR----------------PE  743 (854)
T ss_dssp            HHHHHTTTEECCSSSCCEECTTEEEEEECCTTHHHHHHHHHTTCCHHHHHHHHHHHTTSC----------------HH
T ss_pred            HHHHhccCceeCCCCCEEecceeeEeecCccChHHHHHhhccCCCchHHHHHHHHHHHhCC----------------HH


Q ss_pred            HHHHhhcceEEeec
Q lap1           560 LWSRISHLVLPVQP  573 (583)
Q Consensus      560 LISRISh~VLpVqP  573 (583)
                     |+.|| |.|++..|
T Consensus      744 fl~r~~d~iv~F~~  756 (854)
```

```
T lqvr_A          744 FLNRL-DEIVVFRP  756 (854)
T ss_dssp             HHHTC-SBCCBCCC
T ss_pred             HHhhC-CeEEEcCC
```

No 3

>**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=90.98 E-value=2.3 Score=42.90 Aligned_cols=208 Identities=14% Similarity=0.197 Sum_probs=0.0

```
Q ss_pred             HHHHHHHHHhCCCcccCcchHHHHHHHHHHHHhCCCCCHHHHHHHHHHHHHhcCCCCCCCCeEEEEecCc--ccHHHH
Q lap1            345 AALASGSFWFFSTPEVETTAVQEFQNQMNQLKNKYQGQDEKLWKRSQTFLEKHLNSSHPRSQPAILLLTAAR--DAEEAL  422 (583)
Q Consensus       345 lai~vg~~~~~~~Pqv~~tave~f~~~~~qLKskFPsQse~LWkrlr~~LekhLNts~Pr~ePAVLLLtA~~~~Ae~TL  422 (583)
                      |+=+|.-+..-+.-.+.....+.+.+.-+.|+++.=+|+.-+=+.....-.++...++++||++..  +-...+
T Consensus        11 i~~vi~~~tgip~~~~~~~~~~l~~l~~~L~~~IiGQ~~ai~~i~~~l~~~~~l~~~~p~~~~l~~GpsG~GKT~la   90 (339)
T 4lj9_A           11 IAEIVSRWTGIPVSKLLEGEREKLLRLEEELHKRVVGQDEAIRAVADAIRRARAGLKDPNRPIGSFLFLGPTGVGKTELA   90 (339)
T ss_dssp             HHHHHHHHHCCCHHHHTHHHHHHHSCHHHHHHTTCCSCHHHHHHHHHHHHHHTTCSCTTSCSEEEEEESCTTSSHHHHH
T ss_pred             HHHHHHHHHCCCchhcCHHHHHHHHHHHHHcCeeeCHHHHHHHHHHHHHHHhCCCCCCCCCeEEEEcCCCCCHHHHH

Q ss_pred             HHHHHHHHHHcccccCceeEecCcccccccChhH-------------HHHHHHHHHHHHhcCCcEEEEeehhhCCHHHH
Q lap1            423 RCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDT-------------VKLEVDQELSNGFKNGQNAAVVHRFESFPAGST  489 (583)
Q Consensus       423 qCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~-------------vKleIDeqLks~F~~g~kaAVVh~LE~LPP~Aa  489 (583)
                      ++|+..|...-..+     +.+|...+....+..              .+..|-+.+++   +...+.++=+||..++...
T Consensus        91 ~~la~~L~~~~~~~-----~~id~s~~~~~~~~~l~Gs~~GYvG~~~~~L~~~l~~-------VIllDEieK~~~~v~  162 (339)
T 4lj9_A           91 KTLAATLFDTEEAM-----IQIDMTEYMEKHAVSRLIGAPPGYVGYEEGGQLTEAVRR---RPYSVILFDEIEKAHPDVF  162 (339)
T ss_dssp             HHHHHHHHSSGGGE-----EEEEGGGCCSTTHHHHHCCCTTSTTTTTCCHHHHHHH---CSSCEEEEESGGGSCHHHH
T ss_pred             HHHHHHcCCccchh-----ceeccccccchhHHHHcCCCCCCcCcCcCCHHHHHHH---CCCeEEEEechhhCCHHHH

Q ss_pred             HHHHHHcCC--------CCcCcccceEEEEEEeccccccccCCcCHHHHHHHHHHHHHHcccccccccccCChhhcchHH
Q lap1            490 LIFYKYCDH--------ENAAFKDVALVLTVLLEEETLGTSLGLKEVEEKVRDFLKVKFTNSNTPNSYNHMDPDKLNGLW  561 (583)
Q Consensus       490 LIFH~YCDh--------ENA~fKdVaLfLTV~Leeetl~~s~slkEvEEkV~dfL~~k~~~s~~~~swn~Md~DkLdpLI  561 (583)
                      .+|..+.|.        ..--+.++++|+|-.+-.+.+.............+.....+.        +.+.++    |+
T Consensus       163 ~~Ll~il~~G~~~d~~g~~i~~~n~iii~tsn~g~~~i~~~~~~~~~~~~~~~~~~l~--------~~f~~e----~l  230 (339)
T 4lj9_A          163 NILLQILDDGRLTDSHGRTVDFRNTVIILTSNLGSPLILEGLQKGWPYERIRDEVFKVLQ--------QHFRPE----FL  230 (339)
T ss_dssp             HHHHHHHHHSEEECTTSCEEECTTCEEEEECCTTHHHHHHHHHTCCHHHHHHHHHHHH--------HHCCHH----HH
T ss_pred             HHHHHHhcCcEEECCCCCEecCcccEEecccccchHHHHhhhcccchhhhHHHHHHHH--------HhCCHH----HH

Q ss_pred             HHhhcceEEeec
Q lap1            562 SRISHLVLPVQP  573 (583)
Q Consensus       562 SRISh~VLpVqP  573 (583)
                      .|| +.|++..|
T Consensus       231 ~R~-~~ii~f~~  241 (339)
T 4lj9_A          231 NRL-DEIVVFRP  241 (339)
T ss_dssp             TTS-SEEEECCC
T ss_pred             ccC-CEEEEecC
```

No 4

>**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=89.53 E-value=2 Score=42.11 Aligned_cols=123 Identities=11% Similarity=0.056 Sum_probs=0.0

```
Q ss_pred             cCCCCHHHHHHHHHHHHHhccCCCCCCCeEEEEecCcccHHHH-HHHHHHHH----------------HHhcccccCce
Q lap1            379 YQGQDEKLWKRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEAL-RCLSEQIA----------------DAYSSFRSVRA  441 (583)
Q Consensus       379 FPsQse~LWkrlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TL-qCLae~IA----------------daySs~~s~~a  441 (583)
                      ||=|.+ +|+.+...+++.--      .-|+||-.....++.++ +.+|..|-                ..+.....-+.
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-DFEKLVASYQAGRG------HHALLIQALPGMGDDALIYALSRYLLCQQPQGHKSCGHCRGCQLMQAGTHPDY   76 (334)
T ss_dssp             CGGGHH-HHHHHHHHHHTTCC------CSEEEEECCTTSCHHHHHHHHHHHTCSSCBTTBCCSCSHHHHHHHTCCTTE
T ss_pred             CcccHH-HHHHHHHHHHcCCc------cccccccCCCCCcHHHHHHHHHHHHHcCCCCCCCCCCCCHHHHHHHcCCCCCe

Q ss_pred             eEecCcccccccCh-hHHHHHHHHHHHHHHhcCCCcEEEEEeehhhCCHHHHHHHHHhcCCCCcCcccceEEEEE
Q lap1            442 IRIDGTDKATQDS-DTVKLEVDQELSNGFKNGQNAAVVHRFESFPAGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus       442 I~IDG~~~a~~DS-D~vKleIDeqLks~F~~g~kaAVVh~LE~LPP~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                      +.+...+....=. |+++.-++.-....+.++.|++||.+.|.+...|+.+|=++-+-   +-+++++||+
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             EEECCCTTCSSBCHHHHHHHHHTTSCCTTSSCEEEEESCGGGBCHHHHHHHHHHTS---CCTTEEEEEE
T ss_pred             ecccchhccCCCCHHHHHHHHHHHHHhhhhCCCEEEEEeCchhhhHHHHHHHHHHcC---CCCCceeEee
```

No 5

>**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=89.00 E-value=5.9 Score=39.15 Aligned_cols=158 Identities=14% Similarity=0.173 Sum_probs=0.0

```
Q ss_pred             HHHHHHHHHHhcCCCCCCCCeEEEEEecCcccHHHHHHHHHHHHH--------------------hcccccCceeEecCc
Q lap1            388 KRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEALRCLSEQIADA--------------------YSSFRSVRAIRIDGT  447 (583)
Q Consensus       388 krlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAda--------------------ySs~~s~~aI~IDG~  447 (583)
                      +.....|.+.++...   -|-.+||++..+.-.+  .+|..||..                      +.+..+.+.+.+++.
T Consensus        22 ~~~~~~l~~~~~~~~~~~~ha~L~~G~~G~GK~~-~~a~~~a~~l~~~~~~~~~~~~~~~~~~~~~~~~~~d~~~~~~~   96 (373)
T 1jr3_A           22 EHVLTALANGLSLGR---IHHAYLFSGTRGVGKT--SIARLLAKGLNCETGITATPCGVCDNCREIEQGRFVDLIEIDAA   96 (373)
T ss_dssp             HHHHHHHHHHHHHTC---CCSEEEEESCTTSSHH--HHHHHHHHHSCTTCSCSSCCSSSHHHHHHHTSCCSSCEEEETT
T ss_pred             HHHHHHHHHHHHcCC---CCeeeeeECCCCCCHH--HHHHHHHHHCCCCCCCcCCCCcchHHHHHHcCCCCCeEEEeccc

Q ss_pred             cccccChhHHHHHHHHHHHHHhcCCcEEEEEeehhhCCHHHHHHHHHcCCCCcCcccceEEEEEEecccccccC------
Q lap1            448 DKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESFPAGSTLIFYKYCDHENAAFKDVALVLTVLLEEETLGT------  521 (583)
Q Consensus       448 ~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~LPP~AaLIFH~YCDhENA~fKdVaLfLTV~Leeetl~~------  521 (583)
```

```
                        .....  |+++.-++.--...+.++.|++||.+.|.+..+++.+|-++=+   -+-+++++||+-.-...-+.+
T Consensus         97 ~~~~i---~~ir~l~~~~~~~~~~~~ki~ii~~~~~l~~~~~n~llk~lE---ep~~~~~~il~~~~~~~ll~tI~SRc~  171 (373)
T 1jr3_A            97 SRTKV--EDTRDLLDNVQYAPARGRFKVYLIDEVHMLSRHSFNALLKTLE---EPPEHVKFLLATTDPQKLPVTILSRCL  171 (373)
T ss_dssp              CSCCS--SCHHHHHHHTTSCCSSSSSEEEEEECGGGSCHHHHHHHHHHH---SCCSSEEEEEEESCGGGSCHHHHTTSE
T ss_pred              ccCCH--HHHHHHHHHHhhcccCCCCeEEEEECcCcCCHHHHHHHHHHh---CCCcCeEEEEecCChHhChHHHhhhh


Q ss_pred              -----CcCHHHHHHHHHHHHHHHhcccccccccccCChhcc-hHHHHHhc
Q lap1             522 -----SLGLKEVEEKVRDFLKVKFTNSNTPNSYNHMDPDKLN-GLWSRISH  566 (583)
Q Consensus        522 -----s~slkEvEEkV~dfL~~k~~~s~~~~swn~Md~DkLd~pLISRISh  566 (583)
                           .++..++++.+......           .+++.|.=. .+|.|+|+
T Consensus        172 ~i~f~~l~~~~i~~~L~~~~~~~~~~~~~~e~~~i~~~al~~Ia~~s~  211 (373)
T 1jr3_A           172 QFHLKALDVEQIRHQLEHILNE-----------EHIAHEPRALQLLARAAE  211 (373)
T ss_dssp              EEECCCCCHHHHHHHHHHHHH-----------HTCCBCHHHHHHHHHSS
T ss_pred              ccccccCCcHHHHHHHHHHHh-----------cCCCcCHHHHHHHHHcC
```

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=88.02  E-value=2.4  Score=41.02  Aligned_cols=113  Identities=15%  Similarity=0.099  Sum_probs=0.0

Q ss_pred              HHHHHHHHHcCCCCCCCCeEEEEecCcccHHHH-HHHHHHHHHHhcccccCceeEecCcccccccChhHHHHHHHHHHHH
Q lap1             390 SQTFLEKHLNSSHPRSQPAILLLTAARDAEEAL-RCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNG  468 (583)
Q Consensus        390 lr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TL~qCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~  468 (583)
                       ....|.+++....   .|++||-.....+..++ .+++..|  ...+..+-+.++|+..+.. ..-|+++.-+..--...
T Consensus          5 ~~~~l~~~~~~~~~~~~~l~~g~~g~gk~~~a~~~~~~i~~~~~~~HpD~~~i~~~~~~-I~Id~IR~l~~~~~~p   78 (305)
T 2gno_A             5 QLETLKRIIEKSE---GISILINGEDLSYPREVSLELPEYV--EKFPPKASDVLEIDPEGEN-IGIDDIRTIKDFLNYSP   78 (305)
T ss_dssp              HHHHHHHHHTCS---SEEEEEECSSSSHHHHHHHHHHH--HTSCCCTTTEEEECCSSSC-BCHHHHHHHHHHTSCC
T ss_pred              HHHHHHHHHCCC---CCeEEEECCCCCCHHHHHHHHHHH--hcccccCCCCEEEEeCCCCC-CCHHHHHHHHHHhcc


Q ss_pred              hhcCCcEEEEeehhhCCHHHHHHHHHcCCCCCcCcccEEEEE
Q lap1             469 FKNGQNAAVVHRFESFPAGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus        469 F~~g~kaAVVh~LE~LPP~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                       ++++.|++||.+.|.+...|+.+|=+   +-.-+-+++++||+
T Consensus         79 ~~g~~KVvIId~ad~m~~~AaNALLK---tLEEPp~~t~fIL~  118 (305)
T 2gno_A            79 ELYTRKYVIVHDCERMTQQAANAFLK---ALEEPPEYAVIVLN  118 (305)
T ss_dssp              SSSSSEEEEETTGGGBCHHHHHHTHH---HHHSCCTTEEEEEE
T ss_pred              ccCCCceEEEEeChhhcCHHHHHHHH---HhhcCCCCcccccc
```

No 7

```
>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=84.16  E-value=20  Score=40.85  Aligned_cols=206  Identities=14%  Similarity=0.143  Sum_probs=0.0

Q ss_pred              HHHHHHHHHhcCCcccCcchHHHHHHHHHHHHHhcCCCCHHHHHHHHHHHHHHhcCCCCCCCCeEEEEecCcccHHHHHH
Q lap1             345 AALASGSFWFFSTPEVETTAVQEFQNQMNQLKNKYQGQDEKLWKRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEALRC  424 (583)
Q Consensus        345 lai~vg~~~~~~Pqv~~tave~f~~~~qLKskFPsQse~LWkrlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqC  424 (583)
                       ++=++.-+-.-+.-.+....-+.+.+.-+.|+.+.-+|++-+=.........-..=.+|+.+-++|||++..+      .
T Consensus        426 i~~vv~~~tgip~~~~~~~~~~l~~L~~~l~~rviGQ~~Av~~v~~al~~~~~gl~~~~rP~gsfLf~GPtG------v  499 (758)
T 1r6b_X           426 IESVVARIARIPEKSVSQSDRDTLKNLGDRLKMLVFGQDKAIEALTEAIKMARAGLGHEHKPVGSFLFAGPTG------V  499 (758)
T ss_dssp              HHHHHHHHSCCCCCCSSSSHHHHHHHHHHHTTTSCSCHHHHHHHHHHHHHHTTCSCTTSCSEEEEEECSTT------S
T ss_pred              HHHHHHHHhCCCccccccchHHHHHHHHHHHHhhhcCcHHHHHHHHHHHHHHhcCCCCCCCCceEEEEEeCCc------c


Q ss_pred              HHHHHHHHhcccccCceeEecCcccc---------ccChhHHHHHHHHHHHHHhcCCcEEE-EeehhhCCHHHHHHHHH
Q lap1             425 LSEQIADAYSSFRSVRAIRIDGTDKA---------TQDSDTVKLEVDQELSNGFKNGQNAAV-VHRFESFPAGSTLIFYK  494 (583)
Q Consensus        425 Lae~IAdaySs~~s~~aI~IDG~~~a----------~~DSD~vKleIDeqLks~F~~g~kaAV~Vh~LE~LPP~AaLIFH~  494 (583)
                       ==..+|.+..+.+....|.||-.+|.         +--+..++.+=.-.|-++.+....+.| +-+||.--|..-.+|..
T Consensus        500 GKTelAk~LA~~lf~~liriDMsEy~e~~svsrLiGsppGyvG~~e~g~Lte~Vr~~P~sVvLlDEIEKAhp~V~~lllq  579 (758)
T 1r6b_X           500 GKTEVTVQLSKALGIELLRFDMSEYMERHTVSRLIGAPPGYVGFDQGGLLTDAVIKHPHAVLLLDEIEKAHPDVFNILLQ  579 (758)
T ss_dssp              SHHHHHHHHHHHTCEEEEEEGGGCSSSSCCSSSCCCCSCSHHHHHTTHHHHHHHHCSSEEEEEETGGGSCHHHHHHHH
T ss_pred              cHHHHHHHHHHHHhhhhEEeccccccchhHHHHhcCCCCCCCCCCCCCCccchhhhcCCCceEEEeccchhhcCHHHHHHHH


Q ss_pred              hcCC--------CCcCcccceEEEEEEecccccccCC---cCHHHHHHHHHHHHHHhcccccccccccCChhccchHHHH
Q lap1             495 YCDh--------ENAAFKDVALVLTVLLEEETLGTS---LGLKEVEEKVRDFLKVKFTNSNTPNSYNHMDPDKLNGLWSR  563 (583)
Q Consensus        495 YCDh--------ENA~fKdVaLfLTV~Leeetl~~s~~~slkEvEEkV~dfL~~k~~~s~~~~swn~Md~DkLdpLISR  563 (583)
                       +.|.        ...-|+|++||||=.+-.+.....   .+..+....+.+.|...|.                .-|+.|
T Consensus        580 ildeG~ltD~~Gr~vdF~ntIiImTSN~G~~~~~~~~g~~~~~~~~~~~~l~~~Fr----------------PEflnR  643 (758)
T 1r6b_X           580 VMDNGTLTDNNGRKADFRNVVLVMTTNAGVRETERKSIGLIHQDNSTDAMEEIKKIFT----------------PEFRNR  643 (758)
T ss_dssp              HHHHSEEEETTTEEEECTTEEEEEEECSSCC-----------------CHHHHHHHSC----------------HHHHTT
T ss_pred              HhccCeEECCCCCCEEeccccCEEEecccccHHHHHhcccCcccchhhHHHHHHHHHHhCC----------------HHHHhh


Q ss_pred              hhcceEEeec
Q lap1             564 ISHLVLPVQP  573 (583)
Q Consensus        564 ISh~VLpVqP  573 (583)
                       | |.|++..|
T Consensus        644 i-D~iv~F~~  652 (758)
T 1r6b_X           644 L-DNIIWFDH  652 (758)
T ss_dssp              C-SEEEECCC
T ss_pred              C-CeEEECCC
```

No 8

```
>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=81.71  E-value=4.7  Score=39.11  Aligned_cols=115  Identities=7%  Similarity=0.028  Sum_probs=0.0

Q ss_pred              HHHHHHHHHHccCCCCCCCeEEEEecCcccHHHHHHHHHHHHHHccccc-CceeEecCcccccccChhHHHHHHHHHH
Q lap1             388 KRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEALRCLSEQIADAYSSFRS-VRAIRIDGTDKATQDSDTVKLEVDQELS  466 (583)
Q Consensus        388 krlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s-~~aI~IDG~~~a~~DSD~vKleIDeqLk  466 (583)
```

```
                      ......|...+..    ....-+||++..+.=.|.  ||..||.+...+.. .....+++.+....+.............
T Consensus        31 ~~~~~~l~~~l~~~~~~~~~~lLl~Gp~G~GKtt--la~~la~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  104 (327)
T 1iqp_A           31 EHIVKRLKHYVKT----GSMPHLLFAGPPGVGKTT--AALALARELFGENWRHNFLELNASDERGINVIREKVKEFARTK  104 (327)
T ss_dssp             HHHHHHHHHHHHH----TCCCEEEEESCTTSSHHH--HHHHHHHHHHGGGHHHHEEEEETTCHHHHHTTHHHHHHHHSC
T ss_pred             HHHHHHHHHHHHc----CCCCeEEEECcCCCCHHH--HHHHHHHhhhhcccccceeeeeccCCCChHHHHHHHHHHHHh


Q ss_pred             HHHhcCCcEEEEeehhhCCHHHHHHHHHcCCCCcCcccceEEEEE
Q 1apl            467 NGFKNGQNAAVVHRFESFPAGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus       467 s~F~~g~kaAVVh~LE~LPP~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                      ..+.+..++.||-++|.++.++..+|-++.+...   +++.+||+
T Consensus       105 ~~~~~~~kviiide~d~l~~~~~~~Ll~~lE~~~~~~~~~~Il~  146 (327)
T 1iqp_A          105 PIGGASFKIIFLDEADALTQDAQQALRRTMEMFS---SNVRFILS  146 (327)
T ss_dssp             CGGGCSCEEEEEETGGGSCHHHHHHHHHHHHTT---TTEEEEEE
T ss_pred             hcccCCCeEEEEechhhCCHHHHHHHHHHhCCC---CCeEEEEe
```

No 9

>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=76.87 E-value=15 Score=34.74 Aligned_cols=117 Identities=15% Similarity=0.130 Sum_probs=0.0

```
Q ss_pred             HHHHHHHHHHhccCCCCCCCeEEEEecCcccHHHH-HHHHHHHH----------------HHhcccccCceeEecCcccc
Q 1apl            388 KRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEAL-RCLSEQIA----------------DAYSSFRSVRAIRIDGTDKA  450 (583)
Q Consensus       388 krlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TL-qCLae~IA----------------daySs~~s~~aI~IDG~~~a  450 (583)
                      +.....|.+.+.....  +++||-.-...++.++ ++++..+.                 .........+.+.+++....
T Consensus        29 ~~~~~~L~~~~~~~~~~~~~lLl~Gp~G~GKttla~~~~~l~~~~~~~~~~~~~~~~~~i~~~~~~~~~e~~~~~~~  106 (250)
T 1njg_A           29 EHVLTALANGLSLGRIH--HAYLFSGTRGVGKTSIARLLAKGLNCETGITATPCGVCDNCREIEQGRFVDLIEIDAASRT  106 (250)
T ss_dssp             HHHHHHHHHHHHTCCC--SEEEEECSTTSCHHHHHHHHHHHCTTCSCSSCCSCSHHHHHHTTCCSSEEEEETTCGG
T ss_pred             HHHHHHHHHHHcCCCC--cEEEEECCCCCCcHHHHHHHHHHhCCccccccCCccccccHHHHHHHcCCCCCeEEecchhcC


Q ss_pred             ccChhHHHHHHHHHHHHHhcCCCcEEEEeehhhCCHHHHHHHHhcCCCCcCcccceEEEEE
Q 1apl            451 TQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESFPAGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus       451 ~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~LPP~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                      ..  +.++..+..-......++.++.||.++|.|+.++..+|.++++   -..+++.+||+
T Consensus       107 ~~~~~~ir~li~~~~~~~~~~~kviiIdeid~l~~~a~~~Ll~~le~~~~~~~~~~Il~  162 (250)
T 1njg_A          107 KV--EDTRDLLDNVQYAPARGRFKVYLIDEVHMLSRHSFNALLKTLE---EPPEHVKFLLA  162 (250)
T ss_dssp             GH--HHHHHHHHSCCCSCSSSSSEEEEEETGGGSCHHHHHHHHHHH---SCCTTEEEEEE
T ss_pred             CH--HHHHHHHHHHhccccCCCEEEEEeCcCcCCHHHHHHHHHHH---hCCCCEEEEEe
```

No 10

>1gvn_B Zeta; postsegregational killing system, plasmid; 1.95A {Streptococcus pyogenes} SCOP: c.37.1.21 PDB: 3q8x _B*
Probab=72.52 E-value=37 Score=32.09 Aligned_cols=119 Identities=15% Similarity=0.111 Sum_probs=0.0

```
Q ss_pred             HHHHHHHHHHHHHHHhcCCCCCCCCeEEEEecCcccHHHHHHHHHHHHHHhcccccCceeEecCcccccccChh--------
Q 1apl            384 EKLWKRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSD--------  455 (583)
Q Consensus       384 e~LWkrlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD--------  455 (583)
                      +++=+++...+..++....+...|..+||++.+++=.|+  |+..||+.+...+    +.|++.++......
T Consensus        10 ~e~~~~~~~~~~~~~~~~~~~~P~~ill~GppGsGKT~~~la~~la~~~~~~~~~~v~i~~d~~~~~~~~~~~~~~~~~   83 (287)
T 1gvn_B           10 KQFENRLNDNLEELIQGKKAVESPTAFLLGGQPGSGKTS--LRSAIFEETQGNV----IVIDNDTFKQQHPNFDELVKLY   83 (287)
T ss_dssp             HHHHHHHHHHHHHHTTCCCCCSSCEEEEEECCTTSCTHH--HHHHHHHHTTTCC----EEECTHHHHTTSTTHHHHHHHH
T ss_pred             HHHHHHHHHHHHHHhcCCCCCCCCCEEEEEeCCCCcCHHH--HHHHHHHHhcCCCc----eeecHHHHHHhccchhHHHHHh


Q ss_pred             ----------HHHHHHHHHHHHHHhcCCCcEEEEeehhhCCHHHHHHHHHHhcCCCCcCcccceEEEEEE
Q 1apl            456 ----------TVKLEVDQELSNGFKNGQNAAVVHRFESFPAGSTLIFYKYCDHENAAFKDVALVLTV  512 (583)
Q Consensus       456 -----------vKleIDeqLks~F~~g~kaAVVh~LE~LPP~AaLIFH~YCDhENA~fKdVaLfLTV  512 (583)
                                .....+...+..++.++.+  ++.+-..--++..+.+-..+...+..+  +++++++
T Consensus        84 ~~~~~~~~~~~~~~~~~~~~~a~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~gy~v~~~v~~~a~  146 (287)
T 1gvn_B           84 EKDVVKHVTPYSNRMTEAIISRLSDQGYN--LVIEGTGRTTDVPIQTATMLQAKGYET--KMYVMAV  146 (287)
T ss_dssp             GGGCHHHHHHHHHHHHHHHHHHHHTCC--EEECCCCCCSHHHHHHHHHHTTTCEE--EEEEECC
T ss_pred             hHHHHHHhhccchhHHHHHHHHHhCCCC--CCCCCCccccHHHHHHHHHHHHhCCCeE--EEEEEEC
```

No 11

>3zh9_B Delta; hydrolase, replication; 2.10A {Bacillus subtilis}
Probab=71.25 E-value=9.6 Score=37.56 Aligned_cols=106 Identities=12% Similarity=0.056 Sum_probs=0.0

```
Q ss_pred             HHHHHHhccCCCCCCCeEEEEecCcccHHHHHHHHHHH-HHhccccc-CceeEecCccccccChhHHHHHHHHHHHHHh
Q 1apl            392 TFLEKHLNSSHPRSQPAILLLTAARDAEEALRCLSEQIA-DAYSSFRS-VRAIRIDGTDKATQDSDTVKLEVDQELSNGF  469 (583)
Q Consensus       392 ~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCLae~IA-daySs~~s-~~aI~IDG~~~a~~DSD~vKleIDeqLks~F  469 (583)
                      .-|.++|++....  |++||....   .-=.+-.+..|+ .+..... -+.++++|.+.   |.+.+..++.   ..-|
T Consensus         3 ~~l~~~i~~~~l~~~~yll~G~e~~~~l~~~~~~l~~~~~~~~~~~~~~~~d~~~~~~~~~~l~~~~~~~~~pl   71 (347)
T 3zh9_B            3 FDVWKSLKKGEVH--PVYCLYGKE---TYLLQETVSRIRQTVVDQETKDFNLSVFDLEED---PLDQAIADAE---TFPF   71 (347)
T ss_dssp             HHHHHHHTTCCC--SEEEEESSC---HHHHHHHHHHHHHHCCGGGHHHHEEEEETTTS---CHHHHHHHT---SCCS
T ss_pred             HHHHHHHcCCCC--ceEEEEcCc---HHHHHHHHHHHHHcCCCCccccCCeEEEeCCCC---CHHHHHHHc---CCCC


Q ss_pred             hcCCcEEEEeehhhCCH--------HHHHHHHHhcCCCCcCcccceEEEEE
Q 1apl            470 KNGQNAAVVHRFESFPA--------GSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus       470 ~~g~kaAVVh~LE~LPP--------~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                      -+++++.+|.+.+.|..        .+.-+|-+|+.+   +-++++++||+
T Consensus        72 f~~~kvvii~~~~~l~~~~~~~~~~~~~aLl~~le~~~p~~~~~lIl~  118 (347)
T 3zh9_B           72 MGERRLVIVKNPYFLTGEKKKEKIEHNVSALESYIQS---PAPYTVFVLL  118 (347)
T ss_dssp             SSSCEEEEEECCGGGSCSCTTSSCCCCHHHHHHHHS---CCTTTEEEEEE
T ss_pred             CCCCeEEEEEChhhhhcccccccccccHHHHHHHHhC---CCCCeEEEEE
```

No 12

>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=68.11  E-value=9.8  Score=33.69  Aligned_cols=135  Identities=13%  Similarity=0.063  Sum_probs=0.0

Q ss_pred                HHHHhhcCCccccC---cchHHHHHHHHHHHHHHhcCCCCHHHHHHHHHHHHHHhccCCCCCCCeEEEEecCccccHHHHHHH
Q lap1             349 SGSFWFFSTPEVE---TTAVQEFQNQMNQLKNKYQGQDEKLWKRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEALRCL  425 (583)
Q Consensus        349 vg~~~~~~~Pqv~---~tave~f~~~~~qLKskFPsQse~LWkrlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCL  425 (583)
                         +|+..|...+.+.   ..........++.|+..+|+-...+++.+...++...+...++..-.+|||+.+.........+
T Consensus        44 vgvv~fs~~~~~~~~~l~~~~~~~~~~~i~~~~~~~~~~G~T~~~~al~~~~~~l~~~~~~~~~~~~~iilltDG~~~~~~~~~~~  123 (182)
T 1shu_X          44 LSFIVFSSQATIILPLTGDRGKISKGLEDLKRVSPVGETYIHEGLKLANEQIQKAGGLKTSSIIIALTDGKLDGLVPSYA  123 (182)
T ss_dssp                EEEEEESSSEEEEEEEECCHHHHHHHHHHHHTCCCCSCCCHHHHHHHHHHHHHHHHTGGGSCEEEEEEECCCCCTTHHHHH
T ss_pred                EEEEEEcCCceEeccccccchHHHHHHHhhhcccCCCCCchHHHHHHHHHHHHHHhcccCCCCceEEEEecCCCCCCCccHHH


Q ss_pred                HHHHHHHhcccccCceeEecCcccccccChhHHHHHHHHHHHHHHHHhhcCCCcEEEE-eehhhCCHHHHHHHHHhc
Q lap1             426 SEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVV-HRFESFPAGSTLIFYKYC  496 (583)
Q Consensus        426 ae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVV-h~LE~LPP~AaLIFH~YC  496 (583)
                         ......+.......-+|-|+....             .+|+..-....+.+.+ .+++.|+--.-.+.-++|
T Consensus       124 ~~~a~~~~~~~~i~v~~vgig~~~~-------------~~L~~ia~~~~~~f~~~~~~~~~L~~i~~~i~~~iC  182 (182)
T 1shu_X         124 EKEAKISRSLGASVYCVGVLDFEQ-------------AQLERIADSKEQVFPVKGGFQALKGIINSILAQSC  182 (182)
T ss_dssp                HHHHHHHHHTTCEEEEEECSSCCH-------------HHHHHHSSSGGGEEESSSTTHHHHHHHHHHHHTBC
T ss_pred                HHHHHHHHHCCCEEEEEECCccCH-------------HHHHHHhCCCCCeEEecCCHHHHHHHHHHHHHHHhhC
```

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=61.02  E-value=41  Score=32.33  Aligned_cols=104  Identities=14%  Similarity=0.201  Sum_probs=0.0

Q ss_pred                CHHHHHHHHHHHHHHHHhccCCCCCCCeEEEEec-CcccHHHH-HHHHHHHHHHhcccccCceeEecCcccccccChhHHHHHH
Q lap1             383 DEKLWKRSQTFLEKHLNSSHPRSQPAILLLTA-ARDAEEAL-RCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLE  460 (583)
Q Consensus        383 se~LWkrlr~~LekhLNts~Pr~ePAVLLLtA-~~~Ae~TL-qCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKle  460 (583)
                         .+.+.+.++..+.       ..+ .|..+||.+ ...++.++ ++|+..+         +...+.+++.+..          ...
T Consensus        31 ~~~~~~~l~~~l~~------~~~~~~~~~L~~G~~G~GKT~la~~la~~l--------~~~~~~~~~i~~~~~~~--------~~~~  88 (324)
T 3u61_B          31 PAFDKETFKSITS------KGK-IPHIILHSPSPGTGKTTVAKALCHDV--------NADMMFVNGSDCK-------IDF   88 (324)
T ss_dssp                CHHHHHHHHHHHH------TTC-CCSEEEECSSTTSSHHHHHHHHHHHT--------TEEEEEEETTTCC-------HHH
T ss_pred                cHHHHHHHHHHHH------cCC-CCeEEEeeCcCCCCHHHHHHHHHHHHh--------CCCEEEEcccccC-------HHH


Q ss_pred                HHHHHHHHhhc-----CCcEEEEeehhhCC-HHHHHHHHHhcCCCCCcCccceEEEEE
Q lap1             461 VDQELSNGFKN-----GQNAAVVHRFESFP-AGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus        461 IDeqLks~F~~-----g~kaAVVh~LE~LP-P~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                         +...+......     +.++.+|-+++.|+ ..+.-+|+++-+...   .++.+|+|
T Consensus        89 i~~~~~~~~~~~~~~~~~~vliiDEi~~l~~~~~~~~~L~~~le~~~---~~~~~~iI~~  142 (324)
T 3u61_B          89 VRGPLTNFASAASFDGRQKVIVIDEFDRSGLAESQRHLRSFMEAYS---SNCSIIIT  142 (324)
T ss_dssp                HHTHHHHHHHBCCCSSCEEEEEEESCCCGGGHHHHHHHHHHHHHHHG---GGCEEEEE
T ss_pred                HHHHHHHHHhhcccCCCCeEEEEECCcccCcHHHHHHHHHHHHHHhCC---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=60.25  E-value=28  Score=34.21  Aligned_cols=115  Identities=11%  Similarity=0.179  Sum_probs=0.0

Q ss_pred                HHHHHHHHHHhccCCCCCCCeEEEEecCccccHHHH-HHHHHHHHHHhcccccCceeEecCcccccccChhHHHHHHHHHHHH
Q lap1             388 KRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEAL-RCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELS  466 (583)
Q Consensus        388 krlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TL-qCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLk  466 (583)
                         ......|...+....    -|.+||..-...++.|+ ++||..+   +....+...+.+++.+....+........-....
T Consensus        31 ~~~~~~L~~~i~~~~~~~~~~~lLl~Gp~G~GKTtla~~la~~~---~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  104 (340)
T 1sxj_C          31 NEVITTVRKFVDEGK---LPHLLFYGPPGTGKTSTIVALAREI---YGKNYSNMVLELNASDDRGIDVVRNQIKDFASTR  104 (340)
T ss_dssp                HHHHHHHHHHHHTTC---CCCEEEECSSSSHHHHHHHHHHHH---HTTSHHHHEEECTTSCCSHHHHHTHHHHHHHBC
T ss_pred                HHHHHHHHHHHHCCC---CCEEEEECcCCCCHHHHHHHHHHhh---ccCCcccceeeecccCCChhHHHHHHHHHHHhh


Q ss_pred                HHhhcCCCcEEEEeehhhCCHHHHHHHHHhcCCCCCcCccceEEEEE
Q lap1             467 NGFKNGQNAAVVHRFESFPAGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus        467 s~F~~g~kaAVVh~LE~LPP~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                         ....++.++.+|.+++.+.+.+..+|.++-+..   -+.+.++||
T Consensus       105 ~~~~~~~~kiiiiDe~d~l~~~~q~aLl~~le~~~---~~~~~~~il~  146 (340)
T 1sxj_C         105 QIFSKGFKLIILDEADAMTNAAQNALRRVIERY---TKNTRFCVL  146 (340)
T ss_dssp                CSSSCSCEEEEETTGGGSCHHHHHHHHHHHHHHHT---TTTEEEEEE
T ss_pred                hccCCCeEEEEEeccccCCHHHHHHHHHHHHhcC---CCCeEEEee
```

No 15

>3t15_A Ribulose bisphosphate carboxylase/oxygenase activ chloroplastic; photosynthesis, rubisco activase, AAA+ protein; 2.95A {Nicotiana tabacum} PDB: 3zw6 _A

```
Probab=56.48  E-value=56  Score=31.78  Aligned_cols=117  Identities=10%  Similarity=0.143  Sum_probs=0.0

Q ss_pred                HHHHHHHHHHhccCCCCCCCeEEEEecCccccHHHHHHHHHHHHHHHHhcccccCceeEecCcccccccChhHHHHHHHHHHHH
Q lap1             388 KRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSN  467 (583)
Q Consensus        388 krlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks  467 (583)
                         +.....+...++....+ .|..+||++.++.=.|.  |+..||...    ....+.++..++...........|...++.
T Consensus        18 ~~~~~~~k~~l~~~~~~~-p~~lLl~GppGtGKT~--la~aiA~~l----~~~~~~i~v~~~~~l~~~~~~~g~~~~~i~~~f~~  90 (293)
T 3t15_A          18 KLVVHITKNFLKLPNIK-VPLILGIWGGKGQGKSF--QCELVFRKM----GINPIMMSAGELESGNAGEPAKLIRQRYRE   90 (293)
T ss_dssp                HHHHHHHHTTSCCTTCC-CCSEEEEEECTTSCHHH--HHHHHHHHH----TCCCEEEEHHHHHCC---HHHHHHHHHHHH
T ss_pred                HHHHHHHHHHHHhcCCCC-CCeEEEEECCCCCCHHH--HHHHHHHHh----CCCEEEEeHHHhhccCCchhHHHHHHHHHH


Q ss_pred                Hh----hcCCcEEEEeehhhCCHHHH-------------HHHHHhcCCCC----------cCccceEEEEE
Q lap1             468 GF----KNGQNAAVVHRFESFPAGST-------------LIFYKYCDHEN----------AAFKDVALVLT  511 (583)
Q Consensus        468 ~F----~~g~kaAVVh~LE~LPP~Aa-------------LIFH~YCDhEN----------A~fKdVaLfLT  511 (583)
                         +.    .....+.+|-++|.+-+...             -.|..++|...           ....++++++|.|
T Consensus        91 a~~~~~~~~~~~vl~iDEiD~~~~~~~~~~~~~~~~~~~v~~~Ll~~ld~~~~~~~~~~~~~~~~~v~vI~t  161 (293)
T 3t15_A          91 AAEIIRKGNMCCLFINDLDAGAGRMGGTTQYTVNNQMVNATLMNIADNPTNVQLPGMYNKQENARVPIIVT  161 (293)
T ss_dssp                HHHHHTTSSCCCEEEEECCC-------------CHHHHHHHHHHHHHHCCC-----------CCCCCCEEEE
T ss_pred                HHHHHhcCCCeEEEEechhhhcCCCCCccccccchHHHHHHHHHHHHhcccccccccCCCCCeEEEe
```

No 16

>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=52.39 E-value=1.4e+02 Score=28.59 Aligned_cols=119 Identities=15% Similarity=0.261 Sum_probs=0.0

```
Q ss_pred             HHHHHHHHHHhccCCCCCCCeEEEEecCcccHHHH-HHHHHHH---------------------HHHhccccCCceeEec
Q lap1         388 KRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEAL-RCLSEQI---------------------ADAYSSFRSVRAIRID  445 (583)
Q Consensus    388 krlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TL-qCLae~I---------------------AdaySs~~s~~aI~ID  445 (583)
                     +.....|.+.+.  ..+..|..||..-...++.|+ ++||..|                     -........+...+.+.
T Consensus     20 ~~~~~~L~~~~~~--~~~~~p~lLl~Gp~G~GKTt~a~~la~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  97 (354)
T 1sxj_E        20 EELTNFLKSLSD--QPRDLPHLLLYGPNGTGKKTRCMALLESIFGPGVYRLKIDVRQFVTASNRKLELNVVSSPYHLEIT  97 (354)
T ss_dssp             HHHHHHHHTTTT--CTTCCCCEEEECSTTSSHHHHHHTHHHHHSCTTCCC------------------CCEECSSEEEEC
T ss_pred             HHHHHHHHHHHh--CCCCCCeEEEECCCCcCHHHHHHHHHHHHhcCCcccccccccccccccchhhhccccCCCceeee


Q ss_pred             CcccccccChhHHHHHHHHHH----------HHHHhhcCCcEEEEeehhhCCHHHHHHHHHHhcCCCCcCcccceEEEEE
Q lap1         446 GTDKATQDSDTVKLEVDQE----------LSNGFKNGQNAAVVHRFESFPAGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus    446 G~~~a~~DSD~vKleIDeq----------Lks~F~~g~kaAVVh~LE~LPP~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                     ..+....+...++..+...            ....+.+..++.|+.++|.+...+..+|.+..+...   +++.++||
T Consensus     98 ~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~kiiide~d~l~~~~~~~~~l~~~~le~~~~----~~~~~~il~  170 (354)
T 1sxj_E        98 PSDMGNNDRIVIQELLKEVAQMEQVDFQDSKDGLAHRYKCVIINEANSLTKDAQAALRRTMEKYS---KNIRLIMV  170 (354)
T ss_dssp             CC----CCHHHHHHHHHHHTTTTC------------CCEEEEEECTTSSCHHHHHHHHHHHHHHST---TTEEEEEE
T ss_pred             ccccccCCcceeehhhhhHHhhhhhhhhcccccCCCCeEEEEecccccchHhhHHHHHHHHHHHcc---cceEEeec
```

No 17

>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=51.59 E-value=42 Score=31.93 Aligned_cols=115 Identities=10% Similarity=0.100 Sum_probs=0.0

```
Q ss_pred             HHHHHHHHHHhccCCCCCCCeEEEEecCcccHHHH-HHHHHHHHHHhccccCCceeEecCcccccccChhHHHHHHHHHHH
Q lap1         388 KRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEAL-RCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELS  466 (583)
Q Consensus    388 krlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TL-qCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLk  466 (583)
                     +.....|...+...+   -|.+||......++.++ ++||..+   ...........+++.+....+.-...........
T Consensus     23 ~~~~~~L~~~~~~~~~~~~~~~~~lL~~Gp~G~GKttla~~lak~l---~~~~~~~~~~~~~~~~~~s~~~~~~~~~~~~~~~~~  96 (319)
T 2chq_A        23 DEVIQRLKGYVERKN---IPHLLFSGPPGTGKTATAIALARDL---FGENWRDNFIEMNASDERGIDVVRHKIKEFARTA  96 (319)
T ss_dssp             HHHHHHHHTTTTTC---CCCEEEESSSSSHHHHHHHHHHHHH---HTTCHHHHCEEEETTSTTCTTTSSHHHHHHHHSC
T ss_pred             HHHHHHHHHHHHCCC---CCEEEEECCCCCHHHHHHHHHHHHh---ccccccccccceeecccCCcHHHHHHHHHHHHHHhh


Q ss_pred             HHhhcCCcEEEEeehhhCCHHHHHHHHHHhcCCCCcCcccceEEEEE
Q lap1         467 NGFKNGQNAAVVHRFESFPAGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus    467 s~F~~g~kaAVVh~LE~LPP~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                     .......++.+|.+++.+..++..+|.++++...   +.+.+||+
T Consensus     97 ~~~~~~~~viide~d~l~~~~~~~~l~~~~e~~~~~~~~~~~~~~il~  138 (319)
T 2chq_A        97 PIGGAPFKIIFLDEADALTADAQAALRRTMEMYS---KSCRFILS  138 (319)
T ss_dssp             CSSSCCCEEEEETGGGSCHHHHHTTGGGTSSSS---SSEEEEEE
T ss_pred             hccCCceEEEEEeccccccHHHHHHHHHHHhhCC---ccceeecc
```

No 18

>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=50.26 E-value=59 Score=28.25 Aligned_cols=99 Identities=12% Similarity=-0.012 Sum_probs=0.0

```
Q ss_pred             HHHHhccCCCCCCCeEEEEecCcccHHHHHHHHHHHHHHHHhccccCCceeEecCcccccccChhHHHHHHHHHHHHHHHH-----
Q lap1         394 LEKHLNSSHPRSQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNG-----  468 (583)
Q Consensus    394 LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~-----  468 (583)
                     |.++|+++.+.     +.|.+|.+.--.-+++..-...+....+....+...+.+.            .+++-+...
T Consensus      9 L~~~L~~~l~~-----vYll~G~E~~l~~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~t~pl  73 (140)
T 1jql_B         9 LRAQLNEGLRA-----AYLLLGNDPLLLQESQDAVRQVAAAQGFEEHHTFSIDPNT----------DWNAIFSLCQAMSL  73 (140)
T ss_dssp             HHHHHHHCCCS-----EEEEESSCHHHHHHHHHHHHHHHHHHHHTTCCEEECCCCSTTC----------CHHHHHHHHHCCCT
T ss_pred             HHHHHHccCCc-----EEEEeCcHHHHHHHHHHHHHHHHHhcCCchhhhhhccCCCC----------CHHHHHHHHhcCCC


Q ss_pred             hhcCCcEEEEeehh-hCCHHHHHHHHHHhcCCCCcCcccceEEEEE
Q lap1         469 FKNGQNAAVVHRFE-SFPAGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus    469 F~~g~kaAVVh~LE-~LPP~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                     | +++++.+|+..+ .++....-+|..||.+-++   +++|||+
T Consensus     74 F-~~~klv~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~L~~y~~~~~~~~~~~~~~~~~~ili~~  113 (140)
T 1jql_B        74 F-ASRQTLLLLPENGPNAAINEQLLTLTGLLHD---DLLLIVR  113 (140)
T ss_dssp             T-CCCEEEEEECCTTCSCTTHHHHHHHHHHHCCS---SCCEEEE
T ss_pred             C-cCceeeeccccCCCCCHHHHHHHHHHhcCCCC---CEEEEEE
```

No 19

>2x8a_A Nuclear valosin-containing protein-like; nuclear protein; 2.60A {Homo sapiens}
Probab=50.22 E-value=1.3e+02 Score=28.87 Aligned_cols=100 Identities=13% Similarity=0.120 Sum_probs=0.0

```
Q ss_pred             CCCeEEEEecCcccHHHHHHHHHHHHHHHHhccccCCceeEecCcccccccChhHHHHHHHHHHHHHHHHHHHhhcCCCcEEEEEeehhhC
Q lap1         405 SQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESF  484 (583)
Q Consensus    405 ~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~L  484 (583)
                     ..|.-+||++..+.=.|  -|+..||..+...+    +.+++........++....|..-+..+-.....+.++-+++.|
T Consensus     42 ~~~~giLl~GppGtGKT--~la~aia~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~g~~~~~~l~~~~f~~a~~~~p~il~~d~~d~l  115 (274)
T 2x8a_A        42 VTPAGVLLAGPPGCGKT--LLAKAVANESGLNF----ISVKGPELLNMYVGESERAVRQVFQRAKNSAPCVIFFDEVDAL  115 (274)
T ss_dssp             CCCSEEEEESSTTSCHH--HHHHHHHHHTTCEE----EEEETTTTCSSTTHHHHHHHHHHHHHHHHTCSEEEEEETCTTT
T ss_pred             CCCceEEEECCCCCHH--HHHHHHHHhhcccc----eEEehhhcccccchhHHHHHHHHHHHHHHHcCCcEEeehhhhh


Q ss_pred             CHH-----------HHHHHHHhcCCCCcCcccceEEEEE
Q lap1         485 PAG-----------STLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus    485 PP~-----------AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
```

```
                        -+.           ....|-+++|..... +++++|.|
T Consensus       116 ~~~~~~~~~~~~~~~~~ll~~~~~~~~~~~~v~vIat  152 (274)
T 2x8a_A          116 CPRRSDRETGASVRVVNQLLTEMDGLEAR-QQVFIMAA  152 (274)
T ss_dssp             CC---------CTTHHHHHHHHHTCCST-TCEEEEEE
T ss_pred             hccccCCCCcHHHHHHHHHHHHcccCC-CCEEEEEc
```

No 20

>**4hqf_A** Thrombospondin-related anonymous protein, trap; malaria, parasite motility, I domain, TSR domain, receptor O sporozoite, vaccine target; 2.20A {Plasmodium falciparum} PDB: **4hqk _A** **2bbx _A**
Probab=42.81 E-value=1.7e+02 Score=27.93 Aligned_cols=117 Identities=7% Similarity=-0.087 Sum_probs=0.0

```
Q ss_pred             HHHHHHHHHHH-HhCCCCHHHHHHHHHHHHHHhcc-CCCCCCCeEEEEecCcccHHHHHHHHHHHHHhcccccCceeE
Q lap1            366 QEFQNQMNQLK-NKYQGQDEKLWKRSQTFLEKHLNS-SHPRSQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIR  443 (583)
Q Consensus       366 e~f~~~~qLK-skFPsQse~LWkrlr~~LekhLNt-s~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~  443 (583)
                      +.+...++.|+ ..+++-.-.+...|..+++...+. ..+....++|||+-+.....  ..+...+..+...-...-+|-
T Consensus        87 ~~l~~~i~~l~~~~~~~G~T~~~~aL~~a~~~l~~~~~r~~~~~iilllTDG~~~d~--~~~~~~~~~l~~~gv~i~~ig  164 (281)
T 4hqf_A           87 EKALIIIKSLLSTNLPYGKTSLTDALLQVRKHLNDRINRENANQLVVILTDGIPDSI--QDSLKESRKLSDRGVKIAVFG  164 (281)
T ss_dssp             HHHHHHHHHHHHTTGGGCSCCHHHHHHHHHHHHHTSCCCTTCEEEEEEEESSCCSCH--HHHHHHHHHHHTTCEEEEEE
T ss_pred             HHHHHHHHHHhcCCCCCCcccHHHHHHHHHHHHHhcccccccCEEEEEEecCCCCCc--HHHHHHHHHHHCCCEEEEEe


Q ss_pred             ecCccccccChhHHHHHHHHHHHHHhcC-----CcEEEEeehhhCCHHHHHHHHHc
Q lap1            444 IDGTDKATQDSDTVKLEVDQELSNGFKNG-----QNAAVVHRFESFPAGSTLIFYKYC  496 (583)
Q Consensus       444 IDG~~a~~DSD~vKleIDeqLks~F~~g-----~kaAVVh~LE~LPP~AaLIFH~YC  496 (583)
                      |+....            .+.|+..-...     .+++.+.+++.|+.-.-.+....|
T Consensus       165 iG~~~~~~~~~~~~~~~L~~iA~~~~~g~~~~~~~~~~~L~~~~~l~~~iC  210 (281)
T 4hqf_A          165 IGQGIN~~~~~~~~~~~~VAFNRFLVGCHPSDGKCNLYADSAWENVKNVIGPFMKAVC  210 (281)
T ss_dssp             ESSSCC~~~~~~~~~~~~HHHHHHHTTSCSSSSCCTTEEEECGGGHHHHHHHHHHHH
T ss_pred             CCCccC~~~~~~~~~~~~HHHHHhhhCCCCCCCCCCeEEecchhhhhcccCCccccccC
```

No 21

>**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=41.81 E-value=2.1e+02 Score=25.79 Aligned_cols=158 Identities=9% Similarity=0.060 Sum_probs=0.0

```
Q ss_pred             HHHHHHHHHHHcccCCCCCCCeEEEEecCcccHHHHHHHHHHHHHHccccc-CceeEecCcccccccChhHHHHHHHHHH
Q lap1            388 KRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEALRCLSEQIADAYSSFRS-VRAIRIDGTDKATQDSDTVKLEVDQELS  466 (583)
Q Consensus       388 krlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLk  466 (583)
                      ..+...|...++...   -|.+||.....++.++   |..+|........ ...+.++..+....+.-.....-.....
T Consensus        23 ~~~~~~l~~~i~~~~~~~~~lll~Gp~G~GKTt~~~~a~~i~k~l~~~~~~~~~~~~~~s~~~~~~~~~~~~~~~~~~~  96 (226)
T 2chg_A           23 DEVIQRLKGYVERKN---IPHLLFSGPPGTGKTAT---AIALARDLFGENWRDNFIEMNASDERGIDVVRHKIKEFARTA  96 (226)
T ss_dssp             HHHHHHHHHHHHTTC---CCCEEEECSTTSSHHHH---HHHHHHHHHGGGGGGGEEEEETTCTTCHHHHHHHHHHHTSC
T ss_pred             HHHHHHHHHHHCCC---CCeEEEECCCCCCHHHH---HHHHHHHHhcccccccccceeeccccCCcHHHHHHHHHHHhh


Q ss_pred             HHhhcCCCcEEEEEeehhhCCHHHHHHHHHHcCCCCCcCcccceEEEEEEecccccccC-----------CcCHHHHHHHHHH
Q lap1            467 NGFKNGQNAAVVHRFESFPAGSTLIFYKYCDHENAAFKDVALVLTVLLEEETLGT-----------SLGLKEVEEKVRDP  535 (583)
Q Consensus       467 s~F~~g~kaAVVh~LE~LPP~AaLIFH~YCDhENA~fKdVaLfLTV~Leeetl~~~~~~~~~~~~s~slkEvEEkV~df  535 (583)
                      ....+..++.+|.+++.++.++..+|..+-+..+   +...+|++-.-...-..+           .++..++...+.+.
T Consensus        97 ~~~~~~~~iiide~d~l~~~~~~~ll~~le~~~~~~~~~~i~~~~~~~~l~~~l~sr~~~i~~~~~~~~~~~~l~~i  173 (226)
T 2chg_A           97 PIGGAPFKIIFLDEADALTADAQAALRRTMEMYS---KSCRFILSCNYVSRIIEPIQSRCAVFRFKPVPKEAMKKRLLEI  173 (226)
T ss_dssp             CSTTCSCEEEEEETGGGSCHHHHHHHHHHHHTT---TTEEEEEEESCGGGSCHHHHTTSEEEECCCCCHHHHHHHHHHH
T ss_pred             hhcCCCeeEeehhhhhhcCHHHHHHHHhhhcccC---cceEEEecCCChHhCchhHhhhhhhhhhhcccccHHHHHHHHH


Q ss_pred             HHHHhcccccccccccCChhhcchHHHH
Q lap1            536 LKVKFTNSNTPNSYNHMDPDKLNGLWSR  563 (583)
Q Consensus       536 L~~k~~~s~~~~swn~Md~DkLdpLISR  563 (583)
                      +..         -.-.++++.++-|+.+
T Consensus       174 ~~~~~~~~~~~~~~i~~~~l~~i~~~  192 (226)
T 2chg_A          174 CEK---------EGVKITEDGLEALIYI  192 (226)
T ss_dssp             HHH---------HTCCBCHHHHHHHHHH
T ss_pred             HHH---------hCCCCCHHHHHHHHHH
```

No 22

>**1d2n_A** N-ethylmaleimide-sensitive fusion protein; hexamerization domain, ATPase, transport; HET: ANP; 1.75A {Cricetulus griseus} SCOP: **c.37.1.20** PDB: **1nsf _A***
Probab=41.69 E-value=2.7e+02 Score=27.04 Aligned_cols=120 Identities=16% Similarity=0.192 Sum_probs=0.0

```
Q ss_pred             HHHHHHHHHHHHHHcccCCCCCCCeEEEEecCcccHHHHHHHHHHHHHHcccccCceeEecCcccccccChhHHH-HHHH
Q lap1            384 EKLWKRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVK-LEVD  462 (583)
Q Consensus       384 e~LWkrlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vK~leID  462 (583)
                      +.+=..+...++..+-+  .....|.-+||++.++.=.|+  ||..||......+    +.|++.+...-..+.-+ ..|.
T Consensus        43 ~~i~~~~~~~~~~~~~~~~~~~~~vLL~GppGtGKT~~~la~~lA~~~~~~~~~~~~i~~~~~~~g~~~~~~~~l~  114 (272)
T 1d2n_A           43 TRVLDDGELLVQQTKN--SDRTPLVSVLLEGPPHSGKTA--LAAKIAEESNFPF----IKICSPDKMIGFSETAKCQAMK  114 (272)
T ss_dssp             HHHHHHHHHHHHHHH--CSSCSEEEEEEECSTTSSHHH--HHHHHHHHHTCSE----EEEECGGGCTTCCHHHHHHHHH
T ss_pred             HHHHHHHHHHHHHHc--cCCCCCCeEEEECCCCCCHHH--HHHHHHHHhCCCe----Eeecchhhhcccccchhhhhhh


Q ss_pred             HHHHHHHhcCCcEEEEeehhhC----------CHHHHHHHHHcCCCCCcCcccceEEEEE
Q lap1            463 QELSNGFKNGQNAAVVHRFESF----------PAGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus       463 eqLks~F~~g~kaAVVh~LE~L----------PP~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                      +-++.+.+.+....+.+|-++|.|          .-.....|-.+=|.....-.++++|.|
T Consensus       115 ~~F~~A~~~~p~vl~iDEid~l~~~~~~~~~~~~~~~~l~~~l~~~~~~~~v~vI~t  173 (272)
T 1d2n_A          115 KIFDDAYKSQLSCVVVDDIERLLDYVPIGPRFSNLVLQALLVLLKKAPPQGRKLLIIGT  173 (272)
T ss_dssp             HHHHHHHTSSEEEEEECCHHHHTTCBTTTTBCCHHHHHHHHHHTTCCCSTTCEEEEEEE
T ss_pred             HHHHHHHhcCCeeEEEecchhcccCCCCCchHHHHHHHHHHHHHhCCccccCCCEEEEEc
```

No 23

>**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=37.32  E-value=2.5e+02  Score=26.91  Aligned_cols=127  Identities=13%  Similarity=0.153  Sum_probs=0.0

Q ss_pred              HHHHHHhCCCCCHHHHHHHHHHHHHccCCCCCCCCeEEEEecCcccHHHHHHHHHHHHHcccccCceeEecCccccc
Q lap1            372 MNQLKNKYQGQDEKLWKRSQTFLEKHLNSSHPRSQPAIIIIITAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKAT  451 (583)
Q Consensus       372 ~~qLKskFPsQse~LWkrlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~  451 (583)
                      |.++++..=+++ ..|+.++..+.+.+.-..    ..| |||..-..+++..+=.+++.    +|.-.....+.++.   ..
T Consensus         1 ~~~~~~liG~S-~~~~~~~~~i~~~a~~~~~~p-vlI~GE~GtGK~~lA~~ih~-----s~~~~~~~~~~~~~~~   67 (265)
T 2bjv_A            1 MAEYKDNLLGEA-NSFLEVLEQVSHLAPL----DKP-VLIIGERGTGKELIASRLHY----LSSRWQGPFISLNC---AA   67 (265)
T ss_dssp             ---------CCC-HHHHHHHHHHHHTTS----CSC-EEEECCTTSCHHHHHHHHHH----TSTTTTSCEEEEEG---GG
T ss_pred             CCccccCeEEcC-HHHHHHHHHHHHhCC----CCC-EEEECCCCcCHHHHHHHHH----hcccCCCCeEEec---cc


Q ss_pred              cChhHHHHHHHHHHHHhhcCCc------------EEEEeehhhCCHHHHHHHHHcCC--------CCcCcccceEEEEE
Q lap1            452 QDSDTVKLEVDQELSNGFKNGQN------------AAVVHRFESFPAGSTLIFYKYCDH--------ENAAFKDVALVLT  511 (583)
Q Consensus       452 ~DSD~vKleIDeqLks~F~~g~k------------aAVVh~LE~LPP~AaLIFH~YCDh--------ENA~fKdVaLfLT  511 (583)
                      .+.+.....+.......|....+           +.++.+++.||+..-..|..|.++         .++.-.++-||++
T Consensus        68 ~~~~~~~~l~g~~~~~~~~~~~~~g~le~a~~GtL~l~~i~~L~~~~Q~~L~~~L~~~~~~~~~~~~~~~~riI~s  147 (265)
T 2bjv_A           68 LNENLLDSELFGHEAGAFTGAQKRHPGRFERADGGTLFLDELATAPMMVQEKLLRVIEYGELERVGGSQPLQVNVRLVCA  147 (265)
T ss_dssp             SCHHHHHHHHCCC---------CCCCHHHHTTTSEEEEESGGGSCHHHHHHHHHHHHCEECCCCC--CEECCCEEEEE
T ss_pred             ccccHHHHHHhCCCcCCcCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

No 24
>4b4t_H 26S protease regulatory subunit 7 homolog; hydrolase, AAA-atpases, protein degradation, ubiquitin-prote
pathway; 7.40A {Saccharomyces cerevisiae} PDB:  4bgr _H
Probab=35.89  E-value=1.5e+02  Score=31.48  Aligned_cols=101  Identities=9%  Similarity=0.095  Sum_probs=0.0

Q ss_pred              CCCeEEEEecCcccHHHHHHHHHHHHHHhcccccCceeEecCcccccccCHHHHHHHHHHHHHHHhhcCCcEEEEeehhhC
Q lap1            405 SQPAIIIIITAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESF  484 (583)
Q Consensus       405 ~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~L  484 (583)
                      ..|.-+||++..+.=.|+  ||..||......|    +.+++.++...-.......+...+..+......+.+|=.++.|
T Consensus       241 ~~~~~vLL~GppGtGKT~--lAraiA~~~~~~f----i~v~~s~l~~~~~g~~~~~i~~~f~~a~~~~p~ILfIDEId~l  314 (467)
T 4b4t_H          241 DPPKGIIIYGPPGTGKTL--CARAVANRTDATF----IRVIGSELVQKYVGEGARMVRELFEMARTKKACIIFFDEIDAV  314 (467)
T ss_dssp             CCCSEEEECSCTTSSHHH--HHHHHHHHHTCEE----EEEEGGGGCCCSSSHHHHHHHHHHHHHHHTCSEEEEEECCTTT
T ss_pred             CCCCeeEEECCCCcCHHH--HHHHHHHHcccCCE----EEEehhHhhhhhhccHHHHHHHHHHHHHHCCCeEEEEECcHHH


Q ss_pred              -----------CHHHHHHHHHHcCCCCcC--cccceEEEEE
Q lap1            485 -----------PAGSTLIFYKYCDHENAA--FKDVALVLT  511 (583)
Q Consensus       485 -----------PP~AaLIFH~YCDhENA~~~fKdVaLfLT  511 (583)
                                +.....+|..+.+...-.  -.+++||+|
T Consensus       315 ~~~r~~~~~~~~~~q~~Ll~lL~~ld~~~~~~v~vI~a  354 (467)
T 4b4t_H          315 GGARFDDGAGGDNEVQRTMLELITQLDGFDPRGNIKVMFA  354 (467)
T ss_dssp             SBCCSSSSCGGGGHHHHHHHHHHHHHHSSCCTTTEEEEEE
T ss_pred             hcccccCCcccCHHHHHHHHHHHHHhCcccCCCeEEEEe

No 25
>2lco_A WALP19-P8 peptide; proline distortion, transmembrane, membrane protein; HET: ETA; NMR {Synthetic}
Probab=35.22  E-value=27  Score=24.01  Aligned_cols=17  Identities=35%  Similarity=0.659  Sum_probs=0.0

Q ss_pred              hhHHHHHHHHHHHHHh
Q lap1            337 RWWLLPLIAALASGSFW  353 (583)
Q Consensus       337 ~~~~i~vilai~vg~~~  353 (583)
                      ||+-++-.+|+++++||
T Consensus         3 wwlalapalalalalww   19 (26)
T 2lco_A            3 WWLALAPALALALALWW   19 (26)
T ss_pred             hHHHHHHHHHHHHHHH

No 26
>1jr3_D DNA polymerase III, delta subunit; processivity, processivity clamp, clamp loader, AAA+ ATPase,
transferase; HET: DNA; 2.70A {Escherichia coli} SCOP: a.80.1.1 c.37.1.20 PDB:  1jqj _C*  1xxh _A*  1xxi _A*  3glf _A*  3glg
 3glh _A*  3gli _A*
Probab=33.64  E-value=3.7e+02  Score=26.26  Aligned_cols=105  Identities=12%  Similarity=0.050  Sum_probs=0.0

Q ss_pred              HHHHhcCCCCCCCeEEEEecCcccHHHHHHHHHHHHHcccccCceeEecCccccccChHHHHHHHHHHHHHHhcCC
Q lap1            394 LEKHLNSSHPRSQPAIIIIITAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQ  473 (583)
Q Consensus       394 LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~  473 (583)
                      |.++++++   ..|++||....   .-.++.....|..++.........++..  ...|.+.+-..+.   .-.|=+++
T Consensus         9 l~~~l~~~~~~l~~vyli~G~e~~~~l~~~~~~~i~~~~~~~~~e~~~~~~~~~~~~~~~~l~~~~~~~~s~sLF~~~   77 (343)
T 1jr3_D            9 LRAQLNEG---LRAAYLLLGND---PLLLQESQDAVRQVAAAQGFEEHHTFSID--PNTDWNAIFSLCQ---AMSLFASR   77 (343)
T ss_dssp             HHHHHHHC---CCSEEEEEESC---HHHHHHHHHHHHHHHHTCCEEEEEECC--TTCCHHHHHHHHH---HHHHCCSC
T ss_pred             HHHHHhCC---CCcEEEEEcCh---HHHHHHHHHHHHHHHhCCCccccccccc--CCCCHHHHHHHHh---CCCCCCcc


Q ss_pred              cEEEEeehh-hCCHHHHHHHHHhcCCCCcCcccceEEEEEE
Q lap1            474 NAAVVHRFE-SFPAGSTLIFYKYCDHENAAFKDVALVLTV  512 (583)
Q Consensus       474 kaAVVh~LE-~LPP~AaLIFH~YCDhENA~fKdVaLfLTV  512 (583)
                      ++++|++.+ .++.....+|-.||++-+   .++++|+.+
T Consensus        78 ~~i~i~~~~~~~~~~~~l~~~~~~~~~~~~~li~~~  114 (343)
T 1jr3_D           78 QTLLLLLPENGPNAAINEQLLTLTGLLH---DDLLLIVRG  114 (343)
T ss_dssp             EEEEEECCSSCCCTTHHHHHHHHHTTCB---TTEEEEEEE
T ss_pred             eeeccccccCCCHHHHHHHHHHhCCC---CCcEEEEEEc

No 27
>2lcn_A WALP19-P10 peptide; proline distortion, transmembrane, membrane protein; HET: ETA; NMR {Synthetic}
Probab=33.46  E-value=30  Score=23.79  Aligned_cols=17  Identities=41%  Similarity=0.812  Sum_probs=0.0

Q ss_pred              hhHHHHHHHHHHHHHh
Q lap1            337 RWWLLPLIAALASGSFW  353 (583)
Q Consensus       337 ~~~~i~vilai~vg~~~  353 (583)
```

```
                        ||+-+++.-|+++++||
T Consensus           3 wwlalalapalalalww   19 (26)
T 2lcn_A              3 WWLALALAPALALALWW   19 (26)
T ss_pred               HHHHHHHHHHHHHHHHH
```

No 28

>3lp5_A Putative cell surface hydrolase; structural genom PSI2, MCSG, protein structure initiative, midwest center FO structural genomics; 2.00A {Lactobacillus plantarum}
Probab=32.24 E-value=1.1e+02 Score=27.15 Aligned_cols=73 Identities=8% Similarity=0.189 Sum_probs=0.0

```
Q ss_pred               CCCCCeEEEEecCcccHHHHHHHHHHHHHhcccccCceeEecCcccccc----------------------------cC
Q lap1            403 PRSQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKAT----------------------------QD  453 (583)
Q Consensus       403 Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~----------------------------D  453 (583)
                      .|..| ||||.+.........-|+..|++.|-..+.+-++-+-|.+...                              .-
T Consensus         2 ~r~~P-vlliHG~~~~~~~~~~~~~L~~~~~~~~~via~D~~g~G~S~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~   80 (250)
T 3lp5_A            2 TRMAP-VIMVPGSSASQNRFDSLITELGKETPKKHSVLKLTVQTDGTIKYSGSIAANDNEPFIVIGFANNRDGKANIDKQ   80 (250)
T ss_dssp               CSCCC-EEEECCCGGGHHHHHHHHHHHHSSSCCCEEEEEECTTSCEEEEECCCTTCSSCEEEEEESCCCCSHHHHHHH
T ss_pred               CCCCC-EEEECCcccCHHHHHHHHHHHHcCCCCceEEEEECCCCCCcCCCCcccccccccceeecccccccccCCHHHH

Q ss_pred               hhHHHHHHHHHHHHHhcCCcEEEE
Q lap1            454 SDTVKLEVDQELSNGFKNGQNAAVV  478 (583)
Q Consensus       454 SD~vKleIDeqLks~F~~g~kaAVV  478 (583)
                      .+.++..|+ .|...+ +..++.+|
T Consensus        81 ~~~l~~~i~-~l~~~~-~~~~~lv  103 (250)
T 3lp5_A           81 AVWLNTAFK-ALVKTY-HFNHFYAL  103 (250)
T ss_dssp               HHHHHHHHH-HHHTTS-CCSEEEEE
T ss_pred               HHHHHHHHH-HHHHHh-CCCeEEEE
```

No 29

>3syl_A Protein CBBX; photosynthesis, rubisco activase, AAA+ protein, calvin cycle chaperone; 3.00A {Rhodobacter sphaeroides} PDB: 3syk _A 3zuh _A*
Probab=32.08 E-value=3.5e+02 Score=25.47 Aligned_cols=138 Identities=7% Similarity=0.052 Sum_probs=0.0

```
Q ss_pred               HHHHHHHHHHhcCCCCHHHHHHHHHHHHHHhccCC-------CCCCCeEEEEecCcccHHHHHHHHHHHHHHhcccccCc
Q lap1            368 FQNQMNQLKNKYQGQDEKLWKRSQTFLEKHLNSSH-------PRSQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVR  440 (583)
Q Consensus       368 f~~~~~qLKskFPsQse~LWkrlr~~LekhLNts~-------Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~  440 (583)
                      +.+-++.|...+-+|++-.-.........-.++...       +.+...+||......++.++=..............+..
T Consensus        22 ~~~~~~l~~~i~G~~~~~~l~~~~~~~~~~~~~~g~~~~~~~~vll~G~~GtGKT~la~~la~~l~~~~~~~~~  101 (309)
T 3syl_A           22 AKEVLEELDRELIGLKPVKDRIRETAALLLVERARQKLGLAHETPTLHMSFTGNPGTGKTTVALKMAGLLHRLGYVRKGH  101 (309)
T ss_dssp               HHHHHHHHHHHSSSCHHHHHHHHHHHHHHHHHHHHHHTCCSSCCCCEEEEEECTTSSHHHHHHHHHHHHHTTSSSSCC
T ss_pred               HHHHHHHHHHcccChHHHHHHHHHHHHHHHHHHHHHHcCCCCCCCCCceEEEECCCCCCHHHHHHHHHHHHHcCCcCCCc

Q ss_pred               eeEecCcccccccChhHHHHHHHHHHHHHhcCCcEEEEeehhhC---------CHHHHHHHHHcCCCCcCcccceEEEEE
Q lap1            441 AIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESF---------PAGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus       441 aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~L---------PP~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                      .+.++..++...-.......+...+...   ...+.+|-+++.|         +..+...|..+.|...   .++++|+|
T Consensus       102 ~~~~~~~l~~~~~g~~~~~~~~~~~~~---~~vl~iDEid~l~~~~~~~~~~~~~~~Ll~~l~~~~~~~~~~i~~  175 (309)
T 3syl_A          102 LVSVTRDDLVGQYIGHTAPKTKEVLKRA---MGGVLFIDEAYYLYRPDNERDYGQEAIEILLQVMENNR---DDLVVILA  175 (309)
T ss_dssp               EEEECGGGTCCSSTTCHHHHHHHHHHH---TTSEEEEETGGGSCCCC---CCTHHHHHHHHHHHCT---TTCEEEEE
T ss_pred               EEEEcHHHhhhccccchHHHHHHHHhc---CCCEEEEEChhhhccCCCCccccchHHHHHHHHHHcCC---CCEEEEEe
```

No 30

>4b4t_K 26S protease regulatory subunit 6B homolog; hydrolase, AAA-atpases, protein degradation, ubiquitin-prote pathway; 7.40A {Saccharomyces cerevisiae} PDB: 4bgr _K
Probab=30.16 E-value=2.3e+02 Score=29.61 Aligned_cols=101 Identities=13% Similarity=0.186 Sum_probs=0.0

```
Q ss_pred               CCCeEEEEecCcccHHHHHHHHHHHHHHhcccccCceeEecCcccccccChhHHHHHHHHHHHHHhcCCcEEEEeehhhC
Q lap1            405 SQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESF  484 (583)
Q Consensus       405 ~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~L  484 (583)
                      ..|.-+||++..+.=.|.  |+..||......+    +.+++..+...-.......+...+..+......+.++=.++.|
T Consensus       204 ~~~~gvLl~Gp~GtGKT~~~lakala~~~~~~~~~~i~v~~~~l~~~~~g~~~~~~~~~~~a~~~~p~vL~lDEid~l  277 (428)
T 4b4t_K          204 DPPRGVLLYGPPGTGKTM--LVKAVANSTKAAF----IRVNGSEFVHKYLGEGPRMVRDVFRLARENAPSIIFIDEVDSI  277 (428)
T ss_dssp               CCCCEEEEESCTTTTHHH--HHHHHHHHHTCEE----EEEEGGGTCCSSCSHHHHHHHHHHHHHTCSEEEEEECTHHH
T ss_pred               CCCCceEEECCCCCcHHH--HHHHHHHHhCCCE----EEEchHHHHHHHcCcchHHHHHHHHHHHcCCCEEEEEChhhh

Q ss_pred               -----------CHHHHHHHHHcCCCC--cCcccceEEEEE
Q lap1            485 -----------PAGSTLIFYKYCDHEN--AAFKDVALVLT  511 (583)
Q Consensus       485 -----------PP~AaLIFH~YCDhEN--A~fKdVaLfLT  511 (583)
                                .+....+|..+.+...  ..-.++.+|+|
T Consensus       278 ~~~r~~~~~~~~~~~~~l~~lL~~~~~~~~~~v~vI~t  317 (428)
T 4b4t_K          278 ATKRFDAQTGSDREVQRILIELLTQMDGFDQSTNVKVIMA  317 (428)
T ss_dssp               HCSCSSSCSCCCCHHHHHHHHHHHHHHSCSSCSEEEEEE
T ss_pred               hcccCCCCCCCCHHHHHHHHHHHHhcccccCCCEEEEEe
```

No 31

>2kog_A Vesicle-associated membrane protein 2; synaptobrevin, VAMP2, DPC micelle, snare, coiled coil, membrane fusion, transmembrane; NMR {Rattus norvegicus}
Probab=29.93 E-value=30 Score=30.71 Aligned_cols=21 Identities=14% Similarity=0.029 Sum_probs=0.0

```
Q ss_pred               chhhhHHHHHHHHHHHHHHh
Q lap1            334 KRNRWWLLPLIAALASGSFWF  354 (583)
Q Consensus       334 ~~k~~~~i~vilai~vg~~~~  354 (583)
                      ++|+|++|++++++++.++++
T Consensus        95 ~~K~~ii~~~v~~i~l~~ii~  115 (119)
T 2kog_A           95 NLKMMIILGVICAIILIIIIV  115 (119)
T ss_dssp               HHHHHHHHHHHHHHHHHHHH
T ss_pred               HHHHHHHHHHHHHHHHHHhh
```

No 32

```
>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=29.76  E-value=1.3e+02  Score=28.99  Aligned_cols=116  Identities=9%  Similarity=0.155  Sum_probs=0.0

Q ss_pred            CHHHHHHHHHHHHHHccCCCCCCCeEEEEecCcccHHHH-HHHHHHHHHHhcccccCceeEecCcccccccCh-hHHHHH
Q lap1           383 DEKLWKRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEAL-RCLSEQIADAYSSFRSVRAIRIDGTDKATQDS-DTVKLE  460 (583)
Q Consensus      383 se~LWkrlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TL-qCLae~IAdaySs~~s~~aI~IDG~~~a~~DS-D~vKle  460 (583)
                     ++++.+.++..+.      ..+ -|.+||......++.|+ ++||..+   +...+....+.++..+...... ......
T Consensus       26 ~~~~~~L~~~l~~~~~~~~~~~~Ll~Gp~G~GKttla~~la~e~~~~~~~~~~~~~~~~s~~~~~~~~~~~~~~   95 (323)
T 1sxj_B          26 NKETIDRLQQIAK------DGN~MPHMIISGMPGIGKTTSVHCLAHEL---LGRSYADGVLELNASDDRGIDVVRNQIKH   95 (323)
T ss_dssp            CTHHHHHHHHHH------SCC-CCCEEEECSTTSSHHHHHHHHHHH---HGGGHHHHEEEECTTSCCSHHHHHTHHHH
T ss_pred            cHHHHHHHHHHH------CCC-CCEEEEECcCCCCHHHHHHHHHHh---cCCCCCCceeeecccccchhhhhhhhhh


Q ss_pred            HHHHHHHHhhcCCcEEEEeehhhCCHHHHHHHHHcCCCCcCcccceEEEEE
Q lap1           461 VDQELSNGFKNGQNAAVVHRFESFPAGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus      461 IDeqLks~F~~g~kaAVVh~LE~LPP~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                     ....-........+++|+-+++.+..++..+|.+..+...   +.+.++||
T Consensus       96 ~~~~~~~~~~~~kviiide~d~l~~~~~~~l~~~~e~~~~~~~~~~il~  143 (323)
T 1sxj_B          96 FAQKKLHLPPGKHKIVILDEADSMTAGAQQALRRTMELYS---NSTRFAFA  143 (323)
T ss_dssp            HHHBCCCCCTTCCEEEEEESGGGSCHHHHHTTHHHHHHTT---TTEEEEEE
T ss_pred            hhhcccccccCCcEEEEEeCcccCCHHHHHHHHHHhhhcc---cceeEeec
```

No 33

```
>4ko8_A Transitional endoplasmic reticulum ATPase; transport protein, hydrolase; HET: AGS; 1.98A {Homo sapiens}
PDB:  3hu3 _A*  4kod _A*  3hu2 _A*  4kln _A*  3hu1 _A*  1e32 _A*  1s3s _A*  3qwz _A*  2pjh _B
Probab=26.67  E-value=3.1e+02  Score=29.09  Aligned_cols=135  Identities=14%  Similarity=0.221  Sum_probs=0.0

Q ss_pred            cccCcchHHHHHHHHHHHH--hCCCCCHHHHHHHHHHHHhcCCCCCCCCeEEEEecCcccHHHHHHHHHHHHhcc
Q lap1           358 PEVETTAVQEFQNQMNQLKN--KYQGQDEKLWKRSQTFLEKHLNSSHPRSQPAILLLTAARDAEEALRCLSEQIADAYSS  435 (583)
Q Consensus      358 Pqv~~tave~f~~~~~qLKs--kFPsQse~LWkrlr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs  435 (583)
                     |++.-..+=+-+++++|+.  .+|....++.+.+           .-. .|--+||.+..+.=.|+  |+..||.....
T Consensus      199 ~~v~~~digGl~~~~~l~e~~~pl~~p~~~~~~~~~~~~g~~~~~GiLL~GPpGtGKT~~~la~aiA~e~~~  264 (489)
T 4ko8_A         199 NEVGYDDIGGCRKQLAQIKEMVELPLRHPALFKAI-----------GVK-PPRGILLYGPPGTGKTL--IARAVANETGA  264 (489)
T ss_dssp            TCCCGGGCCSCHHHHHHHHHTHHHHHCHHHHHH-----------TCC-CCCEEEEECSTTSSHHH--HHHHHHHHCSS
T ss_pred            CCCChhhccCHHHHHHHHHHHHHHhcCHHHHHC-----------CCC-CCceEEEECCCCCChhH--HHHHHHHHhCC


Q ss_pred            cccCceeEecCcccccccChhHHHHHHHHHHHHHhcCCcEEEEeehhhCCHH-----------HHHHHHHhcCCCCcCcc
Q lap1           436 FRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESFPAG-----------STLIFYKYCDHENAAFK  504 (583)
Q Consensus      436 ~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~LPP~-----------AaLIFH~YCDhENA~fK  504 (583)
                     .+    +.+++.+....-.......+...+..+-.....+.++-+++.|-+.           ....|=+.+|..... .
T Consensus      265 ~~-----~i~~~~~s~~~~se~~lr~~f~~a~~~p~Il~iDeid~l~~~~~~~~~~~~~~~~~L~~~~~~~~~~-~  339 (489)
T 4ko8_A         265 FF----FLINGPEIMSKLAGESESNLRKAFEEAEKNAPAIIFIDELDAIAPKREKTHGEVERRIVSQLLTLMDGLKQR-A  339 (489)
T ss_dssp            EE----EEEEHHHHHTSCTTHHHHHHHHHHHHHHTCSEEEEEESGGGTCBCTTSCCCHHHHHHHHHHHHHTSCTT-S
T ss_pred            CE----EEEechhhhhcccccchHHHHHHHHHHHHcCCeEEeeehhhhhcccCCCCCCCchHHHHHHHHHHHhhhhccc-C


Q ss_pred            ceEEEEE
Q lap1           505 DVALVLT  511 (583)
Q Consensus      505 dVaLfLT  511 (583)
                     ++++|.|
T Consensus      340 ~V~vi~t  346 (489)
T 4ko8_A         340 HVIVMAA  346 (489)
T ss_dssp            CEEEEEE
T ss_pred            CEEEEee
```

No 34

```
>3lfh_A Manxa, phosphotransferase system, mannose/fructose-speci component IIA; PTS; 1.80A {Thermoanaerobacter
tengcongensis}
Probab=25.88  E-value=2.5e+02  Score=25.20  Aligned_cols=65  Identities=12%  Similarity=0.242  Sum_probs=0.0

Q ss_pred            EEEEecCcccHHHHHHHHHHHHHhcccccCceeEecCcccccccChhHHHHHHHHHHHHHhcCCcEEEEeeh
Q lap1           409 ILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRF  481 (583)
Q Consensus      409 VLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~L  481 (583)
                     +||.+|+    ...+-|...+.-++-...+..++-+.    ...+.+++...|.+.+++.+.++..+.|+.+|
T Consensus        6 Iii~sHG~~~~lA~gl~~s~~~i~G~~~i~~v~~~~~~~~~~~~~~~i~~~i~~~~~~~~vliltDl  70 (144)
T 3lfh_A           6 VLIITHG~~~~DFGKGLLSGAEVIIGKQENVHTVGLN~~~~LGDNIEVVRKEVEKIIKEKLQEDKEIIIVVDL  70 (144)
T ss_dssp            EEEEEET~~~~THHHHHHHHHHHHCCCSSEEEEEEC~~~~TTCCHHHHHHHHHHHHHHHHHTTTCEEEEEES
T ss_pred            EEEEcCH~~~~HHHHHHHHHHHHcCCCCCeEEEEee~~~~CCCCHHHHHHHHHHHHHHhcCCCCcEEEEEec
```

No 35

```
>3j01_B Preprotein translocase SECE subunit; ribonucleoprotein, nucleotide-binding, PR biosynthesis, translation,
zinc-finger, 70S ribosome, ribos translocon; 7.10A {Escherichia coli 536} PDB:  2akh _Z  2aki _Z
Probab=25.86  E-value=32  Score=30.92  Aligned_cols=26  Identities=8%  Similarity=0.104  Sum_probs=0.0

Q ss_pred            cchhhhHHHHHHHHHHHHHhcCCc
Q lap1           333 VKRNRWWLLPLIAALASGSFWFFSTP  358 (583)
Q Consensus      333 ~~~k~~~~i~vilai~vg~~~~~~P  358 (583)
                     ++.||.+.++++++-++|+||+...+
T Consensus        4 d~~kw~~a~~l~~~~i~~~~~~~~~  29 (116)
T 3j01_B           4 EAMKWVVVVALLLVAIVGNYLYRDIM  29 (116)
T ss_dssp            SCCTTHHHHHHTTHHHHHHHTTTCC
T ss_pred            HHHHHHHHHHHHHHHHHHHHHhhh
```

No 36

```
>4b4t_M 26S protease regulatory subunit 6A; hydrolase, AAA-atpases, protein degradation, ubiquitin-prote pathway;
7.40A {Saccharomyces cerevisiae} PDB:  4bgr _M
Probab=25.76  E-value=3.1e+02  Score=28.63  Aligned_cols=101  Identities=7%  Similarity=0.070  Sum_probs=0.0

Q ss_pred            CCCeEEEEecCcccHHHHHHHHHHHHHHhcccccCceeEecCcccccccChhHHHHHHHHHHHHHHhcCCcEEEEeehhhC
Q lap1           405 SQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESF  484 (583)
Q Consensus      405 ~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~L  484 (583)
                     ..|..+||++..+.=.|+  |+..||..+...+    +.+++.++...-.......+...+..+......+.+|=.++.|
T Consensus      213 ~~~~~vLL~GppGtGKT~--lAraia~~~~~~~----i~v~~~~l~~~~~g~~~~~~~~f~~a~~~~p~IL~iDEid~l  286 (434)
T 4b4t_M         213 RAPKGALMYGPPGTGKTL--LARACAAQTNATF----LKLAAPQLVQMYIGEGAKLVRDAFALAKEKAPTIIFIDELDAI  286 (434)
T ss_dssp            CCCCEEEEESCTTSSHHH--HHHHHHHHHTCEE----EEEEGGGGCSSCSSHHHHHHHHHHHHHHHCSEEEEEECTHHH
T ss_pred            CCCCeeEEECCCCCCHHH--HHHHHHHHcCCCE----EEEehhHhhhhccchHHHHHHHHHHHHHhcCCcEEEEechhhh


Q ss_pred            -----------CHHHHHHHHHhcCCCCc--CcccceEEEEE
Q lap1           485 -----------PAGSTLIFYKYCDHENA--AFKDVALVLT  511 (583)
Q Consensus      485 -----------PP~AaLIFH~YCDhENA--~fKdVaLfLT  511 (583)
                                   .+....+|..+.+....  .-.++++|+|
T Consensus      287 ~~~r~~~~~~~~~~q~~l~~lL~~l~~~~~~~~v~vI~a  326 (434)
T 4b4t_M         287 GTKRFDSEKSGDREVQRTMLELLNQLDGFSSDDRVKVLAA  326 (434)
T ss_dssp            HCCCSSGGGGTTHHHHHHHHHHHHHTTSCSSCSSEEEEE
T ss_pred            ccccCCCCCcccHHHHHHHHHHHHHhcccccCCCEEEEEe
```

No 37

```
>1v54_I STA, cytochrome C oxidase polypeptide VIC; oxidoreductase; HET: FME TPO HEA TGL PGV CHD CDL PEK PSC DMU;
1.80A {Bos taurus} SCOP: f.23.3.1 PDB:  1oco _I*  1occ _I*  1ocz _I*  1ocr _I*  1v55 _I*  2dyr _I*  2dys _I*  2eij _I*  2ei
 2eil _I*  2eim _I*  2ein _I*  2occ _I*  2ybb _T*  2zxw _I*  3abk _I*  3abl _I*  3abm _I*  3ag1 _I*  3ag2 _I* ...
Probab=25.24  E-value=24  Score=29.74  Aligned_cols=43  Identities=16%  Similarity=0.301  Sum_probs=0.0

Q ss_pred            hhhhHHHHHHHHHHHHHHhCCCcccCcchHHHHHHHHHHHH
Q lap1           335 RNRWWLLPLIAALASGSFWFFSTPEVETTAVQEFQNQMNQLKN  377 (583)
Q Consensus      335 ~k~~~~i~vilai~vg~~~~~~~Pqv~~tave~f~~~~~qLKs  377 (583)
                     +|..++++++++++++|....-+-...++.+|....+..+.
T Consensus       17 lk~hiv~a~~~sl~~a~~~kf~v~epRKkaYadFYknYD~~kd   59 (73)
T 1v54_I          17 LRFHIVGAFMVSLGFATFYKFAVAEKRKKAYADFYRNYDSMKD   59 (73)
T ss_dssp            HHHHHHHHHHHHHHHHHHHTHHHHHHHHHHHHTCCHHHH
T ss_pred            HHHHHHHHHHHHHHHHHHHHHhhHHHHHHHHHHcccHHHH
```

No 38

```
>4b4t_I 26S protease regulatory subunit 4 homolog; hydrolase, AAA-atpases, protein degradation, ubiquitin-prote
pathway; 7.40A {Saccharomyces cerevisiae} PDB:  4bgr _I
Probab=25.08  E-value=3.5e+02  Score=28.29  Aligned_cols=101  Identities=14%  Similarity=0.166  Sum_probs=0.0

Q ss_pred            CCCeEEEEecCcccHHHHHHHHHHHHHHhcccccCceeEecCcccccccChhHHHHHHHHHHHHHHhcCCcEEEEeehhhC
Q lap1           405 SQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESF  484 (583)
Q Consensus      405 ~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~L  484 (583)
                     ..|..+||++..+.=.|+  |+..||......+    +.+++.++...-.......+...+..+......+.+|=.++.|
T Consensus      214 ~~~~~vLL~GppGtGKT~--lAraia~~~~~~~----i~v~~~~l~~~~~g~~~~~~~~f~~a~~~~p~IL~iDEid~l  287 (437)
T 4b4t_I         214 KPPKGVILYGAPGTGKTL--LAKAVANQTSATF----LRIVGSELIQKYLGDGPRLCRQIFKVAGENAPSIVFIDEIDAI  287 (437)
T ss_dssp            CCCSEEEEESSTTTTHHH--HHHHHHHHHTCEE----EEEESGGGCCSSSSHHHHHHHHHHHHHHHTCSEEEEEEEESSS
T ss_pred            CCCCCcEEECCCCCcHHH--HHHHHHHHhCCCE----EEEehHHhhhhhccchHHHHHHHHHHHHHhcCCCEEEEechhhh


Q ss_pred            -----------CHHHHHHHHHhcCCCC--cCcccceEEEEE
Q lap1           485 -----------PAGSTLIFYKYCDHEN--AAFKDVALVLT  511 (583)
Q Consensus      485 -----------PP~AaLIFH~YCDhEN--A~fKdVaLfLT  511 (583)
                                   ......+|..+.+...  ..-.++++|+|
T Consensus      288 ~~~r~~~~~~~~~~q~~l~~lL~~ld~~~~~~~v~vI~a  327 (437)
T 4b4t_I         288 GTKRYDSNSGGEREIQRTMLELLNQLDGFDDRGDVKVIMA  327 (437)
T ss_dssp            SCCCSCSSCSSCCHHHHHHHHHHHHHHHCCCSSSEEEEEE
T ss_pred            hccccCCCCcccHHHHHHHHHHHHHhCcCcCCCEEEEEE
```

No 39

```
>4hqo_A Sporozoite surface protein 2; malaria, gliding motility, VWA domain, TSR domain, extensibl ribbon,
receptor on sporozoite, vaccine target; HET: FUC BGC; 2.19A {Plasmodium vivax} PDB:  4hql _A*  4hqn _A*
Probab=24.24  E-value=3e+02  Score=26.15  Aligned_cols=118  Identities=8%  Similarity=-0.050  Sum_probs=0.0

Q ss_pred            HHHHHHHHHHHH-HhcCCCCHHHHHHHHHHHHHHcc-CCCCCCCeEEEEecCcccHHHHHHHHHHHHHHcccccCcee
Q lap1           365 VQEFQNQMNQLK-NKYQGQDEKLWKRSQTFLEKHLNS-SHPRSQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAI  442 (583)
Q Consensus      365 ve~f~~~~~qLK~skFPsQse~LWkrlr~~LekhLNt~s~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI  442 (583)
                     .+.+...++.|+ .-+++-.-.+...|+.+.+..-.. ..+....++|||+-+.....  ..+...+..+...-....-+|
T Consensus       83 ~~~~~~~i~~l~~~~~~G~T~~~~AL~~a~~~l~~~~~r~~~~~~iIllTDG~~~d~~~~~~~~a~~l~~~gi~i~~i  160 (266)
T 4hqo_A          83 KRQALSKVTELRKTYTPYGTTSMTAALDEVQKHLNDRVNREKAIQLVILMTDGVPNSK--YRALEVANKLKQRNVRLAVI  160 (266)
T ss_dssp            HHHHHHHHHHHHCCCCSCCCHHHHHHHHHHHHTTCSCTTSEEEEEEEECSCCSCH--HHHHHHHHHHHTTCEEEEE
T ss_pred            HHHHHHHHHHhhccCCCCCCCHHHHHHHHHHHHhcccccCCCeEEEEEccCCCCCCc--hHHHHHHHHHHCCCEEEEE


Q ss_pred            EecCcccccccChhHHHHHHHHHHHHHhcC-----CcEEEEeehhhCCHHHHHHHHHc
Q lap1           443 RIDGTDKATQDSDTVKLEVDQELSNGFKNG-----QNAAVVHRFESFPAGSTLIFYKYC  496 (583)
Q Consensus      443 ~IDG~~~a~~DSD~vKleIDeqLks~F~~g-----~kaAVVh~LE~LPP~AaLIFH~YC  496 (583)
                     -|+....             .+.|+..-...      .+.+.+.+++.|+.-...++..+|
T Consensus      161 GiG~~~~~~~~~~~~~~~~~L~~iA~~~~~~g~~~~~~~d~~~L~~i~~~l~~~iC  207 (266)
T 4hqo_A         161 GIGQGIN~~~~~~~~~~~~~HQFNRLIAGCRPREPNCKFYSYADWNEAVALIKPFIAKVC  207 (266)
T ss_dssp            ECSSSCC~~~~~~~~~~~~HHHHHHHHTCCTTCSSCTTEECSCHHHHHHHHHHHCCCE
T ss_pred            ecCcccC~~~~~~~~~~~~HHHHHHhCCCCCCCCCCeEEecCHHHHHHHHHHHHhhc
```

No 40

```
>4mdf_A Metallophosphoesterase; RNA repair, P-loop phosphotransferase, transferase, hydrolas complex,
transferase-DNA complex; HET: DNA GTP CIT; 1.73A {Clostridium thermocellum} PDB:  4mde _A*  4jt4 _A*  4jsy _A*  4jt2 _A*  4
 4gp6 _A*  4gp7 _A*
```

```
Probab=24.06  E-value=87  Score=27.41  Aligned_cols=104  Identities=9%  Similarity=0.076  Sum_probs=0.0

Q ss_pred            CCCeEEEEecCcccHHHHHHHHHHHHHHhcccccCceeE--ecCcccccccChhHHHHHHHHHHHHhhcCCcEEEEeehh
Q lap1           405 SQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIR--IDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFE  482 (583)
Q Consensus      405 ~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~--IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE  482 (583)
                     |+|.+|||++...+=++  .||..++.-+ ...+.+.|.  +.+..........+...+...+..++.+|.+  ||-+--
T Consensus        7 p~~~liil~G~pGSGKS--T~a~~l~~~~~~is~D~~r~~~~~~~~~~~~~~~~~~~~~~~~~~l~~g~~~~viid~~   81 (171)
T 4mdf_A           7 PELSLVVLIGSSGSGKS--TFAKKHFKPT-EVISSNFCRGLVSDDENDQTVTGAAFDVLHYIVSKRLQLGKL--TVVDAT   81 (171)
T ss_dssp            ESSEEEEEECCTTSCHH--HHHHHHSCGG-GEEEHHHHHHHHSCTTCGGGHHHHHHHHHHHHHHHHTTCC--EEEESC
T ss_pred            CCCEEEEEECCCCCCHH--HHHHHHhCCC-EEechHHHHHHhCcccchhhhHHHHHHHHHHHHHHHHcCCc--EEeccc


Q ss_pred            hCCHHHHHHHHHcCCCCcCcccceEEEEEEecc
Q lap1           483 SFPAGSTLIFYKYCDHENAAFKDVALVLTVLLE  515 (583)
Q Consensus      483 ~LPP~AaLIFH~YCDhENA~fKdVaLfLTV~Le  515 (583)
                     .+.......|-.++...+..+  ++++|.+..+
T Consensus       82 ~~~~~~r~~~~~~a~~~~~~~~~~v~~~~~~e  112 (171)
T 4mdf_A          82 NVQESARKPLIEIAKDYHCFP--VAVVFNLPEK  112 (171)
T ss_dssp            CCSHHHHHHHHHHHTTCEE--EEEEECCCHH
T ss_pred            cCchHHHHHHHHHHcCCcE--EEEEECCCHH
```

No 41

>2qz4_A Paraplegin; AAA+, SPG7, protease, ADP, structural genomics, structural G consortium, SGC, ATP-binding, nucleotide-binding, hydrolase; HET: ADP; 2.22A {Homo sapiens}

```
Probab=23.83  E-value=5e+02  Score=24.59  Aligned_cols=100  Identities=10%  Similarity=0.068  Sum_probs=0.0

Q ss_pred            CCCeEEEEecCcccHHHHHHHHHHHHHHhcccccCceeEecCcccccccChhHHHHHHHHHHHHHhhcCCcEEEEeehhhC
Q lap1           405 SQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESF  484 (583)
Q Consensus      405 ~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~L  484 (583)
                     ..|-.+||++.++.=.|+  |+..||..+...+    +.+++.++...-..+.-..|..-++.+-.....+.++-++|.|
T Consensus       37 ~~~~gvLL~GPpGtGKT~--la~aia~~~~~~~~~~~~v~~~~l~~~~~g~~~~i~~~F~~a~~~~p~il~ide~d~l  110 (262)
T 2qz4_A          37 KVPKGALLLGPPGCGKTL--LAKAVATEAQVPF----LAMAGAEFVEVIGGLGAARVRSLFKEARARAPCIVYIDEIDAV  110 (262)
T ss_dssp            CCCCEEEEESCTTSSHHH--HHHHHHHHHTCCE----EEEETTTTSSSSTTHHHHHHHHHHHHHTCSEEEEEECC---
T ss_pred            CCCCeEEEECCCCCCHHH--HHHHHHhhhcCCCE----EEEEHHHHhcCCCCchHHHHHHHHHHHcCCCeEEEecchhhh


Q ss_pred            CHH---------------HHHHHHHhcCCCCcCcccceEEEEE
Q lap1           485 PAG---------------STLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus      485 PP~---------------AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                     -+.                 ..-.|-+.=|..... +++++|.|
T Consensus      111 ~~~r~~~~~~~~~~~~~~~ll~~ld~~~~~~~v~vI~t  151 (262)
T 2qz4_A         111 GKKRSTTMSGFSNTEEEQTLNQLLVEMDGMGTT-DHVIVLAS  151 (262)
T ss_dssp            ----------------CHHHHHHHHHHTCCTT-CCEEEEEE
T ss_pred            hcccCCCCCCccchHHHHHHHHHHHHhhCCCCC-CCEEEEEe
```

No 42

>2qp9_X Vacuolar protein sorting-associated protein 4; ATPase domain, beta domain, C-terminal helix, ATP-binding, E nucleotide-binding; 2.90A {Saccharomyces cerevisiae} PDB: 2qpa _A*

```
Probab=23.45  E-value=2.4e+02  Score=28.46  Aligned_cols=100  Identities=10%  Similarity=0.074  Sum_probs=0.0

Q ss_pred            CCeEEEEecCcccHHHHHHHHHHHHHHhcccccCceeEecCcccccccChhHHHHHHHHHHHHHhhcCCcEEEEeehhhC-
Q lap1           406 QPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESF-  484 (583)
Q Consensus      406 ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~L-  484 (583)
                     .|.-+||++.++.=.|+  |+..||..+...+    +.+++.++...........|..-+..+-.....+.+|-++|.|
T Consensus       83 p~~giLL~GPpGtGKT~--laraiA~e~~~~~~~~~~i~~~~l~~~~~g~~e~~i~~~f~~a~~~~p~il~iDeid~l~  156 (355)
T 2qp9_X          83 PTSGILLYGPPGTGKSY--LAKAVATEANSTF----FSVSSSDLVSKWMGESEKLVKQLFAMARENKPSIIFIDQVDALT  156 (355)
T ss_dssp            CCCCEEEECSTTSCHHH--HHHHHHHHHTCEE----EEEEHHHHHSCC---CHHHHHHHHHHHHTSSEEEEEECGGGGT
T ss_pred            CCCeEEEECCCCCCHHH--HHHHHHHHHhcc----eeeeHHHHhcccccHHHHHHHHHHHHHHcCCCeeechhhhhhc


Q ss_pred            ----------CHHHHHHHHHhcCCCCcCcccceEEEEE
Q lap1           485 ----------PAGSTLIFYKYCDHENAAFKDVALVLT  511 (583)
Q Consensus      485 ----------PP~AaLIFH~YCDhENA~fKdVaLfLT  511 (583)
                              .......|-+.=|...-..++|++|.|
T Consensus      157 ~~~~~~~~~~~~~~~~l~~~ld~~~~~~~V~vI~t  193 (355)
T 2qp9_X         157 GTRGEGESEASRRIKTELLVQMNGVGNDSQGVLVLGA  193 (355)
T ss_dssp            C------CTHHHHHHHHHHHHHCC---CCEEEEEE
T ss_pred            cCCCCCCccHHHHHHHHHHHHhcccCCCCeEEEee
```

No 43

>4b4t_L 26S protease subunit RPT4; hydrolase, AAA-atpases, protein degradation, ubiquitin-prote pathway; 7.40A {Saccharomyces cerevisiae} PDB: 4bgr _L

```
Probab=22.45  E-value=3.4e+02  Score=28.35  Aligned_cols=101  Identities=7%  Similarity=0.080  Sum_probs=0.0

Q ss_pred            CCCeEEEEecCcccHHHHHHHHHHHHHHhcccccCceeEecCcccccccChhHHHHHHHHHHHHHhhcCCcEEEEeehhhC
Q lap1           405 SQPAILLLTAARDAEEALRCLSEQIADAYSSFRSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESF  484 (583)
Q Consensus      405 ~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~L  484 (583)
                     ..|.-|||++..+.=.|.  |+..||..+...+    +.++..++...-.......+...+..+.....+.++=.+|.|
T Consensus      213 ~~~~gvLL~Gp~GtGKTt--Lakala~~l~~~~~~~~~i~~s~~~~~~~g~~~~~~~~~~~a~~~~p~vLlLDEid~l  286 (437)
T 4b4t_L         213 KPPKGVLLYGPPGTGKTL--LAKAVAATIGANF----IFSPASGIVDKYIGESARIIREMFAYAKEHEPCIIFMDEVDAI  286 (437)
T ss_dssp            CCCCEEEEESCTTSSHHH--HHHHHHHHHTCEE----EEEEGGGTCCSSSSHHHHHHHHHHHHHHHSCSEEEEEECCCSS
T ss_pred            CCCCeEEEECCCCCCHHH--HHHHHHHHcccc----eeecHHHHhhhhcccccHHHHHHHHHHHHhcCCeEEEEecHHhh


Q ss_pred            -----------CHHHHHHHHHhcCCCCcC--cccceEEEEE
Q lap1           485 -----------PAGSTLIFYKYCDHENAA--FKDVALVLT  511 (583)
Q Consensus      485 -----------PP~AaLIFH~YCDhENA~--fKdVaLfLT  511 (583)
                               .+....+|..+.+...-.  .++++||+|
T Consensus      287 ~~~r~~~~~~~d~~~~~l~~lL~~l~~~~~~~~iI~t  326 (437)
T 4b4t_L         287 GGRRFSEGTSADREIQRTLMELLTQMDGFDNLGQTKIIMA  326 (437)
T ss_dssp            SCCCSSSCCSSTTHHHHHHHHHHHHHSSSCTTSSEEEEE
T ss_pred            cccCCCCCCcCCHHHHHHHHHHHhhcccccCCcEEEEE
```

No 44

```
>3lay_A Zinc resistance-associated protein; salmonella typhimurium L structural genomics, center for structural
genomics of INFE diseases; 2.70A {Salmonella enterica subsp}
Probab=22.32  E-value=1.3e+02  Score=28.27  Aligned_cols=90  Identities=17%  Similarity=0.120  Sum_probs=0.0

Q ss_pred            ccccccccchhhhHHHHHHHHHHHHHh--------------cCCcccCcchHHHHHHHHHHHHhcCCCCHHHH---HH
Q lap1           327 PQNASFVKRNRWWLLPLIAALASGSFWF--------------FSTPEVETTAVQEFQNQMNQLKNKYQGQDEKLW---KR  389 (583)
Q Consensus      327 ~~~~~~~~k~~~~i~vilai~vg~~~~----------------~~~Pqv~~tave~f~~~~~qLKskFPsQse~LW---kr  389 (583)
                     .+.+..-|.+--++|+||+..++++.-.              ...-...-|+  +-+.+|++|..+|-.+...|.   ..
T Consensus       19 ~~~~~~Mk~~~k~~la~~al~~~~l~s~~a~A~~~~G~g~g~~~~~~~~LT~--EQq~ki~~i~~~~~~~~~~Lr~ql~~   96 (175)
T 3lay_A          19 YFQSNAMKRNNKSAIALIALSLLALSSGAAFAGHHWGNNDGMWQQGGSPLTT--EQQATAQKIYDDYYTQTSALRQQLIS   96 (175)
T ss_dssp            ------------------------------------------------CCH--HHHHHHHHHHHHHHHHHHHHHHHH
T ss_pred            HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHcCCCCCCCCCCCCCCCCCCH--HHHHHHHHHHHHHHHHHHHHHHHH


Q ss_pred            HHHHHHHHccCCCCCCCeEEEEecCcccHHHHHHHHHHHHH
Q lap1           390 SQTFLEKHLNSSHPRSQPAILLLTAARDAEEALRCLSEQIADA  432 (583)
Q Consensus      390 lr~~LekhLNts~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAda  432 (583)
                     .+.-|+..+...+|.              +..++.|+..|++.
T Consensus       97 kr~EL~aLl~~~~~D---------------~akI~aL~~EI~~L  125 (175)
T 3lay_A          97 KRYEYNALLTASSPD---------------TAKINAVAKEMESL  125 (175)
T ss_dssp            HHHHHHHHHTSSSCC--------------HHHHHHHHHHHHHH
T ss_pred            HHHHHHHHHcCCCC--------------HHHHHHHHHHHHHH
```

No 45

```
>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=21.78  E-value=69  Score=23.93  Aligned_cols=19  Identities=37%  Similarity=0.387  Sum_probs=0.0

Q ss_pred            hhHHHHHHHHHHHHHHhc
Q lap1           337 RWWLLPLIAALASGSFWFF  355 (583)
Q Consensus      337 ~~~~i~vilai~vg~~~~~  355 (583)
                     |.+++..++||.++.|+|+
T Consensus       19 ~Glllifvl~vlfssyffN   37 (37)
T 3arc_L          19 LGLLLILVLALLFSSYFFN   37 (37)
T ss_dssp            HHHHHHHHHHHHHHHHHC
T ss_pred            HHHHHHHHHHHHHHhhcC
```

No 46

```
>4cn9_A Proximal thread matrix protein 1; structural protein; HET: EDO GOL; 1.90A {Mytilus galloprovincialis}
PDB:  4cn8 _A*  4cnb _A*
Probab=21.67  E-value=4.1e+02  Score=26.95  Aligned_cols=161  Identities=13%  Similarity=0.157  Sum_probs=0.0

Q ss_pred            CcchHHHHHHHHHHHHhcCCCCHHHHHHHHHHHHHHcc----CCCCCCCeEEEEecCcccHHHHHHHHHHHHHhccc
Q lap1           361 ETTAVQEFQNQMNQLKNKYQGQDEKLWKRSQTFLEKHLNS----SHPRSQPAILLLTAARDAEEALRCLSEQIADAYSSF  436 (583)
Q Consensus      361 ~~tave~f~~~~~qLKskFPsQse~LWkrlr~~LekhLNt----s~Pr~ePAVLLLtA~~~Ae~TLqCLae~IAdaySs~  436 (583)
                     .....+.+++.++.| ..+.+....+...|+..++..+..    ..+.-.-++|||+.+..  ....-+.....+...-
T Consensus      118 ~~~~~~~l~~~i~~~~~~gg~t~~~~aL~~~~~~~f~~~~~~~r~~~~~v~vliTDG~s--~~~~~~~~~a~~l~~~g  194 (454)
T 4cn9_A         118 KFKTKEDIKKGIQDM-VPRNGGQTEIGTGLKHVRENSFSGAEGGGNPDKQKIVILMTDGKS--NAGAPPQHEAHKLKAEG  194 (454)
T ss_dssp            SCCSHHHHHHHHTC-CCCCBSSCCHHHHHHHHHTTTSGGGTCCCTTSEEEEEEEESSCC--CSSSCHHHHHHHHHTT
T ss_pred            CCCCHHHHHHHHHh-cccCCCCChHHHHHHHHHHHhhhhhcCCCCCCCeeEEEecCCCC--CccHhhhHHHHHHhcC


Q ss_pred            ccCceeEecCcccccccCHhHHHHHHHHHHHHHhcCCCcEEEEeehhhCCHHHHHHHHhcC---CCCcCcccceEEEEEEe
Q lap1           437 RSVRAIRIDGTDKATQDSDTVKLEVDQELSNGFKNGQNAAVVHRFESFPAGSTLIFYKYCD---HENAAFKDVALVLTVL  513 (583)
Q Consensus      437 ~s~~aI~IDG~~~a~~DSD~vKleIDeqLks~F~~g~kaAVVh~LE~LPP~AaLIFH~YCD---hENA~fKdVaLfLTV~  513 (583)
                     -..-+|-|+..-.            .++|+..-....+++.+.+|+.|+.-...+...+|+   ....-..|++++|-..
T Consensus      195 i~i~~vgig~~~~~~~~~~~~~~~L~~ia~~~~v~~~~~~~L~~~~~v~~~~~~~~~~~~~~~DivfviD~S  262 (454)
T 4cn9_A         195 VTVIAIGIGQGFV----------KTELEQIATMKNYVLTTNSFSELSTLLKLVIDLACEVCVVDCAGHADIAFVFDAS  262 (454)
T ss_dssp            EEEEEEEESSSSC------------HHHHHHSSSGGGEEEESCGGGGGGGHHHHHHHHTEEEEECTTSCEEEEEEECC
T ss_pred            CeEEEEEeCCccC------------HHHHHHHhCCCccEEEeccchhhhhhhhcccccccccccCCCCCcceEEEecCC


Q ss_pred            ccccccccCCcCHHHHHHHHHHHH
Q lap1           514 LEEETLGTSIGLKEVEEKVRDFLK  537 (583)
Q Consensus      514 Leeetl~~s~slkEvEEkV~dfL~  537 (583)
                     -... .......+.+.+.|.+++.
T Consensus      263 ~S~~~~~~~~~~~k~fv~~~v~  285 (454)
T 4cn9_A         263 SSIN-ANNPNNYQLMKNFMKDIVD  285 (454)
T ss_dssp            TTTT-SSCTTHHHHHHHHHHHHH
T ss_pred            cccC-CCchHHHHHHHHHHHHH
```

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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