HHpred

Created: Jul 20, 2017 3:33 PM

ID	Date	Tool
1419573		HHPR
8036569		HHPR
2963036		HHPR
6553686		HHPR
5422889		HHPR

Input Parameters Results (/api/job/result/8036569/hhpred/Results)

Raw Output (HHR) (/api/job/result/8036569/hhpred/Raw Output (HHR))

Probability Plot (/api/job/result/8036569/hhpred/Probability Plot)

Query Template MSA (/api/job/result/8036569/hhpred/Query Template MSA)

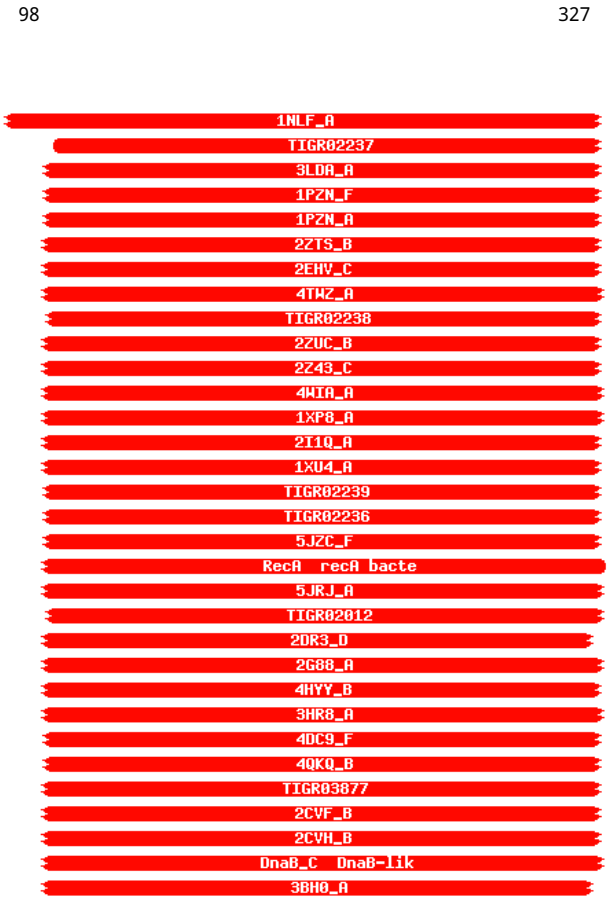
Query MSA (/api/job/result/8036569/hhpred/Query MSA)

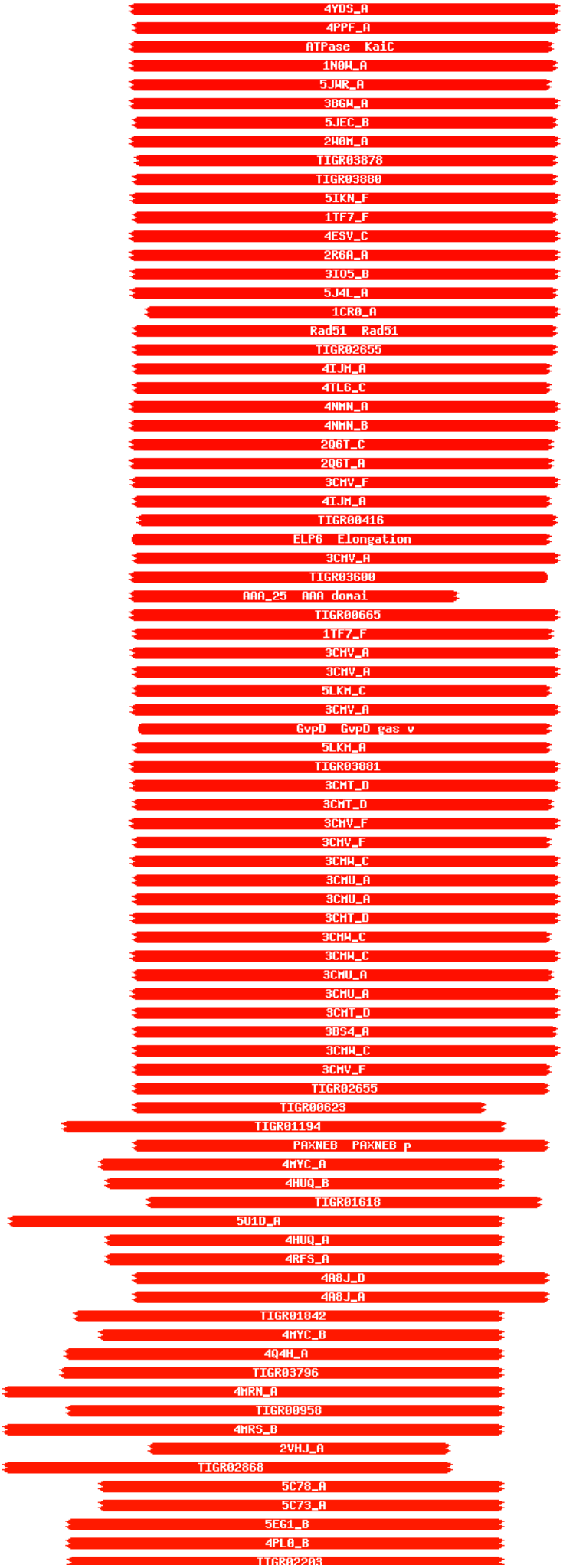
Vis Hits Aln | Select all Forward Forward Query MSA

Number of hits: **250**

Visualization

Resubmit section




4YDS_A
4PPF_A
ATPase KaiC
1N0W_A
5JWR_A
3BGW_A
5JEC_B
2W0M_A
TIGR03878
TIGR03880
5IKN_F
1TF7_F
4ESV_C
2R6A_A
3IO5_B
5J4L_A
1CR0_A
Rad51 Rad51
TIGR02655
4IJM_A
4TL6_C
4NMN_A
4NMN_B
2Q6T_C
2Q6T_A
3CMV_F
4IJM_A
TIGR00416
ELP6 Elongation
3CMV_A
TIGR03600
AAA_25 AAA domai
TIGR00665
1TF7_F
3CMV_A
3CMV_A
5LKM_C
3CMV_A
GvpD GvpD gas v
5LKM_A
TIGR03881
3CMT_D
3CMT_D
3CMV_F
3CMV_F
3CMW_C
3CMU_A
3CMU_A
3CMT_D
3CMW_C
3CMW_C
3CMU_A
3CMU_A
3CMT_D
3BS4_A
3CMW_C
3CMV_F
TIGR02655
TIGR00623
TIGR01194
PAXNEB PAXNEB p
4MYC_A
4HUQ_B
TIGR01618
5U1D_A
4HUQ_A
4RFS_A
4A8J_D
4A8J_A
TIGR01842
4MYC_B
4Q4H_A
TIGR03796
4MRN_A
TIGR00958
4MRS_B
2VHJ_A
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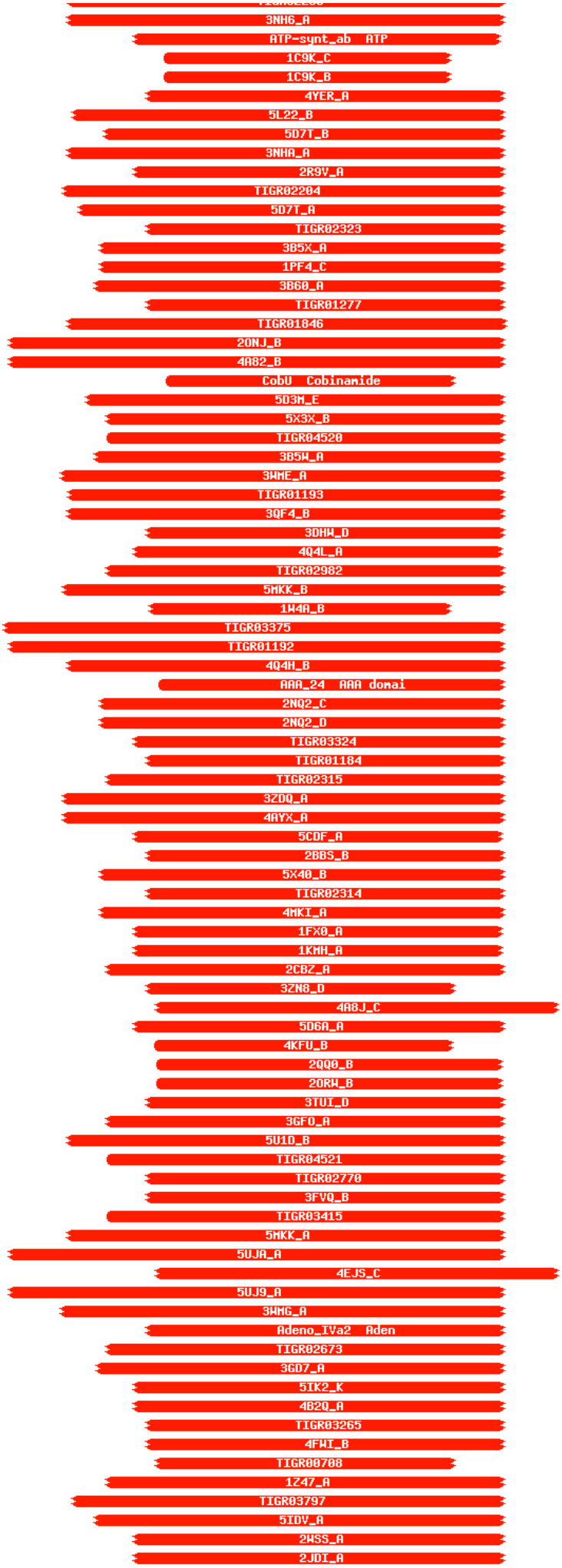
5C78_A
5C73_A
5EG1_B
4PL0_B
TIGR02203


3NH6_A
ATP-synt_ab ATP
1C9K_C
1C9K_B
4YER_A
5L22_B
5D7T_B
3NHA_A
2R9V_A
TIGR02204
5D7T_A
TIGR02323
3B5X_A
1PF4_C
3B60_A
TIGR01277
TIGR01846
2ONJ_B
4A82_B
CobU Cobinamide
5D3M_E
5X3X_B
TIGR04520
3B5W_A
3WME_A
TIGR01193
3QF4_B
3DHW_D
4Q4L_A
TIGR02982
5MKK_B
1W4A_B
TIGR03375
TIGR01192
4Q4M_B
AAA_24 AAA domai
2NQ2_C
2NQ2_D
TIGR03324
TIGR01184
TIGR02315
3ZDQ_A
4AYX_A
5CDF_A
2BBS_B
5X40_B
TIGR02314
4MKI_A
1FX0_A
1KMH_A
2CBZ_A
3ZN8_D
4A8J_C
5D6A_A
4KFU_B
2QQ0_B
2ORW_B
3TUI_D
3GFO_A
5U1D_B
TIGR04521
TIGR02770
3FVQ_B
TIGR03415
5MKK_A
5UJA_A
4EJS_C
5UJ9_A
3WMG_A
Adeno_IVa2 Aden
TIGR02673
3GD7_A
5IK2_K
4B2Q_A
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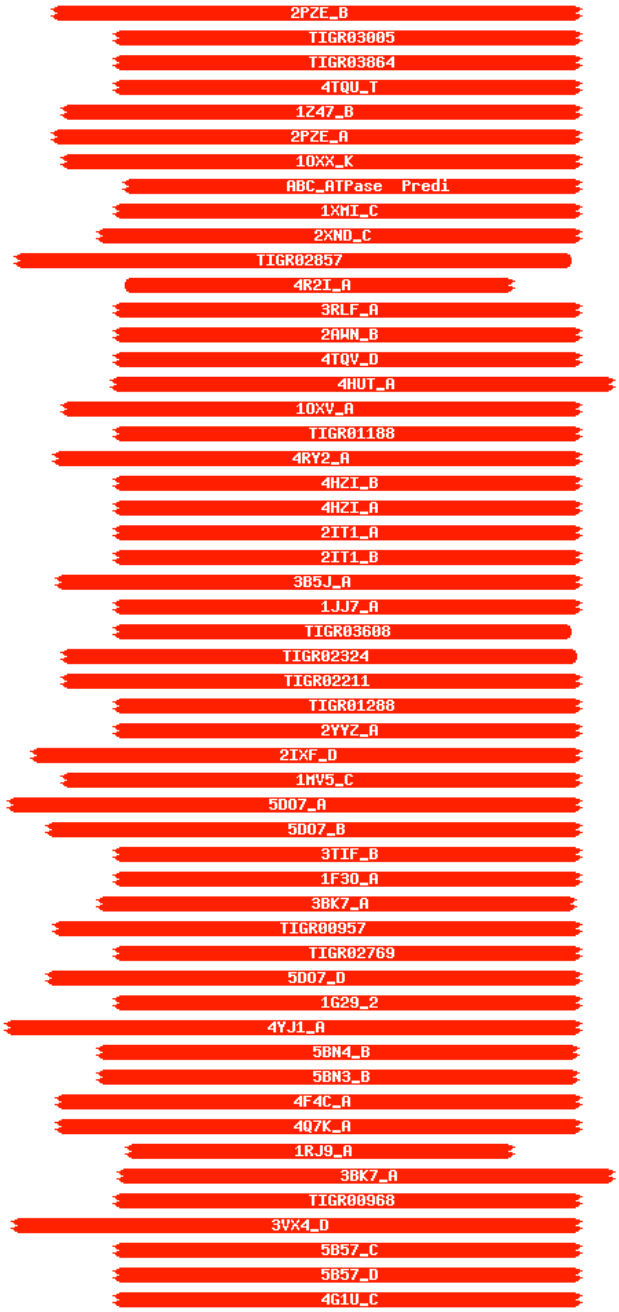
TIGR03797
5IDV_A
2WSS_A
2JDI_A



Hitlist

Show 25 entries

Nr	Hit	Name	Probability
1	1NLF_A (http://pdb.rcsb.org/pdb/explore.do?structureId=1NLF)	Regulatory protein repA; replicative DNA helicase structural changes; HET: SO4; 1.95A {Escherichia coli} SCOP: c.37.1.11	99.47

Nr	Hit	Name	Probability
2	TIGR02237 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR02237)	recomb_radB; DNA repair and recombination protein RadB. This family consists exclusively of archaeal RadB protein, a homolog of bacterial RecA (TIGR02012), eukaryotic RAD51 (TIGR02239) and DMC1 (TIGR02238), and archaeal RadA (TIGR02236).	99.41
3	3LDA_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3LDA)	DNA repair protein RAD51 (E.C.3.1.22.4); DNA BINDING PROTEIN, ATP-binding, DNA; 2.5A {Saccharomyces cerevisiae}	99.38
4	1PZN_F (http://pdb.rcsb.org/pdb/explore.do?structureId=1PZN)	DNA repair and recombination protein; HEPTAMERIC RING HEPTAMER ; HET: IMD, MPD, GOL, SO4; 2.85A {Pyrococcus furiosus} SCOP: c.37.1.11	99.36
5	1PZN_A (http://pdb.rcsb.org/pdb/explore.do?structureId=1PZN)	DNA repair and recombination protein; HEPTAMERIC RING HEPTAMER ; HET: SO4, IMD, GOL, MPD; 2.85A {Pyrococcus furiosus} SCOP: c.37.1.11, a.60.4.1	99.36
6	2ZTS_B (http://pdb.rcsb.org/pdb/explore.do?structureId=2ZTS)	Putative uncharacterized protein PH0186; KaiC like protein, ATP-binding, Nucleotide-binding; HET: ADP; 2.07A {Pyrococcus horikoshii}	99.36
7	2EHV_C (http://pdb.rcsb.org/pdb/explore.do?structureId=2EHV)	Hypothetical protein PH0186; KaiC, RecA ATPase, UNKNOWN FUNCTION; HET: ADP; 2.07A {Pyrococcus horikoshii}	99.36

Nr	Hit	Name	Probability
8	4TWZ_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4TWZ)	PROTEIN RECA; HOMOLOGOUS RECOMBINATION, DNA BINDING, RECOMBINATION; 2.8A {Escherichia coli K12}	99.35
9	TIGR02238 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR02238)	recomb_DMC1; meiotic recombinase Dmc1. This model describes DMC1, a subfamily of a larger family of DNA repair and recombination proteins.	99.35
10	2ZUC_B (http://pdb.rcsb.org/pdb/explore.do?structureId=2ZUC)	DNA repair and recombination protein; ARCHAEA, FILAMENT, LEFT-HANDED, DNA BINDING; 3.3A {Sulfolobus solfataricus}	99.35
11	2Z43_C (http://pdb.rcsb.org/pdb/explore.do?structureId=2Z43)	DNA repair and recombination protein; ARCHAEA, FILAMENT, DNA BINDING, RECOMBINATION; 1.93A {Sulfolobus solfataricus}	99.35
12	4WIA_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4WIA)	Putative flagella-related protein H; archaea, flagella, ATP-binding protein; HET: SO4, MSE; 2.2A {Methanocaldococcus jannaschii DSM 2661}	99.34
13	1XP8_A (http://pdb.rcsb.org/pdb/explore.do?structureId=1XP8)	RecA protein; Recombination, Radioresistance, DNA-repair, ATPase, DNA-binding; HET: AGS; 2.5A {Deinococcus radiodurans} SCOP: d.48.1.1, c.37.1.11	99.33

Nr	Hit	Name	Probability
14	2I1Q_A (http://pdb.rcsb.org/pdb/explore.do?structureId=2I1Q)	DNA repair and recombination protein; ATPASE, RECOMBINASE, ATP COMPLEX, Calcium; HET: ANP; 1.9A {Methanococcus voltae} SCOP: c.37.1.11, a.60.4.1	99.32
15	1XU4_A (http://pdb.rcsb.org/pdb/explore.do?structureId=1XU4)	ATPASE IN COMPLEX WITH AMP-PNP; ATPASE, PROTEIN-ATP COMPLEX, CO-FACTORS, POTASSIUM-DEPENDENCE; HET: ANP; 2.4A {Methanococcus voltae} SCOP: c.37.1.11, a.60.4.1	99.32
16	TIGR02239 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR02239)	recomb_RAD51; DNA repair protein RAD51. This eukaryotic sequence family consists of RAD51, a protein involved in DNA homologous recombination and repair.	99.32
17	TIGR02236 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR02236)	recomb_radA; DNA repair and recombination protein RadA. This family consists exclusively of archaeal RadA protein, a homolog of bacterial RecA (TIGR02012), eukaryotic RAD51 (TIGR02239), and archaeal RadB (TIGR02237).	99.31
18	5JZC_F (http://pdb.rcsb.org/pdb/explore.do?structureId=5JZC)	DNA repair protein RAD51 homolog; cryoEM DNA repair recombinase, CELL; 4.2A {Homo sapiens}	99.3
19	PF00154.20 (http://pfam.xfam.org/family/PF00154.20#tabview=tab0)	; RecA ; recA bacterial DNA recombination protein	99.29

Nr	Hit	Name	Probability
20	5JRJ_A (http://pdb.rcsb.org/pdb/explore.do?structureId=5JRJ)	Protein RecA; DNA-binding protein, ATP-dependent DNA protein; HET: ATP, ADP; 1.7A {Herbaspirillum seropedicae}	99.29
21	TIGR02012 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR02012)	tigrfam_recA; protein RecA. This model describes orthologs of the recA protein. RecA promotes hybridization of homolgous regions of DNA.	99.29
22	2DR3_D (http://pdb.rcsb.org/pdb/explore.do?structureId=2DR3)	UPF0273 protein PH0284; RecA superfamily ATPase, Hexamer, Structural; HET: ADP; 2.0A {Pyrococcus horikoshii}	99.29
23	2G88_A (http://pdb.rcsb.org/pdb/explore.do?structureId=2G88)	Protein recA; RECOMBINATION, DNA-REPAIR; HET: DTP, CIT; 3.2A {Mycobacterium smegmatis}	99.29
24	4HYY_B (http://pdb.rcsb.org/pdb/explore.do?structureId=4HYY)	Meiotic recombination protein DMC1/LIM15 homolog; RecA homolog, DNA strand exchange; 2.603A {Homo sapiens}	99.28
25	3HR8_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3HR8)	Protein recA; Alpha and beta proteins (a/b; 1.95A {Thermotoga maritima}	99.28

Showing 1 to 25 of 250 entries

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Alignments

1. Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/1nlf)
1NLF_A (http://pdb.rcsb.org/pdb/explore.do?structureId=1NLF) Regulatory protein repA; replicative D HET: SO4; 1.95A {Escherichia coli} SCOP: c.37.1.11
Probability: 99.47 E-value: 1.9E-14 Score: 133.86 Aligned Cols: 225 Identities: 17% Similar

```
Q ss_pred              hhhhcccccHHHhcCCCCCccccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCC
Q Klein_Draft   98     SQFRSRFLSVSDIQNMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRN
Q Consensus     98     ~~~~~~~~~~~~~~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~
                       .......+........+.+++++ +.+.+|.+++|+|++|+|||+++..++..+..|..
T Consensus     2      ~~~~~~~~~~~~~~~~~ld~~~-~g~~~g~~~~i~G~~g~GKS~l~~~la~~~~~~~~
T 1NLF_A        2      ATHKPINILEAFAAAPPPLDYVL-PNMVAGTVGALVSPGGAGKSMLALQLAAQIAGGPD
T ss_dssp              CCCCCCCHHHHHHSCCCCCCEEE-TTEETTSEEEEEESTTSSHHHHHHHHHHHHHTCCC
T ss_pred              CCcccccHHHHHhcCCCCCCccc-CcccCCcEEEEECCCCCCHHHHHHHHHHHHHhCcc

Q ss_pred              EEEEECCCcc-cHHHHHHHHHHHHcCc---CccCCEEEEecCcccCcHHHHHHHHHHH
Q Klein_Draft   167    VLYVVAEGVA-GFSSRINAWETAWRQT---LEEGSITFLPVPVNLMSQDVGALVEDIKD
Q Consensus     167    Vl~i~~e~~~-~~~~rl~~~~~~~~~~---~~~~~~~~~~~~~~~~~~~~~~l~~~~~~
                       |+|++.|... .+..++..+.......   .....+.+.............++..+..
T Consensus     71     v~~i~~e~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 1NLF_A        71     VIYLPAEDPPTAIHHRLHALGAHLSAEERQAVADGLLIQPLIGSLPNIMAPEWFDGLKR
T ss_dssp              EEEEESSSCHHHHHHHHHHHHHTTSCHHHHHHHHHHEEECCCTTSCCCTTSHHHHHHHHH
T ss_pred              EEEEeCCCCHHHHHHHHHHHHHcCCHHHHHHHHcCcEEEEeccCCCCCcCCHHHHHHHHH

Q ss_pred              ChHHHcCCCccCCHHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC---------CC
Q Klein_Draft   231    TIARCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE---------KT
Q Consensus     231    ~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~~~
                       ++..++.....    +...+...+..|..+++++++++++++|.+|..         ..
T Consensus     141    ~~~~~~~~~~~~----~~~~~~~~~~~~l~~~~~~~~~~~vi~v~h~~k~~~~~~~~~~~~
T 1NLF_A        141    TLRRFHIEEEN----ASGPMAQVIGRMEAIAADTGCSIVFLHHASKGAAMMGAGDQQQA
T ss_dssp              CGGGGCCSCTT----CHHHHHHHHHHHHHHHHHHCCEEEEEEEC---------------
T ss_pred              CcHHhccccccc----CCHHHHHHHHHHHHHHHHhCCEEEEEcccccchhccCCcccchh

Q ss_pred              cEEEEEEeCCc----------------EEEEEeeecCCCCCCCeeEEEEEec
Q Klein_Draft   292    DTVYFVERGNG----------------ITLTCKKQKDAPEGDRHTLRLQPID  327 (
Q Consensus     292    d~vi~l~~~~~~~~~~~~~~~~~~~~~~l~~~K~r~~~~~~~~~~~~~~~~  327 (
                       |.++.|.+...                +.+...|+|..+.+..+.|.+....
T Consensus     207    d~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~k~r~~~~~~~~~~~~~~~g  258 (
T 1NLF_A        207    RWQSYLSSMTSAEAEEWGVDDDQRRFFVRFGVSKANYGAPFADRWFRRHDGG  258 (
T ss_dssp              SCEEEEEECCHHHHHHTTCCTTSGGGEEEEEEEECSSSSCCCCEEEEECGGG
T ss_pred              eEEEEEEcCCHHHHHHhCCChhHhccEEEEeeccccCCCCcccceEEEcCCe
```

Template alignment

2. **TIGR02237 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR02237) recomb_radB; DNA protein RadB. This family consists exclusively of archaeal RadB protein, a homolog of bacterial RecA (T (TIGR02239) and DMC1 (TIGR02238), and archaeal RadA (TIGR02236).**

Probability: 99.41 E-value: 1.6E-13 Score: 120.85 Aligned Cols: 201 Identities: 17% Similar

```
Q ss_pred              CcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEEECCC
Q Klein_Draft   116    PEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVAEG
Q Consensus     116    ~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~e~
                       +++++.+.+++|.+++|+|++|+|||+++..++..+..          ...+++|++.+.
T Consensus     1      ld~ll~~~~~~g~~~~i~G~~g~GKt~l~~~l~~~~~~~~~~~~~~~~~~v~~~~~~~
T TIGR02237     1      IDELLGGGVERGTITQIYGPPGSGKTNICMILAVNAAR---------QGKKVVYIDTEG
T ss_pred              ChhHccCCCCCCcEEEEECCCCCCHHHHHHHHHHHHHH---------cCCeEEEEECCC

Q ss_pred              HHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC-ccCC
Q Klein_Draft   186    ETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA-EENS
Q Consensus     186    ~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~-~~n~
                       ..............................+...+...++.++|||+++.+.... ....
T Consensus     60     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~iiiD~~~~~~~~~~~~~~
T TIGR02237     60     AEDRPERALSNFIVFEVFDFDEQGVAIQKTSKFIDRDSASLVVVDSFTALYRLELSDDR
T ss_pred              HhcCChHHhhceEEEecCChhhHHHHHHHHHHHHhhcCCeEEEEcChHHHhccccCCCc
```

```
Q ss_pred              HHHHHHcCCCCeEEEEEccCCCCCCC----CCCchhHhccccEEEEEEeCC-cEEEEEe
Q Klein_Draft   255    TRLMDATPDHRGCVLGIHHTGKDEKT----LRGSSAYEGGVDTVYFVERGN-GITLTCK
Q Consensus     255    ~~L~~~~~~~~~~vl~v~H~~k~~~~-----~~Gs~~~~~~~d~vi~l~~~~-~~~l~~~
                       ..|...++..++++++++|..+....    +.|+..+...+|.++.|.... .+.+...
T Consensus     130    ~~l~~~~~~~~~~ii~~~~~~~~~~~~~~~~~~~~~~~~~d~~~~l~~~~~~~~~~~~~
T TIGR02237     130    TLLLSLARKKNLAVVITNQVYTDVNNGTLRPLGGHLLEHWSKVILRLEKFRGRRLATLE
T ss_pred              HHHHHHHHHHcCCEEEEEeCCCcccCCCcccccCChhHHhhcceEEEEEEEeCCeEEEEEE

Q ss_pred              eEEEEEec
Q Klein_Draft   320    TLRLQPID  327 (416)
Q Consensus     320    ~~~~~~~~  327 (416)
                       .|.+...+
T Consensus     200    ~~~i~~~g  207 (209)
T TIGR02237     200    YFRITDDG  207 (209)
T ss_pred              EEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3lda)

3. **3LDA_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3LDA) DNA repair protein RAD51 (E.C.3.1.22.4 binding, DNA; 2.5A {Saccharomyces cerevisiae}**

Probability: 99.38 E-value: 8.2E-14 Score: 136.94 Aligned Cols: 211 Identities: 14% Similar

```
Q ss_pred              CCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   113    MPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     113    ~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       .+.+++++.++++.|.++.|+|++|+|||+|+..++..+..+..+.+   .+.+|+|++
T Consensus     164    ~~~LD~lL~GGi~~G~i~~I~G~sgsGKT~l~~~la~~~~~~~~~~~---~~~~Vlyid
T 3LDA_A        164    SKNLDTLLGGGVETGSITELFGEFRTGKSQLCHTLAVTCQIPLDIGG---GEGKCLYID
T ss_dssp              CHHHHHHTTTSEETTSEEEEEESTTSSHHHHHHHHHHHTTSCGGGTC---CSSEEEEEE
T ss_pred              ChhHHHHcCCCccCCeEEEEECCCCCCHHHHHHHHHHHccchhhCC---CCCeEEEEE

Q ss_pred              HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181    RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                       .+................+........+......+...+...++++||||++..++...
T Consensus     231    ~~~~~~~~~~~~~l~~i~i~~~~~~~~l~~~l~~l~~~~~~~~~~lvIIDsl~~l~~~~
T 3LDA_A        231    SIAQRFGLDPDDALNNVAYARAYNADHQLRLLDAAAQMMSESRFSLIVVDSVMALYRTD
T ss_dssp              HHHHHTTCCHHHHHHTEEEEECCSHHHHHHHHHHHHHHHHHSCEEEEEEETGGGGCC--
T ss_pred              HHHHHcCCCChHHhhhceEEEECCCHHHHHHHHHHHHHHHHcCCceEEEEeChHHHcccc

Q ss_pred              HHHHHHHHHHHHHcCCCCeEEEEEccCCCC----------CCCCCCchhHhccccEEEE
Q Klein_Draft   248    GIVIDSMTRLMDATPDHRGCVLGIHHTGKD----------EKTLRGSSAYEGGVDTVYF
Q Consensus     248    ~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~----------~~~~~Gs~~~~~~~d~vi~
                       ..+...+..|..++++++++|++++|..+.          ...+.|+..+...+|.++.
T Consensus     301    ~~l~~i~~~L~~la~~~~~~VIv~~h~~~~~~~~~~~~~~~~p~gg~~~~~~~~~~i~
T 3LDA_A        301    MHLAKFMRALQRLADQFGVAVVVTNQVVAQVDGGMAFNPDPKKPIGGNIMAYSSTTRLG
T ss_dssp              HHHHHHHHHHHHHHHHHCCEEEEEEEC--------------------CHHHHHCSEEEE
T ss_pred              HHHHHHHHHHHHHHHHHCCEEEEEecCccccCCCCcCCCCCcccCCCChHHhcccEEEE

Q ss_pred              EEeeecCCCCCCCeeEEEEEec
Q Klein_Draft   306    TCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     306    ~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                       .+.|++..+ ...+.|.+...+
T Consensus     371    ~i~Ks~~~~-~~~~~f~I~~~G  391 (400)
T 3LDA_A        371    KVVDSPCLP-EAECVFAIYEDG  391 (400)
T ss_dssp              EEEECSSSC-SCEEEEEEETTE
T ss_pred              EEEeCCCCC-CcEEEEEEeCCe
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/1pzn)

4. **1PZN_F (http://pdb.rcsb.org/pdb/explore.do?structureId=1PZN) DNA repair and recombination protei**
HET: IMD, MPD, GOL, SO4; 2.85A {Pyrococcus furiosus} SCOP: c.37.1.11

Probability: 99.36 E-value: 2.3E-13 Score: 131.4 Aligned Cols: 210 Identities: 12% Similari

```
Q ss_pred                CCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCCcEEEEE
Q Klein_Draft     113    MPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus       113    ~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                         .+.+++++.+++++|.++.|+|++|+|||+|+..++..+..+..+.+   ...+|+|++
T Consensus       117    ~~~lD~ll~ggi~~G~i~~i~G~~gsGKT~l~~~l~~~~~~~~~~~g---~~~~~vl~i~
T 1PZN_F          117    SKSLDKLLGGGIETQAITEVFGEFGSGKTQLAHTLAVMVQLPPEEGG---LNGSVIWID
T ss_dssp                CHHHHHHHTSSEESSEEEEEEEESTTSSHHHHHHHHHHHTTSCGGGTC---CSCEEEEEE
T ss_pred                CHHHHHHhCCCeecCeEEEEECCCCCCHHHHHHHHHHHhCChhhCC---CcceEEEEE

Q ss_pred                HHHHHHHcCcC---ccCCEEEEecCcccCcHHHHHHHHHHHH-----hCCcEEEEeChH
Q Klein_Draft     183    NAWETAWRQTL---EEGSITFLPVPVNLMSQDVGALVEDIKD-----YGFEFIVLDTIA
Q Consensus       183    ~~~~~~~~~~~---~~~~~~~~~~~~~~~~~~~~~l~~~~~~-----~~~~lviiD~l~
                         ..+........   ....................++...+..     .++++||||+++
T Consensus       183    ~~~~~~~~~~~~~~l~~i~~~~~~~~~~~~~~l~~l~~~l~~~~~~~~~~liviDsl~
T 1PZN_F          183    REIAQNRGLDPDEVLKHIYVARAFNSNHQMLLVQQAEDKIKELLNTDRPVKLLIVDSLT
T ss_dssp                HHHHHTTTSCHHHHTTSEEEEECCSHHHHHHHHHHHHHHHHHHHHTSSSCEEEEEEETSS
T ss_pred                HHHHHHcCCCHHHHHcCEEEEECCCHHHHHHHHHHHHHHHHHHHccCCCeEEEEEeCcH

Q ss_pred                -CHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCC-------CCCCCCchhHhccccE
Q Klein_Draft     243    -SARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKD-------EKTLRGSSAYEGGVDT
Q Consensus       243    -~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~-------~~~~~Gs~~~~~~~d~
                          .......+...+..|..++++++++|++++|.++.       ...++|+..+...+|.
T Consensus       253    ~~~~~~~~~~~~~~~L~~la~~~~~~vi~~~~~~~~~~~~~~~~~~~g~~~~~~~~~
T 1PZN_F          253    ALAERQQKLAKHLADLHRLANLYDIAVFVTNQVQARPDAFFGDPTRPIGGHILAHSATL
T ss_dssp                THHHHHHHHHHHHHHHHHHHHHHTTCEEEEEEECC---------------CCCCCTTCSE
T ss_pred                cHHHHHHHHHHHHHHHHHHHHHHcCCEEEEEeccccCCccccCCCcccCChhHHhccceE

Q ss_pred                EEEEEeeecCCCCCCCeeEEEEEec
Q Klein_Draft     303    ITLTCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus       303    ~~l~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                         +.+.+.|++..+.+. +.|.+...+
T Consensus       323    ~~l~v~k~~~~~~~~-~~f~i~~~G  346 (349)
T 1PZN_F          323    RIARLIDAPHLPEGE-AVFSITEKG  346 (349)
T ss_dssp                EEEECSCSSSSCCCE-EEEEEETTE
T ss_pred                EEEEEEECCCCCCeE-EEEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/1pzn)

5. **1PZN_A (http://pdb.rcsb.org/pdb/explore.do?structureId=1PZN) DNA repair and recombination protei**
HET: SO4, IMD, GOL, MPD; 2.85A {Pyrococcus furiosus} SCOP: c.37.1.11, a.60.4.1

Probability: 99.36 E-value: 2.3E-13 Score: 131.4 Aligned Cols: 210 Identities: 12% Similari

```
Q ss_pred                CCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCCcEEEEE
Q Klein_Draft     113    MPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus       113    ~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                         .+.+++++.+++++|.++.|+|++|+|||+|+..++..+..+..+.+   ...+|+|++
T Consensus       117    ~~~lD~ll~ggi~~G~i~~i~G~~gsGKT~l~~~l~~~~~~~~~~~g---~~~~~vl~i~
T 1PZN_A          117    SKSLDKLLGGGIETQAITEVFGEFGSGKTQLAHTLAVMVQLPPEEGG---LNGSVIWID
T ss_dssp                CHHHHHHHTSSEESSEEEEEEEESTTSSHHHHHHHHHHHTTSCGGGTS---CSCEEEEEE
T ss_pred                CHHHHHHhCCCeecCeEEEEECCCCCCHHHHHHHHHHHhCChhhCC---CcceEEEEE

Q ss_pred                HHHHHHHcCcC---ccCCEEEEecCcccCcHHHHHHHHHHHH-----hCCcEEEEeChH
Q Klein_Draft     183    NAWETAWRQTL---EEGSITFLPVPVNLMSQDVGALVEDIKD-----YGFEFIVLDTIA
```

```
Q Consensus     183    ~~~~~~~~~~~---~~~~~~~~~~~~~~~~~~~~~~l~~~~~~-----~~~~lviiD~l~
                       ..+........   ....................++...+..     .++++||||+++
T Consensus     183    ~~~~~~~~~~~~~~l~~i~~~~~~~~~~~~~~~l~~l~~~l~~~~~~~~~~~liviDsl~
T 1PZN_A        183    REIAQNRGLDPDEVLKHIYVARAFNSNHQMLLVQQAEDKIKELLNTDRPVKLLIVDSLT
T ss_dssp              HHHHHTTTCCHHHHGGGEEEEECCSHHHHHHHHHHHHHHHHHSSSSSSCEEEEEEETSS
T ss_pred              HHHHHHcCCCHHHHHcCEEEEECCCHHHHHHHHHHHHHHHHHHhccCCCeEEEEEeCcH

Q ss_pred              -CHHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCC-------CCCCCCchhHhccccE
Q Klein_Draft   243    -SARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKD-------EKTLRGSSAYEGGVDT
Q Consensus     243    -~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~-------~~~~~Gs~~~~~~~d~
                        .......+...+..|..++++++++|++++|.++.       ...++|+..+...+|.
T Consensus     253    ~~~~~~~~~~~~~~~L~~la~~~~~~vi~~~~~~~~~~~~~~~~~~~~g~~~~~~~~~
T 1PZN_A        253    ALAERQQKLAKHLADLHRLANLYDIAVFVTNQVQARPDAFFGDPTRPIGGHILAHSATL
T ss_dssp              THHHHHHHHHHHHHHHHHHHHHHTTCEEEEEEECC---------------CCCCCTTCSE
T ss_pred              cHHHHHHHHHHHHHHHHHHHHHcCCEEEEEeccccCCccccCCCcccCChhHHhccceE

Q ss_pred              EEEEEeeecCCCCCCCeeEEEEEec
Q Klein_Draft   303    ITLTCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     303    ~~l~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                       +.+.+.|++..+.+. +.|.+...+
T Consensus     323    ~~l~v~k~~~~~~~~~-~~f~i~~~G  346 (349)
T 1PZN_A        323    RIARLIDAPHLPEGE-AVFSITEKG  346 (349)
T ss_dssp              EEEEESCSSSSCCSE-EEEEEETTE
T ss_pred              EEEEEEECCCCCCeE-EEEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2zts)

6. **2ZTS_B (http://pdb.rcsb.org/pdb/explore.do?structureId=2ZTS) Putative uncharacterized protein PH01 Nucleotide-binding; HET: ADP; 2.07A {Pyrococcus horikoshii}**

Probability: 99.36 E-value: 2.9E-13 Score: 123.2 Aligned Cols: 202 Identities: 16% Similarit

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHH-cCCCCCCCCCCCCcEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLA-TGRNWQGRETEKVKVLY
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~-~g~~~~g~~~~~~~Vl~
                       ..+.+++++++.+++|.+++|.|++|+|||+|+..++.... .         .+..++|
T Consensus     15     g~~~ld~~~~~~~~~g~~~~i~G~~g~GKs~l~~~l~~~~~~~~~~~~~~~~~~~~~~~
T 2ZTS_B        15     GIPGFDELIEGGFPEGTTVLLTGGTGTGKTTFAAQFIYKGAEE---------YGEPGVF
T ss_dssp              SCTTTGGGGTTSEETTCEEEEECSTTSSHHHHHHHHHHHHHHH---------HCCCEEE
T ss_pred              CCCCHHHHhcCCCCCCcEEEEEcCCCCCHHHHHHHHHHHHHHH---------hCCCEEE

Q ss_pred              HHHHHHHHHHcCcCcccCCEEEEec----------------CcccCcHHHHHHHHHHHh
Q Klein_Draft   180    SRINAWETAWRQTLEEGSITFLPV----------------PVNLMSQDVGALVEDIKDY
Q Consensus     180    ~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                       .++..+............+.+...                ...........+...+...
T Consensus     76     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 2ZTS_B        76     REMASFGWDFEKYEKEGKIAIVDGVSSVVGLPSEEKFVLEDRFNVDNFLRYIYRVVKAI
T ss_dssp              HHHHTTTCCHHHHHHTTSEEEEC-------------------CCHHHHHHHHHHHHHT
T ss_pred              HHHHHcCCCHHHHhhcCCEEEEECcccccCCCcccceeecCCCCHHHHHHHHHHHHHHc

Q ss_pred              HHcCCCccCCHHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCC-CCCCCchhHhccc
Q Klein_Draft   234    RCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-KTLRGSSAYEGGV
Q Consensus     234    ~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-~~~~Gs~~~~~~~
                       .+.....     ....+...+..+...++.+++++++++|..+.. ...+|+..+...+
T Consensus     146    ~~~~~~~~-----~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~
T 2ZTS_B        146    SIALRLE-----EERKIREVLLKLNTILLEMGVTTILTTEAPDPQHGKLSRYGIEEFIA
T ss_dssp              HHHTTSS-----SGGGHHHHHHHHHHHHHHCCEEEEEECCC----CCSSSSSCGGGGC
T ss_pred              Hhhhhcc-----hHHHHHHHHHHHHHHHHcCCEEEEEccCCCCccCCccccChhheEE
```

```
Q ss_pred                 ----cEEEEEeeecCCC-CCCCeeEEEEEec
Q Klein_Draft   302       ----GITLTCKKQKDAP-EGDRHTLRLQPID  327 (416)
Q Consensus     302       ----~~~l~~~K~r~~~~-~~~~~~~~~~~~~  327 (416)
                              .+.+...|.|... ....+.|++...
T Consensus     211       ~~~~~~~l~v~K~r~~~~~~~~~~~~~~~~~g  241 (251)
T 2ZTS_B        211       NIELKRYVLIRKMRETRHSMKKYPFEIGPNG  241 (251)
T ss_dssp                 TTEEEEEEEEEEETTCCCCCBCEEEEEETTE
T ss_pred                  ccceeEEEEEEeccCCCCCCCCeeeEEeCCe
```

[Template alignment](#) | [Template 3D structure](#) | [PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2ehv)](http://www.ebi.ac.uk/pdbe/entry/pdb/2ehv)

7. **[2EHV_C (http://pdb.rcsb.org/pdb/explore.do?structureId=2EHV)](http://pdb.rcsb.org/pdb/explore.do?structureId=2EHV) Hypothetical protein PH0186; KaiC, Re FUNCTION; HET: ADP; 2.07A {Pyrococcus horikoshii}**

Probability: 99.36 E-value: 2.9E-13 Score: 123.2 Aligned Cols: 202 Identities: 16% Similarit

```
Q ss_pred                 CCCCCccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHH-cCCCCCCCCCCCcEEE
Q Klein_Draft   112       NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLA-TGRNWQGRETEKVKVLY
Q Consensus     112       ~~~~~~~l~~~~l~~g~~~~~i~G~~G~GKStl~~~la~~~~-~g~~~~g~~~~~~~~Vl~
                          ..+.+++++++.+++|.+++|.|++|+|||+|+..++.... .         .+..++|
T Consensus     15        g~~~ld~~~~~~~~~~g~~~~~i~G~~g~GKs~l~~~l~~~~~~~---------~~~~~~~~
T 2EHV_C        15        GIPGFDELIEGGFPEGTTVLLTGGTGTGKTTFAAQFIYKGAEE---------YGEPGVF
T ss_dssp                 SCTTTGGGTTTSEETTCEEEEECSTTSSHHHHHHHHHHHHHHH---------HCCCEEE
T ss_pred                  CCCCHHHHhcCCCCCCcEEEEEcCCCCCHHHHHHHHHHHHHHH---------hCCCEEE

Q ss_pred                 HHHHHHHHHHcCcCccCCCEEEEec----------------CcccCcHHHHHHHHHHHHh
Q Klein_Draft   180       SRINAWETAWRQTLEEGSITFLPV----------------PVNLMSQDVGALVEDIKDY
Q Consensus     180       ~rl~~~~~~~~~~~~~~~~~~~~~~~~-----------------~~~~~~~~~~~~l~~~~~~
                          .++..+............+.+...                 ...........+...+...
T Consensus     76        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 2EHV_C        76        REMASFGWDFEKYEKEGKIAIVDGVSSVVGLPSEEKFVLEDRFNVDNFLRYIYRVVKAI
T ss_dssp                 HHHHTTTCCHHHHHHHTTSEEEEECSSSCCTTCCC---------CCHHHHHHHHHHHHHH
T ss_pred                  HHHHHcCCCHHHHhhcCCEEEEEECcccccCCCcccceeecCCCCHHHHHHHHHHHHc

Q ss_pred                 HHcCCCccCCHHHHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCC-CCCCCchhHhccc
Q Klein_Draft   234       RCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-KTLRGSSAYEGGV
Q Consensus     234       ~~~~~~~~~~n~~~~~~~~~~~~~~~l~~L~~~~~~~~~~~~~~vl~v~H~~k~~~-~~~~~Gs~~~~~~~~
                          .+.....     ....+...+..+...++.+++++++++++|..+..  ...+|+..+...+
T Consensus     146       ~~~~~~~~~-----~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~
T 2EHV_C        146       SIALRLE-----EERKIREVLLKLNTILLEMGVTTILTTEAPDPQHGKLSRYGIEEFIA
T ss_dssp                 HHHHTSS-----SGGGHHHHHHHHHHHHHHHHCCEEEEEEECCC----CCSSSSSCGGGGC
T ss_pred                  Hhhhhcc-----hHHHHHHHHHHHHHHHHHHHcCCEEEEEccCCCCCccCCCCCCCCCChhheEE
```



```
Q ss_pred                 ----cEEEEEeeecCCC-CCCCeeEEEEEec
Q Klein_Draft   302       ----GITLTCKKQKDAP-EGDRHTLRLQPID  327 (416)
Q Consensus     302       ----~~~l~~~K~r~~~~-~~~~~~~~~~~~~  327 (416)
                              .+.+...|.|... ....+.|++...
T Consensus     211       ~~~~~~~l~v~K~r~~~~~~~~~~~~~~~~~g  241 (251)
```



```
T 2EHV_C        211       NIELKRYVLIRKMRETRHSMKKYPFEIGPNG  241 (251)
T ss_dssp                 SSBEEEEEEEEEETTCCCCCSCEEEEEETTE
T ss_pred                  ccceeEEEEEEeccCCCCCCCCeeeEEeCCe
```

[Template alignment](#) | [Template 3D structure](#) | [PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4twz)](http://www.ebi.ac.uk/pdbe/entry/pdb/4twz)

8. **[4TWZ_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4TWZ)](http://pdb.rcsb.org/pdb/explore.do?structureId=4TWZ) PROTEIN RECA; HOMOLOGOUS RECOI RECOMBINATION; 2.8A {Escherichia coli K12}**

Probability: 99.35 E-value: 1.5E-13 Score: 132.83 Aligned Cols: 199 Identities: 15% Similar

```
Q ss_pred                 CCCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEE
Q Klein_Draft   112       NMPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLY
```

```
Q Consensus     112    ~~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~
                       ..+.++|++. ++++.|.+++|+|++|+|||+++..++..+..         .+++|+|
T Consensus     43     g~~~ld~~l~~ggi~~g~i~~i~G~~g~GKT~l~~~la~~~~~---------~~~~v~~
T 4TWZ_A        43     GSLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAF
T ss_dssp              SCHHHHHHTSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHHH---------TTCCEEE
T ss_pred              CCHHHHHHHhcCCccCCcEEEEECCCCCcHHHHHHHHHHHHHH---------CCCeEEE

Q ss_pred              HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181    RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                       ++..+..        ....+.............+..++...++++||||++..++...
T Consensus     103    ~~~~~g~---------~~~~l~~~~~~~~~~~~~~~~~~~~~~~lvvID~l~~~~~~~
T 4TWZ_A        103    YARKLGV--------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKA
T ss_dssp              HHHHTTC--------CGGGCEEECCSSHHHHHHHHHHHHHHTCCSEEEEECTTTCCCHH
T ss_pred              HHHHcCC--------CccceEEECCCCHHHHHHHHHHHHcCCceEEEEeCccccCCcc

Q ss_pred              HHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCC-------CCCCCCCchhHhccccEEE
Q Klein_Draft   244    ARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGK-------DEKTLRGSSAYEGGVDTVY
Q Consensus     244    ~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k-------~~~~~~Gs~~~~~~~d~vi
                       ......+...+..|..+++++++++++|.+|       .....+|+.++...+|.++
T Consensus     165    ~~~~~~~~~~~~~l~~~~~~~~~~vi~i~h~~k~~~~~~~~~~~~g~~~~~~~a~~~i
T 4TWZ_A        165    GLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRL
T ss_dssp              HHHHHHHHHHHHHHHHHHHHHHTCEEEEEECBCCCC-----CTTCBTTCHHHHHHCSEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHHhcCcEEEEEeeeehhcccccCCCcccccCHHHheeEEEE

Q ss_pred              ------cEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   302    ------GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     302    ------~~~l~~~K~r~~~~~~~~~~~~~~~~  328 (416)
                             .+.+...|+|..+....+.|.+....+
T Consensus     235    ~~~~~~~~~l~i~K~r~~~~~~~~~~i~~~~g  267 (352)
T 4TWZ_A        235    ENVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  267 (352)
T ss_dssp              TEEEEEEEEEEEEEESSBCSCCEEEEEEETTTE
T ss_pred              CceEeeeEEEEEEecCCCCCCcEEEEEEEeCCc
```

Template alignment

9. **TIGR02238 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR02238) recomb_DMC1; me**
model describes DMC1, a subfamily of a larger family of DNA repair and recombination proteins.

Probability: 99.35 E-value: 1.8E-13 Score: 129.94 Aligned Cols: 210 Identities: 12% Similar

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEEEC
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVA
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~
                       +.+++++.+++++|.++.|+|++|+|||+++..++.....+..+.+   ...+|+|++.
T Consensus     83     ~~lD~~l~Ggl~~g~~~~i~G~~gsGKT~l~~~l~~~~~~~~~~~~---~~~~vl~i~~
T TIGR02238     83     QALDGILGGGIESMSITEVFGEFRCGKTQLSHTLCVTAQLPREMGG---GNGKVAYIDT
T ss_pred              HHHHHHHCCCcCCCcEEEEEcCCCCCHHHHHHHHHHHcccHHHCC---CCCeEEEEEC

Q ss_pred              HHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCc
Q Klein_Draft   182    INAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAE
Q Consensus     182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~
                       +.......................+......+...+...++++||||+++.++....
T Consensus     150    ~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~~l~~l~~~~~~~~~liiiDsl~~~~~~~~
T TIGR02238     150    IAERFGVDPDAVLDNILYARAYTSEHQMELLDYLAAKFSEEPFRLLIVDSIMALFRVDF
T ss_pred              HHHHhCCCHHHHHHhceEEEEeCCCHHHHHHHHHHHHHHHHcCCccEEEEEeChHHHccCc

Q ss_pred              HHHHHHHHHHHHhcCCCCeEEEEEccCCCCCCC----------CCCchhHhccccEEEEE
Q Klein_Draft   249    IVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT----------LRGSSAYEGGVDTVYFV
```

```
Q Consensus     249    ~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~----------~~Gs~~~~~~~d~vi~l
                       .+...+..|..++.++++++++++|..+....          +.|+..+...++.++.+
T Consensus     220    ~~~~~~~~L~~l~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~g~~~~~~~~~~i~l
T TIGR02238     220    KLAQMLSRLNKISEEFNVAVFVTNQVQADPGATMTFIADPKKPIGGHVLAHASTTRILL
T ss_pred              HHHHHHHHHHHHHHHHhCCEEEEEeccCCCcccccccCCCCCCCchHHHHhcccEEEEE

Q ss_pred              EeeecCCCCCCCeeEEEEEec
Q Klein_Draft   307    CKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     307    ~~K~r~~~~~~~~~~~~~~~~  327 (416)
                       +.|++..+... +.|.+...+
T Consensus     290    v~k~~~~~~~~-~~f~i~~~G  309 (313)
T TIGR02238     290    LYDSPDMPEAE-ASFQITEGG  309 (313)
T ss_pred              EEeCCCCCCce-EEEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2zuc)

10. **2ZUC_B (http://pdb.rcsb.org/pdb/explore.do?structureId=2ZUC) DNA repair and recombination protei HANDED, DNA BINDING; 3.3A {Sulfolobus solfataricus}**

Probability: 99.35 E-value: 2.4E-13 Score: 129.88 Aligned Cols: 211 Identities: 13% Similar

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       ..+.+++++.++++.|.++.|+|++|+|||+|+..++..+.....+.+   .+.+|+|+
T Consensus     92     g~~~ld~ll~gg~~~g~i~~i~G~~gsGKT~l~~~l~~~~~~~~~~~~---~~~~vl~i
T 2ZUC_B        92     GSQALDGLLAGGIETRTMTEFFGEFGSGKTQLCHQLSVNVQLPPEKGG---LSGKAVYI
T ss_dssp              SCHHHHHHTTTSEETTSEEEEEESTTSSHHHHHHHHHHHTTSCGGGTS---CSCEEEEE
T ss_pred              CCHHHHHHccCCcccCcEEEEeCCCCCCHHHHHHHHHHHcCCHHHCC---CCCEEEEE

Q ss_pred              HHHHHHHHcCcCc---cCCEEEEecCcccCcHHHHHHHHHHH-HhCCcEEEEeChHHHc
Q Klein_Draft   182    INAWETAWRQTLE---EGSITFLPVPVNLMSQDVGALVEDIK-DYGFEFIVLDTIARCT
Q Consensus     182    l~~~~~~~~~~~~---~~~~~~~~~~~~~~~~~~~~~l~~~~~-~~~~~lviiD~l~~~~
                       +..+...+.....   .............+...+..+...+. ..++++||||+++.++
T Consensus     158    l~~~~~~~~~~~~~~l~~i~~~~~~~~~~~~~~l~~l~~~~~~~~~~lvvIDsl~~~~
T 2ZUC_B        158    IENMAKALGLDIDNVMNNIYYIRAINTDHQIAIVDDLQELVSKDPSIKLIVVDSVTSHF
T ss_dssp              HHHHHHTTTCCHHHHHHTEEEEECCSHHHHHHHHHHHHHHHHSCTTEEEEEEESSHHHH
T ss_pred              HHHHHHHcCCCHHHHHHcEEEEECCCHHHHHHHHHHHHHHHHhhCCCeeEEEEcCchHHh

Q ss_pred              HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCC-------CCCchhHhccccEEEE
Q Klein_Draft   245    RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT-------LRGSSAYEGGVDTVYF
Q Consensus     245    ~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~-------~~Gs~~~~~~~d~vi~
                       .....+...+..|..++.+++++|++++|..+....       +.|+..+...+|.++.
T Consensus     228    ~~~~~~~~~~~~L~~l~~~~~~~vi~~~~~~~~~~~~~~~~~~~gg~~~~~~~~~~l~
T 2ZUC_B        228    VRQQKLNKHLHQLTRLAEVYDIAVIITNQVMARPDMFYGDPTVAVGGHTLYHVPGIRIQ
T ss_dssp              HHHHHHHHHHHHHHHHHHHHHTCEEEEEEECSCCSCC-----------CCCCCCCSEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHHhCCEEEEEeccccCCcccccCCCcccccCchHHhhCCcEEEE

Q ss_pred              EEeeecCCCCCCCeeEEEEEec
Q Klein_Draft   306    TCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     306    ~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                       +..|++..+... +.|.+...+
T Consensus     298    ~i~k~~~~~~~~-~~f~i~~~G  318 (324)
T 2ZUC_B        298    RVVDAPHLPEGE-VVFALTEEG  318 (324)
T ss_dssp              EEEECSSCCCCE-EEEEECSSC
T ss_pred              EEEECCCCCCeE-EEEEEeCCe
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2z43)

11. 2Z43_C (http://pdb.rcsb.org/pdb/explore.do?structureId=2Z43) **DNA repair and recombination protein; BINDING, RECOMBINATION; 1.93A {Sulfolobus solfataricus}**

Probability: 99.35 E-value: 2.4E-13 Score: 129.88 Aligned Cols: 211 Identities: 13% Similar

```
Q ss_pred                CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft     112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus       112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                         ..+.+++++.++++.|.++.|+|++|+|||+|+..++..+.....+.+   .+.+|+|+
T Consensus       92     g~~~ld~ll~gg~~~g~i~~i~G~~gsGKT~l~~~l~~~~~~~~~~~~---~~~~vl~i
T 2Z43_C          92     GSQALDGLLAGGIETRTMTEFFGEFGSGKTQLCHQLSVNVQLPPEKGG---LSGKAVYI
T ss_dssp                SCHHHHHHTTTSEETTEEEEEEESTTSSHHHHHHHHHHHTTSCGGGTS---CSCEEEEE
T ss_pred                CCHHHHHHccCCcccCcEEEEeCCCCCCHHHHHHHHHHHhcCCHHHCC---CCCEEEEE

Q ss_pred                HHHHHHHHcCcCc---cCCEEEEecCcccCcHHHHHHHHHHH-HhCCcEEEEeChHHHc
Q Klein_Draft     182    INAWETAWRQTLE---EGSITFLPVPVNLMSQDVGALVEDIK-DYGFEFIVLDTIARCT
Q Consensus       182    l~~~~~~~~~~~~---~~~~~~~~~~~~~~~~~~~~~l~~~~~-~~~~~lviiD~l~~~~
                         +..+...+.....   .............+...+..+...+. ..++++||||+++.++
T Consensus       158    l~~~~~~~~~~~~~~l~~i~~~~~~~~~~~~~~l~~l~~~~~~~~~~lvvIDsl~~~~
T 2Z43_C          158    IENMAKALGLDIDNVMNNIYYIRAINTDHQIAIVDDLQELVSKDPSIKLIVVDSVTSHF
T ss_dssp                HHHHHHHTTCCHHHHHHTEEEEECCSHHHHHHHHHHHHHHHHHCTTEEEEEEETTTHHH
T ss_pred                HHHHHHHcCCCHHHHHhcEEEEECCCHHHHHHHHHHHHHHHhhCCCeeEEEEcCchHHh

Q ss_pred                HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCC-------CCCchhHhccccEEEE
Q Klein_Draft     245    RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT-------LRGSSAYEGGVDTVYF
Q Consensus       245    ~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~~Gs~~~~~~~d~vi~
                         .....+...+..|..++.+++++|++++|..+....       +.|+..+...+|.++.
T Consensus       228    ~~~~~~~~~~~~L~~l~~~~~~~vi~~~~~~~~~~~~~~~~~~~gg~~~~~~~~~~l~
T 2Z43_C          228    VRQQKLNKHLHQLTRLAEVYDIAVIITNQVMARPDMFYGDPTVAVGGHTLYHVPGIRIQ
T ss_dssp                HHHHHHHHHHHHHHHHHHHHHTCEEEEEEEC-----------------------CCEEEE
T ss_pred                HHHHHHHHHHHHHHHHHHHHhCCEEEEEeccccCCccccCCCccccCchHHhhCCcEEEE

Q ss_pred                EEeeecCCCCCCCeeEEEEEec
Q Klein_Draft     306    TCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus       306    ~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                         +..|++..+... +.|.+...+
T Consensus       298    ~i~k~~~~~~~~-~~f~i~~~G  318 (324)
T 2Z43_C          298    RVVDAPHLPEGE-VVFALTEEG  318 (324)
T ss_dssp                EEEECTTSCCCE-EEEEEETTE
T ss_pred                EEEECCCCCCeE-EEEEEeCCe
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4wia)

12. 4WIA_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4WIA) **Putative flagella-related protein H; ar protein; HET: SO4, MSE; 2.2A {Methanocaldococcus jannaschii DSM 2661}**

Probability: 99.34 E-value: 3.6E-13 Score: 121.58 Aligned Cols: 200 Identities: 17% Similar

```
Q ss_pred                CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft     112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus       112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                         ..|.+++++.+.++.|..++|+|++|+|||+|+..++.....         ...+|+|+
T Consensus       12     g~~~ld~~~~ggl~~g~~~~i~G~~g~GKs~l~~~~~~~~~~~~~~~~~~~~~~vl~~
T 4WIA_A          12     SRDDLDKRIGGGIPHGSLIIIEGEESTGKSVLCQRLAYGFLQ---------NRYSVTYV
T ss_dssp                TTCCHHHHTTSSEETTCEEEEECCTTSSHHHHHHHHHHHHHH---------TTCCEEEE
T ss_pred                CchhHHHHhCCCcCCCcEEEEECCCCCCHHHHHHHHHHHHh---------cCCeEEEE

Q ss_pred                HHHHHHHHHcCcCcccCCEEEEecCcc-----cCcHHHHHHHHHHHhCCcEEEEeChHH
Q Klein_Draft     181    RINAWETAWRQTLEEGSITFLPVPVN-----LMSQDVGALVEDIKDYGFEFIVLDTIAR
Q Consensus       181    rl~~~~~~~~~~~~~~~~~~~~~~~~-----~~~~~~~~l~~~~~~~~~~lviiD~l~~
                         ++.............+.+.+......     ........+...++..++++||||+++.
```

```
T Consensus     73     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~iviD~l~~
T 4WIA_A        73     QMNSLNYSINKKLLSGALLYIPVYPLIADNKKKDGFLKKVMETRAFYEKDVIIFDSISA
T ss_dssp              HHHHTTCCCHHHHHHTSEEEEECHHHHHCTTCCBCHHHHHHHCHHHHTSSEEEEETHHH
T ss_pred              HHHhcCcchhhhhhcCCeeEEecccccCccchhHHHHHHHHHHHcCCCEEEEeChHH

Q ss_pred              HHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeCC---
Q Klein_Draft   246    DVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERGN---
Q Consensus     246    ~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~~---
                       ....+...+..|..++...++++++++|....   ..+.+.+...+|.++.+....
T Consensus     138    ~~~~~~~~~~~l~~l~~~~~~~i~~~~~~~~~---~~~~~~~~~~~~d~vi~l~~~~~~~
T 4WIA_A        138    SEVNVDDLMAFFKRITALKKIIICTVNPKELP---ESVLTIIRTSATMLIRTELFTFGG
T ss_dssp              SSCCHHHHHHHHHHHHTTTCEEEEEECGGGSC---HHHHHHHHHHCSEEEEEEEEETT
T ss_pred              CcchHHHHHHHHHHHHhCCEEEEEeChhcCC---hhHHHHHHHHceEEEEEEEecCc

Q ss_pred              cCCCC--CCCeeEEEEEecC
Q Klein_Draft   311    KDAPE--GDRHTLRLQPIDG  328 (416)
Q Consensus     311    r~~~~--~~~~~~~~~~~~~  328 (416)
                       |....  ...+.|++....|
T Consensus     205    r~~~~~~~~~~~~~~~~~~g  224 (233)
T 4WIA_A        205    NMAPGSYQKNIVFRVEPKIG  224 (233)
T ss_dssp              TTCCSCCCSEEEEEEETTTE
T ss_pred              cCCCCccCCceEEEEecCce
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/1xp8)

13. **1XP8_A (http://pdb.rcsb.org/pdb/explore.do?structureId=1XP8) RecA protein; Recombination, Radiore**
DNA-binding; HET: AGS; 2.5A {Deinococcus radiodurans} SCOP: d.48.1.1, c.37.1.11

Probability: 99.33 E-value: 2.0E-13 Score: 132.76 Aligned Cols: 198 Identities: 16% Similar

```
Q ss_pred              CCCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEE
Q Klein_Draft   112    NMPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLY
Q Consensus     112    ~~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~
                       ..+.+++++. +++++|.++.|+|++|+|||+|+..++..+..         ...+|+|
T Consensus     58     g~~~lD~~l~~ggl~~G~i~~I~G~~gsGKTtl~~~la~~~~~~~~~~~~~~~~v~~
T 1XP8_A        58     GSLSLDLALGVGGIPRGRITEIYGPESGGKTTLALAIVAQAQK---------AGGTCAF
T ss_dssp              SCHHHHHHTSSSSEETTSEEEEEESTTSSHHHHHHHHHHHHHH---------TTCCEEE
T ss_pred              CCHHHHHHhccCCccCCeEEEEECCCCCCHHHHHHHHHHHHHH---------CCCeEEE

Q ss_pred              HHHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCC
Q Klein_Draft   180    SRINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVG
Q Consensus     180    ~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~
                       .+...+          ..-.+.............+..++...++++||||++..+...
T Consensus     119    ~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~liiiDsl~~l~~~
T 1XP8_A        119    ARALGV----------NTDELLVSQPDNGEQALEIMELLVRSGAIDVVVVDSVAALTPR
T ss_dssp              HHHTTC----------CGGGCEEECCSSHHHHHHHHHHHHTTTCCSEEEEECTTTCCCS
T ss_pred              HHHcCC----------CCcceEEECCCCHHHHHHHHHHHHCCCCcEEEEecchhcCCh

Q ss_pred              --HHHHHHHHHHHHHHHcCCCCeEEEEEccCCCC-------CCCCCCchhHhccccEE
Q Klein_Draft   245    --RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKD-------EKTLRGSSAYEGGVDTV
Q Consensus     245    --~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~-------~~~~~Gs~~~~~~~d~v
                         .....+...+..|..++.+++++|++++|.++.       ....+|+.++...+|.+
T Consensus     179    ~~~~~~~~~~~~~~L~~~~~~~~~~vi~i~h~~~~~~~~~~~~~~~Gg~~~~~~a~~~
T 1XP8_A        179    PGLQARLMSQALRKLTAILSKTGTAAIFINQVREKIGVMYGNPETTTGGRALKFYASVR
T ss_dssp              CCHHHHHHHHHHHHHHHHHTTTCCEEEEEEEC---------------CHHHHHHHCSEE
T ss_pred              HHHHHHHHHHHHHHHHHHHHHhHCcEEEEEEecchhcccccCCCcccccchHHhceeeEE

Q ss_pred              ---------EEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   303    ---------ITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
```

```
Q Consensus     303    ----------~~l~~~K~r~~~~~~~~~~~~~~~~  328 (416)
                                +.+.+.|+|..+......|.+....+
T Consensus     249    ~~~~~~~~~~~~~v~Knr~~~~~~~~~~~l~~~~g  283 (366)
T 1XP8_A        249    VGNDAVANTVKIKTVKNKVAAPFKEVELALVYGKG  283 (366)
T ss_dssp              -----CEEEEEEEEEEESSSCCCCEEEEEEETTTE
T ss_pred              cCCCcccceEEEEEEcCCCCCCccEEEEEEEcCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2i1q)

14. **2I1Q_A (http://pdb.rcsb.org/pdb/explore.do?structureId=2I1Q) DNA repair and recombination protein COMPLEX, Calcium; HET: ANP; 1.9A {Methanococcus voltae} SCOP: c.37.1.11, a.60.4.1**

Probability: 99.32 E-value: 1.7E-13 Score: 130.56 Aligned Cols: 215 Identities: 13% Similar

```
Q ss_pred              CCCCCccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCC-------
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETE-------
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~-------
                       ..+.+++++.+++++|.++.|+|++|+|||+++..++..+..+..+++....
T Consensus     83     g~~~ld~~l~ggl~~g~i~~i~G~~g~GKS~l~~~l~~~~~~~~~~~~~~~~~~~~~~
T 2I1Q_A        83     SSSELDSVLGGGLESQSVTEFAGVFGSGKTQIMHQSCVNLQNPEFLFYDEEAVSKGEVA
T ss_dssp              SCHHHHHHTTSSEETTEEEEEEESTTSSHHHHHHHHHHHTTCGGGEECCTTTSCTTTTS
T ss_pred              CCHHHHHHcCCCccCCeEEEEEcCCCCCHHHHHHHHHHHcCchHHcCChhhhccCCCc

Q ss_pred              --cccHHHHHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHH-hCCcEEEEe
Q Klein_Draft   175    --VAGFSSRINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKD-YGFEFIVLD
Q Consensus     175    --~~~~~~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~-~~~~lviiD
                         .......+................+.............+...+.. .++++||||
T Consensus     153    ~~~~~~l~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~~~l~~~~~~~~~~~lvviD
T 2I1Q_A        153    TFRPERIMQMAEHAGIDGQTVLDNTFVARAYNSDMQMLFAEKIEDLIQEGNNIKLVVID
T ss_dssp              CCCHHHHHHHHHHHHTCCHHHHHHTEEEEECSSHHHHHHHHHHTHHHHHHTTCEEEEEEEE
T ss_pred              CCCHHHHHHHHHHHcCCCHHHHHHcEEEEeCCCHHHHHHHHHHHHHHHHHcCCCeEEEEEe

Q ss_pred              ---CCHHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhcc
Q Klein_Draft   242    ---NSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGG
Q Consensus     242    ---n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~
                          +.......+...+..|..++++++++|++++|.++..       ....|+..+...
T Consensus     223    ~~~~~~~~~~~~~~~~~~L~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~g~~~~~~~
T 2I1Q_A        223    GRGKLAERQQKLGRHMATLNKLADLFNCVVLVTNQVSAKPDAFFGMAEQAIGGHIVGHA
T ss_dssp              CTTSHHHHHHHHHHHHHHHHHHHHHHTTCEEEEEECEECC-------CCEESSHHHHHHH
T ss_pred              CCCcHHHHHHHHHHHHHHHHHHHHHhCCEEEEeccccCCCcccccCcccccccchHHHhhe

Q ss_pred              --cEEEEEeeecCCCCCCCeeEEEEEec
Q Klein_Draft   302    --GITLTCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     302    --~~~l~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                         .+++...|.+..+.. .+.|++...+
T Consensus     293    ~~~r~~~~~~~~~~~~~-~~~f~i~~~G  319 (322)
T 2I1Q_A        293    GDKRVAKLYDSPHLPDA-EAIFRITEKG  319 (322)
T ss_dssp              TTEEEEEEEECSSSCCE-EEEEEEETTE
T ss_pred              CCeEEEEEEeCCCCCCc-EEEEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/1xu4)

15. **1XU4_A (http://pdb.rcsb.org/pdb/explore.do?structureId=1XU4) ATPASE IN COMPLEX WITH AMP-PNP; CO-FACTORS, POTASSIUM-DEPENDENCE; HET: ANP; 2.4A {Methanococcus voltae} SCOP: c.37.1.11, a.60.4.**

Probability: 99.32 E-value: 1.7E-13 Score: 130.56 Aligned Cols: 215 Identities: 13% Similar

```
Q ss_pred              CCCCCccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCC-------
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETE-------
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~-------
                       ..+.+++++.+++++|.++.|+|++|+|||+++..++..+..+..+++....
```

```
T Consensus     83      g~~~ld~~l~ggl~~g~i~~i~G~~g~GKS~l~~~l~~~~~~~~~~~~~~~~~~~~~~
T 1XU4_A        83      SSSELDSVLGGGLESQSVTEFAGVFGSGKTQIMHQSCVNLQNPEFLFYDEEAVSKGEVA
T ss_dssp               SCHHHHHHTTTSEETTSEEEEEESTTSSHHHHHHHHHHHTTSGGGEECCTTTSCTGGGS
T ss_pred               CCHHHHHHcCCCccCCeEEEEEcCCCCCHHHHHHHHHHHhcCchHHcCChhhhccCCCc

Q ss_pred               --cccHHHHHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHH-hCCcEEEEe
Q Klein_Draft   175     --VAGFSSRINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKD-YGFEFIVLD
Q Consensus     175     --~~~~~~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~-~~~~lviiD
                          .......+.................+.............+...+.. .++++||||
T Consensus     153     ~~~~~~l~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~~~l~~~~~~~~~~~lvviD
T 1XU4_A        153     TFRPERIMQMAEHAGIDGQTVLDNTFVARAYNSDMQMLFAEKIEDLIQEGNNIKLVVID
T ss_dssp               CCCHHHHHHHHHHHTSCHHHHHHTEEEEECCSHHHHHHHHHTHHHHHHTTCEEEEEEEE
T ss_pred               CCCHHHHHHHHHHcCCCHHHHHhcEEEEeCCCHHHHHHHHHHHHHHHHcCCCeEEEEEe

Q ss_pred               ---CCHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhcc
Q Klein_Draft   242     ---NSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGG
Q Consensus     242     ---n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~
                           +.......+...+..|..++++++++|++++|.++..       ....|+..+...
T Consensus     223     ~~~~~~~~~~~~~~~~~L~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~g~~~~~~~
T 1XU4_A        223     GRGKLAERQQKLGRHMATLNKLADLFNCVVLVTNQVSAKPDAFFGMAEQAIGGHIVGHA
T ss_dssp               STTSHHHHHHHHHHHHHHHHHHHHHTTCEEEEEECEESSCCCSSSCCCEESSHHHHHHH
T ss_pred               CCCcHHHHHHHHHHHHHHHHHHHHHhCCEEEEeccccCCCccccCcccccchHHHhhe

Q ss_pred               --cEEEEEeeecCCCCCCCeeEEEEEec
Q Klein_Draft   302     --GITLTCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     302     --~~~l~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                          .+++...|.+..+.. .+.|++...+
T Consensus     293     ~~~r~~~~~~~~~~~~~-~~~f~i~~~G  319 (322)
T 1XU4_A        293     GDKRVAKLYDSPHLPDA-EAIFRITEKG  319 (322)
T ss_dssp               TTEEEEEEEECSSSCCE-EEEEEEETTE
T ss_pred               CCeEEEEEEeCCCCCCc-EEEEEEeCCc
```

Template alignment

16. **TIGR02239 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR02239) recomb_RAD51; DN eukaryotic sequence family consists of RAD51, a protein involved in DNA homologous recombination a**

Probability: 99.32 E-value: 3.9E-13 Score: 127.71 Aligned Cols: 211 Identities: 12% Similar

```
Q ss_pred               CCCCccccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   113     MPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     113     ~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                        .+.+++++.+++++|.++.|+|++|+|||+|+..++..+..+..+.+   ...+|+|++
T Consensus     82      ~~~ld~~l~ggl~~g~~~~i~G~~g~GKT~l~~~l~~~~~~~~~~~~---~~~~v~~i~
T TIGR02239     82      SKELDKLLGGGIETGSITEIFGEFRTGKTQLCHTLAVTCQLPIDQGG---GEGKALYID
T ss_pred               CHHHHHHhCCCcCCCcEEEEECCCCCCHHHHHHHHHHHccCCcccCC---CCceEEEEE

Q ss_pred               HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181     RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181     rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~
                        .+.................+.......+......+...+...++++||||+++.++...
T Consensus     149     ~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~l~~l~~~~~~~~~~liiID~l~~l~~~~
T TIGR02239     149     AIAERYGLNPEDVLDNVAYARAYNTDHQLQLLQQAAAMMSESRFALLIVDSATALYRTD
T ss_pred               HHHHHcCCCHHHHHHheeEeecCCHHHHHHHHHHHHHHHHhhcCCeEEEEcCHHHHhcCC

Q ss_pred               HHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-----------CCCCCchhHhccccEEE
Q Klein_Draft   248     GIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-----------KTLRGSSAYEGGVDTVY
Q Consensus     248     ~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------------~~~~Gs~~~~~~~d~vi
                        ..+...+..|..++.++++++++++|.++..           ..+.|+..+...+|.++
```

```
T Consensus     219    ~~~~~~~~~L~~la~~~~~~ii~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i
T TIGR02239     219    MHLARFLRSLQRLADEFGVAVVITNQVVAQVDGAGSMFAGDPKKPIGGNIMAHASTTRL
T ss_pred              HHHHHHHHHHHHHHHHHCCEEEEEeCCCcccCCCCcccCCCCCCCCchHHhcccEEE

Q ss_pred              EEEeeecCCCCCCCeeEEEEEec
Q Klein_Draft   305    LTCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     305    l~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                       +...|+|..+... +.|++...+
T Consensus     289    ~~~~k~~~~~~~~~-~~f~i~~~G  310 (316)
T TIGR02239     289    CKIYDSPCLPESE-AMFAIYEDG  310 (316)
T ss_pred              EEEEecCCCCCcc-eeEEEeCCc
```

Template alignment

17. **TIGR02236 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR02236) recomb_radA; DNA protein RadA. This family consists exclusively of archaeal RadA protein, a homolog of bacterial RecA (T (TIGR02239), and archaeal RadB (TIGR02237).**

Probability: 99.31 E-value: 9.9E-13 Score: 124.16 Aligned Cols: 210 Identities: 14% Similar

```
Q ss_pred              CCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   113    MPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     113    ~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       .+.+++++.+.++.|.+++|+|++|+|||+|+..++..+..+..+.+   ...+|+|++
T Consensus     81     ~~~ld~~l~ggl~~g~~~~i~G~~g~GKT~l~~~l~~~~~~~~~~~~---~~~~v~~i~
T TIGR02236     81     SKELDELLGGGIETQAITEVFGEFGSGKTQICHQLAVNVQLPEEKGG---LGGKAVYID
T ss_pred              ChHHHHHcCCCcccCCeEEEEECCCCCCHHHHHHHHHHHccCchHhCC---CCCeEEEEE

Q ss_pred              HHHHHHHcCcCcc---CCEEEEecCcccCcHHHHHHHHHHHHh--CCcEEEEeChHHHc
Q Klein_Draft   183    NAWETAWRQTLEE---GSITFLPVPVNLMSQDVGALVEDIKDY--GFEFIVLDTIARCT
Q Consensus     183    ~~~~~~~~~~~~~---~~~~~~~~~~~~~~~~~~~~l~~~~~~~--~~~lviiD~l~~~~
                       ..+..........   ...................+...+...  ++++||||+++.++
T Consensus     147    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~liiiD~~~~l~
T TIGR02236     147    MQMAEARGLDPDEVLKNIYVARAYNSNHQMLLVEKAEDLIKELNNPVKLLIVDSLTSHF
T ss_pred              HHHHHHCCCCHHHHHHHceeeeCCCchHHHHHHHHHHHHHHHHhCCCcEEEEEeChHHc

Q ss_pred              HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhccccEEEE
Q Klein_Draft   245    RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGVDTVYF
Q Consensus     245    ~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~~d~vi~
                       .....+...+..|..+++++++++++|.++..       ..+.|+..+...+|.++.
T Consensus     217    ~~~~~~~~~~~~l~~l~~~~~~~ii~~~~~~~~~~~~~~~~~~~g~~~~~~~~~~i~
T TIGR02236     217    ERQQKLNKHLHDLLRLADLYNAAVVVTNQVMARPDAFFGDPTRPIGGHILGHAATFRVY
T ss_pred              HHHHHHHHHHHHHHHHHHHhCCEEEEEEecCCCCcccCCCCCCCCCchHHhccceEEEE

Q ss_pred              EEeeecCCCCCCCeeEEEEEec
Q Klein_Draft   306    TCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     306    ~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                       ...|.+..+... +.|.+...+
T Consensus     287    ~~~~~~~~~~~~-~~f~i~~~G  307 (310)
T TIGR02236     287    RLVDSPHLPEGE-AVFRITEKG  307 (310)
T ss_pred              EEEeCCCCCCCc-eEEEEeCCe
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/5jzc)

18. **5JZC_F (http://pdb.rcsb.org/pdb/explore.do?structureId=5JZC) DNA repair protein RAD51 homolog; cry CELL; 4.2A {Homo sapiens}**

Probability: 99.3 E-value: 6.7E-13 Score: 127.64 Aligned Cols: 210 Identities: 12% Similari

```
Q ss_pred              CCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   113    MPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
```

```
Q Consensus     113    ~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       .+.+++++.+++++|.++.|+|++|+|||+|+..++..+..+..+.+   ...+|+|++
T Consensus     106    ~~~lD~~l~ggi~~g~i~~i~G~~gsGKT~l~~~l~~~~~~~~~~~~---~~~~vl~i~
T 5JZC_F        106    SKELDKLLQGGIETGSITEMFGEFRTGKTQICHTLAVTCQLPIDRGG---GEGKAMYID
T ss_dssp              SHHHHHHHTSCSBSSSEEEECCCTTSCHHHHHHHHHHHTTSCGGGTC---CCCBEEEEE
T ss_pred              CHHHHHHcCCCeecceEEEEECCCCCCHHHHHHHHHHHhcCchHhCC---CCceEEEEE

Q ss_pred              HHHHHHHcCcCc---cCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCC
Q Klein_Draft   183    NAWETAWRQTLE---EGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVG
Q Consensus     183    ~~~~~~~~~~~~---~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~
                       ..+.........   .............+......+...+...++++||||++..++..
T Consensus     172    ~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~l~~l~~~~~~~~~~liiIDsi~~~~~~
T 5JZC_F        172    LAVAERYGLSGSDVLDNVAYARAFNTDHQTQLLYQASAMMVESRYALLIVDSATALYRT
T ss_dssp              HHHHHHTTCCHHHHHHHEEEEECCSHHHHHHHHHHHHHHHHHSCBCEEEEECTTHHHHS
T ss_pred              HHHHHHcCCCHHHHHhcEEEEeCCCHHHHHHHHHHHHHHHHhcCeEEEEEeChHHHhcc

Q ss_pred              HHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCC----------CCCCchhHhccccEEE
Q Klein_Draft   247    VGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEK----------TLRGSSAYEGGVDTVY
Q Consensus     247    ~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~~~~~Gs~~~~~~~d~vi
                       ...+...+..|..++++++++|++++|..+...          .+.|+..+...++.++
T Consensus     242    ~~~l~~~~~~L~~l~~~~~~~vl~~~~~~~~~~~~~~~~~~~~~~g~~~~~~~~~~l
T 5JZC_F        242    QMHLARFLRMLLRLADEFGVAVVITNQVVAQVDGAAMFAADPKKPIGGNIIAHASTTRL
T ss_dssp              HHHHHHHHHHHHHHHHHHCCEEEEECCBCCCCC--------CCCCBTTGGGSCTTSCBC
T ss_pred              HHHHHHHHHHHHHHHHHHCCEEEEEeCcccccCCcccccCCCcccccCcHHHHhcceEEE

Q ss_pred              EEEeeecCCCCCCCeeEEEEEec
Q Klein_Draft   305    LTCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     305    l~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                       +...|+|..+. ..+.|.+...+
T Consensus     312    ~~v~ks~~~~~-~~~~f~i~~~G  333 (339)
T 5JZC_F        312    CKIYDSPCLPE-AEAMFAINADG  333 (339)
T ss_dssp              ECCCSCSSSSS-CCCEEEEETTE
T ss_pred              EEEEECCCCCC-cEEEEEEcCCc
```

Template alignment | CDD (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam00154)

19. **PF00154.20 (http://pfam.xfam.org/family/PF00154.20#tabview=tab0) ; RecA ; recA bacterial DNA recom**

Probability: 99.29 E-value: 8.3E-13 Score: 122.02 Aligned Cols: 201 Identities: 12% Similar

```
Q ss_pred              CCCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEE
Q Klein_Draft   112    NMPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLY
Q Consensus     112    ~~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~
                       ..+.+++++. +.+++|.+++|.|++|+|||+++..++..+..         .+.+++|
T Consensus     36     g~~~ld~~~~~~~~~~g~~~~i~G~~g~GKT~l~~~l~~~~~~~~~~~~~~~~~v~~
T PF00154.20    36     GSLGLDVALGIGGLPMGRIVEIFGPESSGKTTLTLSVIAQAQK---------AGKTCAF
T ss_pred              CcHHHHHHHcCCCccCCcEEEEECCCCCCHHHHHHHHHHHHH---------CCCeEEE

Q ss_pred              HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181    RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                       ++..+..        ...................+...+...++++||||+++.++...
T Consensus     96     ~~~~~~~~-------~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vviiD~~~~~~~~~
T PF00154.20    96     YAAKLGV--------DVKELFVSQPDNGEQALEICDALVRSGAIDVIIVDSVAALTPKA
T ss_pred              HHHHcCC--------CchheEEECCCcHHHHHHHHHHHHcCCceEEEEeCchhcCCHH

Q ss_pred              HHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCC-------CCCCchhHhccccEEE
Q Klein_Draft   244    ARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEK-------TLRGSSAYEGGVDTVY
Q Consensus     244    ~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~~~Gs~~~~~~~d~vi
```

```
                         ......+...+..|...+++.++++++++|.++...       ...|++.+...+|.++
T Consensus     158      ~~~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~g~~~~~~~~~~~i
T PF00154.20    158      GLQARLMSQALRKLTGQIKNANCLVVFINQIRMKIGVMFGNPETTTGGNALKFYSSVRL
T ss_pred                HHHHHHHHHHHHHHHHHHHHcCeEEEEEecccccccCccCCCCcccCCchhhheeeEEEE

Q ss_pred                -------EEEEEeeecCCCCCCCeeEEEEEecCCc
Q Klein_Draft   303      -------ITLTCKKQKDAPEGDRHTLRLQPIDGTD  330 (416)
Q Consensus     303      -------~~l~~~K~r~~~~~~~~~~~~~~~~~~  330 (416)
                                +.+.+.|+|..+.+..+.|.+....|.+
T Consensus     228      ~~~~~~~~~l~i~K~r~~~~~~~~~~~~~~~~g~~  262 (262)
T PF00154.20    228      ENIIGNETRVKVVKNKLAAPFRQVDFQILYGEGIS  262 (262)
T ss_pred                CceeeeEEEEEEEeCCCCCCccEEEEEEeecCCCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/5jrj)

20. **5JRJ_A (http://pdb.rcsb.org/pdb/explore.do?structureId=5JRJ) Protein RecA; DNA-binding protein, ATP-ATP, ADP; 1.7A {Herbaspirillum seropedicae}**

Probability: 99.29 E-value: 6.0E-13 Score: 128.69 Aligned Cols: 199 Identities: 15% Similar

```
Q ss_pred                CCCCCcccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEE
Q Klein_Draft   112      NMPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLY
Q Consensus     112      ~~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~
                         ..+.+++++. +++++|.++.|+|++|+|||+|+..++..+..         ....|+|
T Consensus     50       g~~~Ld~~l~~ggi~~G~~~~i~G~~gsGKT~l~~~l~~~~~~~~~~~~~~~~vl~
T 5JRJ_A        50       GSLGLDIALGIGGLPRGRVIEIYGPESSGKTTLTLQSIAEMQK---------LGGTCAF
T ss_dssp                SCHHHHHHTSSSSEETTSEEEEEESTTSSHHHHHHHHHHHHHH---------TTCCEEE
T ss_pred                CCHHHHHHhccCCccCCeEEEEECCCCCCHHHHHHHHHHHHHH---------CCCeEEE

Q ss_pred                HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181      RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181      rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                         ++..+..        ....++.............+..++...++++||||++..+....
T Consensus     110      ~~~~~g~--------~~~~~~~~~~~~~~~~~~~~~~~~~~~~~liviDs~~~l~~~~
T 5JRJ_A        110      YAQKLGV--------NLNDLLISQPDTGEQALEICDALVRSGAVDLIVVDSVAALTPKA
T ss_dssp                HHHHTTC--------CGGGCEEECCSSHHHHHHHHHHHHHTSCCCEEEEECSTTCCCHH
T ss_pred                HHHHcCC--------CchheEEeCCCCHHHHHHHHHHHHCCCCcEEEEechhhhCChh

Q ss_pred                -HHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhccccEEE
Q Klein_Draft   245      -RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGVDTVY
Q Consensus     245      -~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~~d~vi
                          .....+...+..|..++.++++++++++|.++..       ....|+.++...++.++
T Consensus     172      ~~~~~~~~~~~~~l~~~~~~~~~~vi~i~q~~~~~~~~~~~~~~~Gg~~~~~~a~~~i
T 5JRJ_A        172      GLQARLMSQALRKLTGSINRTNTTVIFINQIRMKIGVMFGNPETTTGGNALKFYASVRL
T ss_dssp                ----CHHHHHHHHHHHHHHHHTCEEEEEEEC----------------CCHHHHHCSEEE
T ss_pred                HHHHHHHHHHHHHHHHHHHHcCcCEEEEEecceeccCccCCCcccccCchHHheeEEEE

Q ss_pred                -------EEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   303      -------ITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     303      -------~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                                +.+.+.|+|..+.....|.+....+
T Consensus     242      ~~~~g~~~~~~i~K~r~~~~~~~~~~l~~~~g  274 (351)
T 5JRJ_A        242      DEVIGSETKVKVVKNKVAPPFREAHFDILYGEG  274 (351)
T ss_dssp                TEEEEEEEEEEEEEESSSCSCCEEEEEEETTTE
T ss_pred                CeeeeeEEEEEEEecCCCCCceEEEEEEEeCCC
```

Template alignment

21. TIGR02012 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR02012) **tigrfam_recA; prot orthologs of the recA protein. RecA promotes hybridization of homolgous regions of DNA.**

Probability: 99.29 E-value: 6.5E-13 Score: 126.76 Aligned Cols: 197 Identities: 15% Similar

```
Q ss_pred              CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       +.+++++. +++++|.++.|+|++|+|||+++..++..+..         ....|+|++
T Consensus     41     ~~ld~~l~~ggi~~G~i~~i~G~~gsGKTtl~~~l~~~~~~---------~~~~v~~i~
T TIGR02012     41     LALDLALGVGGLPKGRIIEIYGPESSGKTTLALHAIAEAQK---------AGGTAAFID
T ss_pred              HHHHHHHcCCCcCCCcEEEEECCCCCcHHHHHHHHHHHHH---------CCCeEEEEE

Q ss_pred              HHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCcc
Q Klein_Draft   183    NAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAEE
Q Consensus     183    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~~
                       ..+..        ....+..............+..+++..++++||||++..++.....
T Consensus     101    ~~~~~-------~~~~~~~~~~~~~~~~~~~~~~~~~~~~liviDs~~~l~~~~~~
T TIGR02012     101    RKLGV--------DIDNLLVSQPDTGEQALEIAETLVRSGAVDIIVVDSVAALVPKAEI
T ss_pred              HHhCC--------ChhheEEeCCCCHHHHHHHHHHHHCCCCeEEEEechhhcCCHhHh

Q ss_pred              HHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCC-------CCCCchhHhccccEEEEE
Q Klein_Draft   246    DVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEK-------TLRGSSAYEGGVDTVYFV
Q Consensus     246    ~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~-------~~~Gs~~~~~~~d~vi~l
                       ....+.+.+..|...+++++++++++|.++...       ...|+.++...+|.++.|
T Consensus     163    ~~~~~~~~l~~l~~~~~~~~~~ii~i~~~~~~~~~~~~~~~~~Gg~~~~~~a~~~i~l
T TIGR02012     163    QARLMSQALRKLTGALSKSNTTAIFINQIREKIGVMFGNPETTTGGNALKFYASVRLDI
T ss_pred              HHHHHHHHHHHHHHHHHHcCcEEEEEecccccccccCCCCCCCCCcchhheeeeEEEEE

Q ss_pred              -----EEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   303    -----ITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     303    -----~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                            +.+++.|+|..+....+.|.+....|
T Consensus     233    ~~g~~~~~~i~K~r~~~~~~~~~~~i~~~~G  263 (321)
T TIGR02012     233    VVGNRTKVKVVKNKVAPPFREAEFDILYGEG  263 (321)
T ss_pred              eeCcEEEEEEEecCCCCCCCeEEEEEeCCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2dr3)

22. 2DR3_D (http://pdb.rcsb.org/pdb/explore.do?structureId=2DR3) **UPF0273 protein PH0284; RecA superfa Structural; HET: ADP; 2.0A {Pyrococcus horikoshii}**

Probability: 99.29 E-value: 1.2E-12 Score: 118.45 Aligned Cols: 196 Identities: 14% Similar

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       ..+.+++++.+.+++|.+++|.|++|+|||+++..++..+..         ....++|+
T Consensus     8      g~~~ld~~l~~g~~~g~~~~i~G~~g~GKt~l~~~~~~~~~~---------~~~~v~~~
T 2DR3_D        8      GIPGVDEILHGGIPERNVVLLSGGPGTGKTIFSQQFLWNGLK---------MGEPGIYV
T ss_dssp              CSTTHHHHTTTSEETTCEEEEEECTTSSHHHHHHHHHHHHH---------TTCCEEEE
T ss_pred              CCCCHHHHhCCCcCCCCEEEEECCCCCCHHHHHHHHHHHHH---------cCCCEEEE

Q ss_pred              HHHHHHHHHcCcCccCCEEEEe-----------------cCcccCcHHHHHHHHHHHh
Q Klein_Draft   181    RINAWETAWRQTLEEGSITFLP-----------------VPVNLMSQDVGALVEDIKDY
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                       ++..+.............+..                  ............+...+...
T Consensus     69     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 2DR3_D        69     NMAQFGWDVKPYEEKGMFAMVDAFTAGIGKSKEYEKYIVHDLTDIREFIEVLRQAIRDI
T ss_dssp              HHGGGTCCCHHHHHHTSEEEEECSGGGGCCCCCCCSEECCCCSSSHHHHHHHHHHHHT
T ss_pred              HHHhhCCCcHHHHHcCcEEEEEcccccCCCCcccceeeecCCCCHHHHHHHHHHHHHc
```

```
Q ss_pred             HHcCCCccCCHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhcccc
Q Klein_Draft   234   RCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVD
Q Consensus     234   ~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d
                      .++....       ......+..|...+.+.++++++++|..+. ....|+..+...+|
T Consensus     139   ~~~~~~~~------~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~-~~~~~~~~~~~~~d
T 2DR3_D        139   TLYINKP-------AMARSIILQLKRVLAGTGCTSIFVSQVSVG-ERGFGGPGVEHGVD
T ss_dssp             HHHTTCG-------GGHHHHHHHHHHHHHHTTCEEEEEEECCTT-CCSSSCTTHHHHSS
T ss_pred             hhhcCCH-------HHHHHHHHHHHHHHhhcCCEEEEEEecccC-CCCccccceeEEee

Q ss_pred             ---cEEEEEeeecCCCCC-CCeeEEEE
Q Klein_Draft   302   ---GITLTCKKQKDAPEG-DRHTLRLQ  324 (416)
Q Consensus     302   ---~~~l~~~K~r~~~~~-~~~~~~~~  324 (416)
                         .+.+...|.|..+.. ..+.|+++
T Consensus     201   ~~~~~~~~~~k~r~~~~~~~~~~~~~~  227 (247)
T 2DR3_D        201   GELKRSLIVWKMRGTSHSMRRHPFDIT  227 (247)
T ss_dssp             TEEEEEEEEEEETTSCCCCBCEEEEEE
T ss_pred             CeEEEEEEEEEcCCCCCCCceEEEEEc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2g88)

23. 2G88_A (http://pdb.rcsb.org/pdb/explore.do?structureId=2G88) **Protein recA; RECOMBINATION, DNA-R {Mycobacterium smegmatis}**

Probability: 99.29 E-value: 4.0E-13 Score: 129.86 Aligned Cols: 199 Identities: 15% Similar

```
Q ss_pred             CCCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEE
Q Klein_Draft   112   NMPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLY
Q Consensus     112   ~~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~
                      ..+.+++++. +++++|.+++|+|++|+|||+++..++..+..         ...+|+|
T Consensus     45    g~~~ld~~l~~gg~~~g~i~~i~G~~gsGKT~l~~~~~~~~~~~---------~~~~v~~
T 2G88_A        45    GSISLDVALGIGGLPRGRVIEIYGPESSGKTTVALHAVANAQA---------AGGIAAF
T ss_dssp             SCHHHHHHHTSSSBCSSSEEEEECSTTSSHHHHHHHHHHHHH---------TCCEEEE
T ss_pred             CCHHHHHHhccCCccCCeEEEEECCCCCHHHHHHHHHHHHH---------CCCeEEE

Q ss_pred             HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181   RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181   rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                      ++..+..        ....++.............+..+++..++++||||++..+....
T Consensus     105   ~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~lviiDsl~~l~~~~
T 2G88_A        105   YAKKLGV--------DTDSLLVSQPDTGEQALEIADMLVRSGALDIIVIDSVAALVPRA
T ss_dssp             HHHTTTC--------CGGGCEEECCSSHHHHTHHHHHHHTTCCEEEEEESCSSSCCCTT
T ss_pred             HHHHcCC--------ChhheEEECCCCHHHHHHHHHHHhCCCCeEEEEechhhhCCHH

Q ss_pred             --HHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCC-------CCCCchhHhcccEEE
Q Klein_Draft   246   --DVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEK-------TLRGSSAYEGGVDTVY
Q Consensus     246   --~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~~Gs~~~~~~~d~vi
                        ....+...+..|...++++++++++|.++...       ...|+.++...+|.++
T Consensus     167   ~~~a~~~~~~l~~l~~~~~~~~~~vi~i~q~~~~~~~~~~~~~~~Gg~~~~~~a~~~i
T 2G88_A        167   GLQARLMSQALRKMTGALNNSGTTAIFINQLREKIGVMFGSPETTTGGKALKFYASVRL
T ss_dssp             CHHHHHHHHHHHHHHHHHHTTTCEEEEEECCC------------CCSHHHHHHCSEEE
T ss_pred             HHHHHHHHHHHHHHHHHHHHhCCEEEEEecchhhcCccCCCCccccCchhhceeEEEEE

Q ss_pred             -------EEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   303   -------ITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     303   --------~~l~~~K~r~~~~~~~~~~~~~~~~  328 (416)
                             +.+.+.|+|..+.....|.+....|
T Consensus     237   ~~~~g~~~~~~i~K~r~~~~~~~~~~~i~~~~G  269 (349)
T 2G88_A        237   TDAVGNRTRVKVVKNKVSPPFKQAEFDILYGQG  269 (349)
```

```
T ss_dssp             SSCCCCCEEEEEEEEEETTSCCCEEEEEEEETTTE
T ss_pred             CCccCcEEEEEEEeCCCCCCCcEEEEEEEeCCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4hyy)

24. **4HYY_B (http://pdb.rcsb.org/pdb/explore.do?structureId=4HYY) Meiotic recombination protein DMC1/ DNA strand exchange; 2.603A {Homo sapiens}**

Probability: 99.28 E-value: 1.0E-12 Score: 121.22 Aligned Cols: 212 Identities: 10% Similar

```
Q ss_pred             CCCCCccccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   112   NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112   ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                      ..|.++.++.+++++|.+++|+|++|+|||+++..++..+..+..+..   .+.+|+|+
T Consensus     21    g~~~ld~~l~gg~~~g~~~~i~G~~g~GKs~l~~~l~~~~~~~~~~~~~---~~~~v~~i
T 4HYY_B        21    GSQEFDKLLGGGIESMAITEAFGEFRTGKTQLSHTLCVTAQLPGAGGY---PGGKIIFI
T ss_dssp             SCHHHHHHTTSSEEBSEEEEEEESTTCTHHHHHHHHHHHTTSCCGGGC---CCCEEEEE
T ss_pred             CCHHHHHHhCCCccCCeEEEEECCCCCCHHHHHHHHHHHhCCCcCCC---CCCeEEEE

Q ss_pred             HHHHHHHHHHcCcCcccCCEEEEecCcccCcHHHHHHHHHHHH--hCCcEEEEeChHHHc
Q Klein_Draft   180   SRINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKD--YGFEFIVLDTIARCT
Q Consensus     180   ~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~--~~~~lviiD~l~~~~
                      ..+.............................++...+..  .++.+||||+++.++
T Consensus     88    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~l~~~~~~~~~~~llviD~l~~~~
T 4HYY_B        88    RDIADRFNVDHDAVLDNVLYARAYTSEHQMELLDYVAAKFHEEAGIFKLLIIDSIMALF
T ss_dssp             HHHHHHTTCCHHHHHHTEEEEECCSHHHHHHHHHHHHHHHHHSSSSEEEEEEECSSHHH
T ss_pred             HHHHHHcCCCChHHhHhcEEEEECCCHHHHHHHHHHHHHHHhHhcCCeEEEEEeChhHHH

Q ss_pred             HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCC----------CCCchhHhccccE
Q Klein_Draft   245   RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT----------LRGSSAYEGGVDT
Q Consensus     245   ~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~~~~~Gs~~~~~~~d~
                      .....+...+..|..++.+.++++++++|.++....          +.|+..+...+|.
T Consensus     158   ~~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~g~~~~~~~~~~
T 4HYY_B        158   ERQQKLAQMLSRLQKISEEYNVAVFVTNQMTADPGATMTFQADPKKPIGGHILAHASTT
T ss_dssp             HHHHHHHHHHHHHHHHHHHHTTCEEEEEECBC--------------CBSSHHHHHHHCSE
T ss_pred             HHHHHHHHHHHHHHHHHHHHhCcEEEEEecccCCCCCCCcccCCCCcccCcchhhccCcE

Q ss_pred             EEEEEeeecCCCCCCCeeEEEEEec
Q Klein_Draft   303   ITLTCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     303   ~~l~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                      +.+...|++..+.. .+.|.++..+
T Consensus     228   ~~~~~~k~~~~~~~-~~~f~i~~~g  251 (265)
T 4HYY_B        228   RIAKIYDSPEMPEN-EATFAITAGG  251 (265)
T ss_dssp             EEEEESSCCSCGGG-EEEEECCTTS
T ss_pred             EEEEEEeCCCCCCc-EEEEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3hr8)

25. **3HR8_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3HR8) Protein recA; Alpha and beta proteins maritima}**

Probability: 99.28 E-value: 5.0E-13 Score: 129.53 Aligned Cols: 199 Identities: 16% Similar

```
Q ss_pred             CCCCCcccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEE
Q Klein_Draft   112   NMPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLY
Q Consensus     112   ~~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~
                      ..|.+++++. ++++.|.+++|+|++|+|||+|+|+..++..+..         ....|+|
T Consensus     45    g~~~ld~~l~~gg~~~g~i~~i~G~~gsGKT~l~~~l~~~~~~~~~~~~~~~~~v~~
T 3HR8_A        45    GSLAIDIATGVGGYPRGRIVEIFGQESSGKTTLALHAIAEAQK---------MGGVAAF
T ss_dssp             SCHHHHHHTSSSSEETTEEEEEEESTTSSHHHHHHHHHHHHH---------TTCCEEE
T ss_pred             CCHHHHHHhCCCcccCCcEEEEECCCCCCHHHHHHHHHHHHH---------CCCeEEE
```

```
Q ss_pred              HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181    RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                       ++..+..        ....++.............+..++...++++||||++..++...
T Consensus     105    ~~~~~g~-------~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~liIiDsl~~l~~~~
T 3HR8_A        105    YAKNLGV--------DLKSLLISQPDHGEQALEIVDELVRSGVVDLIVVDSVAALVPRA
T ss_dssp              HHHHHTC--------CGGGCEEECCSSHHHHHHHHHHHHHTSCCSEEEEECTTTCCCHH
T ss_pred              HHHHcCC--------CHHHeEEECCCCHHHHHHHHHHHHCCCCeEEEEechhhhCCHH

Q ss_pred              ---HHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhccccEEE
Q Klein_Draft   247    ---VGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGVDTVY
Q Consensus     247    ---~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~~d~vi
                          ...+.+.+..|...++++++++++|.++..       ....|+.++...+|.++
T Consensus     167    ~~~~~~~~~~l~~l~~~~~~~~~~vi~i~q~~~~~~~~~~~~~~~Gg~~l~~~a~~~i
T 3HR8_A        167    GLQARLMSQALRKIAGSVNKSKAVVIFTNQIRMKIGVMFGSPETTTGGLALKFYATMRM
T ss_dssp              SHHHHHHHHHHHHHHHHHHHTSSCEEEEEEEESSSCSSSSSCSCSSCTHHHHHHHHCSEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHhccCcEEEEeeccchhcCccCCCCccccCChHHhceeEEEE

Q ss_pred              -------EEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   303    -------ITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     303    -------~~l~~~K~r~~~~~~~~~~~~~~~~  328 (416)
                              +.+.+.|+|..+.....+.+....|
T Consensus     237    ~~~~g~~~~i~v~K~r~~~~~~~~~~~~~~~G  269 (356)
T 3HR8_A        237    KDVIGNVISVKIVKNKVAPPFKTAQTYIIYGKG  269 (356)
T ss_dssp              TEEEEEEEEEEEEEESSSCCCCEEEEEEETTTB
T ss_pred              CceeccEEEEEEEeCCCCCCCceEEEEEEcCCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4dc9)

26. **4DC9_F (http://pdb.rcsb.org/pdb/explore.do?structureId=4DC9) DNA repair and recombination protein Homologous Recombination; HET: NO3; 2.6A {Methanococcus voltae}**

Probability: 99.27 E-value: 6.3E-13 Score: 123.09 Aligned Cols: 214 Identities: 13% Similar

```
Q ss_pred              CCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHcCCCCCCCCCC-------C
Q Klein_Draft   113    MPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETE-------K
Q Consensus     113    ~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~-------~
                       .|.+++++.+++++|.+++|+|++|+|||+|+..++..+..+..|+.....       .
T Consensus     28     ~~~ld~~l~gg~~~g~~~~i~G~~g~GKT~l~~~l~~~~~~~~~~~~~~~~~~~~~~~~
T 4DC9_F        28     SSELDSVLGGGLESQSVTEFAGVFGSGKTQIMHQSCVNLQNPEFLFYDEEAVSKGEVAQ
T ss_dssp              CHHHHHHHTSSEETTSEEEEEECTTSSHHHHHHHHHHHTTCGGGEECCTTTSCTTTTSS
T ss_pred              CHHHHHHhCCCcccCeEEEEEcCCCCCHHHHHHHHHHhhCchhhcCChhhhccCCCCC

Q ss_pred              -cccHHHHHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHH-hCCcEEEEeC
Q Klein_Draft   175    -VAGFSSRINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKD-YGFEFIVLDT
Q Consensus     175    -~~~~~~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~-~~~~lviiD~
                        .......+.............................+.+.+.. .++++||||+
T Consensus     98     ~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~iiiD~
T 4DC9_F        98     FRPERIMQMAEHAGIDGQTVLDNTFVARAYNSDMQMLFAEKIEDLIQEGNNIKLVVIDS
T ss_dssp              CCHHHHHHHHHHHTTCCHHHHHHHEEEEECSSHHHHHHHHHHHHHHHHHTTCCEEEEEEEC
T ss_pred              CCHHHHHHHHHHcCCCHHHHHhcEEEEEcCCHHHHHHHHHHHHHHHHhCCCeEEEEEeC

Q ss_pred              CH---HHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhccc
Q Klein_Draft   243    SA---RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGV
Q Consensus     243    ~~---~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~~
                       ..   .....+...+..|..++++++++|++++|.++..       ....|+..+....
T Consensus     168    ~~~~~~~~~~~~~~~~l~~l~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 4DC9_F        168    RGKLAERQQKLGRHMATLNKLADLFNCVVLVTNQVSAKPDAFFGMAEQAIGGHIVGHAA
```

```
T ss_dssp             SSSHHHHHHHHHHHHHHHHHHHHTTCEEEEEECEEC--------CCEETTHHHHHTTC
T ss_pred             CchHHHHHHHHHHHHHHHHHHHHhCcEEEEEeccccCCcccccCceeeccchHhccee

Q ss_pred             -cEEEEEeeecCCCCCCeeEEEEEec
Q Klein_Draft   302   -GITLTCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     302   -~~~l~~~K~r~~~~~~~~~~~~~~~  327 (416)
                       .+.+...|.+..+.. .+.|++...+
T Consensus     238   ~~~~~~~~~~~~~~~-~~~~~i~~~G  263 (266)
T 4DC9_F        238   DKRVAKLYDSPHLPDA-EAIFRITEKG  263 (266)
T ss_dssp             TEEEEEEEECSSSCCE-EEEEEECSSS
T ss_pred             CeEEEEEEecCCCCCc-EEEEEEcccc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4qkq)

27. **4QKQ_B (http://pdb.rcsb.org/pdb/explore.do?structureId=4QKQ) DNA repair and recombination prote ATPase; HET: NO3, 35N; 2.0A {Methanococcus voltae}**

Probability: 99.27 E-value: 6.3E-13 Score: 123.09 Aligned Cols: 214 Identities: 13% Similar

```
Q ss_pred             CCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCC-------C
Q Klein_Draft   113   MPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETE-------K
Q Consensus     113   ~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~-------~
                      .|.+++++.+++++|.+++|+|++|+|||+|+..++..+..+..|+.....       .
T Consensus     28    ~~~ld~~l~gg~~~g~~~~i~G~~g~GKT~l~~~l~~~~~~~~~~~~~~~~~~~~~~~~
T 4QKQ_B        28    SSELDSVLGGGLESQSVTEFAGVFGSGKTQIMHQSCVNLQNPEFLFYDEEAVSKGEVAQ
T ss_dssp             CHHHHHHTTTSEETTSEEEEECSTTSSHHHHHHHHHHHHTCGGGEECCTTTSCTTTTSS
T ss_pred             CHHHHHHhCCCcccCeEEEEEcCCCCCHHHHHHHHHHHhCchhhcCChhhhccCCCCC

Q ss_pred             -cccHHHHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHH-hCCcEEEEeC
Q Klein_Draft   175   -VAGFSSRINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKD-YGFEFIVLDT
Q Consensus     175   -~~~~~~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~-~~~~lviiD~
                       .......+.................................+.+.+.. .++++||||+
T Consensus     98    ~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~iiiD~
T 4QKQ_B        98    FRPERIMQMAEHAGIDGQTVLDNTFVARAYNSDMQMLFAEKIEDLIQEGNNIKLVVIDS
T ss_dssp             CCHHHHHHHHHHTTTCCHHHHHHTEEEEECSSHHHHHHHHHHHHHHHHTTCEEEEEEEEC
T ss_pred             CCHHHHHHHHHHcCCCHHHHHhcEEEEEcCCHHHHHHHHHHHHHHHHhCCCeEEEEEeC

Q ss_pred             CH---HHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCC-------CCCCCchhHhccc
Q Klein_Draft   243   SA---RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGV
Q Consensus     243   ~~---~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~~
                      ..   .....+...+..|..++++++++|++++|.++..       ....|+..+....
T Consensus     168   ~~~~~~~~~~~~~~~~l~~l~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 4QKQ_B        168   RGKLAERQQKLGRHMATLNKLADLFNCVVLVTNQVSAKPDAFFGMAEQAIGGHIVGHAA
T ss_dssp             TTTHHHHHHHHHHHHHHHHHHHHHTTCEEEEEECEEC--------CCEETTHHHHHTTC
T ss_pred             CchHHHHHHHHHHHHHHHHHHHHhCcEEEEEeccccCCcccccCceeeccchHhccee

Q ss_pred             -cEEEEEeeecCCCCCCeeEEEEEec
Q Klein_Draft   302   -GITLTCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     302   -~~~l~~~K~r~~~~~~~~~~~~~~~  327 (416)
                       .+.+...|.+..+.. .+.|++...+
T Consensus     238   ~~~~~~~~~~~~~~~-~~~~~i~~~G  263 (266)
T 4QKQ_B        238   DKRVAKLYDSPHLPDA-EAIFRITEKG  263 (266)
T ss_dssp             TEEEEEEEECSSSCCE-EEEEEECSSC
T ss_pred             CeEEEEEEecCCCCCc-EEEEEEcccc
```

Template alignment

28. TIGR03877 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR03877) **thermo_KaiC_1; Ka**
Members of this family contain a single copy of the KaiC domain (pfam06745) that occurs in two copies
kinase KaiC itself.

Probability: 99.27 E-value: 1.9E-12 Score: 116.03 Aligned Cols: 199 Identities: 15% Similar

```
Q ss_pred                CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft   112      NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112      ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                         ..+.+++++.+.+++|..++|.|++|+|||+++..++..+..          ....++|+
T Consensus     6        g~~~ld~~l~~~~~~g~~~~i~G~~g~GKt~l~~~l~~~~~~---------~~~~v~~~
T TIGR03877     6        GIPGMDEILHGGIPERNVVLLSGGPGTGKSIFSQQFLWNGLQ---------MGEPGIYV
T ss_pred                CcccHHHHhcCCCCCCCEEEEECCCCCCHHHHHHHHHHhhhh---------cCCCEEEE

Q ss_pred                HHHHHHHHHcCcCcccCCEEEEec-----------------CcccCcHHHHHHHHHHHh
Q Klein_Draft   181      RINAWETAWRQTLEEGSITFLPV-----------------PVNLMSQDVGALVEDIKDY
Q Consensus     181      rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                         ++..+.............+...                  ...........+...+...
T Consensus     67       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T TIGR03877     67       NMAQFGWDVRKYEEEGKFAIVDAFTGGIGEAAEREKYVVKDPTDVRELIDVLRQAIRDI
T ss_pred                HHHHhCcchhhhhhcCCceehhhhcccCcchhhhhcceecCCCCHHHHHHHHHHHHHc

Q ss_pred                HHcCCCccCCHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhcccc
Q Klein_Draft   234      RCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVD
Q Consensus     234      ~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d
                         .++....       ......+..|...+++.++++++++|..+. ....|++.+...+|
T Consensus     137      ~~~~~~~~------~~~~~~~~~~l~~~~~~~~~~ii~~~~~~~~~-~~~~~~~~~~~~~d
T Consensus     137      TLYITKP-------AMARSIVMQLKRVLSGLGCTSIFVSQVSVG-ERGFGGPGVEHAVD
T ss_pred                HhccCCH-------HHHHHHHHHHHHHHHhhCCEEEEEecCCCC-CCCCCCcchHhhcC

Q ss_pred                ---cEEEEEeeecCCCCC-CCeeEEEEEec
Q Klein_Draft   302      ---GITLTCKKQKDAPEG-DRHTLRLQPID  327 (416)
Q Consensus     302      ---~~~l~~~K~r~~~~~-~~~~~~~~~~~  327 (416)
                            .+.+...|.|..+.. ..+.|.+....
T Consensus     199      ~~~~~~~~~~k~~~~~~~~~~~~~~~~~~~  228 (237)
T TIGR03877     199      GELKRSLIVWKMRGTKHSMRRHPFEITDKG  228 (237)
T ss_pred                CceEEEEEEEeeCCCCCCCCceEEEEcCCe
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2cvf)

29. 2CVF_B (http://pdb.rcsb.org/pdb/explore.do?structureId=2CVF) **DNA repair and recombination protein**
homologous recombination; 2.6A {Thermococcus kodakarensis}

Probability: 99.27 E-value: 1.4E-12 Score: 115.85 Aligned Cols: 200 Identities: 18% Similar

```
Q ss_pred                CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft   112      NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112      ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                         ..+.+++++.+.++.|.+++|+|++|+|||+++..++..             ...+++|+
T Consensus     5        g~~~l~~~l~~~~~~g~~~~i~G~~g~GKt~l~~~l~~~~~~~~~~~~~~~~v~~i
T 2CVF_B        5        GTKSLDSLLGGGFAPGVLTQVYGPYASGKTTLALQTGLL------------SGKKVAYV
T ss_dssp                SSHHHHHHHSSSSCSSSCBCCBCSSTTHHHHHHHHHHHH------------TSSEEEEE
T ss_pred                CCHHHHHHhCCCCCCCeEEEEECCCCCcHHHHHHHHHHh------------CCCeEEEE

Q ss_pred                HHHHHHHHHHcCcCcccCCEEEEecCcccCcHHHHHHHHHHHH--hCCcEEEEeChHHHc
Q Klein_Draft   180      SRINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKD--YGFEFIVLDTIARCT
Q Consensus     180      ~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~--~~~~lviiD~l~~~~
                         ..+.................+.............+..+...  .++.+||||+++.++
T Consensus     60       ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~liiD~~~~~~
T 2CVF_B        60       ERLVQMAETRGLNPEEALSRFILFTPSDFKEQRRVIGSLKKTVDSNFALVVVDSITAHY
T ss_dssp                STHHHHHHHHSSCHHHHHHHEEEECCSSTHHHHHHHHHHTTSCSTTEEEEEECCSCCSC
```

```
T ss_pred             HHHHHHHHHcCCCHHHHHhccEEECCCCHHHHHHHHHHHHHHccCCccEEEEeChHHhc

Q ss_pred             HHHHHHHHHHHHhcCCCCeEEEEEccCCCCC----CCCCCchhHhccccEEEEEEeCC-
Q Klein_Draft   248   GIVIDSMTRLMDATPDHRGCVLGIHHTGKDE----KTLRGSSAYEGGVDTVYFVERGN-
Q Consensus     248   ~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~----~~~~Gs~~~~~~~d~vi~l~~~~-
                      ..+...+..+...+++.++++++++|..+..    ..++|+..+...+|.++.+....
T Consensus     129   ~~~~~~~~~l~~~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~d~vi~l~~~~~
T 2CVF_B        129   AELSRQLQVLLWIARKHNIPVIVINQVHFDSRTEMTKPVAEQTLGYRCKDILRLDKLPK
T ss_dssp             HHHHHHHHHHHHHHHHHTTCCCBBCCCEEECTTTTSSEETTTTTHHHHSCCCEEEEECSS
T ss_pred             HHHHHHHHHHHHHHHHHcCCcEEEEeccccCCCCcccCCchhHhhhccceEEEEEEeCCC

Q ss_pred             cCCCCCCCeeEEEEEec
Q Klein_Draft   311   KDAPEGDRHTLRLQPID  327 (416)
Q Consensus     311   r~~~~~~~~~~~~~~~~  327 (416)
                      |..+....+.|++...+
T Consensus     199   ~~~~~~~~~~~~i~~~g  215 (220)
T 2CVF_B        199   RFRPEGLMAYFRITERG  215 (220)
T ss_dssp             SSSCSCCEEEEBCCTTS
T ss_pred             cCCCCCCeEEEEEeCCe
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2cvh)

30. **2CVH_B (http://pdb.rcsb.org/pdb/explore.do?structureId=2CVH) DNA repair and recombination protei homologous recombination; 2.2A {Thermococcus kodakarensis}**

Probability: 99.27 E-value: 1.4E-12 Score: 115.85 Aligned Cols: 200 Identities: 18% Similar

```
Q ss_pred             CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft   112   NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112   ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                      ..+.+++++.+.++.|.+++|+|++|+|||+++..++..            ...+++|+
T Consensus     5     g~~~l~~~l~~~~~~g~~~~i~G~~g~GKt~l~~~l~~~~~~~~~~~~~~~~v~~i
T 2CVH_B        5     GTKSLDSLLGGGFAPGVLTQVYGPYASGKTTLALQTGLL------------SGKKVAYV
T ss_dssp             SCHHHHHHTTSSBCTTSEEEEECSTTSSHHHHHHHHHHH------------HCSEEEEE
T ss_pred             CCHHHHHHhCCCCCCCeEEEEECCCCCcHHHHHHHHHHh------------CCCeEEEE

Q ss_pred             HHHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHH--hCCcEEEEeChHHHc
Q Klein_Draft   180   SRINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKD--YGFEFIVLDTIARCT
Q Consensus     180   ~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~--~~~~lviiD~l~~~~
                      ..+.................+.............+..+...  .++.+||||+++.++
T Consensus     60    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~liiD~~~~~~
T 2CVH_B        60    ERLVQMAETRGLNPEEALSRFILFTPSDFKEQRRVIGSLKKTVDSNFALVVVDSITAHY
T ss_dssp             HHHHHHHHHHTTCCHHHHHHHEEEECCCSSHHHHHHHHHHHHHCCTTEEEEEEECCSCSB
T ss_pred             HHHHHHHHHcCCCHHHHHhccEEECCCCHHHHHHHHHHHHHccCCccEEEEeChHHHc

Q ss_pred             HHHHHHHHHHHHhcCCCCeEEEEEccCCCCC----CCCCCchhHhccccEEEEEEeCC-
Q Klein_Draft   248   GIVIDSMTRLMDATPDHRGCVLGIHHTGKDE----KTLRGSSAYEGGVDTVYFVERGN-
Q Consensus     248   ~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~----~~~~Gs~~~~~~~d~vi~l~~~~-
                      ..+...+..+...+++.++++++++|..+..    ..++|+..+...+|.++.+....
T Consensus     129   ~~~~~~~~~l~~~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~d~vi~l~~~~~
T 2CVH_B        129   AELSRQLQVLLWIARKHNIPVIVINQVHFDSRTEMTKPVAEQTLGYRCKDILRLDKLPK
T ss_dssp             HHHHHHHHHHHHHHHHHTCCEEEEECSSSSCCSSCCCSSCSTTHHHHCSEEEEEEECSS
T ss_pred             HHHHHHHHHHHHHHHHHcCCcEEEEeccccCCCCcccCCchhHhhhccceEEEEEEeCCC

Q ss_pred             cCCCCCCCeeEEEEEec
Q Klein_Draft   311   KDAPEGDRHTLRLQPID  327 (416)
Q Consensus     311   r~~~~~~~~~~~~~~~~  327 (416)
                      |..+....+.|++...+
T Consensus     199   ~~~~~~~~~~~~i~~~g  215 (220)
```

```
T 2CVH_B        199    RFRPEGLMAYFRITERG  215 (220)
T ss_dssp              SSSCTTCEEEEEEETTE
T ss_pred              cCCCCCCeEEEEEeCCe
```

Template alignment | CDD (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam03796)

31. **PF03796.14 (http://pfam.xfam.org/family/PF03796.14#tabview=tab0) ; DnaB_C ; DnaB-like helicase C te**

Probability: 99.26 E-value: 9.5E-13 Score: 120.04 Aligned Cols: 204 Identities: 17% Similar

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       ..|.++.++ +.+++|.+++|+|++|+|||+|+..++..+...        .+.+++|+
T Consensus     5      g~~~ld~~~-~~~~~g~~~~i~G~~g~GKS~l~~~l~~~~~~~-------~~~~v~~~
T PF03796.14    5      GFAEFDRMT-AGLQPSDLILIAARPAMGKTSFALNIVQHAALR--------AGVPVAIF
T ss_pred              CchHHHHhh-cCCCCCcEEEEEcCCCCCHHHHHHHHHHHHHHH--------cCCCEEEE

Q ss_pred              HHHHHHHHHcCcCcccC--------------------CEEEEecCcccCcHHHHHHHHH
Q Klein_Draft   181    RINAWETAWRQTLEEG--------------------SITFLPVPVNLMSQDVGALVED
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~
                       ++.............                     .+.+.............+...
T Consensus     66     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~l~~~
T PF03796.14    66     RMICSEAMIDSHKLRTGNLEDEEWKKFAKALALLSNAPIYIDDTPAITVSEMRAKCRRL
T ss_pred              HHHHHHhCCCHHHHhcCCCCHHHHHHHHHHHHHHhcCCeEEeCCCCCCHHHHHHHHHH

Q ss_pred              EEeChHHHcCCCccCCHHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCC-----
Q Klein_Draft   228    VLDTIARCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTL-----
Q Consensus     228    iiD~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~-----
                       |||+++.++....  .......+...+..|..+++++++++++|..+.....
T Consensus     135    viD~~~~~~~~~~--~~~~~~~~~~~~~~~l~~~~~~~~~~ii~~~~~~~~~~~~~~~~~
T PF03796.14    135    MVDYLQLMTARGR--FESKQQEIAEISRSLKALARELNVPVLALSQLSRAPETRADHRP
T ss_pred              EEechhhccCCCC--CCCHHHHHHHHHHHHHHHHHHhCCCEEEEEccCCCcccCCCCCC

Q ss_pred              hccccEEEEEEeCC--c--------EEEEEeeecCCCCCCeeEEEEEecC
Q Klein_Draft   288    EGGVDTVYFVERGN--G--------ITLTCKKQKDAPEGDRHTLRLQPIDG  328 (4
Q Consensus     288    ~~~~d~vi~l~~~~~~~~~~~~~~~~~~l~~~K~r~~~~~~~~~~~~~~~~  328 (4
                       ...+|.++.|....  .        +.+...|.|.+..+ .+.+.++...+
T Consensus     203    ~~~~d~v~~l~~~~~~~~~~~~~~~~~~l~~~K~R~~~~~-~~~~~~~~~~~  252 (2
T PF03796.14    203    EQDADIVAFLYRDEYYNPDTDKKHIAELIIAKHRNGPTG-TIELLFLDKHT  252 (2
T ss_pred              hhhCCEEEEEechhhcCCCCCCCceEEEEEEccCCCCCE-EEEEEEECccc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3bh0)

32. **3BH0_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3BH0) B.subtilis phage SPP1 DNA sequence; 2.35A {Bacillus phage SPP1}**

Probability: 99.26 E-value: 9.0E-13 Score: 125.34 Aligned Cols: 200 Identities: 14% Similar

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       ..+.++.++. .+.+|++++|.|++|+|||+|+..++..++.         .+.+|+|+
T Consensus     54     g~~~ld~~~~-g~~~g~~~~i~G~~g~GKT~l~~~la~~~~~---------~~~~v~~~
T 3BH0_A        54     GFTELDRMTY-GYKRRNFVLIAARPSMGKTAFALKQAKNMSD---------NDDVVNLH
T ss_dssp              SCHHHHHHHS-SBCTTCEEEEECCTTSSHHHHHHHHHHHHHT---------TTCEEEEE
T ss_pred              CcHHHHHHc-CcccCcEEEEEecccccHHHHHHHHHHHHc---------CCCeEEEE

Q ss_pred              HHHHHHHHHcCc-----------------------CccCCEEEEecCcccCcHHHHHHH
Q Klein_Draft   181    RINAWETAWRQT-----------------------LEEGSITFLPVPVNLMSQDVGALV
```

```
Q Consensus     181    rl~~~~~~~~~~-----------------------~~~~~~~~~~~~~~~~~~~~~~l~
                       ++.........                        +....+.+.............+.
T Consensus     114    r~~~~~~~~~~~~l~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~
T 3BH0_A        114    RLIVTAGSINAQKIKAARRDFASEDWGKLSMAIGEISNSNINIFDKAGQSVNYIWSKTR
T ss_dssp              HHHHHHTTCCHHHHHSCHHHHCSSCHHHHHHHHHHHHHTSCEEEECCSCCBHHHHHHHHH
T ss_pred              HHHHHHcCCCHHHHHhccccCCHHHHHHHHHHHHHHHhcCCcEEEeCCCCCHHHHHHHHH

Q ss_pred              EEEEeChHHHcCCCccCCHHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCC-----
Q Klein_Draft   226    FIVLDTIARCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEK-----
Q Consensus     226    lviiD~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~-----
                       +||||+++.+.......+  ....+...+..|..++++++++|++++|.++...
T Consensus     184    lviID~l~~~~~~~~~~--~~~~~~~~~~~l~~~a~~~~~~ii~~~~~~~~~~~~~~~
T 3BH0_A        184    IVMIDYLQLLEPAKANDS--RTNQISQISRDLKKMARELDVVVIALSQLSRQVEQRQDK
T ss_dssp              EEEEECGGGSBCSCTTSC--HHHHHHHHHHHHHHHHHHHTCEEEEEECCCGGGTTSSSC
T ss_pred              EEEEeCHHHcCccccCCC--HHHHHHHHHHHHHHHHHHhCCEEEEEecCCcchhcCCCC

Q ss_pred              hHhccccEEEEEEeCC----------cEEEEEeeecCCCCCCeeEEEE
Q Klein_Draft   286    AYEGGVDTVYFVERGN----------GITLTCKKQKDAPEGDRHTLRLQ  324 (416
Q Consensus     286    ~~~~~~d~vi~l~~~~----------~~~l~~~K~r~~~~~~~~~~~~~  324 (416
                       .+...+|.++.|.+..          ...+.+.|+|.++.+ .+.+.++
T Consensus     252    ~~~~~ad~v~~l~~~~~~~~~~~~~~~~l~v~K~R~g~~~-~~~l~~~  299 (315
T 3BH0_A        252    QLEQDADIIEFLYRDDYYDKESESKNIVEVIIAKHRDGPVG-TVSLAFI  299 (315
T ss_dssp              HHHHHCSEEEEEEEHHHHCTTCTTTTEEEEEEEEETTSCCE-EEEEEEE
T ss_pred              cHHHhCCEEEEEecHHHcCCccccCcEEEEEEEecCCCCCe-EEEEEEE
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4yds)

33. **4YDS_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4YDS) Flagella-related protein H; RecA super ATP; 2.3A {Sulfolobus acidocaldarius}**

Probability: 99.25 E-value: 3.2E-12 Score: 114.72 Aligned Cols: 198 Identities: 14% Similar

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       ..+.+++++ +.+++|.+++|.|++|+|||+|+..++..+..         ...+|+|+
T Consensus     6      g~~~ld~~l-~g~~~g~~~~i~g~~g~GKt~l~~~l~~~~~~~~~~~~~~~~~v~~~
T 4YDS_A        6      GNDDLDRRL-GGIPYPASIMIEGDHGTGKSVLSAQFVLGFLL---------SDKKGYVI
T ss_dssp              SCHHHHHHH-CSEESSCEEEEEECTTSSHHHHHHHHHHHHHH---------TTCCEEEE
T ss_pred              CCHHHHHHh-CCCCCCCEEEEEcCCCCCHHHHHHHHHHHHhh---------CCCCEEEE

Q ss_pred              HHHHHHHHHcCcCccCCEEEEecCccc-------CcHHHHHHHHHHHHhCCcEEEEeCh
Q Klein_Draft   181    RINAWETAWRQTLEEGSITFLPVPVNL-------MSQDVGALVEDIKDYGFEFIVLDTI
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~~-------~~~~~~~l~~~~~~~~~~lviiD~l
                       ++...............+.+.......       .......+...++..++.+||||++
T Consensus     66     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 4YDS_A        66     KMKEIKIDLIPYFIRGKLRIAPLNTKKFNWNSSLAEKILDVIVNFIRSKNIDFIVIDSL
T ss_dssp              HHHHTTCCCHHHHHTTSEEEEECCSSSSCCCHHHHHHHHHHHHHHHHHTSCCSEEEEECC
T ss_pred              HHHhcCCcchHhhcCcEEEEEcccCcccCCcccHHHHHHHHHHHHHhcCCCEEEEeCh

Q ss_pred              HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeCCc
Q Klein_Draft   244    ARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERGNG
Q Consensus     244    ~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~~~
                       ......+...+..+..    .++++++++|..+.  ...+...+...+|.++.+.....
T Consensus     133    ~~~~~~~~~~l~~~~~---~~~~vi~~~~~~~~--~~~~~~~~~~~~~d~~i~l~~~~~
T 4YDS_A        133    EKQLLQFMKDIRVLVN----TGKMILFTIHPDTF--DEEMKSKITSIVDVYLKLSAATI
T ss_dssp              HHHHHHHHHHHHHHHH----TTCEEEEEECTTSS--CHHHHHHHHHHSSEEEEEEEES
T ss_pred              HHHHHHHHHHHHHHHh----cCCEEEEEECCCCC--ChHHHhHHHHhccEEEEEeeeee
```

```
Q ss_pred              eecCCCCC-CCeeEEEEEecC
Q Klein_Draft   309    KQKDAPEG-DRHTLRLQPIDG  328 (416)
Q Consensus     309    K~r~~~~~-~~~~~~~~~~~~  328 (416)
                       |.|..+.. ..+.|++++..|
T Consensus     197    k~~~~~~~~~~~~~~~~~~~g  217 (228)
T 4YDS_A        197    KTTGGISGSDTISFDVDPALG  217 (228)
T ss_dssp              ECSSCCCCCCCEEEEEETTTE
T ss_pred              EecCCCcccceEEEEEeCCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4ppf)

34. **4PPF_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4PPF) Protein RecA, 1st part, 2nd; HOMOLOG REPAIR, ATPASE; HET: FLC, EDO; 2.3A {Mycobacterium tuberculosis}**

Probability: 99.24 E-value: 1.2E-12 Score: 126.56 Aligned Cols: 197 Identities: 14% Similar

```
Q ss_pred              CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       +.+++++. ++++.|.++.|+|++|+|||+++..++..+..         .+.+|+|++
T Consensus     46     ~~Ld~~l~~gg~~~G~i~~i~G~~gsGKT~l~~~~~~~~~~----------~~~~v~~i~
T 4PPF_A        46     IALDVALGIGGLPRGRVIEIYGPESSGKTTVALHAVANAQA---------AGGVAAFID
T ss_dssp              HHHHHHTSSSSEETTSEEEEEESTTSSHHHHHHHHHHHHHH---------TTCCEEEEE
T ss_pred              HHHHHHhcCCCccCCeEEEEECCCCCcHHHHHHHHHHHHHH---------CCCeEEEEE

Q ss_pred              HHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCcc
Q Klein_Draft   183    NAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAEE
Q Consensus     183    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~~
                       ..+..        ....++.............+..+++..++++||||++..+......
T Consensus     106    ~~~g~--------~~~~~~~~~~~~~~e~~~~~l~~~~~~~~~~lvviDsl~~l~~~~~~
T 4PPF_A        106    KKLGV--------DTDSLLVSQPDTGEQALEIADMLIRSGALDIVVIDSVAALVPRAEL
T ss_dssp              HHHTC--------CGGGCEEECCSSHHHHHHHHHHHHHTSCCSEEEEECGGGCCCHHHH
T ss_pred              HHcCC--------ChhhEEEECCCCHHHHHHHHHHHhCCCCcEEEEechHhhCCHHHh

Q ss_pred              HHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCC-------CCCchhHhccccEEEEE
Q Klein_Draft   246    DVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT-------LRGSSAYEGGVDTVYFV
Q Consensus     246    ~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~-------~~Gs~~~~~~~d~vi~l
                       ....+...+..|..+++++++++++|.++....       ..|+.++...++.++.+
T Consensus     168    ~~~~~~~~~~~L~~~~~~~~~~vi~i~q~~~~~~~~~~~~~~~Gg~~~~~~a~~~i~l
T 4PPF_A        168    QARLMSQALRKMTGALNNSGTTAIFINQLRDKIGVMFGSPETTTGGKALKFYASVRMDV
T ss_dssp              HHHHHHHHHHHHHHHHHHHHTCEEEEEEECC-------------CCHHHHHHHCSEEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHCCEEEEEeccccccccccCCCccCCCChhhcceeEEEEEE

Q ss_pred              -----EEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   303    -----ITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     303    ------~~l~~~K~r~~~~~~~~~~~~~~~~  328 (416)
                            +.+.+.|+|..+.....|.+....|
T Consensus     238    ~~g~~~~~~i~K~r~~~~~~~~~~~i~~~~G  268 (350)
T 4PPF_A        238    AVGNRTRVKVVKNKCSPPFKQAEFDILYGKG  268 (350)
T ss_dssp              EEEEEEEEEEEEESSSCSCCEEEEEEETTTE
T ss_pred              ccccEEEEEEEeCCCCCCccEEEEEEEeCCc
```

Template alignment | CDD (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam06745)

35. **PF06745.12 (http://pfam.xfam.org/family/PF06745.12#tabview=tab0) ; ATPase ; KaiC**

Probability: 99.22 E-value: 4.2E-12 Score: 113.65 Aligned Cols: 199 Identities: 15% Similar

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
```

```
                        ..+.+++++.+.+++|..++|+|++|+|||+++..++.....         ....++|+
T Consensus     4       g~~~ld~~~~~~~~~g~~~~i~G~~g~GKs~l~~~l~~~~~~~~~~~~~~~~~~v~~~
T PF06745.12    4       GIPGFDFLSDGGLPLGRATLIAGTAGSAKTIFASQFLVEGIQ---------RGENGVFV
T ss_pred               CCCCHHHHcCCCccCCcEEEEECCCCCCHHHHHHHHHHHHHH---------CCCCEEEE

Q ss_pred               HHHHHHHHHcCcCccCCEEEEecC-----------cccCcHHHHHHHHHHHhCCcEEE
Q Klein_Draft   181     RINAWETAWRQTLEEGSITFLPVP-----------VNLMSQDVGALVEDIKDYGFEFIV
Q Consensus     181     rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~lvi
                        ++..+.............+....           ..........+...+...++.+||
T Consensus     65      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ii
T PF06745.12    65      NMRGFGWDIQQWENEGKWVFVDASPQPGDRPIVSGEYDLGALIARIEHAVRKYKASRIS
T ss_pred               HHHhcCCCHHHHHhcCCEEEEECCCCCCCCCcccCCCCHHHHHHHHHHHHHHhCCCEEE

Q ss_pred               ccCCHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCCCCCCchhHhc-cccEEEEE
Q Klein_Draft   240     EENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEG-GVDTVYFV
Q Consensus     240     ~~n~~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~-~~d~vi~l
                        .     ......+.+..|...+++.++++++++|..+. ....+...+.. .+|.++.+
T Consensus     135     ~-----~~~~~~~~~~~~l~~~~~~~~~~ii~~~~~~~~-~~~~~~~~~~~~~~~d~~i~l
T PF06745.12    135     S-----DSAQVRSDLFRLASALRELGVTAIMTAERVEE-YGEISRYGVEEFVADNVVIV
T ss_pred               C-----CHHHHHHHHHHHHHHHHHcCCEEEEEeccccc-cccccccchhHhhccEEEEE

Q ss_pred               EEEEeeecCCCCC-CCeeEEEEE
Q Klein_Draft   304     TLTCKKQKDAPEG-DRHTLRLQP  325 (416)
Q Consensus     304     ~l~~~K~r~~~~~-~~~~~~~~~  325 (416)
                        .+.+.|.|..+.. ..+.|++..
T Consensus     199     ~~~i~k~~~~~~~~~~~~~~i~~  221 (232)
T PF06745.12    199     TIEILKYRGTDHQKGEFPFTIIN  221 (232)
T ss_pred               EEEEEEcCCCCCCCceEEEEEEc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/1n0w)

36. **1N0W_A (http://pdb.rcsb.org/pdb/explore.do?structureId=1N0W) DNA repair protein RAD51 homolog; recombination, breast; HET: MSE, EDO; 1.7A {Homo sapiens} SCOP: c.37.1.11**

Probability: 99.22 E-value: 3.6E-12 Score: 115.43 Aligned Cols: 212 Identities: 12% Similar

```
Q ss_pred               CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft   112     NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112     ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                        ..+.+++++.+.+++|..++|+|++|+|||+++..++..+..+..+.+   ....++|+
T Consensus     9       ~~~~ld~~l~~~~~~g~~~~i~G~~g~GKs~l~~~~~~~~~~~~~~~~~---~~~~v~~i
T 1N0W_A        9       GSKELDKLLQGGIETGSITEMFGEFRTGKTQICHTLAVTCQLPIDRGG---GEGKAMYI
T ss_dssp               SCHHHHHHTTTSEETTSEEEEECCTTSSHHHHHHHHHHHTTSCGGGTC---CSSEEEEE
T ss_pred               CCHHHHHHhCCCccCCeEEEEECCCCCCHHHHHHHHHHHcCChhhCC---CCceEEEE

Q ss_pred               HHHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCC
Q Klein_Draft   180     SRINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVG
Q Consensus     180     ~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~
                        ..+.............................+...+...++.+||||+++.++..
T Consensus     76      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviD~~~~~~~~
T 1N0W_A        76      LAVAERYGLSGSDVLDNVAYARAFNTDHQTQLLYQASAMMVESRYALLIVDSATALYRT
T ss_dssp               HHHHHHTTCCHHHHHHTEEEEECCSHHHHHHHHHHHHHHHHHSCEEEEEEETSSGGGC-
T ss_pred               HHHHHHcCCChHHHhcCEEEEecCCHHHHHHHHHHHHHHHHhhcccEEEEEeChhHHhcc

Q ss_pred               HHHHHHHHHHHHHhcCCCCeEEEEEccCCC----------CCCCCCCchhHhccccEEE
Q Klein_Draft   247     VGIVIDSMTRLMDATPDHRGCVLGIHHTGK----------DEKTLRGSSAYEGGVDTVY
Q Consensus     247     ~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k----------~~~~~~Gs~~~~~~~d~vi
                        ...+...+..|..+++++++++++++|..+          ......|+..+...+|.++
T Consensus     146     ~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i
```

```
T 1N0W_A        146    QMHLARFLRMLLRLADEFGVAVVITNQVVAQVDGAAMFAADPKKPIGGNIIAHASTTRL
T ss_dssp              HHHHHHHHHHHHHHHHHHCCEEEEEC------------------------CCTTCEEE
T ss_pred              HHHHHHHHHHHHHHHHHHCCEEEEEecceeeccccccccCCCCCccchHhhhcCeEEE

Q ss_pred              EEEeeecCCCCCCCeeEEEEEec
Q Klein_Draft   305    LTCKKQKDAPEGDRHTLRLQPID  327 (416)
Q Consensus     305    l~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                       +...|+|..+... +.|.+...+
T Consensus     216    ~~~~k~r~~~~~~-~~~~~~~~g  237 (243)
T 1N0W_A        216    CKIYDSPCLPEAE-AMFAINADG  237 (243)
T ss_dssp              EEECCBTTBSCEE-EEEEEETTE
T ss_pred              EEEEeCCCCCCce-EeeEEecCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/5jwr)

37. **5JWR_A (http://pdb.rcsb.org/pdb/explore.do?structureId=5JWR) Circadian clock protein kinase KaiC; Tı foldswitch; HET: PO4; 2.61A {Thermosynechococcus elongatus}**

Probability: 99.21 E-value: 5.6E-12 Score: 114.11 Aligned Cols: 200 Identities: 13% Similar

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       ..+.+++++.+.+++|.+++|+|++|+|||+++..++..+...        ....++|+
T Consensus     17     g~~~ld~~l~~~~~~g~~~~i~G~~g~GKs~l~~~l~~~~~~~~-------~~~~v~~~
T 5JWR_A        17     MIEGFDDISHGGLPQGATTLVSGTSGTGKTLFAVQFLYNGITI--------FNEPGIFV
T ss_dssp              CCTTHHHHTTSSEETTSEEEEEESTTSSHHHHHHHHHHHHHHT--------TCCCEEEE
T ss_pred              CCccHHHHcCCCCCCCcEEEEEcCCCCCHHHHHHHHHHHhhhH--------cCcCEEEE

Q ss_pred              HHHHHHHHHcCcCccCCEEEEecCcc----------cCcHHHHHHHHHHHHhCCcEEEE
Q Klein_Draft   181    RINAWETAWRQTLEEGSITFLPVPVN----------LMSQDVGALVEDIKDYGFEFIVL
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~----------~~~~~~~~l~~~~~~~~~~lvii
                       ++..+.............+......          ........+...+...++.+|||
T Consensus     79     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~iii
T 5JWR_A        79     NALSFGWNLQSLIDQGKLFILDASPDPDGQEVAGDFDLSALIERIQYAIRKYKATRVSI
T ss_dssp              HHHTTTCCHHHHHHTTSEEEEECSCCTTCEEECSCCBCHHHHHHHHHHHHHTTCSEEEE
T ss_pred              HHHhcCCChHHHhhcCCEEEEEcCCCCCCccccCCCCHHHHHHHHHHHHHhhCCCEEEE

Q ss_pred              cCCHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEe
Q Klein_Draft   241    ENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVER
Q Consensus     241    ~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~
                            ....+...+..+...+++.++++++++|..+......|+..+...+|.++.+..
T Consensus     149    -----~~~~~~~~~~~~~~~~~~~~~~ii~~~~~~~~~~~~~~~~~~~~~d~vi~l~~
T 5JWR_A        149    -----AASVVRREIFRLAFRLAQLGVTTIMTTERVDEYGPVARFGVEEFVSDNVVILRN
T ss_dssp              -----CHHHHHHHHHHHHHHHHHTTCEEEEEEECSCSSSCSSGGGTTTTSCSEEEEEEE
T ss_pred              -----CHHHHHHHHHHHHHHHHHcCCEEEEEecccCCCCCccccCcHhhccCeEEEEEE

Q ss_pred              EEeeecCCC-CCCCeeEEEE
Q Klein_Draft   306    TCKKQKDAP-EGDRHTLRLQ  324 (416)
Q Consensus     306    ~~~K~r~~~-~~~~~~~~~~  324 (416)
                       .+.|.|... ....+.|++.
T Consensus     214    ~v~K~~~~~~~~~~~~~~~~  233 (247)
T 5JWR_A        214    EILKLRGTTHMKGEYPFTIN  233 (247)
T ss_dssp              EEEEETTSCCCCSEEEEEES
T ss_pred              EEEEcCCCCCCCceEEEEEc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3bgw)

38. [3BGW_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3BGW)](http://pdb.rcsb.org/pdb/explore.do?structureId=3BGW) **DNAB-Like Replicative Helicase; ATP phage SPP1}**

Probability: 99.2 E-value: 1.9E-12 Score: 129.29 Aligned Cols: 204 Identities: 13% Similarit

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       ..|.++.++. ++.+|.+++|+|++|+|||+|+..++..++.         .+.+|+|+
T Consensus     183    g~~~Ld~~~~-g~~~G~l~~i~g~~g~GKS~l~~~l~~~~~~~---------~~~~vl~~
T 3BGW_A        183    GFTELDRMTY-GYKRRNFVLIAARPSMGKTAFALKQAKNMSD---------NDDVVNLH
T ss_dssp              SCHHHHHHHS-SBCSSCEEEEEECSSSSHHHHHHHHHHHHH---------TTCEEEEE
T ss_pred              CchHHHHHhh-cccCCeEEEEEeCCCCCHHHHHHHHHHHHHc---------CCCeEEEE

Q ss_pred              HHHHHHHHHcCc-----------------------CccCCEEEEecCcccCcHHHHHHH
Q Klein_Draft   181    RINAWETAWRQT-----------------------LEEGSITFLPVPVNLMSQDVGALV
Q Consensus     181    rl~~~~~~~~~~-----------------------~~~~~~~~~~~~~~~~~~~~~l~
                       ++.........                        .....+.+.............+.
T Consensus     243    r~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~i~
T 3BGW_A        243    RLIVTAGSINAQKIKAARRDFASEDWGKLSMAIGEISNSNINIFDKAGQSVNYIWSKTR
T ss_dssp              HHHHHHSCCCHHCCCCCGGGTCCSCHHHHHHHHHHHHTSCEEEECCSSCBHHHHHHHHH
T ss_pred              HHHHHHcCCCHHHHHhcccCCCHHHHHHHHHHHHHHHcCCcEEEcCCCCCHHHHHHHHH

Q ss_pred              EEEEeChHHHcCCCccCCHHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCC-----
Q Klein_Draft   226    FIVLDTIARCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEK-----
Q Consensus     226    lviiD~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~-----
                       +||||++..+.....  .......+...+..|..+++++++++++|.++...
T Consensus     313    lvvID~l~~~~~~~~--~~~~~~~~~~~~~~L~~la~~~~~~vi~~~q~~~~~~~~~~
T 3BGW_A        313    IVMIDYLQLLEPAKA--NDSRTNQISQISRDLKKMARELDVVVIALSQLSRQVEQRQDK
T ss_dssp              EEEEECSTTSBCSCS--SSCHHHHHHHHHHHHHHHHHHHTCEEEEEEECCGGGGGSSCC
T ss_pred              EEEEeCHHHcCCccc--CCCHHHHHHHHHHHHHHHHHHhCCEEEEEecCCcchhhCCCC

Q ss_pred              hHhccccEEEEEEeCC----------cEEEEEeeecCCCCCCeeEEEEEecC
Q Klein_Draft   286    AYEGGVDTVYFVERGN----------GITLTCKKQKDAPEGDRHTLRLQPIDG  328
Q Consensus     286    ~~~~~~d~vi~l~~~~~~~~~~~~~~l~~~K~r~~~~~~~~~~~~~~~~~~  328
                       .+...+|.++.+.+..          ...+.+.|+|.++.+ .+.+.++...+
T Consensus     381    ~~~~~ad~vi~l~~~~~~~~~~~~~~~~l~i~K~R~g~~~-~~~~~~~~~~~  432
T 3BGW_A        381    QLEQDADIIEFLYRDDYYDKESESKNIVEVIIAKHRDGPVG-TVSLAFIKEYG  432
T ss_dssp              HHHHHCSEEEECCBGGGTCTTCSSTTEEEEEEEEESSSCCE-EEEEEEETTTT
T ss_pred              cHHHhCCEEEEEECHHHcCCcccCCceEEEEEEecCCCCCe-EEEEEEeccce
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/5jec)

39. [5JEC_B (http://pdb.rcsb.org/pdb/explore.do?structureId=5JEC)](http://pdb.rcsb.org/pdb/explore.do?structureId=5JEC) **DNA repair and recombination protein; drug; HET: SO4; 2.34A {Pyrococcus furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1)}**

Probability: 99.2 E-value: 9.7E-12 Score: 111.43 Aligned Cols: 204 Identities: 11% Similarit

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEEEC
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVA
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~
                       |.+++++.+.+++|..++|+|++|+|||+++..++..+..+..|.+   ....++|++.
T Consensus     12     ~~ld~~~~~~~~~g~~~~i~G~~gsGKt~l~~~l~~~~~~~~~~~~~---~~~~v~~~~~
T 5JEC_B        12     KSLDKLLGGGIETQAITEVFGEFGSGKTQLAHTLAVMVQLPPEEGG---LNGKAMYIDT
T ss_dssp              HHHHHHHTSSEETTEEEEEEECTTSSHHHHHHHHHHHHTTSCGGGTC---CSCEEEEEES
T ss_pred              HHHHHHhCCCCcCCeEEEEECCCCCCHHHHHHHHHHHHcCChhHCC---CCCeEEEEEC

Q ss_pred              HHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHH--------hCCcEEEEeChHH
Q Klein_Draft   184    AWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKD--------YGFEFIVLDTIAR
Q Consensus     184    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~lviiD~l~~
                       ..............................+..+...        .++.+||||+++.
```

```
T Consensus     78      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~liiiD~~~~
T 5JEC_B        78      EIAQNRGLSGSDVLDNVAYARAFNSNHQMLLVQQASDMMVELLNTDRPYKLLIVDSLTS
T ss_dssp               HHHHHTTCCHHHHHHTEEEEECCSHHHHHHHHHHHHHHHHHHTTSSSCEEEEEEECSSH
T ss_pred               HHHHhCCCChhhhhcCEEEEEcCCHHHHHHHHHHHHHHHHHHcCCCCEEEEEEeChHH

Q ss_pred               CHHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeCC
Q Klein_Draft   243     SARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERGN
Q Consensus     243     ~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~~
                        ...........+..|..+++.+++++++++|..+.     +...+...+|.++.+....
T Consensus     148     ~~~~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~-----~~~~~~~~~~d~~i~l~~~~
T 5JEC_B        148     LAERQQKLAKHLADLHRLANLYDIAVFVTNQVQAN-----GGHILAHSATLRVYLRKGK
T ss_dssp               HHHHHHHHHHHHHHHHHHHHHHHTCEEEEEEECCSS-----CCCCCCTTCSEEEEEEECS
T ss_pred               HHHHHHHHHHHHHHHHHHHHHHcCcEEEEEeccccc-----CcchhhccceEEEEEEECC

Q ss_pred               cCCCCCCCeeEEEEEec
Q Klein_Draft   311     KDAPEGDRHTLRLQPID  327 (416)
Q Consensus     311     r~~~~~~~~~~~~~~~~  327 (416)
                        |..+... +.|.+...+
T Consensus     213     ~~~~~~~-~~~~i~~~g  228 (231)
T 5JEC_B        213     PHLPEGE-AVFSITEKG  228 (231)
T ss_dssp               SSSCSCE-EEEEEETTE
T ss_pred               CCCCCce-EEEEEcCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2w0m)

40. **2W0M_A (http://pdb.rcsb.org/pdb/explore.do?structureId=2W0M) SSO2452; SSO2452, RECA, SULFOLOB**
{SULFOLOBUS SOLFATARICUS P2}

Probability: 99.19 E-value: 6.4E-12 Score: 112.4 Aligned Cols: 200 Identities: 14% Similarit

```
Q ss_pred               CCCCCccccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft   112     NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112     ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                        ..+.+++++.+.+++|..++|.|++|+|||+++..++..+..         ...+++|+
T Consensus     8       ~~~~ld~~~~~~~~~g~~~~i~G~~g~GKs~l~~~l~~~~~~---------~~~~v~~~
T 2W0M_A        8       GILDFDKLIQGGIPQGFFIALTGEPGTGKTIFSLHFIAKGLR---------DGDPCIYV
T ss_dssp               SCHHHHGGGTTSEETTCEEEEECSTTSSHHHHHHHHHHHHH---------HTCCEEEE
T ss_pred               CCccHHHHHcCCCCCCCEEEEEcCCCCCHHHHHHHHHHHhh---------cCCCEEEE

Q ss_pred               HHHHHHHHHcCcCccCCEEEEecCc----------ccCcHHHHHHHHHHH--hCCcEE
Q Klein_Draft   181     RINAWETAWRQTLEEGSITFLPVPV----------NLMSQDVGALVEDIKD--YGFEFI
Q Consensus     181     rl~~~~~~~~~~~~~~~~~~~~~~~~----------~~~~~~~~~l~~~~~~--~~~~lv
                        ++..+....................          .........+...++.  .++.+|
T Consensus     69      ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l
T 2W0M_A        69      QAKQFNWDFEEYIEKKLIIIDALMKEKEDQWSLVNLTPEELVNKVIEAKQKLGYGKARL
T ss_dssp               HHHHTTCCCGGGBTTTEEEEECCC----CTTBCSSCCHHHHHHHHHHHHHHHCSSCEEE
T ss_pred               HHHHcCCCChHHHhhcCeEEEeccccccccccccCCCCHHHHHHHHHHHHHHhCCCccEE

Q ss_pred               CccCCHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEE
Q Klein_Draft   239     AEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFV
Q Consensus     239     ~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l
                        ..       ......+..+...+.+.++++++++|..+. ...+|+..+...+|.++.+
T Consensus     139     ~~-------~~~~~~~~~l~~~~~~~~~~ii~~~~~~~~-~~~~~~~~~~~~~d~~i~l
T 2W0M_A        139     KP-------AMARKISYYLKRVLNKWNFTIYATSQYAIT-TSQAFGFGVEHVADGIIRF
T ss_dssp               CG-------GGHHHHHHHHHHHHHHTTEEEEEEEC------------CHHHHCSEEEEE
T ss_pred               CH-------HHHHHHHHHHHHHHHhcCCEEEEEeecCcc-cccccccccceeeecEEEEE

Q ss_pred               EEEEeeecCCCCC-CCeeEEEEEecC
Q Klein_Draft   304     TLTCKKQKDAPEG-DRHTLRLQPIDG  328 (416)
```

```
Q Consensus     304    ~l~~~K~r~~~~~-~~~~~~~~~~~~~  328 (416)
                       .+...|.|..... ..+.|++....|
T Consensus     201    ~l~~~k~r~~~~~~~~~~~~~~~~~~g  226 (235)
T 2W0M_A        201    YILIEKMRQTDHDKHVWEIDIVNGKG  226 (235)
T ss_dssp              EEEEEEETTCCCCCSCEEEEEETTTE
T ss_pred              EEEEEecCCCCCCceeeEEEEECCce
```

Template alignment

41. **TIGR03878 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR03878) thermo_KaiC_2; Ka family. This KaiC domain-containing protein family occurs sporadically across a broad taxonomic rang Dictyoglomi, Epsilonproteobacteria, and Firmicutes), but exclusively in thermophiles.**

Probability: 99.19 E-value: 1.5E-11 Score: 112.66 Aligned Cols: 197 Identities: 15% Similar

```
Q ss_pred              CCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEECC
Q Klein_Draft   115    KPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVAE
Q Consensus     115    ~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~e
                       +..|++.+.+++|.+++|+|++|+|||+++..++.....         ....++|++.+
T Consensus     24     ~~~~~~~~~i~~g~~~~i~G~~g~GKs~l~~~l~~~~~~~~~~~~~~~~~~~~v~~~~~~
T TIGR03878     24     KIVRKPLGGIPAYSVINITGVSDTGKSLMVEQFAIKQAS---------RGNRVLFVTVE
T ss_pred              ceeeccCCCCCCCeEEEEEcCCCCCHHHHHHHHHHHHHh---------cCCeEEEEEcC

Q ss_pred              HHHHHHcCcCccCCEEEEecCccc-------CcHHHHHHHHHHHHhCCcEEEEeChHHH
Q Klein_Draft   184    AWETAWRQTLEEGSITFLPVPVNL-------MSQDVGALVEDIKDYGFEFIVLDTIARC
Q Consensus     184    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-------~~~~~~~l~~~~~~~~~~lviiD~l~~~
                       .+..............+.......       .......+...+...++.+||||+++.+
T Consensus     85     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~liiiD~~~~~
T TIGR03878     85     LRANAMGVDFDKIEDNIILIDAASSTKLRENVPNLLATLAYAIKEYKVKNTVIDSITGL
T ss_pred              HHHHHcCCCHHHhhhceEEeecccccccccccHHHHHHHHHHHHHHcCCeEEEEeCcccc

Q ss_pred              HHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCC----CCCCchhHhccccEEEEEEe--
Q Klein_Draft   247    VGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEK----TLRGSSAYEGGVDTVYFVER--
Q Consensus     247    ~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~----~~~Gs~~~~~~~d~vi~l~~--
                       ...+...+..|...++..++++++++|.++...    ...|+..+...+|.++.+..
T Consensus     148    ~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~d~~i~l~~~~
T TIGR03878     148    EMMAREIVRQLYNFMKKWYQTALFVSQKRSGHEELSAEAAGGYAVSHIVDGTIVLAKEL
T ss_pred              HHHHHHHHHHHHHHHHHHhCCEEEEEEeCCCCChhhhhhcccchHHHHhCCEEEEEechh

Q ss_pred              ----CCcEEEEEeeecCCC-CCCCeeEEEEEec
Q Klein_Draft   300    ----GNGITLTCKKQKDAP-EGDRHTLRLQPID  327 (416)
Q Consensus     300    ----~~~~~l~~~K~r~~~-~~~~~~~~~~~~~  327 (416)
                           ...+.+...|.|..+ ....+.|.+...+
T Consensus     218    ~~~~~~~~~~~i~k~r~~~~~~~~~~~~i~~~g  250 (259)
T TIGR03878     218    KPIGEIVRLFRIDGCRMCGHDTKTHFLEITETG  250 (259)
T ss_pred              CCCCCeEEEEEEEeecCCCCCCCeEEEEEeCCc
```

Template alignment

42. **TIGR03880 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR03880) KaiC_arch_3; KaiC This model represents a rather narrowly distributed archaeal protein family in which members have a**

Probability: 99.16 E-value: 4.2E-11 Score: 106.8 Aligned Cols: 199 Identities: 12% Similarit

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEEC
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVA
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~
                       |.+++++++.+++|.+++|+|++|+|||+|+..++.....         ....++|++.
T Consensus     3      ~~ld~~l~~~i~~g~~~~i~G~~g~GKs~l~~~l~~~~~~~~~~~~~~~~~~~~v~~~~~
T TIGR03880     3      PGLDEMLGGGFPEGHVIVVIGEYGTGKTTFSLQFLYQGLK---------NGEKAMYISL
T ss_pred              CchHHHccCCCCCCcEEEEEcCCCCCHHHHHHHHHHHhhh---------CCCeEEEEeC
```

```
Q ss_pred              HHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHH----hCCcEEEEeChHHHcC
Q Klein_Draft   183    NAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKD----YGFEFIVLDTIARCTV
Q Consensus     183    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~----~~~~lviiD~l~~~~~
                       ............. .+++.............+...+..    ..+.++|||++..+ .
T Consensus     64     ~~~~~~~~~~~~~-~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~iiid~~~~l-~
T TIGR03880     64     KSKGWDLEDYIDK-SLYIVRLDPSDFKTSLNRIKNELPILIKELGASRVVIDPISLL-E
T ss_pred              HHcCCChHHhhcc-ceEEEecCcccchHhHHHHHHHHHHHHHHHHHCCeEEEECChhHH-h

Q ss_pred              HHHHHHHHHHHhcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeCC------
Q Klein_Draft   249    IVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERGN------
Q Consensus     249    ~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~~------
                       .+...+..+...    ++++++++|..+......+...+...+|.++.+....
T Consensus     132    ~l~~l~~~~~~~~---~~~~vi~~~~~~~~~~~~~~~~~~~~~d~~~~l~~~~~~~~~~
T TIGR03880     132    ELFRFYSSLRET----GVTTILTSEADKTNVFASKYGLIEYLADGVIILKYVRNSDLRD
T ss_pred              HHHHHHHHHHHHh----CCEEEEEecCCccccchhhhHHHHhCCEEEEEEeccCCcccc

Q ss_pred              CC-CCCCCeeEEEEEec
Q Klein_Draft   312    DA-PEGDRHTLRLQPID  327 (416)
Q Consensus     312    ~~-~~~~~~~~~~~~~~  327 (416)
                       .. +....+.|.+....
T Consensus     198    ~~~~~~~~~~~~~~~~~  214 (224)
T TIGR03880     198    RSKHSREIKPYEITDSG  214 (224)
T ss_pred              CCCCCCcceeEEEECCe
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/5ikn)

43. **5IKN_F (http://pdb.rcsb.org/pdb/explore.do?structureId=5IKN) DNA-directed DNA polymerase (E.C.2.7 TRANSFERASE; 4.802A {Enterobacteria phage T7}**

Probability: 99.15 E-value: 1.5E-11 Score: 123.96 Aligned Cols: 205 Identities: 16% Similar

```
Q ss_pred              CCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   113    MPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     113    ~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       .|.++.++ +.+++|++++|.|++|+|||+|+..++..+..+        ...+|+|++
T Consensus     229    ~~~ld~~~-~gl~~g~~~~i~G~~g~GKS~l~~~l~~~~~~~--------~~~~v~~~~
T 5IKN_F        229    CTGINDKT-LGARGGEVIMVTSGSGMGKSTFVRQQALQWGTA--------MGKKVGLAM
T ss_dssp              CTTHHHHH-CSCCTTCEEEEECSSSSSSHHHHHHHHHHHHHT--------TCCCEEEEE
T ss_pred              CchHHHhh-cCcccCCeEEEEECCCCCCHHHHHHHHHHHHHh--------cCCeEEEEE

Q ss_pred              HHHHHHHHcCcCcc-----------------------CCEEEEecCcccCcHHHHHHHH
Q Klein_Draft   182    INAWETAWRQTLEE-----------------------GSITFLPVPVNLMSQDVGALVE
Q Consensus     182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~
                       +.............                       ...................+..
T Consensus     290    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 5IKN_F        290    LIGLHNRVRLRQSDSLKREIIENGKFDQWFDELFGNDTFHLYDSFAEAETDRLLAKLAY
T ss_dssp              HHHHHTTSCGGGCHHHHHHHHHTTHHHHHHHHHHHTTSCEEECCCCSCCCSTTTHHHHHH
T ss_pred              HHHHHcCCccccChhhhhHHhcccchHHHHHHHhCCCcEEEEcCCccCCHHHHHHHHHH

Q ss_pred              EeChHHHcCCCccCCHHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCC------
Q Klein_Draft   229    LDTIARCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTL------
Q Consensus     229    iD~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~------
                       ||++..++....  .......+...+..|..+++.++++|++++|.+|.....
T Consensus     360    iD~~~~~~~~~~--~~~~~~~~~~~~~~l~~l~~~~~~~vi~~~h~~k~~~~~~~~~~
T 5IKN_F        360    LDHISIVVSASG--ESDERKMIDNLMTKLKGFAKSTGVVLVVICHLKNPDKGKAHEEGR
T ss_dssp              EECSCCCCSSTT--SSCTHHHHHHHHHHHHHHHHHHTCEEEEEECBCCCCSSSCSTBCC
T ss_pred              EccHHHhccCCC--cchHHHHHHHHHHHHHHHHHHCCEEEEEEecCCCCCCCCccCCC
```

```
Q ss_pred              hHhccccEEEEEEeCCc------EEEEEeeecC-CCCCCCeeEEEEEecC
Q Klein_Draft   286    AYEGGVDTVYFVERGNG------ITLTCKKQKD-APEGDRHTLRLQPIDG  328 (41
Q Consensus     286    ~~~~~~d~vi~l~~~~~------~~l~~~K~r~-~~~~~~~~~~~~~~~  328 (41
                       .+...+|.++.+.....      +.+.+.|+|. +..+....+.++...+
T Consensus     428    ~~~~~~d~v~~l~~~~~~~~~~~~~l~v~K~r~~g~~~~~~~~~~~~~~  477 (48
T 5IKN_F        428    ALRQLSDTIIALERNQQGDMPNLVLVRILKCRFTGDTGIAGYMEYNKETG  477 (48
T ss_dssp              SHHHHCSEEEEEECBTTSSCTTEEEEEEEEETTTCCCEEEEEEEECTTTC
T ss_pred              HHHHHCCEEEEEEecCCCCCCCeEEEEEEeccCCCCcceeEEEEEeCCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/1tf7)

44. **1TF7_F (http://pdb.rcsb.org/pdb/explore.do?structureId=1TF7) KaiC; homohexamer, hexamer, CIRCAD**
2.8A {Synechococcus sp.} SCOP: c.37.1.11

Probability: 99.13 E-value: 1.1E-11 Score: 126.6 Aligned Cols: 199 Identities: 11% Similarit

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEEC
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVA
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~
                       +.+++++.+.+++|.+++|.|++|+|||+++..++.....         .+.+|+|++.
T Consensus     268    ~~ld~~~~gg~~~g~~~~i~g~~g~GKs~l~~~~~~~~~~----------~~~~v~~i~~
T 1TF7_F        268    VRLDEMCGGGFFKDSIILATGATGTGKTLLVSRFVENACA---------NKERAILFAY
T ss_dssp              HHHHHHTTSSEESSCEEEEEESTTSSHHHHHHHHHHHHHH---------TTCCEEEEES
T ss_pred              ccHHHHcCCCccCCcEEEEEcCCCCCHHHHHHHHHHHHHH---------CCCCEEEEEC

Q ss_pred              HHHHHHHcCcCccCCEEEEecCccc--CcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   183    NAWETAWRQTLEEGSITFLPVPVNL--MSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     183    ~~~~~~~~~~~~~~~~~~~~~~~~--~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                       ..+..........+.+.+.......  .......+...+...++++||||+++.+....
T Consensus     329    ~~~g~~~~~~~~~~l~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~vviD~l~~l~~~~
T 1TF7_F        329    YSWGMDFEEMERQNLLKIVCAYPESAGLEDHLQIIKSEINDFKPARIAIDSLSALARGV
T ss_dssp              HHTSCCHHHHHHTTCEEECCCCGGGSCHHHHHHHHHHHHHTTCCSEEEEECHHHHTSSS
T ss_pred              HHcCCCHHHHHHcCCEEEEEeChhhcCHHHHHHHHHHHHHhhCCCEEEEeChHHHHhcC

Q ss_pred              HHHHHHHHHHcCCCCeEEEEEccCCCCC-CCCCCchhHhccccEEEEEEeCC-----cE
Q Klein_Draft   251    IDSMTRLMDATPDHRGCVLGIHHTGKDE-KTLRGSSAYEGGVDTVYFVERGN-----GI
Q Consensus     251    ~~~l~~L~~~~~~~~~~vl~v~H~~k~~-~~~~Gs~~~~~~~d~vi~l~~~~-----~~
                       .+.+..|..+++++++++++++|.++.. ....|+..+...+|.+|.+....     .+
T Consensus     393    ~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~aD~vi~l~~~~~~~~~~~
T 1TF7_F        393    RQFVIGVTGYAKQEEITGLFTNTSDQFMGAHSITDSHISTITDTIILLQYVEIRGEMSR
T ss_dssp              HHHHHHHHHHHHHHTTCEEEEEEECSSSSCCCSSCSSCCTTTCSEEEEEEEEECSSBEEE
T ss_pred              HHHHHHHHHHHHHHcCcEEEEEecCccccCCccCCcccHHHHeeEEEEEEEeeeCCeEEE

Q ss_pred              CC-CCeeEEEEEec
Q Klein_Draft   315    EG-DRHTLRLQPID  327 (416)
Q Consensus     315    ~~-~~~~~~~~~~~  327 (416)
                       .. ..+.|.+....
T Consensus     463    ~~~~~~~~~i~~~g  476 (525)
T 1TF7_F        463    HDKAIREFMISDKG  476 (525)
T ss_dssp              CCCBEEEEEECSSC
T ss_pred              CCCceEEEEeeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4esv)

45. **4ESV_C (http://pdb.rcsb.org/pdb/explore.do?structureId=4ESV) Replicative helicase/DNA Complex; Rec**
DNA complex; HET: GDP, MES, ALF, CA; 3.2A {Geobacillus stearothermophilus}

Probability: 99.13 E-value: 5.5E-12 Score: 126.17 Aligned Cols: 206 Identities: 18% Similar

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
```

```
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       ..|.++.++ +.+++|.+++|+|++|+|||+++..++..+..+        .+.+|+|+
T Consensus     189    g~~~ld~~~-~gl~~G~~~~i~G~~g~GKS~l~~~l~~~~~~~--------~g~~vl~~
T 4ESV_C        189    GFTELDRMT-SGFQRSDLIIVAARPSVGKTAFALNIAQNVATK--------TNENVAIF
T ss_dssp              SCHHHHHHH-CSCCTTCEEEEECSTTSSHHHHHHHHHHCCCCC--------SSCCEEEE
T ss_pred              CchHHHHHh-ccccCCcEEEEEeCCCCcHHHHHHHHHHHHHHH--------CCCcEEEE

Q ss_pred              HHHHHHHHHcCc---------------------CccCCEEEEecCcccCcHHHHHHHHH
Q Klein_Draft   181    RINAWETAWRQT---------------------LEEGSITFLPVPVNLMSQDVGALVED
Q Consensus     181    rl~~~~~~~~~~---------------------~~~~~~~~~~~~~~~~~~~~~l~~~
                       ++..........                     .....+++.............+...
T Consensus     250    r~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~i~~~
T 4ESV_C        250    RMLCAEGNINAQNLRTGKLTPEDWGKLTMAMGSLSNAGIYIDDTPSIRVSDIRAKCRRL
T ss_dssp              HHHHHHHTCCHHHHHHTCCCHHHHHHHHHHHHHHHTTCEEEECCSCCBHHHHHHHHHH
T ss_pred              HHHHHHcCCCHHHHhcCCCCHHHHHHHHHHHHHHhcCcEEcCCCCCCHHHHHHHHHHH

Q ss_pred              eChHHHcCCCccCCHHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCC---------
Q Klein_Draft   230    DTIARCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEK---------
Q Consensus     230    D~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~---------
                       |++..+... ..........+...+..|..++++++++|++++|.++...
T Consensus     320    D~l~~~~~~-~~~~~~~~~~~~~~~~L~~la~~~~~~vi~~~~~~~~~~~~~~~~~~~
T 4ESV_C        320    DYLQLIQGS-GRSKENRQQEVSEISRSLKALARELEVPVIALSQLSRSVEQRQDKRPMM
T ss_dssp              SCGGGSBCC-SSCSCCHHHHHHHHHHHHHHHHHHHHTSCEEEEECBCGGGGTSSSCCCCG
T ss_pred              eChhhcCCC-CCCCcCHHHHHHHHHHHHHHHHHHHhCCCEEEEecCCcChhcCCCCCCCH

Q ss_pred              cccEEEEEEeCC----------cEEEEEeeecCCCCCCeeEEEEEecC
Q Klein_Draft   290    GVDTVYFVERGN----------GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416
Q Consensus     290    ~~d~vi~l~~~~----------~~~l~~~K~r~~~~~~~~~~~~~~~~  328 (416
                       .+|.++.+....          ...+.+.|+|.++.+ .+.+.++...+
T Consensus     389    ~ad~v~~l~~~~~~~~~~~~~~~~l~v~K~R~g~~~-~~~~~~~~~~~  436 (454
T 4ESV_C        389    DADIVAFLYRDDYYNKDSENKNIIEIIIAKQRNGPVG-TVQLAFIKEYN  436 (454
T ss_dssp              HCSEEEEEECHHHHCSSCSSCSEEEEEEEEESSSCCE-EEEEEEEGGGT
T ss_pred              hCCEEEEEEcHHHcCCCccCCcEEEEEEecCCCCCE-EEEEEEeccce
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2r6a)

46. **2R6A_A (http://pdb.rcsb.org/pdb/explore.do?structureId=2R6A) Replicative helicase/DnaG Primase, He Primase, Replication, dnaB, dnaG; HET: SO4; 2.9A {Geobacillus stearothermophilus}**

Probability: 99.13 E-value: 5.5E-12 Score: 126.17 Aligned Cols: 206 Identities: 18% Similar

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       ..|.++.++ +.+++|.+++|+|++|+|||+++..++..+..+        .+.+|+|+
T Consensus     189    g~~~ld~~~-~gl~~G~~~~i~G~~g~GKS~l~~~l~~~~~~~--------~g~~vl~~
T 2R6A_A        189    GFTELDRMT-SGFQRSDLIIVAARPSVGKTAFALNIAQNVATK--------TNENVAIF
T ss_dssp              SCHHHHHHH-SSBCTTCEEEEECCTTSCHHHHHHHHHHHHHHH--------SSCCEEEE
T ss_pred              CchHHHHHh-ccccCCcEEEEEeCCCCcHHHHHHHHHHHHHHH--------CCCcEEEE

Q ss_pred              HHHHHHHHHcCc---------------------CccCCEEEEecCcccCcHHHHHHHHH
Q Klein_Draft   181    RINAWETAWRQT---------------------LEEGSITFLPVPVNLMSQDVGALVED
Q Consensus     181    rl~~~~~~~~~~---------------------~~~~~~~~~~~~~~~~~~~~~l~~~
                       ++..........                     .....+++.............+...
T Consensus     250    r~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~i~~~
T 2R6A_A        250    RMLCAEGNINAQNLRTGKLTPEDWGKLTMAMGSLSNAGIYIDDTPSIRVSDIRAKCRRL
T ss_dssp              HHHHHHHTCCHHHHHTSCCCHHHHHHHHHHHHHHHSSCEEEECCTTCCHHHHHHHHHH
T ss_pred              HHHHHHcCCCHHHHhcCCCCHHHHHHHHHHHHHHhcCcEEcCCCCCCHHHHHHHHHHH
```

```
Q ss_pred              eChHHHcCCCccCCHHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCC---------
Q Klein_Draft   230    DTIARCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEK---------
Q Consensus     230    D~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~---------
                       |++..+... ..........+...+..|..++++++++|++++|.++...
T Consensus     320    D~l~~~~~~-~~~~~~~~~~~~~~~~~L~~la~~~~~~vi~~~~~~~~~~~~~~~~~~~
T 2R6A_A        320    DYLQLIQGS-GRSKENRQQEVSEISRSLKALARELEVPVIALSQLSRSVEQRQDKRPMM
T ss_dssp              ECGGGSCCS-CC----CHHHHHHHHHHHHHHHHHHTCCEEEEECCCTTSTTC---CCCT
T ss_pred              eChhhcCCC-CCCCcCHHHHHHHHHHHHHHHHHHhCCCEEEEecCCcChhcCCCCCCCH

Q ss_pred              cccEEEEEEeCC----------cEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   290    GVDTVYFVERGN----------GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416
Q Consensus     290    ~~d~vi~l~~~~----------~~~l~~~K~r~~~~~~~~~~~~~~~~  328 (416
                       .+|.++.+....          ...+.+.|+|.++.+ .+.+.++...+
T Consensus     389    ~ad~v~~l~~~~~~~~~~~~~~~~~l~v~K~R~g~~~-~~~~~~~~~~~  436 (454
T 2R6A_A        389    DADIVAFLYRDDYYNKDSENKNIIEIIIAKQRNGPVG-TVQLAFIKEYN  436 (454
T ss_dssp              HCSEEEEEEETTC-------CCEEEEEEEEESSSCCE-EEEEEEETTTT
T ss_pred              hCCEEEEEEcHHHcCCCccCCcEEEEEEEecCCCCCE-EEEEEEeccce
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3io5)

47. **3IO5_B (http://pdb.rcsb.org/pdb/explore.do?structureId=3IO5) Recombination and repair protein; stor conformation, RecA; HET: PO4; 2.4A {Enterobacteria phage T4}**

Probability: 99.12 E-value: 1.9E-11 Score: 117.43 Aligned Cols: 200 Identities: 15% Similar

```
Q ss_pred              CCCCccccc----CcccCCCEEEEEcCCCCCHHHHHHHHHHHH--HcCCCCCCCCCCC
Q Klein_Draft   113    MPKPEPLIE----GVFNRGSTALLYGRWGTSKSFIALDWACSL--ATGRNWQGRETEKV
Q Consensus     113    ~~~~~~l~~----~~l~~g~~~~i~G~~G~GKStl~~~la~~~--~~g~~~~g~~~~~~
                       .|.+++++.    +++++| ++.|+|++|+|||+|+..++..+  ..          ...
T Consensus     11     ~~~LD~~l~~~~~gGl~~G-~~~i~G~~gsGKTtl~~~l~~~~~~~~~~~~~~~~~~~~
T 3IO5_B        11     IPMMNIALSGEITGGMQSG-LLILAGPSKSFKSNFGLTMVSSYMRQY---------PDA
T ss_dssp              CHHHHHHHHSSTTCCCCSE-EEEEEEESSSSHHHHHHHHHHHHHHHC---------TTC
T ss_pred              CHHHHHHhcCCCCCCcCCc-EEEEECCCCCCHHHHHHHHHHHHHHHC---------CCC

Q ss_pred              cHHHHHHHHHHHHcCcCccCCEEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHH
Q Klein_Draft   177    GFSSRINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARC
Q Consensus     177    ~~~~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~
                       ..     .+...++.... ....................+..+...++++||||++..+
T Consensus     71     ~~-----~~~~~~g~~~~-~~~~~~~~~~e~~~~~~~~~l~~~~~~~~~~livIDsi~~l
T 3IO5_B        71     TP-----AYLRSMGVDPE-RVIHTPVQSLEQLRIDMVNQLDAIERGEKVVVFIDSLGNL
T ss_dssp              CH-----HHHHHTTCCGG-GEEEEECSBHHHHHHHHHHHHHHTCCTTCCEEEEEECSTTC
T ss_pred              CH-----HHHHHCCCCHH-hcEEEeCCCcHHHHHHHHHHHHHHhhcCCcEEEEEeChHHh

Q ss_pred              -------HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCC-----CCCCCCchhHhccc
Q Klein_Draft   245    -------RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKD-----EKTLRGSSAYEGGV
Q Consensus     245    -------~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~-----~~~~~Gs~~~~~~~
                              .....+...+..|..++.++++++++++|.++.     .....|+.....+
T Consensus     135    ~~~~~d~~~~~~l~~~~~~l~~~~~~~~~~ii~i~q~~~~~~~~~~~~~gG~~~~~~~~
T 3IO5_B        135    EKVVSDMTRAKTMKSLFRIVTPYFSTKNIPCIAINHTYETQEMFSKTVMGGGTGPMYSA
T ss_dssp              -------CHHHHHHHHHHHHHHHHHHTTCEEEEEEEEC--------------CCGGGGS
T ss_pred              hccccHHHHHHHHHHHHHHHHHHhCCCcEEEEecccccccccCccccCCCchhhcce

Q ss_pred              ---------cEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   302    ---------GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     302    ----------~~~l~~~K~r~~~~~~~~~~~~~~~~  328 (416)
                                .+.+.+.|+|..+....+.|.+....|
T Consensus     205    ~~~~~~~g~~~~i~i~K~R~~~~~~~~~~~i~~~~G  240 (333)
T 3IO5_B        205    KDGSDLQGYQFVLNVEKSRTVKEKSKFFIDVKFDGG  240 (333)
T ss_dssp              ----------EEEEEEECSSBCTTCEEEECBCTTSC
T ss_pred              cCCCcccceEEEEEEecCCCCCcceEEEEEecCCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/5j4l)

48. **5J4L_A (http://pdb.rcsb.org/pdb/explore.do?structureId=5J4L) DNA repair and recombination protein; drug; 1.13A {Pyrococcus furiosus (strain ATCC 43587 / DSM 3638 / JCM 8422 / Vc1)}**

Probability: 99.09 E-value: 3.2E-11 Score: 107.71 Aligned Cols: 206 Identities: 12% Similar

```
Q ss_pred                CCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCCcEEEEE
Q Klein_Draft     113    MPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus       113    ~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                         .+.+++++.+.+.+|..++|+|++|+|||+++..++..+..+..+.+   ....++|++
T Consensus       11     ~~~ld~~~~~~~~~g~~~~i~G~~g~GKs~l~~~~~~~~~~~~~~~~---~~~~~~~~~~
T 5J4L_A          11     SKSLDKLLGGGIETQAITEVFGEFGSGKTQLAHTLAVMVQLPPEEGG---LNGSAMYID
T ss_dssp                CHHHHHHTTTSEESSEEEEEEESTTSSHHHHHHHHHHHTTSCGGGTC---CSCEEEEEE
T ss_pred                cHHHHHHhCCCCccceEEEEECCCCCCHHHHHHHHHHHcCCcccCC---CCCeeEEEE

Q ss_pred                HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHH-----hCCcEEEEeChHH
Q Klein_Draft     181    RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKD-----YGFEFIVLDTIAR
Q Consensus       181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~-----~~~~lviiD~l~~
                         .+.............................+...+..     .++.+||||++..
T Consensus       78     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~liiiD~~~~
T 5J4L_A          78     EIAQNRGLDPDEVLDNVAYARAFNSNHQMLLVQQAEDMIKELLNTDRPVKLLIVDSLTS
T ss_dssp                HHHHHTTCCHHHHHHTEEEEECCSHHHHHHHHHHHHHHHHHHTTSSSCEEEEEEETTTH
T ss_pred                HHHHhcCCCHHHhhccEEEEeCCCHHHHHHHHHHHHHHHHHHccCCCCeEEEEEeChHH

Q ss_pred                CHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeCC
Q Klein_Draft     243    SARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERGN
Q Consensus       243    ~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~~
                         ...........+..|..+++..++++++++|.++.     |...+...+|.++.+..+.
T Consensus       148    ~~~~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~-----~~~~~~~~~~d~~i~l~~~~
T 5J4L_A          148    LAERQQKLAKHLADLHRLANLYDIAVFVTNQVQAN-----GGHILAHSATLRVYLRKGK
T ss_dssp                HHHHHHHHHHHHHHHHHHHHHHHTCEEEEEEECC---------CCCCCCCSEEEEEEECG
T ss_pred                HHHHHHHHHHHHHHHHHHHHHHCCeEEEEEeccccc-----cCcchhcccEEEEEEEECC

Q ss_pred                cCCCCCCCeeEEEEEec
Q Klein_Draft     311    KDAPEGDRHTLRLQPID  327 (416)
Q Consensus       311    r~~~~~~~~~~~~~~~~  327 (416)
                         |..+.+. +.|++....
T Consensus       213    ~~~~~~~-~~~~~~~~g  228 (231)
T 5J4L_A          213    PHLPEGE-AVFSITEKG  228 (231)
T ss_dssp                TTSCCCE-EEEEEETTE
T ss_pred                CCCCCcE-EEEEEecCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/1cr0)

49. **1CR0_A (http://pdb.rcsb.org/pdb/explore.do?structureId=1CR0) DNA PRIMASE/HELICASE (E.C.2.7.7.-); R TRANSFERASE; HET: SO4; 2.3A {Enterobacteria phage T7} SCOP: c.37.1.11**

Probability: 99.09 E-value: 5.9E-11 Score: 110.9 Aligned Cols: 199 Identities: 17% Similarit

```
Q ss_pred                ccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEECCCcc-c
Q Klein_Draft     120    IEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVAEGVA-G
Q Consensus       120    ~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~e~~~-~
                         +...+.+|++++|.|++|+|||+++..++..+..+        ...+++|++.+... .
T Consensus       28     ~~~~i~~g~~~~i~G~~g~GKs~l~~~l~~~~~~~~~~~~~~~~v~~~~~e~~~~~
T 1CR0_A          28     KTLGARGGEVIMVTSGSGMGKSTFVRQQALQWGTA--------MGKKVGLAMLEESVEE
T ss_dssp                HHCSBCTTCEEEEEESTTSSHHHHHHHHHHHHHT--------SCCCEEEEESSSCHHH
T ss_pred                HhcCCCCCeEEEEECCCCCCHHHHHHHHHHHHHH--------cCCcEEEEEcCCCHHH
```

```
Q ss_pred             HcCcCcc-----------------------CCEEEEecCcccCcHHHHHHHHHHHHhCC
Q Klein_Draft   189   WRQTLEE-----------------------GSITFLPVPVNLMSQDVGALVEDIKDYGF
Q Consensus     189   ~~~~~~~-----------------------------~~~~~~~~~~~~~~~~~~l~~~~~~~~~
                      .......                        ...................+...+...++
T Consensus     90    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 1CR0_A        90    VRLRQSDSLKREIIENGKFDQWFDELFGNDTFHLYDSFAEAETDRLLAKLAYMRSGLGC
T ss_dssp             CCGGGCHHHHHHHHHHTHHHHHHHHHHSSSCEEEECCCCSCCHHHHHHHHHHHHHTTCC
T ss_pred             CCcccCchhhhHHHhccchHHHHHHHhCCCcEEEecCCCcCCHHHHHHHHHHHHhccCC

Q ss_pred             cCCCccCCHHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCC-------------CC
Q Klein_Draft   236   TVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEK-------------TL
Q Consensus     236   ~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~~~~~~~~~
                      +....  ...........+..|..+++.+++++++++|.++...              ..
T Consensus     160   ~~~~~--~~~~~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~
T 1CR0_A        160   VSASG--ESDERKMIDNLMTKLKGFAKSTGVVLVVICHLKNPDKGKAHEEGRPVSITDL
T ss_dssp             -----------CHHHHHHHHHHHHHHHHHCCEEEEEEECC-----------------CC
T ss_pred             ccCCC--CCcHHHHHHHHHHHHHHHHHHHCCEEEEEEeccCcCCCCCcccCCCCCcHHHh

Q ss_pred             EEEEEEeCC------cEEEEEeeecC-CCCCCCeeEEEEEecC
Q Klein_Draft   293   TVYFVERGN------GITLTCKKQKD-APEGDRHTLRLQPIDG  328 (416)
Q Consensus     293   ~vi~l~~~~~~~~~~~~l~~~K~r~-~~~~~~~~~~~~~~~~  328 (416)
                      .++.+....      .+.+...|.|. ++.+..+.+.+....+
T Consensus     228   ~v~~l~~~~~~~~~~~~~~~~~K~r~~g~~~~~~~~~~~~~~~  270 (296)
T 1CR0_A        228   TIIALERNQQGDMPNLVLVRILKCRFTGDTGIAGYMEYNKETG  270 (296)
T ss_dssp             EEEEEEEC-------CEEEEEEEETTTCCCEEEEEEEECTTTC
T ss_pred             EEEEEeccCCCCCCCeEEEEEEeeCCCCCcCceEEEEECCCC
```

Template alignment | CDD (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam08423)

50. **PF08423.10 (http://pfam.xfam.org/family/PF08423.10#tabview=tab0) ; Rad51 ; Rad51**

Probability: 99.08 E-value: 5.9E-11 Score: 108.62 Aligned Cols: 203 Identities: 12% Similar

```
Q ss_pred             CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCC------CCc
Q Klein_Draft   114   PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETE------KVK
Q Consensus     114   ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~------~~~
                      +.+++++.+.++.|.+++|+|++|+|||+++..++.....         .      ...
T Consensus     24    ~~ld~~l~~~l~~g~~~~i~G~~gsGKT~l~~~l~~~~~~---------~~~~~~~~~~
T PF08423.10    24    RELDKLLCGGFETGSITELFGEFRTGKTQLCHQLCVTCQL---------GIENGGTEGR
T ss_pred             HHHHHHhcCCccCCeEEEEECCCCCCHHHHHHHHHHHhhh---------chHhCCCCCe

Q ss_pred             HHHHHHHHHHHHcCcCc---cCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChH
Q Klein_Draft   178   FSSRINAWETAWRQTLE---EGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIA
Q Consensus     178   ~~~rl~~~~~~~~~~~~---~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~
                       ..++..+...+.....   ...................+...+...++.+||||+++
T Consensus     85    -~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~liiiD~~~
T PF08423.10    85    -PERLTQIAEKYGLNSEEALNNVAVARAHNTEHQMQLLQMASGLMAKERYGLLIIDSAT
T ss_pred             -HHHHHHHHHHHhCCChHHHHhcEEEEECCCHHHHHHHHHHHHHHHhhcCceEEEEecHH

Q ss_pred             CCHHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCCC-----------CCCchhHhc
Q Klein_Draft   242   NSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT-----------LRGSSAYEG
Q Consensus     242   n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~~~~~~~~~Gs~~~~~
                      +.......+...+..|..++++.++++++++|..+....           +.|+..+..
T Consensus     154   ~~~~~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~g~~~~~
T PF08423.10    154   ELASRQMHLAKFLRALQRIADEFSVAVVLTNQVVAQVDGQASMFGGDTKKPVGGNIIAH
T ss_pred             chHHHHHHHHHHHHHHHHHHHHhCCEEEEEeccEeecCCCcccccCCceeecchhHHhh

Q ss_pred             C--cEEEEEeeecCCCCCCCeeEEEEEec
Q Klein_Draft   301   N--GITLTCKKQKDAPEGDRHTLRLQPID  327 (416)
```

```
Q Consensus     301    ~--~~~l~~~K~r~~~~~~~~~~~~~~~~  327 (416)
                       .  .+.++..|.+..+... +.|.+...+
T Consensus     224    ~~~~~~~~~~~~~~~~~~~-~~~~i~~~G  251 (255)
T PF08423.10    224    KGEARICKVYDSPCLPESE-ASFAITTNG  251 (255)
T ss_pred              CCCcEEEEEEeCCCCCCcE-EEEEEeCCc
```

Template alignment

51. **TIGR02655 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR02655) circ_KaiC; circadia**
this family are the circadian clock protein KaiC, part of the kaiABC operon that controls circadian rhytl

Probability: 99.06 E-value: 6.2E-11 Score: 119.19 Aligned Cols: 199 Identities: 11% Similar

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEEC
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVA
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~
                       +...+++.+.++++..+++.|++|+|||+++..++.....         .+.+|+|++.
T Consensus     250    ~~~~~~~~~~~~~~~~~i~g~~~~gkt~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~~
T TIGR02655     250    VRLDEMCGGGFFKDSIILATGATGTGKTLLVSKFLENACA---------NKERAILFAY
T ss_pred              CcHHhhcCCCccCCcEEEEEcCCCCCHHHHHHHHHHHHhh---------CCCcEEEEEc

Q ss_pred              HHHHHHHcCcCccCCEEEEecCcccCc--HHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   183    NAWETAWRQTLEEGSITFLPVPVNLMS--QDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     183    ~~~~~~~~~~~~~~~~~~~~~~~~~~~--~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                       ..+.............+.+........+  .....+.+.+...++.+||||+++.++...
T Consensus     311    ~~~g~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~iiiD~~~~~~~~~~
T TIGR02655     311    YSWGIDFEEMEQQGLLKIICAYPESAGLEDHLQIIKSEIADFKPARIAIDSLSALARGV
T ss_pred              HHcCCCHHHHHHcccEEEEecCCccCCHHHHHHHHHHHHHHcCCCEEEEeCHHHHhhcC

Q ss_pred              HHHHHHHHHHcCCCCeEEEEEccCCCCC-CCCCCchhHhccccEEEEEEeCC-----cE
Q Klein_Draft   251    IDSMTRLMDATPDHRGCVLGIHHTGKDE-KTLRGSSAYEGGVDTVYFVERGN-----GI
Q Consensus     251    ~~~l~~L~~~~~~~~~~vl~v~H~~k~~-~~~~Gs~~~~~~~d~vi~l~~~~-----~~
                       ...+..|...+++.++++++++|..+.. ...+|++.+...+|.+|.+....     .+
T Consensus     375    ~~~l~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~ad~vi~l~~~~~~~~~~~
T TIGR02655     375    RQFVIGVTGYAKQEEITGFFTNTSDQFMGSHSITDSHISTITDTILMLQYVEIRGEMSR
T ss_pred              HHHHHHHHHHHHHhcCcEEEEEEeCCcccCCccCCcchHHHhCCEEEEEeecccCCeEEE

Q ss_pred              CC-CCeeEEEEEec
Q Klein_Draft   315    EG-DRHTLRLQPID  327 (416)
Q Consensus     315    ~~-~~~~~~~~~~~  327 (416)
                       .. ..+.|.+....
T Consensus     445    ~~~~~~~~~i~~~g  458 (484)
T TIGR02655     445    HDKGIREFMISDKG  458 (484)
T ss_pred              CCCceEEEEEeCCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4ijm)

52. **4IJM_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4IJM) Circadian clock protein kinase KaiC; ATI**
auto-kinase; HET: PO4, ATP; 3.352A {Synechococcus elongatus}

Probability: 99.02 E-value: 8.4E-11 Score: 119.55 Aligned Cols: 196 Identities: 11% Similar

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEEC
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVA
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~
                       +.+++.+.+.+++|..++|.|++|+|||+++..++.....         ...+|+|++.
T Consensus     255    ~~l~~~~~~~~~g~~~~i~g~~~~gkt~l~~~~~~~~~~~~~~~~~~~~~~~v~~i~~
T 4IJM_A        255    VRLDEMCGGGFFKDSIILATGATGTGKTLLVSRFVENACA---------NKERAILFAY
T ss_dssp              HHHHHHTTSSEESSCEEEEEECTTSCHHHHHHHHHHHHHH---------TTCCEEEEES
T ss_pred              ccHHHHcCCCccCCcEEEEECCCCCCHHHHHHHHHHHHHH---------CCCCEEEEEc
```

```
Q ss_pred              HHHHHHHcCcCccCCEEEEecCccc--CcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   183    NAWETAWRQTLEEGSITFLPVPVNL--MSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     183    ~~~~~~~~~~~~~~~~~~~~~~~~~--~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                       ..+.............+.+.......  .......+.+.+...++++||||+++.++...
T Consensus     316    ~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~lviiD~l~~~~~~~
T 4IJM_A        316    YSWGMDFEEMERQNLLKIVCAYPESAGLEDHLQIIKSEINDFKPARIAIDSLSALARGV
T ss_dssp              HTTSCCHHHHHHTTSEEECCCCGGGSCHHHHHHHHHHHHHTTCCSEEEEECHHHHTSSS
T ss_pred              HHcCCCHHHHHHcCCEEEEEEeChhhcCHHHHHHHHHHHHHhhCCCEEEEeCHHHHHhcC

Q ss_pred              HHHHHHHHHHcCCCCeEEEEEccCCCCC-CCCCCchhHhccccEEEEEEeCC-----cE
Q Klein_Draft   251    IDSMTRLMDATPDHRGCVLGIHHTGKDE-KTLRGSSAYEGGVDTVYFVERGN-----GI
Q Consensus     251    ~~~l~~L~~~~~~~~~~vl~v~H~~k~~-~~~~Gs~~~~~~~d~vi~l~~~~-----~~
                       ...+..|...++++++++++|..+.. ....|+..+...||.++.+....     .+
T Consensus     380    ~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~ad~vi~l~~~~~~~~~~
T 4IJM_A        380    RQFVIGVTGYAKQEEITGLFTNTSDQFMGVHSITDSHISTITDTIILLQYVEIRGEMSR
T ss_dssp              HHHHHHHHHHHHHHTTCEEEEEEECSSSSCCCCSCTTCCGGGCSEEEEEEEEEETTEEEE
T ss_pred              HHHHHHHHHHHHHhcCcEEEEEecCCcccCCccCCchhHHHHccEEEEEEEeeeCCeEEE

Q ss_pred              C-CCCeeEEEE
Q Klein_Draft   315    E-GDRHTLRLQ  324 (416)
Q Consensus     315    ~-~~~~~~~~~~  324 (416)
                       . ...+.|.+.
T Consensus     450    ~~~~~~~~~i~  460 (512)
T 4IJM_A        450    HDKAIREFMIS  460 (512)
T ss_dssp              CCCBCEEEEEE
T ss_pred              CCCceEEEEEc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4tl6)

53. **4TL6_C (http://pdb.rcsb.org/pdb/explore.do?structureId=4TL6) Circadian clock protein kinase KaiC; Se**
TRANSFERASE; HET: ANP; 1.763A {Synechococcus elongatus (strain PCC 7942)}

Probability: 99.02 E-value: 1.4E-10 Score: 105.27 Aligned Cols: 198 Identities: 13% Similar

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEEC
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVA
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~
                       +.++.+..+.+++|.+++|.|++|+|||+|+..++.....        ....+++++.
T Consensus     26     ~~l~~~~~g~~~~g~~~~i~G~~g~GKs~l~~~~~~~~~~~~--------~~~~~i~~~~
T 4TL6_C        26     EGFDDISHGGLPIGRSTLVSGTSGTGKTLFSIQFLYNGIIE--------FDEPGVFVTF
T ss_dssp              BTHHHHTTSSEETTSEEEEEESTTSSHHHHHHHHHHHHHH--------HCCCEEEEES
T ss_pred              cCHHHHhcCCCCCCcEEEEEeCCCCCHHHHHHHHHHHcchh--------cCccEEEEEC

Q ss_pred              HHHHHHHcCcCccCCEEEEecCcc----------cCcHHHHHHHHHHHHhCCcEEEEeC
Q Klein_Draft   183    NAWETAWRQTLEEGSITFLPVPVN----------LMSQDVGALVEDIKDYGFEFIVLDT
Q Consensus     183    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~
                       ................+......          ........+...+...+++++|||+
T Consensus     88     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~liiD~
T 4TL6_C        88     RSFGWDLAKLVDEGKLFILDASPDPEGQEVVGGFDLSALIERINYAIQKYRARRVSIDS
T ss_dssp              GGGTCCHHHHHHTTSEEEEECCCCCC--------CHHHHHHHHHHHHHHHTCSEEEEEC
T ss_pred              HHcCCCHHHHhhcCCEEEEeCCCCcccceecCCCCHHHHHHHHHHHHHHhCCcEEEEeC

Q ss_pred              CHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeCC
Q Klein_Draft   243    SARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERGN
Q Consensus     243    ~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~~
                          ........+..+...+++.++++++++|..+.....+|++.+...+|.++.+....
T Consensus     156    ---~~~~~~~~~l~~l~~~~~~~~~ii~~~~~~~~~~~~~~~~~~~~d~~i~l~~~~
T 4TL6_C        156    ---ASSVVRRELFRLVARLKQIGATTVMTTERIEEYGPIARYGVEEFVSDNVVILRNVL
T ss_dssp              ---CHHHHHHHHHHHHHHHHHTCEEEEEEECSCTTSCSSTTSCHHHHCSEEEEEEEEE
```

```
T ss_pred             ---ChHHHHHHHHHHHHHHHcCCEEEEEecccccCCccccChHHHhcCEEEEEEeec

Q ss_pred             eeecCCC-CCCCeeEEEE
Q Klein_Draft   308   KKQKDAP-EGDRHTLRLQ  324 (416)
Q Consensus     308   ~K~r~~~-~~~~~~~~~~  324 (416)
                      .|.|..+ ....+.|.+.
T Consensus     223   ~k~r~~~~~~~~~~~~~~  240 (253)
T 4TL6_C        223   LKLRGTSHMKGEYPFTIT  240 (253)
T ss_dssp             EEETTSCCCCSEEEEEEE
T ss_pred             EEcCCCCCCCceEEEEEe
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4nmn)

54. **4NMN_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4NMN) Replicative DNA helicase; RecA-type helicase; HET: ADP; 3.301A {Aquifex aeolicus}**

Probability: 99.01 E-value: 6.5E-11 Score: 117.7 Aligned Cols: 204 Identities: 17% Similarit

```
Q ss_pred             CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHH-cCCCCCCCCCCCCcEEE
Q Klein_Draft   112   NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLA-TGRNWQGRETEKVKVLY
Q Consensus     112   ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~-~g~~~~g~~~~~~~Vl~
                      ..|.++.+. +.+++|++++|+|++|+|||+++..++..+. .         .+.+|+|
T Consensus     179   g~~~ld~~~-~g~~~g~~~~i~g~~g~GKS~l~~~l~~~~~~~~---------~g~~v~~
T 4NMN_A        179   GFTELDLKT-TGFHPGDLIILAARPGMGKTAFMLSIIYNLAKD---------EGKPSAV
T ss_dssp             SCHHHHHHH-CCBCTTCEEEEEECTTSSHHHHHHHHHHHHHHH---------SCCCEEE
T ss_pred             CchHHHHhc-CcccCCCcEEEEEcCCCCCHHHHHHHHHHHHHHH---------cCCCEEE

Q ss_pred             HHHHHHHHHHcCc---------------------CccCCEEEEecCcccCcHHHHHHHH
Q Klein_Draft   180   SRINAWETAWRQT---------------------LEEGSITFLPVPVNLMSQDVGALVE
Q Consensus     180   ~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~
                      .++..........                     ......+...............+..
T Consensus     239   ~r~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~~~~~~~~
T 4NMN_A        239   MRLLSMMSEVPLFKIRSGSISNEDLKKLEASAIELAKYDIYLDDTPALTTTDLRIRARK
T ss_dssp             HHHHHHHHCCCHHHHHHTCCCHHHHHHHHHHHHHHHHSCEEEECCSSCBHHHHHHHHHH
T ss_pred             HHHHHHHhCCCHHHhhcCCCCHHHHHHHHHHHHHHHhCCcEecCCCCCCHHHHHHHHHH

Q ss_pred             EeChHHHcCCCccCCHHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCC--------
Q Klein_Draft   229   LDTIARCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEK--------
Q Consensus     229   iD~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~---------
                      ||++..+.....  .......+...+..|..++++++++|++++|.++...
T Consensus     309   iD~~~~~~~~~~--~~~~~~~~~~~~~~~L~~l~~~~~~~vi~~~~~~~~~~~~~~~~~~
T 4NMN_A        309   VDYLQLLRPPVR--KSPRQEEVAEVSRNLKALAKELRIPVMALAQLSREVEKRSDKRPQ
T ss_dssp             EECGGGCBCSSC--CSSHHHHHHHHHHHHHHHHHHHTSCEEEEEECCGGGTTSTTCSCC
T ss_pred             EeCHHHcCCCCC--CCCHHHHHHHHHHHHHHHHHHhCCcEEEEEeCCcchhcCCCCCCC

Q ss_pred             ccccEEEEEEe------------CCcEEEEEeeecCCCCCCeeEEEEEecC
Q Klein_Draft   289   GGVDTVYFVER------------GNGITLTCKKQKDAPEGDRHTLRLQPIDG  328 (
Q Consensus     289   ~~~d~vi~l~~-------------~~~~~l~~~K~r~~~~~~~~~~~~~~~~  328 (
                      ..+|.++.+..             .....+.+.|+|.++.+ .+.|.+.....
T Consensus     377   ~~ad~vi~l~~~~~~~~~~~~~~~~~~~l~~~K~R~g~~~-~~~~~~~~~~~  427 (
T 4NMN_A        377   QDADLILFLHRPEYYTKKPNPEEQGIAEVIIAKQRQGPTD-IVKLAFIKEYT  427 (
T ss_dssp             GGCSEEEEEECHHHHCSCCC--CCSEEEEEEEECSSSCCE-EEEEEEETTTT
T ss_pred             HHCCEEEEEeCHHHcCCCCCCcccCCeEEEEEEEcCCCCCc-EEEEEEEcccc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4nmn)

55. **4NMN_B (http://pdb.rcsb.org/pdb/explore.do?structureId=4NMN) Replicative DNA helicase; RecA-type helicase; HET: ADP; 3.301A {Aquifex aeolicus}**

Probability: 99.01 E-value: 6.5E-11 Score: 117.7 Aligned Cols: 204 Identities: 17% Similarit

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHH-cCCCCCCCCCCCCcEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLA-TGRNWQGRETEKVKVLY
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~-~g~~~~g~~~~~~~Vl~
                       ..|.++.+. +.+++|++++|+|++|+|||+++..++..+. .         .+.+|+|
T Consensus     179    g~~~ld~~~-~g~~~g~~~~i~g~~g~GKS~l~~~l~~~~~~~~---------~g~~v~~
T 4NMN_B        179    GFTELDLKT-TGFHPGDLIILAARPGMGKTAFMLSIIYNLAKD---------EGKPSAV
T ss_dssp              SCHHHHHHS-CCBCTTCEEEEEECTTSSHHHHHHHHHHHHHHH---------SCCCEEE
T ss_pred              CchHHHHhc-CcccCCCcEEEEEcCCCCCHHHHHHHHHHHHHHH---------cCCCEEE

Q ss_pred              HHHHHHHHHHcCc---------------------CccCCEEEEecCcccCcHHHHHHHH
Q Klein_Draft   180    SRINAWETAWRQT---------------------LEEGSITFLPVPVNLMSQDVGALVE
Q Consensus     180    ~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~
                       .++..........                     ......+...............+..
T Consensus     239    ~r~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~~~~~~~~
T 4NMN_B        239    MRLLSMMSEVPLFKIRSGSISNEDLKKLEASAIELAKYDIYLDDTPALTTTDLRIRARK
T ss_dssp              HHHHHHHHTCCHHHHHHTCCCHHHHHHHHHHHHHHHHHSCEEEECCSSCBHHHHHHHHHH
T ss_pred              HHHHHHHHhCCCHHHhhcCCCCHHHHHHHHHHHHHHHHhCCcEecCCCCCCHHHHHHHHHH

Q ss_pred              EeChHHHcCCCccCCHHHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCC--------
Q Klein_Draft   229    LDTIARCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEK--------
Q Consensus     229    iD~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~
                       ||++..+.....  .......+...+..|..++++++++|++++|.++...
T Consensus     309    iD~~~~~~~~~~--~~~~~~~~~~~~~~L~~l~~~~~~~vi~~~~~~~~~~~~~~~~~~
T 4NMN_B        309    VDYLQLLRPPVR--KSPRQEEVAEVSRNLKALAKELRIPVMALAQLSREVEKRSDKRPQ
T ss_dssp              EECGGGCBCSSC--CSSSHHHHHHHHHHHHHHHHHHTSCEEEEEECC--------CCCC
T ss_pred              EeCHHHcCCCCC--CCCHHHHHHHHHHHHHHHHHHhCCcEEEEEeCCcchhcCCCCCCC

Q ss_pred              ccccEEEEEEe------------CCcEEEEEeeecCCCCCCeeEEEEEecC
Q Klein_Draft   289    GGVDTVYFVER------------GNGITLTCKKQKDAPEGDRHTLRLQPIDG  328 (
Q Consensus     289    ~~~d~vi~l~~-------------~~~~~l~~~K~r~~~~~~~~~~~~~~~~  328 (
                       ..+|.++.+..             .....+.+.|+|.++.+ .+.|.+.....
T Consensus     377    ~~ad~vi~l~~~~~~~~~~~~~~~~~~l~~~K~R~g~~~-~~~~~~~~~~~  427 (
T 4NMN_B        377    QDADLILFLHRPEYYTKKPNPEEQGIAEVIIAKQRQGPTD-IVKLAFIKEYT  427 (
T ss_dssp              TTCSEEEEEECHHHHC----CCCCCEEEEEEEEESSSCCE-EEEEEEETTTT
T ss_pred              HHCCEEEEEeCHHHcCCCCCCccCCeEEEEEEcCCCCCc-EEEEEEEcccc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2q6t)

56. **2Q6T_C (http://pdb.rcsb.org/pdb/explore.do?structureId=2Q6T) DnaB replication fork helicase (E.C.3.6. HYDROLASE; HET: SO4; 2.9A {Thermus aquaticus}**

Probability: 99.01 E-value: 7.3E-11 Score: 117.71 Aligned Cols: 203 Identities: 18% Similar

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHH-cCCCCCCCCCCCCcEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLA-TGRNWQGRETEKVKVLY
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~-~g~~~~g~~~~~~~Vl~
                       ..|.++.++ +.+++|++++|.|++|+|||+++..++..+. .         .+.+|+|
T Consensus     186    g~~~ld~~~-~g~~~G~~~~i~g~~g~GKS~l~~~l~~~~~~~~---------~g~~v~~
T 2Q6T_C        186    GFKELDQLI-GTLGPGSLNIIAARPAMGKTAFALTIAQNAALK---------EGVGVGI
T ss_dssp              CCHHHHHHH-CSCCTTCEEEEEECTTSSHHHHHHHHHHCCCCC---------CCCEEEE
T ss_pred              ChHHHHHHh-cCcCCCcEEEEEcCCCCCHHHHHHHHHHHHHHH---------hCCeEEE

Q ss_pred              HHHHHHHHHHcCcC---------------------ccCCEEEEecCcccCcHHHHHHHH
Q Klein_Draft   180    SRINAWETAWRQTL--------------------EEGSITFLPVPVNLMSQDVGALVE
Q Consensus     180    ~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~
                       .++..........                     ....+.+..............+..
T Consensus     246    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~
T 2Q6T_C        246    LRMMCSEARIDMNRVRLGQLTDRDFSRLVDVASRLSEAPIYIDDTPDLTLMEVRARARR
T ss_dssp              HHHHHHHTTCCCC----------CCHHHHHHHHHHTTSCEEEECCSSCBHHHHHHHHHT
```

```
T ss_pred              HHHHHHHhCCCHHHHhcCCCCHHHHHHHHHHHHHHHhCCeEEECCCCCCHHHHHHHHHH

Q ss_pred              EeChHHHcCCC-ccCCHHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCCC------
Q Klein_Draft   229    LDTIARCTVGA-EENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT------
Q Consensus     229    iD~l~~~~~~~-~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~------
                       ||++..+.... ..........+...+..|..+++++++++++|.++....
T Consensus     316    iD~~~~~~~~~~~~~~~~~~~~~~~~~L~~la~~~~~~ii~~~~~~~~~~~~~~~~~
T 2Q6T_C        316    IDYLQLMSGPGSGKSGENRQQEIAAISRGLKALARELGIPIIALSQLSRAVEARPNKRP
T ss_dssp              EETGGGCBCC-------CHHHHHHHHHHHHHHHHHHHTSCEEEEEECCTTGGGSSCCCC
T ss_pred              EEChhhcCCCCCCCCCCHHHHHHHHHHHHHHHHHHHCCCEEEEeeCCcchhcCCCCCC

Q ss_pred              hccccEEEEEEe----------CCcEEEEEeeecCCCCCCeeEEEEE
Q Klein_Draft   288    EGGVDTVYFVER----------GNGITLTCKKQKDAPEGDRHTLRLQP  325 (416)
Q Consensus     288    ~~~~d~vi~l~~----------~~~~~l~~~K~r~~~~~~~~~~~~~~  325 (416)
                       ...+|.++.+..          .+...+.+.|.|.++.+ .+.+.+..
T Consensus     386    ~~~ad~vi~l~~~~~~~~~~~~~~~~l~~~K~R~g~~~-~~~~~~~~  432 (444)
T 2Q6T_C        386    EQDADLVMFIYRDEYYNPHSEKAGIAEIIVGKQRNGPTG-TVELQFHA  432 (444)
T ss_dssp              TTTCSEEEEEEEHHHHCTTSSCSSEEEEEEEECSSSCCE-EEEEEEET
T ss_pred              HHhCCEEEEEeCHHHcCCCcccCCeEEEEEEEeCCCCCE-EEEEEEec
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2q6t)

57. **2Q6T_A (http://pdb.rcsb.org/pdb/explore.do?structureId=2Q6T) DnaB replication fork helicase (E.C.3.6. HYDROLASE; HET: SO4; 2.9A {Thermus aquaticus}**

Probability: 99.01 E-value: 7.3E-11 Score: 117.71 Aligned Cols: 203 Identities: 18% Similar

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHH-cCCCCCCCCCCCCcEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLA-TGRNWQGRETEKVKVLY
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~-~g~~~~g~~~~~~~Vl~
                       ..|.++.++ +.+++|++++|.|++|+|||+++..++..+. .         .+.+|+|
T Consensus     186    g~~~ld~~~-~g~~~G~~~~i~g~~g~GKS~l~~~l~~~~~~~~~~~~~~~~g~~v~~
T 2Q6T_A        186    GFKELDQLI-GTLGPGSLNIIAARPAMGKTAFALTIAQNAALK---------EGVGVGI
T ss_dssp              SCHHHHHHH-CCCCTTCEEEEEECTTSCHHHHHHHHHHCCCCC---------CCCCEEE
T ss_pred              ChHHHHHHh-cCcCCCcEEEEEcCCCCCHHHHHHHHHHHHHHH---------hCCeEEE

Q ss_pred              HHHHHHHHHHcCcC---------------------ccCCEEEEecCcccCcHHHHHHHH
Q Klein_Draft   180    SRINAWETAWRQTL---------------------EEGSITFLPVPVNLMSQDVGALVE
Q Consensus     180    ~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~
                       .++...........                     ....+.+.............+..
T Consensus     246    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~
T 2Q6T_A        246    LRMMCSEARIDMNRVRLGQLTDRDFSRLVDVASRLSEAPIYIDDTPDLTLMEVRARARR
T ss_dssp              HHHHHHHTTCCTTTCCGGGCCHHHHHHHHHHHHHHHTSCEEEECCTTCBHHHHHHHHH
T ss_pred              HHHHHHHhCCCHHHHhcCCCCHHHHHHHHHHHHHHHhCCeEEECCCCCCHHHHHHHHH

Q ss_pred              EeChHHHcCCC-ccCCHHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCCC------
Q Klein_Draft   229    LDTIARCTVGA-EENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT------
Q Consensus     229    iD~l~~~~~~~-~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~------
                       ||++..+.... ..........+...+..|..+++++++++++|.++....
T Consensus     316    iD~~~~~~~~~~~~~~~~~~~~~~~~~L~~la~~~~~~ii~~~~~~~~~~~~~~~~~
T 2Q6T_A        316    IDYLQLMSGPGSGKSGENRQQEIAAISRGLKALARELGIPIIALSQLSRAVEARPNKRP
T ss_dssp              EECGGGCBCC-------CHHHHHHHHHHHHHHHHHHHTSCEEEEEECCGGGGSSSSCSC
T ss_pred              EEChhhcCCCCCCCCCCHHHHHHHHHHHHHHHHHHHCCCEEEEeeCCcchhcCCCCCC

Q ss_pred              hccccEEEEEEe----------CCcEEEEEeeecCCCCCCeeEEEEE
Q Klein_Draft   288    EGGVDTVYFVER----------GNGITLTCKKQKDAPEGDRHTLRLQP  325 (416)
Q Consensus     288    ~~~~d~vi~l~~----------~~~~~l~~~K~r~~~~~~~~~~~~~~  325 (416)
                       ...+|.++.+..          .+...+.+.|.|.++.+ .+.+.+..
T Consensus     386    ~~~ad~vi~l~~~~~~~~~~~~~~~~l~~~K~R~g~~~-~~~~~~~~  432 (444)
```

```
T 2Q6T_A        386    EQDADLVMFIYRDEYYNPHSEKAGIAEIIVGKQRNGPTG-TVELQFHA  432 (444)
T ss_dssp              GGGCSEEEEEEEGGGTCSSSSCCSEEEEEEEECSSSCCE-EEEEEEET
T ss_pred              HHhCCEEEEEeCHHHcCCCcccCCeEEEEEEEeCCCCCE-EEEEEEec
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmv)

58. **3CMV_F (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMV) PROTEIN recA; homologous recombir MG; 4.3A {Escherichia coli}**

Probability: 98.99 E-value: 6.5E-11 Score: 134.39 Aligned Cols: 197 Identities: 15% Similar

```
Q ss_pred              CCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft   113    MPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     113    ~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       .|.+++++. ++++.|.+++|+|++|+|||+++..++..+..         .+.+|+|+
T Consensus     1067   ~~~ld~~~~~gg~~~g~~~~l~G~~g~GKS~l~~~~a~~~~~---------~~~~vl~i
T 3CMV_F        1067   SLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFI
T ss_dssp              CSSHHHHSSSSSEETTSEEEEECCTTSSHHHHHHHHHHHHHT---------TSCCEEEE
T ss_pred              cHHHHHHhcCCCccCCeEEEEECCCCCCHHHHHHHHHHHHH---------cCCeEEEE

Q ss_pred              HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181    RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                       +....          ....+.............+.++++..++++||||++..+....
T Consensus     1128   ~~~~~----------~~~~i~~~~~~~~~~~~~~~~~~~~~~~lviiD~l~~~~~~~
T 3CMV_F        1128   RKLGV----------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKA
T ss_dssp              HHHTC----------CGGGCCCBCCSSHHHHHHHHHHHHHSSSCCEEEETTGGGCCC--
T ss_pred              HHcCC----------CcccEEEeCCCCHHHHHHHHHHHHcCCceEEEEechHHcCCHh

Q ss_pred              HHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCC-------CCCchhHhccccEEE
Q Klein_Draft   244    ARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT-------LRGSSAYEGGVDTVY
Q Consensus     244    ~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~---------~~Gs~~~~~~~d~vi
                       ......+.+.+..|..++.+++++|++++|.+|....       .+|++++...+|.++
T Consensus     1188   ~~~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~g~~~~~~~~~~~~
T 3CMV_F        1188   GLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRL
T ss_dssp              -CTTTTHHHHHHHHHHHHHHCCEEEEEEC----------------CCSTHHHHCSEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHhcCEEEEEEecccccccCccCCCCccccCcHHHHhceEEEE

Q ss_pred              -----CcEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   301    -----NGITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     301    -----~~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                            ..+.+.+.|+|..+....+.|.+....+
T Consensus     1258   ~~~~~~~~~~~~~K~r~~~~~~~~~~~~~~~~g  1290 (1357)
T 3CMV_F        1258   ENVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  1290 (1357)
T ss_dssp              SCBCEEEEEEEEEEESSSCCSCEEEEEEETTTE
T ss_pred              CcccceEEEEEEEeCCCCCCcccEEEEEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4ijm)

59. **4IJM_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4IJM) Circadian clock protein kinase KaiC; ATI auto-kinase; HET: PO4, ATP; 3.352A {Synechococcus elongatus}**

Probability: 98.99 E-value: 1.1E-10 Score: 118.81 Aligned Cols: 197 Identities: 13% Similar

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCC-CCcEEEEE
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETE-KVKVLYVV
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~-~~~Vl~i~
                       |.+++++.+.+++|..++|+|++|+|||+|+..++.....         . ...++|++
T Consensus     13     ~~ld~~l~ggl~~g~~~~i~G~~GsGKT~l~~~~~~~~~~---------~~~~~v~~v~
T 4IJM_A        13     EGFDDISHGGLPIGRSTLVSGTSGTGKTLFSIQFLYNGII---------EFDEPGVFVT
T ss_dssp              TTHHHHTTSSEETTSEEEEEESTTSSHHHHHHHHHHHHHH---------HHCCCEEEEE
```

```
T ss_pred             CCHHHHhcCCccCCcEEEEEcCCCCCHHHHHHHHHHhchh---------hcCCCEEEEE

Q ss_pred             HHHHHHHHcCcCccCCEEEEecCcc----------cCcHHHHHHHHHHHhCCcEEEEe
Q Klein_Draft   182   INAWETAWRQTLEEGSITFLPVPVN----------LMSQDVGALVEDIKDYGFEFIVLD
Q Consensus     182   l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                      +..+...........+.+......          ......+.+.+.+...++++||||
T Consensus     74    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 4IJM_A        74    ARSFGWDLAKLVDEGKLFILDASPDPEGQEVVGGFDLSALIERINYAIQKYRARRVSID
T ss_dssp             HTTTTCCHHHHHHTTSEEEEECCCCSSCCSCCSSHHHHHHHHHHHHHHHHHHTCSEEEEE
T ss_pred             HHhcCCCHHHHcccCCEEEEeCCCCcCCccccCCCCHHHHHHHHHHHHHHHhCCCEEEEc

Q ss_pred             CCHHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeC
Q Klein_Draft   242   NSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERG
Q Consensus     242   n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~~d~vi~l~~~
                          ........+..+...+++.++++++++|.........+...+...+|.++.+...
T Consensus     143   ----~~~~~~~~~l~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~d~vi~l~~~
T 4IJM_A        143   ----ASSVVRRELFRLVARLKQIGATTVMTTERIEEYGPIARYGVEEFVSDNVVILRNV
T ss_dssp             ----CHHHHHHHHHHHHHHHHHHTCEEEEEEECSSSSSCSSSSSCHHHHSSEEEEEEEE
T ss_pred             ----ChHHHHHHHHHHHHHHHHcCCEEEEEecCccccCCccccCcHHheeceEEEEEee

Q ss_pred             EeeecCCCCC-CCeeEEEE
Q Klein_Draft   307   CKKQKDAPEG-DRHTLRLQ  324 (416)
Q Consensus     307   ~~K~r~~~~~-~~~~~~~~  324 (416)
                      ..|.+..+.. ....|.+.
T Consensus     209   i~k~r~~~~~~~~~~~~i~  227 (512)
T 4IJM_A        209   ILKLRGTSHMKGEYPFTIT  227 (512)
T ss_dssp             EEEETTSCCCCSCEEEEEE
T ss_pred             EEECCCCCCCCeEEEEEEE
```

Template alignment

60. **TIGR00416 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR00416) sms; DNA repair p**
codes for a probable ATP-dependent protease involved in both DNA repair and degradation of proteins

Probability: 98.96 E-value: 2.0E-10 Score: 115.15 Aligned Cols: 191 Identities: 20% Similar

```
Q ss_pred             CcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEEECCC
Q Klein_Draft   116   PEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVAEG
Q Consensus     116   ~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~e~
                      ++.++.+.+++|..++|+|++|+|||+++..++..+..          ...+++|++.+.
T Consensus     83    ld~~l~g~~~~g~~~~i~G~~G~GKT~l~~~l~~~~~~~~~~~~~~~~~~v~~i~~~~
T TIGR00416     83    LDRVLGGGIVPGSLILIGGDPGIGKSTLLLQVACQLAK---------NQMKVLYVSGEE
T ss_pred             HHHHhCCCCCCCeEEEEECCCCCcHHHHHHHHHHHHHh---------CCCEEEEEeChh

Q ss_pred             HHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCccCCH
Q Klein_Draft   186   ETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAEENSA
Q Consensus     186   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~~n~~
                      ..............        .....+.+...+...++++||||+++.++........
T Consensus     141   ~~~~~~~~~~~~~~~-------~~~~~~~l~~~~~~~~~~liviD~~~~~~~~~~~~~~
T TIGR00416     141   AIRLGLPEPNLYVL--------SETNWEQICANIEEENPQACVIDSIQTLYSPDISSAP
T ss_pred             HHHcCCCCCcceeC--------CcccHHHHHHHHHHCCCEEEEeCcccccCCCccCCC

Q ss_pred             HHHHhcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeCC---cEEEEEeeec
Q Klein_Draft   256   RLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERGN---GITLTCKKQK
Q Consensus     256   ~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~~d~vi~l~~~~---~~~l~~~K~r
                      .|..+++..++++++++|..+. ....|+..+...+|.++.+..+.   .+.+...|.|
T Consensus     203   ~l~~~~~~~~~~vi~~~~~~~~-~~~~g~~~~~~~~d~~i~l~~~~~~~~r~l~i~k~~
T TIGR00416     203   ELMRLAKTRGIAIFIVGHVTKE-GSIAGPKVLEHMVDTVLYFEGDRDSRFRILRSVKNR
T ss_pred             HHHHHHHHHhCCEEEEEcccCCC-CCCCChhHHHhhcCEEEEEeCCcccceEEEEEEecC
```

```
Q ss_pred              EEEec
Q Klein_Draft   323    LQPID  327 (416)
Q Consensus     323    ~~~~~  327 (416)
                       +....
T Consensus     272    i~~~g  276 (454)
T TIGR00416     272    MTEQG  276 (454)
T ss_pred              Ecccc
```

Template alignment | CDD (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam09807)

61. **PF09807.8 (http://pfam.xfam.org/family/PF09807.8#tabview=tab0) ; ELP6 ; Elongation complex protein**

Probability: 98.96 E-value: 1.8E-10 Score: 106.41 Aligned Cols: 197 Identities: 12% Similar

```
Q ss_pred              CCCCccccccC---cccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEE
Q Klein_Draft   113    MPKPEPLIEG---VFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVL
Q Consensus     113    ~~~~~~l~~~---~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl
                       .+.++.++.+   ++++|.+++|.| +|+|||+|+..++...+.         .+.+|+
T Consensus     1      ~~~LD~~l~g~~~gl~~g~~~li~g-~~sgKs~l~~~~~~~~~~~~~~~~~~~~~~~v~
T PF09807.8     1      FTELNSILNTSPESFTPGEFILLSD-RQSDASFLIHHFLSFYLK---------ARCKVC
T ss_pred              CchHHHHhCCCCCCCCCCcEEEEEe-CCCCccHHHHHHHHHHHh---------cCCeEE

Q ss_pred              HHHHHHHHHHHcCcCccCCEEEEecCccc------------------------CcHHH
Q Klein_Draft   179    SSRINAWETAWRQTLEEGSITFLPVPVNL------------------------MSQDV
Q Consensus     179    ~~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                       ..++.............+.+.+.......                         +....
T Consensus     61     ~~~~~~~g~~~~~~~~~~~l~~~d~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~
T PF09807.8     61     HAVSQRLGVSLTQAKEKGQLIFLEGLKESLSVFLPQEENAGHQAMSFLRDPAAGLRSLY
T ss_pred              HHHHHHhCCChhHHHhcCcEEEEeCchhhhhhcCCcccccccccccchhcCcchHHHHHH

Q ss_pred              ---------hCCcEEEEeChHHHcCCCccCCHHHHHHHHHHHHHHHHcC-CCCeEEEE
Q Klein_Draft   222    ---------YGFEFIVLDTIARCTVGAEENSARDVGIVIDSMTRLMDATP-DHRGCVLG
Q Consensus     222    ---------~~~~lviiD~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~-~~~~~vl~
                                .++.+||||+++.++....     ....+...+..|...++ .++.++++
T Consensus     131    ~~~~~~~~~~~~~~vvIDsl~~l~~~~~-----~~~~~~~~~~~L~~~~~~~~~~~~i~
T PF09807.8     131    GGGGASAEQWGPPVLLMDDVSVLLSLGV-----RVGAVLDFSHYCRTTVCSQLQGNVVM
T ss_pred              CCCCCchhcCCCCEEEEeCHHHHHHcCC-----CHHHHHHHHHHHHHHHhhcCCceEEE

Q ss_pred              CCC-----CCchhHhccccEEEEEEeCC-------cEEEEEeeecCC-----CCCCCee
Q Klein_Draft   279    KTL-----RGSSAYEGGVDTVYFVERGN-------GITLTCKKQKDA-----PEGDRHT
Q Consensus     279    ~~~------~Gs~~~~~~~d~vi~l~~~~-------~~~l~~~K~r~~-----~~~~~~~
                       ...     .++..+...+|.+|.+....       ...+.+.|.|..     +....+.
T Consensus     196    ~~~~~~~~~~~~~~~~ad~vi~l~~~~~~~~~~~~~~l~v~k~~~~~~~~~~~~~~~~
T PF09807.8     196    DADDEGSEQLMRGLTHQSCLTLHVQGLPTGYCRDIHGQVEFCWKKRQSDGQHAPKKVFQ
T ss_pred              cCCcchhHHHHHHHHHHCCEEEEEcCCCCCceeecCeEEEEEECCCCCCCCCCCcEEEE
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmv)

62. **3CMV_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMV) PROTEIN recA; homologous recombi ANP; 4.3A {Escherichia coli}**

Probability: 98.95 E-value: 1.9E-10 Score: 130.81 Aligned Cols: 197 Identities: 14% Similar

```
Q ss_pred              CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       +.+++++. ++++.|.++.|+|+||+|||+|+..++..+..         .+.+|+|++
T Consensus     1068   ~~lD~~l~~gGl~~g~~~~i~G~~g~GKT~l~~~la~~~~~~~~~~~~~~~~vl~i~
T 3CMV_A        1068   LSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFID
T ss_dssp              SSHHHHSSSSSEETTSEEEEECCTTSSHHHHHHHHHHHHHT---------TSCCEEEEC
```

```
T ss_pred             HHHHHHHcCCCcccCCeEEEEECCCCCCHHHHHHHHHHHHHH---------CCCeEEEEe

Q ss_pred             HHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCC---
Q Klein_Draft   183   NAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVG---
Q Consensus     183   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~---
                      .         .......+.............+..+++..++++||||++..+...
T Consensus     1129  ~---------~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~lvviDsl~~l~~~~~~
T 3CMV_A        1129  K---------LGVDIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAEI
T ss_dssp             H---------HTCCGGGCCCBCCSSHHHHHHHHHHHHHSSSSCCEEEETTGGGCCC----
T ss_pred             H---------cCCCcccEEEeCCCCHHHHHHHHHHHHHcCCcEEEEEcchhhcCCHhHH

Q ss_pred             HHHHHHHHHHHHHHHcCCCCeEEEEEccCCCC-------CCCCCCchhHhccccEEEEE
Q Klein_Draft   246   DVGIVIDSMTRLMDATPDHRGCVLGIHHTGKD-------EKTLRGSSAYEGGVDTVYFV
Q Consensus     246   ~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~-------~~~~~Gs~~~~~~~d~vi~l
                      ....+...+..|..++++++++|++++|.++.       .....|+.++...++.++.+
T Consensus     1190  ~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~gg~~~~~~~~~~~~l
T 3CMV_A        1190  AARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDI
T ss_dssp             TTTTHHHHHHHHHHHHHHHCCEEEEEEC----------------CCSTHHHHCSEEEEE
T ss_pred             HHHHHHHHHHHHHHHHHHcCeEEEEEecceecCCcccCCCcccccCchHHHhceEEEEEE

Q ss_pred             ---CcEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   301   ---NGITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     301   ---~~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                         ..+.+.+.|+|..+......|.+....+
T Consensus     1260  ~~~~~~~l~~~K~r~~~~~~~~~~~i~~~~g  1290 (1357)
T 3CMV_A        1260  VVGSETRVKVVKNKIAAPFKQAEFQILYGEG  1290 (1357)
T ss_dssp             BCEEEEEEEEEEEESSSCCSCEEEEEEETTTE
T ss_pred             eeceEEEEEEEeCCCCCCccEEEEEEEecCc
```

Template alignment

63. **TIGR03600 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR03600) phage_DnaB; phag family, HK022 subfamily. Members of this family are phage (or prophage-region) homologs of the bact helicase DnaB.**

Probability: 98.91 E-value: 4.2E-10 Score: 111.04 Aligned Cols: 198 Identities: 20% Similar

```
Q ss_pred             CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHH-cCCCCCCCCCCCcEEE
Q Klein_Draft   112   NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLA-TGRNWQGRETEKVKVLY
Q Consensus     112   ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~-~g~~~~g~~~~~~~Vl~
                      ..+.++.+.. .+.+|++++|.|++|+|||+++..++..+. .         ...+|+|
T Consensus     179   g~~~l~~~~~-gi~~g~~~~i~g~~g~GKS~l~~~l~~~~~~~~---------~~~~v~~
T TIGR03600     179   GLPKLDRLTN-GLVKGDLIVIGARPSMGKTTLALNIAENVALR---------EGKPVLF
T ss_pred             CchhhhhhC-CcccCCcEEEEEcCCCCCHHHHHHHHHHHHHH---------CCCCEEE

Q ss_pred             HHHHHHHHHHcCc---------------------CccCCEEEEecCcccCcHHHHHHHH
Q Klein_Draft   180   SRINAWETAWRQT---------------------LEEGSITFLPVPVNLMSQDVGALVE
Q Consensus     180   ~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~
                      .++..........                     .....+.+.............+..
T Consensus     239   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T TIGR03600     239   ERLLASKSGINTGNIRTGRFNDSEFNRLLNAVDRLSEKDLYIDDTGGLTVAQIRSIARR
T ss_pred             HHHHHHhhCCCcccccCCCCCHHHHHHHHHHHHHccCCcEecCCCCCCHHHHHHHHHH

Q ss_pred             EEeChHHHcCCCccCCHHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC--------
Q Klein_Draft   228   VLDTIARCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE--------
Q Consensus     228   iiD~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~---------
                      |||++....   .............+..|..+++++++++++|.++..
T Consensus     309   iiD~~~~~~---~~~~~~~~~~~~~~~~~l~~l~~~~~~~ii~~~q~~~~~~~~~~~~
T TIGR03600     309   VVDYIQLMA---PARGRDRNEELGGISRGLKALAKELDVPVVLLAQLNRGSEKRTDKRP
T ss_pred             EEcchhhcC---CcCCCChhHHHHHHHHHHHHHHHHcCCcEEEEEeCCCCCCccCCCCC
```

```
Q ss_pred             hccccEEEEEEeC----------CcEEEEEeeecCCCCCCCeeEEE
Q Klein_Draft   288   EGGVDTVYFVERG----------NGITLTCKKQKDAPEGDRHTLRL  323 (416)
Q Consensus     288   ~~~~d~vi~l~~~-----------~~~~l~~~K~r~~~~~~~~~~~~  323 (416)
                      ...+|.++.+..+          +...+.+.|+|.++.+. +.+.|
T Consensus     376   ~~~ad~v~~l~~~~~~~~~~~~~~~~~~~~k~R~g~~g~-~~~~~  420 (420)
T TIGR03600     376   EQDADVIGLIHREGYYDAREPPAGIAELILAKNRHGPTGT-VELLF  420 (420)
T ss_pred             HHhCCEEEEEEcCCcCCCCCCCCCEEEEEEEeecCCCCCc-eeecC
```

Template alignment | CDD (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam13481)

64. **PF13481.5 (http://pfam.xfam.org/family/PF13481.5#tabview=tab0) ; AAA_25 ; AAA domain**

Probability: 98.9 E-value: 6.0E-10 Score: 96.65 Aligned Cols: 157 Identities: 18% Similarity

```
Q ss_pred             CCCCCccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCC--CCCCCCcEE
Q Klein_Draft   112   NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQG--RETEKVKVL
Q Consensus     112   ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g--~~~~~~~~Vl
                      ..+.+++++.+.++ |.+++|+|++|+|||+++..++..+. |..+++  ++....+++
T Consensus     14    ~~~~~~~~~~~~~~-g~~~~i~G~~g~GKs~l~~~l~~~~~-g~~~~~~~~~~~~~~v~
T PF13481.5     14    EPAAPRWVIPGFIG-HGLVIIAGAHGAGKTTALLPLALVAA-GLHPPGDPLAPLHWRRV
T ss_pred             CCCCCcccccccccC-CcEEEEEcCCCCCHHHHHHHHHHHHc-CCCCCCCCCCCCCCceE

Q ss_pred             HHHHH-HHHHHcCcCccC----CEEEEecCcccCc------HHHHHHHHHHHH-hCCcE
Q Klein_Draft   180   SRINA-WETAWRQTLEEG----SITFLPVPVNLMS------QDVGALVEDIKD-YGFEF
Q Consensus     180   ~rl~~-~~~~~~~~~~~~~----~~~~~~~~~~~~~~~------~~~~~l~~~~~~-~~~~l
                      .++.. +...+.......    ...+.........      .....+...+.. .++++
T Consensus     81    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T PF13481.5     81    RRILAGVLSHAQYRPALDLVRDRLRVVEARRLPPAEVVEVAGDYAHLRRDVDGVELLPL
T ss_pred             HHHHHHHHHhcccCeeeeeccCceeeeeccCCCCcchhhhhhHHHHHHHHHcCCCCCE

Q ss_pred             CCccCCHHHH-HHHHHHHHHHHHcCCCCeEEEEEccCCCC
Q Klein_Draft   238   GAEENSARDV-GIVIDSMTRLMDATPDHRGCVLGIHHTGKD  277 (416)
Q Consensus     238   ~~~~η~~~~~-~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~  277 (416)
                      . ..++..++ ..+...+..     .++++++++++|.+|.
T Consensus     151   ~-~~~~~~~~~~~~~~~l~~-----~~~~~~vi~~~~~~k~  185 (187)
T PF13481.5     151   L-EEENSNSEASAAVAMLKQ-----RFAGLPVWLVGHVAKA  185 (187)
T ss_pred             c-cccCChHHHHHHHHHHH-----HhhCCCEEEEeccccc
```

Template alignment

65. **TIGR00665 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR00665) DnaB; replicative I describes the helicase DnaB, a homohexameric protein required for DNA replication.**

Probability: 98.9 E-value: 5.4E-10 Score: 110.8 Aligned Cols: 205 Identities: 19% Similarity

```
Q ss_pred             CCCCCccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft   112   NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112   ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                      ..|.++.+. +.+.+|++++|.|++|+|||+++..++..+...        .+.+++|+
T Consensus     180   g~~~l~~~~-~g~~~g~~~~i~g~~g~GKS~l~~~l~~~~~~~~~~~~~~g~~v~~~
T TIGR00665     180   GFTDLDKLT-SGLQPSDLIILAARPSMGKTAFALNIAENAAIK--------EGKPVAFF
T ss_pred             CCchHHHhh-cCCCCCCEEEEEcCCCCCHHHHHHHHHHHHHH--------CCCCEEEE

Q ss_pred             HHHHHHHHHcCc---------------------CccCCEEEEecCcccCcHHHHHHHHH
Q Klein_Draft   181   RINAWETAWRQT---------------------LEEGSITFLPVPVNLMSQDVGALVED
Q Consensus     181   rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~
                      ++..........                     .....+.+.............+...
T Consensus     241   r~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T TIGR00665     241   RMLSSESRVDSQKLRTGRLSDEDWEKLTEAAGELSEAPLYIDDTPGLTITELRAKARRL
```

```
T ss_pred              HHHHhccCCCHHHHhcCCCCHHHHHHHHHHHHHhcCCcEecCCCCCCHHHHHHHHHHH

Q ss_pred              eChHHHcCCCccCCHHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCC--------
Q Klein_Draft   230    DTIARCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT--------
Q Consensus     230    D~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~---------
                       |++..+.....  .......+...+..|..+++.+++++++++|.++....
T Consensus     311    D~~~~~~~~~~--~~~~~~~~~~~~~~~L~~la~~~~~~ii~~~q~~~~~~~~~~~~~~~
T TIGR00665     311    DYLQLMSGSGR--SENRQQEVSEISRSLKALAKELNVPVIALSQLSRSVEQREDKRPQL
T ss_pred              cchhhhcCCCC--CccHHHHHHHHHHHHHHHHHHhCCCEEEEecCChhhccccCcCCch

Q ss_pred              cccEEEEEEeCC----------cEEEEEeeecCCCCCCeeEEEEEecC
Q Klein_Draft   290    GVDTVYFVERGN----------GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416
Q Consensus     290    ~~d~vi~l~~~~----------~~~l~~~K~r~~~~~~~~~~~~~~~~  328 (416
                       .+|.++.+....          .+.+.+.|+|.++.+ .+.+.++...+
T Consensus     379    ~ad~vi~l~~~~~~~~~~~~~~~~~~i~K~R~g~~~-~~~~~~~~~~~  426 (432
T TIGR00665     379    DADIVMFLYRDEYYNPDSEDKGIAEIIIAKQRNGPTG-TVKLAFLGEYT  426 (432
T ss_pred              cccEEEEEecCCCCCCCCcCcEEEEEEEeecCCCCc-eEEEEEECCcc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/1tf7)

66. **1TF7_F (http://pdb.rcsb.org/pdb/explore.do?structureId=1TF7) KaiC; homohexamer, hexamer, CIRCAD**
2.8A {Synechococcus sp.} SCOP: c.37.1.11

Probability: 98.87 E-value: 5.7E-10 Score: 114.02 Aligned Cols: 198 Identities: 13% Similar

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCC-CCcEEEEE
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETE-KVKVLYVV
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~-~~~Vl~i~
                       |.++.++.+.+++|..++|+|++|+|||+|+..++.....         . ..+++|++
T Consensus     26     ~~ld~~~~ggl~~g~~~~i~G~~GsGKT~l~~~~~~~~~~~---------~~~~~~~~i~
T 1TF7_F        26     EGFDDISHGGLPIGRSTLVSGTSGTGKTLFSIQFLYNGII---------EFDEPGVFVT
T ss_dssp              TTHHHHTTSSEETTSEEEEEESTTSSHHHHHHHHHHHHHH---------HHCCCEEEEE
T ss_pred              CCHHHHcCCCccCCCEEEEEeCCCCCHHHHHHHHHHhchh---------HcCCCEEEEE

Q ss_pred              HHHHHHHHcCcCccCCEEEEecCcc----------cCcHHHHHHHHHHHHhCCcEEEEe
Q Klein_Draft   182    INAWETAWRQTLEEGSITFLPVPVN----------LMSQDVGALVEDIKDYGFEFIVLD
Q Consensus     182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                       +..+.....+.+.....          ........+...+...++++||||
T Consensus     87     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 1TF7_F        87     ARSFGWDLAKLVDEGKLFILDASPDPEGQEVVGGFDLSALIERINYAIQKYRARRVSID
T ss_dssp              HGGGTCCHHHHHHTTSEEEEECCCCTTCCSCCTTHHHHHHHHHHHHHHHHHTCCEEEEE
T ss_pred              HHHcCCCHHHhhhcCCEEEEeCCCCCCCccccCCCCHHHHHHHHHHHHHHHhCCCEEEEe

Q ss_pred              CCHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeC
Q Klein_Draft   242    NSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERG
Q Consensus     242    n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~
                           ........+..+...+++.++++++++|..+.....++..+...+|.++.+...
T Consensus     156    ----~~~~~~~~~l~~l~~~l~~~~~~vi~~~~~~~~~~~~~~~~~~~~~d~vi~l~~~
T 1TF7_F        156    ----ASSVVRRELFRLVARLKQIGATTVMTTERIEEYGPIARYGVEEFVSDNVVILRNV
T ss_dssp              ----CHHHHHHHHHHHHHHHHHHTCEEEEEEECSSSSSCSSTTSCHHHHSSEEEEEEEE
T ss_pred              ----ChHHHHHHHHHHHHHHHHcCCEEEEEecCccccCCccccCcHHheeceEEEEEEe

Q ss_pred              EeeecCCCCC-CCeeEEEEE
Q Klein_Draft   307    CKKQKDAPEG-DRHTLRLQP  325 (416)
Q Consensus     307    ~~K~r~~~~~-~~~~~~~~~  325 (416)
                       ..|.|..... ....+.+..
T Consensus     222    v~k~r~~~~~~~~~~~~~~  241 (525)
T 1TF7_F        222    ILKLRGTSHMKGEYPFTITD  241 (525)
T ss_dssp              EEEETTSCCCCSEEEEEEET
```

```
T ss_pred              EEECCCCCCCCeEEEEEEEC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmv)

67. **3CMV_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMV) PROTEIN recA; homologous recombi ANP; 4.3A {Escherichia coli}**

Probability: 98.85 E-value: 4.0E-10 Score: 128.16 Aligned Cols: 197 Identities: 15% Similar

```
Q ss_pred              CCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   113    MPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     113    ~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       .|.+++++. ++++.|.+++|+|+||+|||+|+..++..++.         .+.+|+|+
T Consensus     19     ~~~lD~~l~~gG~~~g~i~~i~G~~g~GKT~l~~~la~~~~~---------~~~~vl~i
T 3CMV_A        19     SLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFI
T ss_dssp              CHHHHHHHSSSSEETTSEEEEECSSSSSHHHHHHHHHHHHHT---------TSCCEEEE
T ss_pred              CHHHHHHHccCCCCCCcEEEEECCCCCCHHHHHHHHHHHHH---------CCCeEEEE

Q ss_pred              HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181    RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                       +...+          ....+.............+...+...++++||||+++.+....
T Consensus     80     ~~~~~----------~~~~i~~~~~~~~~~~~~~i~~~~~~~~~~lvvIDsl~~l~~~~
T 3CMV_A        80     RKLGV----------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKA
T ss_dssp              HHHTC----------CGGGEEEECCSSHHHHHHHHHHHHHSSSCCEEEEECGGGCCCHH
T ss_pred              HHcCC----------ChhhEEEeCCCCHHHHHHHHHHHHHcCCcEEEEEechhhcCCHH

Q ss_pred              HHHHHHHHHHHHHHHHHcCCCCeEEEEEcccCCCC-------CCCCCCchhHhccccEEE
Q Klein_Draft   244    ARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKD-------EKTLRGSSAYEGGVDTVY
Q Consensus     244    ~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~-------~~~~~Gs~~~~~~~d~vi
                       ......+.+.+..|..++++++++|++++|.++.       .....|+..+...++..+
T Consensus     140    ~~~~~~~~~~l~~L~~~a~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 3CMV_A        140    GLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRL
T ss_dssp              TTHHHHHHHTTHHHHHTTTTTTCEEEEEEC----------------CCTTHHHHEEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHHcCEEEEEEecccccccCCcCCCCccCCCchHHHheeEEEE

Q ss_pred              -----CcEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   301    -----NGITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     301    -----~~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                            ..+.+...|+|..+....+.|.+....+
T Consensus     210    ~~~~~~~~~~~i~k~~~~~~~~~~~~~~~~~~  242 (1357)
T 3CMV_A        210    ENVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  242 (1357)
T ss_dssp              SCCCCCEEEEEEEEESSSCCSCEEEEEEETTTE
T ss_pred              CceeceeEEEEEEeCCCCCCceEEEEEEecCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmv)

68. **3CMV_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMV) PROTEIN recA; homologous recombi ANP; 4.3A {Escherichia coli}**

Probability: 98.8 E-value: 9.6E-10 Score: 125.13 Aligned Cols: 196 Identities: 15% Similarit

```
Q ss_pred              CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       +.+++++. ++++.|.+++|+|+||+|||+|+..++..+..         .+.+|+|++
T Consensus     369    ~~lD~~l~~gGi~~g~~~~l~G~~g~GKT~l~~~la~~~~~---------~~~~vl~i~
T 3CMV_A        369    LSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFID
T ss_dssp              HHHHHHHSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHHT---------TTCCCEEEE
T ss_pred              HHHHHHHccCCccCCeEEEEECCCCCCHHHHHHHHHHHHH---------CCCeEEEEe
```

```
Q ss_pred              HHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCc
Q Klein_Draft   182    INAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAE
Q Consensus     182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~
                       ....          ....+.............+...+...++++||||+++.+.....
T Consensus     430    ~~~~----------~~~~i~~~~~~~~~~~~~~~~~~~~~~~lvviD~l~~l~~~~~
T 3CMV_A        430    KLGV----------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAE
T ss_dssp              HHTC----------CGGGCEEECCSCHHHHHHHHHHHHTTSSCCEEEEECGGGCCCHHH
T ss_pred              HcCC----------CcccEEEeCCCCHHHHHHHHHHHHcCCceEEEEechhHcCCHHH

Q ss_pred              HHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhccccEEEE
Q Klein_Draft   245    RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGVDTVYF
Q Consensus     245    ~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~~d~vi~
                       .....+.+.+..|..++++++++|++++|.++..       ....|+..+...++..+.
T Consensus     490    ~~~~~~~~~l~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~
T 3CMV_A        490    LAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLD
T ss_dssp              TTTHHHHHHHHHHHHHHHHTTTCEEEEEEECCBSCSSSCCCCCBSCSSCTTHHHHCSEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHhcCEEEEEEcCCcccCCCcCCCCcccCCCchHHheeeEEEEE

Q ss_pred              ----CcEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   301    ----NGITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     301    ----~~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                           ..+.+...|+|..+......|.+....+
T Consensus     560    ~~~~~~~~~~i~K~~~~~~~~~~~~~~~~~~g  591 (1357)
T 3CMV_A        560    NVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  591 (1357)
T ss_dssp              EECEEEEEEEEEEESSSCTTCEEEEEEETTTE
T ss_pred              ceeeeEEEEEEEeCcCCCCceEEEEEEecCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/5lkm)

69. **5LKM_C (http://pdb.rcsb.org/pdb/explore.do?structureId=5LKM) DNA repair protein RadA; Helicase, re protein, Lon-protease; HET: TYD; 3.5A {Streptococcus pneumoniae}**

Probability: 98.78 E-value: 1.1E-9 Score: 109.72 Aligned Cols: 188 Identities: 20% Similarit

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHcCCCCCCCCCCCcEEEEEC
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVA
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~
                       +.+..++.+.+.+|..++|+|+||+|||+++..++..+.          ....++|++.
T Consensus     75     ~~l~~~~~~~~~g~~~ll~G~~G~GKT~l~~~la~~~~~~~~~~~~~~~~~~~~~i~~
T 5LKM_C        75     EEFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLS----------QVGTVLYVSG
T ss_dssp              HHHHHHTTSSBCSSEEEEEEECTTSSHHHHHHHHHHHHT----------TTSCEEEECS
T ss_pred              HHHHHHhCCCcCCCeEEEEEcCCCCcHHHHHHHHHHHHh----------cCCCEEEEeC

Q ss_pred              HHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHcCCcEEEEeChHHHcCCCcc
Q Klein_Draft   183    NAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAEE
Q Consensus     183    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~~
                       .            ................+.+.+.+...++++||||+++.++.....
T Consensus     135    ~------------~~~~~~~~~~~~~~~~~~l~~~~~~~~~~iliiDe~~~~~~~~~~
T 5LKM_C        135    E------------RLGDIDSEFYLYAETNMQSVRAEVERIQPDFLIIDSIQTIMSPEIS
T ss_dssp              H------------HHSCCSSSEEEECCCSSHHHHHHHHHHCCSEEEESCSTTCCCC---
T ss_pred              H------------HhCCCCcceEEeeCCCHHHHHHHHHHHHCCCEEEEECcchhCcccC

Q ss_pred              HHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeCC---cEEEEEe
Q Klein_Draft   253    SMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERGN---GITLTCK
Q Consensus     253    ~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~~---~~~l~~~
                       .+..|...+...+.++++++|.++. ....|...+...+|.++.+....   ...+...
T Consensus     193    ~l~~l~~~~~~~~~~viii~~~~~~-~~~~~~~~~~~~~~d~~i~l~~~~~~~~~~l~~~
T 5LKM_C        193    VTAELMQLAKTNNIAIFIVGHVTKE-GTLAGPRMLEHMVDTVLYFEGERHHTFRILRAV
T ss_dssp              HHHHHHHHHHHHTTCEEEEEEECC--------CCSSGGGSSEEEEEECCSSCCEEEEEEE
```

```
T ss_pred             HHHHHHHHHHHhCCCEEEEEeeeCCC-CCCCChhHHhhhcceEEEEecCCcccceEEEEEE

Q ss_pred             eEEEE
Q Klein_Draft   320   TLRLQ  324 (416)
Q Consensus     320   ~~~~~  324 (416)
                      .|.+.
T Consensus     262   ~~~~~  266 (452)
T 5LKM_C        262   IFEMQ  266 (452)
T ss_dssp             EEEEC
T ss_pred             EEEee
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmv)

70. **3CMV_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMV) PROTEIN recA; homologous recombi ANP; 4.3A {Escherichia coli}**

Probability: 98.78 E-value: 1.3E-9 Score: 124.08 Aligned Cols: 197 Identities: 15% Similari

```
Q ss_pred             CCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   113   MPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     113   ~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                      .+.+++++. +++++|.+++|+|+||+|||+|+..++..+..         .+.+|+|+
T Consensus     717   ~~~lD~~l~~gG~~~g~~~~i~G~~g~GKT~l~~~~a~~~~~---------~~~~vl~i
T 3CMV_A        717   SLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFI
T ss_dssp             CHHHHHHHSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHHT---------SSCCEEEE
T ss_pred             CHHHHHHhcCCCccCceEEEEECCCCCCHHHHHHHHHHHHHH---------CCCeEEEE

Q ss_pred             HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181   RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181   rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                      +....          ....+.............+...++..++++||||+++.+....
T Consensus     778   ~~~~~---------~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~lvviDsl~~l~~~~
T 3CMV_A        778   RKLGV----------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKA
T ss_dssp             HHHTC----------CGGGCEEECCSCHHHHHHHHHHHHTTSCCCEEEEECGGGCCCTT
T ss_pred             HHhCC----------CccceEEeCCCCHHHHHHHHHHHHcCCceEEEEeChhhcCCHH

Q ss_pred             HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCC-------CCCchhHhccccEEE
Q Klein_Draft   244   ARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT-------LRGSSAYEGGVDTVY
Q Consensus     244   ~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~~~Gs~~~~~~~d~vi
                      ......+...+..|..++++++++|++++|..+....       ..|+..+...++..+
T Consensus     838   ~~~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 3CMV_A        838   GLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRL
T ss_dssp             CCCCHHHHHTHHHHHHHTTTTTCEEEEEEC----------------CCTTHHHHEEEEE
T ss_pred             HHHHHHHHHHHHHHHHHHHHcCEEEEEEcCCcccCCCcCCCCcccCCchHHheeeEEEE

Q ss_pred             -----CcEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   301   -----NGITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     301   -----~~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                            ..+.+...|+|..+......|.+....+
T Consensus     908   ~~~~~~~~~~~i~K~~~~~~~~~~~~~~~~~~~  940 (1357)
T 3CMV_A        908   ENVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  940 (1357)
T ss_dssp             SSEEEEEEEEEEEEESSSCCSCEEEEEEETTTE
T ss_pred             cceeeeeEEEEEEcCCCCCCcceEEEEEEeCCc
```

Template alignment | CDD (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam07088)

71. **PF07088.10 (http://pfam.xfam.org/family/PF07088.10#tabview=tab0) ; GvpD ; GvpD gas vesicle protein**

Probability: 98.77 E-value: 2.3E-9 Score: 109.49 Aligned Cols: 189 Identities: 16% Similari

```
Q ss_pred              CccccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEECCC
Q Klein_Draft   116    PEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVAEG
Q Consensus     116    ~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~e~
                       ++.++.+  ++|+.++|.|++|+|||+|+..++.. ..         .+.+++|++.+.
T Consensus     1      l~~~l~g--~~G~~vlI~G~~GsGKTtl~~~l~~~-l~---------~~~~v~yvs~e~
T PF07088.10    1      LSQFFMG--DAGETLLINGAPGTGKTLFTIRGLDV-LD---------RDSDVLYVSTRV
T ss_pred              CchhcCC--CCCcEEEEECCCCCCHHHHHHHHHHH-Hc---------CCCCEEEEECCC

Q ss_pred              -------HHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHH
Q Klein_Draft   183    -------NAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIAR
Q Consensus     183    -------~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~
                              ..+.........................+.+...+...++++||||+++.
T Consensus     59     ~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~s~~~l~~~l~~~~~~~~p~llvID~i~~
T PF07088.10    59     DHSSLDTTAILDLFQDPFELPLDVDVPFEKLDLDSLLEWIQEINAATTQLTIAFDSWEL
T ss_pred              ccCCCCChHHHHHhccCCcCCCCCCCCCcccCCHHHHHHHHHHHHHHcCCCEEEEeCHHH

Q ss_pred              HHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeCC---
Q Klein_Draft   246    DVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERGN---
Q Consensus     246    ~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~~---
                       ....+...+..|...+++.++++++++|..+       ...+...+|.++.|....
T Consensus     128    ~~~~~~~~l~~L~~~~~~~g~~iIli~~~~~~~~~~~~~i~~~aD~vi~L~~~~~~~
T PF07088.10    128    DPPDIKTVTNQLAVLAREENIRLMLVTETAA-------PSSLEYIVDGVVTLQVKEDDR
T ss_pred              ChHHHHHHHHHHHHHHHHcCCEEEEEEeCCC-------CcchHHhcCEEEEEEEcccCC

Q ss_pred              ecCCCCC-CCeeEEEE
Q Klein_Draft   310    QKDAPEG-DRHTLRLQ  324 (416)
Q Consensus     310    ~r~~~~~-~~~~~~~~  324 (416)
                       .|..... ..+.|.+.
T Consensus     191    ~R~~~~~~~~~~f~i~  206 (514)
T PF07088.10    191    LRGVRIGNRLQPFTLA  206 (514)
T ss_pred              CCCCCCCCceEEEEEe
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/5lkm)

72. **5LKM_A (http://pdb.rcsb.org/pdb/explore.do?structureId=5LKM) DNA repair protein RadA; Helicase, re protein, Lon-protease; HET: TYD; 3.5A {Streptococcus pneumoniae}**

Probability: 98.77 E-value: 1.0E-9 Score: 110.01 Aligned Cols: 188 Identities: 20% Similarit

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEEC
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVA
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~
                       +.+..++.+.+.+|..++|+|+||+|||+|+..++..+.          ....++|++.
T Consensus     75     ~~~~~~~~~~~~~g~~~ll~G~~G~GKT~l~~~la~~~~~~~~~~~~~~~~~~~~i~~
T 5LKM_A        75     EEFNRVLGGGVVPGSLVLIGGDPGIGKSTLLLQVSTQLS----------QVGTVLYVSG
T ss_dssp              HHHHHHTTSSBCSSEEEEEEECTTSSHHHHHHHHHHHHT----------TTSCEEEEES
T ss_pred              HHHHHHhCCCcCCCeEEEEEcCCCCcHHHHHHHHHHHh----------ccCCEEEEcC

Q ss_pred              HHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCcc
Q Klein_Draft   183    NAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAEE
Q Consensus     183    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~~
                       .            ................+.+...+...++++||||+++.++.....
T Consensus     135    ~------------~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~ilviDe~~~~~~~~~~
T 5LKM_A        135    E------------RLGDIDSEFYLYAETNMQSVRAEVERIQPDFLIIDSIQTIMSPEIS
T ss_dssp              H------------HHSCCSSSEEEECCCBHHHHHHHHHHHHCCSEEEEECGGGCBCCC--
T ss_pred              H------------HhCCCCcceEEeeCCCHHHHHHHHHHHHCCCEEEEeCccccccCccC

Q ss_pred              HHHHHHHhcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeCC---cEEEEEe
Q Klein_Draft   253    SMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERGN---GITLTCK
```

```
Q Consensus     253    ~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~~---~~~l~~~
                       .+..|...+...+.++++++|.++. ....|...+...+|.++.+....   ...+...
T Consensus     193    ~l~~l~~~~~~~~~~vii~~~~~~~-~~~~~~~~~~~~~d~~i~l~~~~~~~~~~l~~~
T 5LKM_A        193    VTAELMQLAKTNNIAIFIVGHVTKE-GTLAGPRMLEHMVDTVLYFEGERHHTFRILRAV
T ss_dssp              HHHHHHHHHHHHTTCEEEEEEECCSC-C----CCSSGGGSSEEEEEECCSSCSEEEEEEE
T ss_pred              HHHHHHHHHHHhCCCEEEEEeecCCC-CCCCChHHHHhhcceEEEEecCCcccceEEEEE

Q ss_pred              eEEEE
Q Klein_Draft   320    TLRLQ  324 (416)
Q Consensus     320    ~~~~~  324 (416)
                       .|.+.
T Consensus     262    ~~~~~  266 (452)
T 5LKM_A        262    IFEMQ  266 (452)
T ss_dssp              EEEEC
T ss_pred              EEEEc
```

Template alignment

73. **TIGR03881 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR03881) KaiC_arch_4; KaiC (**
Members of this protein family are archaeal single-domain KaiC_related proteins, homologous to the (
cycle protein KaiC, an autokinase/autophosphorylase that has two copies of the domain.

Probability: 98.76 E-value: 3.6E-9 Score: 94.12 Aligned Cols: 200 Identities: 16% Similarity

```
Q ss_pred              CCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   112    NMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     112    ~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       ..+.+++++++.+++|.+++|.|++|+|||+|+..++.....         ....++|+
T Consensus     5      g~~~l~~~~~~~~i~~g~~~~i~G~~g~GKs~l~~~l~~~~~~---------~~~~~~~~
T TIGR03881     5      GVEGLDKLLEGGIPRGFFVAVTGEPGTGKTIFCLHFAYKGLR---------DGDPVIYV
T ss_pred              CchhHHHHHhCCCCCCcEEEEEcCCCCCHHHHHHHHHHhccc---------CCCCEEEE

Q ss_pred              HHHHHHHHHcCcCcccCCEE-----------EEecCcccCcHHHHHHHHHHHHh--CCcE
Q Klein_Draft   181    RINAWETAWRQTLEEGSIT-----------FLPVPVNLMSQDVGALVEDIKDY--GFEF
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~----------~~~~~~~~~~~~~~~l~~~~~~~~--~~~l
                       +...+.............           ...............+...+...  +..+
T Consensus     66     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T TIGR03881     66     QAAQFGMDFEKAIEEGKLVIIDALMKEKEDEWSLRELSIEELLNKVIEAKKYLGYGHAR
T ss_pred              HHHHhCCCHHHHHHcCcchHHHHHHhhcccccccccCCHHHHHHHHHHHHHHhCCCceE

Q ss_pred              CCccCCHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEE
Q Klein_Draft   238    GAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYF
Q Consensus     238    ~~~~n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~
                       .       +.......+..+...+++.++++++++|..+. ...+++..+...+|.++.
T Consensus     136    ~-------~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~-~~~~~~~~~~~~~d~~~~
T TIGR03881     136    D-------KPAMARKYSYYLKRVLNRWNFTILLTSQYAIT-TSQAFGFGIEHVADGIIR
T ss_pred              C-------CHHHHHHHHHHHHHHHhhcCcEEEEEcCCchh-cCcccccchhHhcCEEEE

Q ss_pred              EEEEEeeecCCCCC-CCeeEEEEEecC
Q Klein_Draft   303    ITLTCKKQKDAPEG-DRHTLRLQPIDG  328 (416)
Q Consensus     303    ~~l~~~K~r~~~~~-~~~~~~~~~~~~  328 (416)
                       ..+...|.|..... ..+.|.+....|
T Consensus     198    ~~l~~~k~~~~~~~~~~~~~~~~~~g  224 (229)
T TIGR03881     198    RYLIVEKMRQTNHDKRAWEIDIVPGKG  224 (229)
T ss_pred              EEEEEEecCCCCCCcceEEEEEeCCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmt)

74. 3CMT_D (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMT) **PROTEIN recA/DNA Complex; homolc binding, DNA damage; HET: ALF, ADP, MG; 3.15A {Escherichia coli}**

Probability: 98.73 E-value: 1.9E-9 Score: 125.29 Aligned Cols: 198 Identities: 13% Similarit

```
Q ss_pred                CCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft     113    MPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus       113    ~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                         .+.+++++. ++++.|..++|+|+||+|||+|+..++..+..         .+.+|+|+
T Consensus       1416   ~~~ld~~l~~gGl~~g~~~~l~G~~g~GKT~l~~~~a~~~~~---------~~~~v~~i
T 3CMT_D          1416   SLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFI
T ss_dssp                CHHHHHHTSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHHT---------TTCCEEEE
T ss_pred                cHHHHHHhcCCCccCCeEEEEECCCCCcHHHHHHHHHHHHHH---------CCCeEEEE

Q ss_pred                HHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHc----
Q Klein_Draft     182    INAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCT----
Q Consensus       182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~----
                         ...+....      ..+.+...  .........+...++..++++||||++..+.
T Consensus       1476   ~~~~g~~~------~~~~~~~~--~~~~~~~~~~~~~~~~~~~lvviD~l~~~~~~~~
T 3CMT_D          1476   ARKLGVDI------DNLLCSQP--DTGEQALEICDALARSGAVDVIVVDSVAALTPKAE
T ss_dssp                HHHTTCCG------GGCEEECC--SSHHHHHHHHHHHHHHTCCSEEEESCSTTCCCHHH
T ss_pred                HHHcCCCh------hhEEEECC--CCHHHHHHHHHHHHHcCCceEEEEcChhHhCcHHH

Q ss_pred                HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhccccEEEE
Q Klein_Draft     245    RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGVDTVYF
Q Consensus       245    ~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~~d~vi~
                         .....+.+.+..|..++.+++++|++++|.++..       ....|+.++...++..+.
T Consensus       1538   ~~~~~~~~~l~~l~~~~~~~~~~vi~~~q~~~~~~~~~~~~~~~~g~~~~~~~~~~~~~
T 3CMT_D          1538   LAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLD
T ss_dssp                HHHHHHHHHHHHHHHHHHHHHTCEEEEEECEEECSSCCSSCCEEESSCSHHHHHEEEEEE
T ss_pred                HHHHHHHHHHHHHHHHHHHcCEEEEEEecccccCCccCCCCcccccchHHHHHHhEEeEE

Q ss_pred                -----cEEEEEeeecCCCCCCeeEEEEEecC
Q Klein_Draft     302    -----GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus       302    -----~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                              .+.+.+.|+|.++......|.+....+
T Consensus       1608   ~~~g~~~~~~v~K~r~~~~~~~~~~~~~~~~g  1639 (1706)
T 3CMT_D          1608   NVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  1639 (1706)
T ss_dssp                EEEEEEEEEEEEEEESSSCSCCEEEEEEETTTE
T ss_pred                ceeceeEEEEEEeCCCCCCceEEEEEEeeCCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmt)

75. 3CMT_D (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMT) **PROTEIN recA/DNA Complex; homolc binding, DNA damage; HET: ALF, ADP, MG; 3.15A {Escherichia coli}**

Probability: 98.73 E-value: 1.4E-9 Score: 126.56 Aligned Cols: 194 Identities: 14% Similarit

```
Q ss_pred                CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft     114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus       114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                         |.+++++. +++++|.+++|+|+||+|||+|+.+++..++.         .+.+|+|++
T Consensus       20     ~~lD~~l~~gGl~~g~~~~i~G~~GsGKT~la~~la~~~~~---------~~~~vlyi~
T 3CMT_D          20     LSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFID
T ss_dssp                HHHHHHTSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHHT---------TTCCEEEEC
T ss_pred                HHHHHHHhcCCcCCCcEEEEECCCCCCHHHHHHHHHHHHH---------CCCeEEEEE

Q ss_pred                HHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCc-
Q Klein_Draft     183    NAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAE-
Q Consensus       183    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~~-
                         ..+..        ....+.............+...+...++++||||+++.++....
```

```
T Consensus     80    ~~~~~--------~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lvvIDsl~~l~~~~~~
T 3CMT_D        80    RKLGV--------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAEI
T ss_dssp             HHTTC--------CTTTCEEECCSSHHHHHHHHHHHHHHTCCSEEEESCSTTCCCHHHH
T ss_pred             HHcCC--------chhheeeeCCCCHHHHHHHHHHHHHcCCceEEEEeCccccCChhHH

Q ss_pred             HHHHHHHHHHHHHHhcCCCCeEEEEEccCCCC-------CCCCCCchhHhccccEEEEE
Q Klein_Draft   246   DVGIVIDSMTRLMDATPDHRGCVLGIHHTGKD-------EKTLRGSSAYEGGVDTVYFV
Q Consensus     246   ~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~-------~~~~~Gs~~~~~~~d~vi~l
                      ....+...+..|..++++++++|++++|.++.       .....++..+...++..+.+
T Consensus     142   ~~~~~~~~~~~L~~~a~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~l
T 3CMT_D        142   AARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDI
T ss_dssp             HHHHHHHHHHHHHHHHHHHHTCEEEEEECEEECSSCCSSCCEEESSCSHHHHHEEEEEEE
T ss_pred             HHHHHHHHHHHHHHHHHHhcCcEEEEEeccccccCcccCCcccCCCcchhheeeeEEEEE

Q ss_pred             ----cEEEEEeeecCCCCCCCeeEEEEE
Q Klein_Draft   302   ----GITLTCKKQKDAPEGDRHTLRLQP  325 (416)
Q Consensus     302   ----~~~l~~~K~r~~~~~~~~~~~~~~  325 (416)
                          .+.+...|.|..+......|.+..
T Consensus     212   ~~~~~~~~~i~k~~~~~~~~~~~~~~~~  239 (1706)
T 3CMT_D        212   VVGSETRVKVVKNKIAAPFKQAEFQILY  239 (1706)
T ss_dssp             EEEEEEEEEEEEESSSCSCCEEEEEEET
T ss_pred             eecceEEEEEecCCCCCceEEEEEec
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmv)

76. **3CMV_F (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMV) PROTEIN recA; homologous recombir MG; 4.3A {Escherichia coli}**

Probability: 98.73 E-value: 1.8E-9 Score: 122.85 Aligned Cols: 198 Identities: 15% Similarit

```
Q ss_pred             CCCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEE
Q Klein_Draft   112   NMPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLY
Q Consensus     112   ~~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~
                      ..+.+++++. ++++.|..++|+|+|+||+|||+|+..++..+..         .+.+|+|
T Consensus     367   g~~~ld~~l~~gg~~~g~~~ll~G~~G~GKT~l~~~la~~~~~~~~~~~~~~~~vl~
T 3CMV_F        367   GSLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAF
T ss_dssp             SCHHHHHHHSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHHT---------TTCCCEE
T ss_pred             CcHHHHHHhcCCCccCCeEEEEECCCCCCHHHHHHHHHHHHH---------CCCeEEE

Q ss_pred             HHHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCC
Q Klein_Draft   180   SRINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVG
Q Consensus     180   ~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~
                      .+....          ....+.............+...++..++++||||++..+...
T Consensus     428   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~llviD~i~~l~~~
T 3CMV_F        428   ARKLGV----------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPK
T ss_dssp             HHHHTC----------CGGGCEEECCSSHHHHHHHHHHHHTTSSCCEEEEECGGGCCCH
T ss_pred             HHHcCC----------CcccEEEeCCCCHHHHHHHHHHHHhcCCceEEEEecccccCCH

Q ss_pred             CHHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCC-------CCCCCchhHhccccEE
Q Klein_Draft   243   SARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGVDTV
Q Consensus     243   ~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~~Gs~~~~~~~d~v
                      .......+...+..|..++.+++++|++++|.++..       ....|+..+...++.+
T Consensus     488   ~~~~~~~~~~~l~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 3CMV_F        488   MGLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVR
T ss_dssp             SSCTTHHHHHHHHHHHHHHHTTTCEEEEEEC----------------CCTTHHHHCSEE
T ss_pred             hHHHHHHHHHHHHHHHHHHhcCEEEEEEecccccCcccCCCCcccCCCchheeeEEEE

Q ss_pred             -------cEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   302   -------GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
```

```
Q Consensus     302    --------~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                              .+.+...|++..+....+.|.+....+
T Consensus     558    ~~~~~~~~~~i~i~k~~~~~~~~~~~~~~~~~~~  591 (1357)
T 3CMV_F        558    GENVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  591 (1357)
T ss_dssp              TTEECEEEEEEEEEEESSSCTTCEEEEEEETTTE
T ss_pred              CcceEeeEEEEEEEeCccCCCceEEEEEEecCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmv)

77. **3CMV_F (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMV) PROTEIN recA; homologous recombir MG; 4.3A {Escherichia coli}**

Probability: 98.73 E-value: 1.4E-9 Score: 123.62 Aligned Cols: 192 Identities: 15% Similarit

```
Q ss_pred              CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       |.+++++. ++++.|..++|+|+||+|||+|+..++..+..         .+.+|+|++
T Consensus     20     ~~ld~~l~~gg~~~g~~~li~G~~G~GKT~l~~~l~~~~~~---------~~~~v~~i~
T 3CMV_F        20     LSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFID
T ss_dssp              HHHHHHHSSSSEETTSEEEEECSSSSSHHHHHHHHHHHHHT---------TSCCEEEEE
T ss_pred              HHHHHHhccCCCCCCcEEEEECCCCCCHHHHHHHHHHHHHH---------cCCEEEEEe

Q ss_pred              HHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCc
Q Klein_Draft   182    INAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAE
Q Consensus     182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~
                       ...+....          +.............+.+.++..++++||||+++.++....
T Consensus     81     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~liiiD~i~~~~~~~~
T 3CMV_F        81     KLGVDIDN----------LLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAE
T ss_dssp              HHTCCGGG----------EEEECCSSHHHHHHHHHHHHHSSSCCEEEEECGGGCCCHHH
T ss_pred              HcCCChhh----------eEEeCCCCHHHHHHHHHHHHHcCCcEEEEEeCccccCCHHH

Q ss_pred              HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCC-------CCCchhHhccccEEEE
Q Klein_Draft   245    RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT-------LRGSSAYEGGVDTVYF
Q Consensus     245    ~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~~Gs~~~~~~~d~vi~
                       .....+.+.+..|...+.+++++|++++|.++....       ..|+..+...++..+.
T Consensus     141    ~~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 3CMV_F        141    LAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLD
T ss_dssp              SHHHHHHHTTHHHHHTTTTTTCEEEEEEC----------------CCTTHHHHEEEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHhcCEEEEEEecccccCCCcCCCCcccCCcchhheeEEEEEE

Q ss_pred              ----CcEEEEEeeecCCCCCCCeeEEEE
Q Klein_Draft   301    ----NGITLTCKKQKDAPEGDRHTLRLQ  324 (416)
Q Consensus     301    ----~~~~l~~~K~r~~~~~~~~~~~~~  324 (416)
                           ..+.+...|.|..+....+.|.+.
T Consensus     211    ~~~~~~~~~~~~k~~~~~~~~~~~~~~~  238 (1357)
T 3CMV_F        211    NVVGSETRVKVVKNKIAAPFKQAEFQIL  238 (1357)
T ss_dssp              CCCCCEEEEEEEEESSSCCSCEEEEEEE
T ss_pred              ceeeeEEEEEEEeCCCCCCceEEEEEEe
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmw)

78. **3CMW_C (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMW) PROTEIN recA/DNA Complex; homo recombination-DNA COMPLEX; HET: ALF, ADP, MG; 2.8A {Escherichia coli}**

Probability: 98.72 E-value: 2.1E-9 Score: 124.97 Aligned Cols: 198 Identities: 13% Similarit

```
Q ss_pred              CCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   113    MPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     113    ~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       .+.+++++. ++++.|..+.|+|+||+|||+|+..++..+..         .+++|+|+
```

```
T Consensus     1416   ~~~ld~~l~~gG~~~g~~~~l~G~~g~GKT~l~~~~a~~~~~~~~~~~~~~~~v~~i
T 3CMW_C        1416   SLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFI
T ss_dssp              CHHHHHHTSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHHH---------TTCCEEEE
T ss_pred              cHHHHHHhcCCCccCCeEEEEECCCCCcHHHHHHHHHHHHHH---------CCCeEEEE

Q ss_pred              HHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHc----
Q Klein_Draft   182    INAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCT----
Q Consensus     182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~----
                       ...+....      ..+.+...  .........+...++..++++||||++..+.
T Consensus     1476   ~~~~g~~~~------~~~~~~~~~--~~~~~~~~~~~~~~~~~~~~lvviD~l~~l~~~~~
T 3CMW_C        1476   ARKLGVDI------DNLLCSQP--DTGEQALEICDALARSGAVDVIVVDSVAALTPKAE
T ss_dssp              HHHTTCCG------GGCEEECC--SSHHHHHHHHHHHHHHTCCSEEEESCSTTCCCTTT
T ss_pred              HHHcCCCh------hhEEEECC--CCHHHHHHHHHHHHHcCCceEEEEeChhHhCcHHH

Q ss_pred              HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhccccEEEE
Q Klein_Draft   245    RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGVDTVYF
Q Consensus     245    ~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~~d~vi~
                       .....+...+..|..++.+++++|++++|.++..       ...+|+.++...++..+.
T Consensus     1538   ~~~~~~~~~l~~l~~~~~~~~~~vi~~~q~~~~~~~~~~~~~~~~gg~~~~~~~~~~~~
T 3CMW_C        1538   LAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLD
T ss_dssp              HHHHHHHHHHHHHHHHHHHHHTCEEEEEECBC--------CCCCBSSCSHHHHHEEEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHcCEEEEEEecccccCCccCCCCCcccChHHHHHHHeeeEE

Q ss_pred              -----cEEEEEeeecCCCCCCeeEEEEEecC
Q Klein_Draft   302    -----GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     302    -----~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                            .+.+.+.|+|.++......|.+....+
T Consensus     1608   ~~~g~~~~~~v~K~r~~~~~~~~~~~l~~~~g  1639 (1706)
T 3CMW_C        1608   NVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  1639 (1706)
T ss_dssp              EEEEEEEEEEEEEEEESSSCSCCEEEEEEETTTE
T ss_pred              ceeceeEEEEEEeCCCCCCceEEEEEEecCCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmu)

79. **3CMU_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMU) PROTEIN recA/DNA Complex; homol**
recombination-DNA COMPLEX; HET: ADP, ALF; 4.2A {Escherichia coli}

Probability: 98.72 E-value: 2.1E-9 Score: 126.98 Aligned Cols: 195 Identities: 15% Similarit

```
Q ss_pred              CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       +.+++++. +++++|.++.|+|+||+|||+|+.+++.....         .+.+|+|++
T Consensus     1067   ~~lD~~l~~gG~~~g~~~~i~G~~g~GKT~la~~~a~~~~~~~~~~~~~~~~vlyi~
T 3CMU_A        1067   LSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFID
T ss_dssp              HHHHHHHSSSSEETTSEEEEECCTTSSHHHHHHHHHHHHHT---------TTCCEEEEC
T ss_pred              HHHHHHhcCCCccCCcEEEEECCCCCCHHHHHHHHHHHHH---------CCCeEEEEe

Q ss_pred              HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181    RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                       .+.           .....++.............+...++..++++||||+++.+....
T Consensus     1128   ~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~i~~~~~~~~~~lvviDsl~~l~~~~
T 3CMU_A        1128   KLG-----------VDIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKA
T ss_dssp              HTT-----------CCTTTCEEECCSSHHHHHHHHHHHHHHTCCSEEEESCGGGCCCHH
T ss_pred              HcC-----------CCccceEEeCCCCHHHHHHHHHHHHcCCCcEEEEeCchhcCCHH

Q ss_pred              HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhccccEEEE
Q Klein_Draft   244    ARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGVDTVY
```

```
Q Consensus     244    ~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~~d~vi
                       ......+...+..|..++.+++++|++++|.++..       ....|+..+...++.++
T Consensus     1187   ~~~~~~~~~~~~~L~~~a~~~~~~vi~~~q~~~~~~~~~~~~~~~gg~~~~~~~~~~i
T 3CMU_A        1187   GLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRL
T ss_dssp              THHHHHHHHHHHHHHHHHHTTTCEEEEEECCEECTTCCSSCCEECSSHHHHHHHEEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHHhCeEEEEEeccccCCccCCCCcccCCcHHHheeEEEE

Q ss_pred              ------cEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   302    ------GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     302    ------~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                             .+.+...|+|..+......|.+....+
T Consensus     1257   ~~~~~~~~~~~i~K~r~~~~~~~~~~~~~~~~g  1289 (2050)
T 3CMU_A        1257   ENVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  1289 (2050)
T ss_dssp              TEEEEEEEEEEEEEESSSCSCCEEEEEEETTTE
T ss_pred              ceeEeeEEEEEEEeCCCCCCccEEEEEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmu)

80. **3CMU_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMU) PROTEIN recA/DNA Complex; homol**
recombination-DNA COMPLEX; HET: ADP, ALF; 4.2A {Escherichia coli}

Probability: 98.67 E-value: 3.7E-9 Score: 124.92 Aligned Cols: 196 Identities: 15% Similarit

```
Q ss_pred              CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       +.++.++. +++++|.++.|+|++|+|||+|+..++..+..         .+.+|+|++
T Consensus     718    ~~lD~~l~~GGl~~g~~~~i~G~~g~GKT~l~~~la~~~~~~~~~~~~~~~~vl~i~
T 3CMU_A        718    LSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFID
T ss_dssp              HHHHHHHSSSSEETTSEEEEECCTTSSHHHHHHHHHHHHHT---------TTCCEEEEC
T ss_pred              HHHHHHhcCCccCCeEEEEECCCCCcHHHHHHHHHHHHHH---------CCCeEEEEE

Q ss_pred              HHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCc
Q Klein_Draft   182    INAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAE
Q Consensus     182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~
                       ........          +..............+...+...++++||||++..++....
T Consensus     779    ~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~lvviDsl~~l~~~~~
T 3CMU_A        779    KLGVDIDN----------LLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAE
T ss_dssp              HTTCCTTT----------CEEECCSSHHHHHHHHHHHHHHTCCSEEEESCGGGCCCHHH
T ss_pred              HcCCCHHH----------eEEeCCCCHHHHHHHHHHHHhcCCceEEEEeCchhcCChhH

Q ss_pred              HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCC-------CCCchhHhccccEEEE
Q Klein_Draft   245    RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT-------LRGSSAYEGGVDTVYF
Q Consensus     245    ~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~~~Gs~~~~~~~d~vi~
                       .....+.+.+..|..++++++++|++++|..+....       ..|+..+...++.++.
T Consensus     839    ~~~~~~~~~l~~L~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~gg~~~~~~~~~~l~
T 3CMU_A        839    LAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLD
T ss_dssp              HHHHHHHHHHHHHHHHHHHTTTCEEEEEECCEECTTCCSSCCEECSSHHHHHHHEEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHhCeEEEEEeccccCCCCCCCcccCCccHHheeeEEEEE

Q ss_pred              -----cEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   302    -----GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     302    -----~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                            .+.+...|+|..+......|.+....+
T Consensus     909    ~~~~~~~~~~v~K~r~~~~~~~~~~~~~~~~~  940 (2050)
T 3CMU_A        909    NVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  940 (2050)
T ss_dssp              EEEEEEEEEEEEEESSSCSCCEEEEEEETTTE
T ss_pred              eEeceEEEEEEEecCCCCCCcEEEEEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmt)

81. **3CMT_D (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMT) PROTEIN recA/DNA Complex; homolc binding, DNA damage; HET: ALF, ADP, MG; 3.15A {Escherichia coli}**

Probability: 98.66 E-value: 3.7E-9 Score: 122.96 Aligned Cols: 197 Identities: 15% Similarit

```
Q ss_pred                CCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft     113    MPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus       113    ~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                         .+.++.++. +++++|.++.|+|+||+|||+|+.+++..+..         .+.+|+|+
T Consensus       717    ~~~lD~~l~~gGl~~g~~~~i~G~~g~GKT~la~~~~~~~~~~---------~~~~vl~i
T 3CMT_D          717    SLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFI
T ss_dssp                CHHHHHHTSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHHT---------TTCCEEEE
T ss_pred                CHHHHHHhcCCCccCCeEEEEECCCCCCHHHHHHHHHHHHHH---------CCCeEEEE

Q ss_pred                HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft     181    RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus       181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                         +....          ....+.............+...++..++++||||++..+....
T Consensus       778    ~~~~~---------~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lvviDsi~~l~~~~
T 3CMT_D          778    RKLGV----------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKA
T ss_dssp                HHTTC----------CGGGCEEECCSSHHHHHHHHHHHHHHTCCSEEEESCSTTCCCHH
T ss_pred                HHcCC----------CcccceEEeCCCCHHHHHHHHHHHHcCCceEEEEeCchhcCCHH

Q ss_pred                HHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhccccEEE
Q Klein_Draft     244    ARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGVDTVY
Q Consensus       244    ~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~~d~vi
                         ......+...+..|..+++++++++++|..+..       ....|+..+...++..+
T Consensus       838    ~~~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 3CMT_D          838    GLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRL
T ss_dssp                THHHHHHHHHHHHHHHHHHHHTCEEEEEECEEECSSCCSSCCEEESSCSHHHHHEEEEE
T ss_pred                HHHHHHHHHHHHHHHHHHHHcCeEEEEEecccccCCccCCCcccccCCchhheeeEEEE

Q ss_pred                ------cEEEEEeeecCCCCCCeeEEEEEecC
Q Klein_Draft     302    ------GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus       302    ------~~~l~~~K~r~~~~~~~~~~~~~~~~  328 (416)
                               .+.+...|+|..+.....+.+....+
T Consensus       908    ~~~~~~~~~~~i~k~r~~~~~~~~~~~~~~~~g  940 (1706)
T 3CMT_D          908    ENVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  940 (1706)
T ss_dssp                TEEEEEEEEEEEEEESSSCSCCEEEEEEETTTE
T ss_pred                cceeceeEEEEEEcCCCCCCccEEEEEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmw)

82. **3CMW_C (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMW) PROTEIN recA/DNA Complex; homo recombination-DNA COMPLEX; HET: ALF, ADP, MG; 2.8A {Escherichia coli}**

Probability: 98.66 E-value: 2.5E-9 Score: 124.36 Aligned Cols: 193 Identities: 15% Similarit

```
Q ss_pred                CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft     114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus       114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                         |.+++++. +++++|.+++|+|+||+|||+|+.+++..++.         ...+|+|++
T Consensus       20     ~~lD~~l~~gGl~~g~~~~i~G~~GsGKT~l~~~la~~~~~---------~~~~vlyi~
T 3CMW_C          20     LSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFID
T ss_dssp                HHHHHHTSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHHH---------TTCCEEEEC
T ss_pred                HHHHHHHhcCCcCCCcEEEEECCCCCCHHHHHHHHHHHHHH---------CCCeEEEEE

Q ss_pred                HHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCcc
Q Klein_Draft     183    NAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAEE
```

```
Q Consensus     183    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~~
                       ..+..        ....+.............+...+...++++||||+++.++.....
T Consensus     80     ~~~~~--------~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~livIDsl~~l~~~~~~
T 3CMW_C        80     RKLGV--------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAEI
T ss_dssp              HHTTC--------CGGGCEEECCSSHHHHHHHHHHHHHHTCCSEEEESCSTTCCCHHHH
T ss_pred              HHcCC--------CHHheEEeCCCCHHHHHHHHHHHHcCCceEEEEeCchhcCChhHH

Q ss_pred              HHHHHHHHHHHHHHHcCCCCeEEEEEccCCCC-------CCCCCCchhHhccccEEEEE
Q Klein_Draft   246    DVGIVIDSMTRLMDATPDHRGCVLGIHHTGKD-------EKTLRGSSAYEGGVDTVYFV
Q Consensus     246    ~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~-------~~~~~Gs~~~~~~~d~vi~l
                       ....+...+..|..++++++++|++++|.++.       .....++..+...++..+.+
T Consensus     142    ~~~~~~~~~~~L~~~a~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~l
T 3CMW_C        142    AARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDI
T ss_dssp              HHHHHHHHHHHHHHHHHHHTCEEEEEECEEECTTCCSSCCEEESSCSHHHHHEEEEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHcCcEEEEEeccccccCcccCCCccccCCCchhceeeeEEEEE

Q ss_pred              --CCcEEEEEeeecCCCCCCCeeEEEE
Q Klein_Draft   300    --GNGITLTCKKQKDAPEGDRHTLRLQ  324 (416)
Q Consensus     300    --~~~~~l~~~K~r~~~~~~~~~~~~~  324 (416)
                         ...+.+...|.|..+......|.+.
T Consensus     212    ~~~~~~~~~i~k~~~~~~~~~~~~~~~  238 (1706)
T 3CMW_C        212    VVGSETRVKVVKNKIAAPFKQAEFQIL  238 (1706)
T ss_dssp              EEEEEEEEEEEEESSSCSCCEEEEEEE
T ss_pred              eecceEEEEEecCCCCCceEEEEEEe
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmw)

83. **3CMW_C (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMW) PROTEIN recA/DNA Complex; homo recombination-DNA COMPLEX; HET: ALF, ADP, MG; 2.8A {Escherichia coli}**

Probability: 98.66 E-value: 4.1E-9 Score: 122.65 Aligned Cols: 197 Identities: 15% Similarit

```
Q ss_pred              CCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHcCCCCCCCCCCCcEEEE
Q Klein_Draft   113    MPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     113    ~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       .+.++.++. +++++|.++.|+|+||+|||+|+..++..+..         .+.+|+|+
T Consensus     717    ~~~lD~~l~~gG~~~g~~~~i~G~~g~GKT~l~~~~~~~~~~~~~~~~~~~~~~~~vl~i
T 3CMW_C        717    SLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFI
T ss_dssp              CHHHHHHTSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHHH---------TTCCEEEE
T ss_pred              CHHHHHHHhcCCccCceEEEEECCCCCCHHHHHHHHHHHHHH---------CCCeEEEE

Q ss_pred              HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181    RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~
                       +...+          ....+.............+...++..++++||||++..+....
T Consensus     778    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~vviDsl~~l~~~~
T 3CMW_C        778    RKLGV----------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKA
T ss_dssp              HHTTC----------CGGGCEEECCSSHHHHHHHHHHHHHHTCCSEEEESCSTTCCCHH
T ss_pred              HHcCC----------CccceEEeCCCCHHHHHHHHHHHHcCCceEEEEechhhcCCHH

Q ss_pred              HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhccccEEE
Q Klein_Draft   244    ARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGVDTVY
Q Consensus     244    ~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~~d~vi
                       ......+...+..|..+++++++++++++|..+..       ....|+..+...++..+
T Consensus     838    ~~~~~~~~~~~~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 3CMW_C        838    GLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRL
T ss_dssp              THHHHHHHHHHHHHHHHHHHHTCEEEEEECEEECTTCCSSCCEEESSCSHHHHHEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHHcCeEEEEEecccccCCcccCCCceeccCcchhceeeEEEE
```

```
Q ss_pred              ------cEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   302    ------GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     302    ------~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                             .+.+...|+|..+......+.+....+
T Consensus     908    ~~~~~~~~~~~i~k~r~~~~~~~~~~~~~~~~g  940 (1706)
T 3CMW_C        908    ENVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  940 (1706)
T ss_dssp              TEEEEEEEEEEEEEESSSCSCCEEEEEEETTTE
T ss_pred              cceeceEEEEEEEcCCCCCCCcEEEEEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmu)

84. **3CMU_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMU) PROTEIN recA/DNA Complex; homol recombination-DNA COMPLEX; HET: ADP, ALF; 4.2A {Escherichia coli}**

Probability: 98.66 E-value: 4.8E-9 Score: 123.95 Aligned Cols: 194 Identities: 14% Similarit

```
Q ss_pred              CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       |.+++++. +++++|.+++|+|+||+|||+|+.+++..++.         .+.+|+|++
T Consensus     20     ~~lD~~l~~gGi~~g~~~lI~G~~GsGKT~la~~la~~~~~~~~~~~~~~~~vl~i~
T 3CMU_A        20     LSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFID
T ss_dssp              HHHHHHHSSSSEETTSEEEEECCTTSSHHHHHHHHHHHHHT---------TTCCEEEEC
T ss_pred              HHHHHHHhcCCCCCCcEEEEECCCCCCHHHHHHHHHHHHHH---------CCCeEEEEE

Q ss_pred              HHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCc-
Q Klein_Draft   183    NAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAE-
Q Consensus     183    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~-
                       ..+..        ....+.............+...+...++++||||+++.++....
T Consensus     80     ~~~~~-------~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~livID~l~~l~~~~~~
T 3CMU_A        80     RKLGV--------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAEI
T ss_dssp              HHTTC--------CTTTCEEECCSSHHHHHHHHHHHHHHTCCSEEEESCGGGCCCHHHH
T ss_pred              HHhcc--------ChhheEeeCCCCHHHHHHHHHHHHhcCCceEEEEeChhhhcChhHh

Q ss_pred              HHHHHHHHHHHHHHHcCCCCeEEEEEccCCCC-------CCCCCCchhHhccccEEEEE
Q Klein_Draft   246    DVGIVIDSMTRLMDATPDHRGCVLGIHHTGKD-------EKTLRGSSAYEGGVDTVYFV
Q Consensus     246    ~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~-------~~~~~Gs~~~~~~~d~vi~l
                       ....+...+..|..++.+++++|++++|.++.       ...+.++..+...++.++.+
T Consensus     142    ~~~~~~~l~~~L~~l~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~l
T 3CMU_A        142    AARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLDI
T ss_dssp              HHHHHHHHHHHHHHHHHHTTTCEEEEEECCEECTTCCSSCCEECSSHHHHHHHEEEEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHhCCEEEEEeccccccccccCCCccccCCcccceecceEEEEE

Q ss_pred              -----EEEEEeeecCCCCCCCeeEEEEE
Q Klein_Draft   303    -----ITLTCKKQKDAPEGDRHTLRLQP  325 (416)
Q Consensus     303    ------~~l~~~K~r~~~~~~~~~~~~~  325 (416)
                            +.+...|.|..+......|.+..
T Consensus     212    ~~~~~~~i~~~k~r~~~~~~~~~~~~~  239 (2050)
T 3CMU_A        212    VVGSETRVKVVKNKIAAPFKQAEFQILY  239 (2050)
T ss_dssp              EEEEEEEEEEEEESSSCSCCEEEEEEET
T ss_pred              eecceEEEEEEecCCCCCccEEEEEEEe
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmu)

85. **3CMU_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMU) PROTEIN recA/DNA Complex; homol recombination-DNA COMPLEX; HET: ADP, ALF; 4.2A {Escherichia coli}**

Probability: 98.64 E-value: 4.7E-9 Score: 124.08 Aligned Cols: 197 Identities: 15% Similarit

```
Q ss_pred              CCCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   113    MPKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYV
```

```
Q Consensus     113    ~~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       .+.+++++. +++++|.+++|+|+||+|||+|+..++.....         .+.+|+|+
T Consensus     368    ~~~lD~~l~~gG~~~g~~~~i~G~~GsGKT~la~~la~~~~~---------~~~~v~~i
T 3CMU_A        368    SLSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFI
T ss_dssp              CHHHHHHHSSSSEETTSEEEEECCTTSSHHHHHHHHHHHHHT---------TTCCEEEE
T ss_pred              CHHHHHHhcCCCccCCcEEEEECCCCCCHHHHHHHHHHHHH---------CCCeEEEE

Q ss_pred              HHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCC
Q Klein_Draft   181    RINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGA
Q Consensus     181    rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~
                       +...+          ....++.............+...++..++++||||+++.+....
T Consensus     429    ~~~~~----------~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~liviDsl~~l~~~~
T 3CMU_A        429    RKLGV----------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKA
T ss_dssp              HHTTC----------CTTTCEEECCSSHHHHHHHHHHHHHHTCCSEEEESCGGGCCCHH
T ss_pred              HHcCC----------CcccEEEeCCCCHHHHHHHHHHHHcCCCeEEEEeCchhcCCHH

Q ss_pred              HHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCC-------CCCCCchhHhccccEEE
Q Klein_Draft   244    ARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDE-------KTLRGSSAYEGGVDTVY
Q Consensus     244    ~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~-------~~~~Gs~~~~~~~d~vi
                       ......+...+..|..++++++++|++++|..+..       ....|+..+...++..+
T Consensus     489    ~~~~~~~~~~l~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i
T 3CMU_A        489    GLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRL
T ss_dssp              THHHHHHHHHHHHHHHHHHHTTTCEEEEEECCEECTTCCSSCCEECSSHHHHHHHEEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHHHhCeEEEEEecccccccCccCCCCccccCccHHhheeEEEE

Q ss_pred              ------cEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   302    ------GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     302    ------~~~l~~~K~r~~~~~~~~~~~~~~~~  328 (416)
                             .+.+...|+|..+......|.+....+
T Consensus     559    ~~~~~~~~~~i~K~r~~~~~~~~~~~~~~~~g  591 (2050)
T 3CMU_A        559    ENVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  591 (2050)
T ss_dssp              TEEEEEEEEEEEEEESSSCSCCEEEEEEETTTE
T ss_pred              CceeeeEEEEEEEecCCCCCCcEEEEEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmt)

86. **3CMT_D (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMT) PROTEIN recA/DNA Complex; homolc binding, DNA damage; HET: ALF, ADP, MG; 3.15A {Escherichia coli}**

Probability: 98.63 E-value: 6.1E-9 Score: 121.25 Aligned Cols: 196 Identities: 15% Similarit

```
Q ss_pred              CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       +.+++++. ++++.|.+++|+|+||+|||+|+..++..+.+..         .+.+|+|++
T Consensus     369    ~~lD~~l~~gG~~~g~~~~i~G~~G~GKT~l~~~~a~~~~~---------~~~~v~~i~
T 3CMT_D        369    LSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFID
T ss_dssp              HHHHHHTSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHT---------TTCCEEEEC
T ss_pred              HHHHHHHhcCCccCCeEEEEECCCCCHHHHHHHHHHHHH---------CCCeEEEEe

Q ss_pred              HHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCc
Q Klein_Draft   182    INAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAE
Q Consensus     182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~
                       ....          ....+.............+...+...++++||||++..+.....
T Consensus     430    ~~~~----------~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~lviiDsl~~l~~~~~
T 3CMT_D        430    KLGV----------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAE
T ss_dssp              HTTC----------CGGGCEEECCSSHHHHHHHHHHHHHHTCCSEEEESCSTTCCCHHH
T ss_pred              HcCC----------CcccEEEeCCCCHHHHHHHHHHHHcCCCeEEEEechhHcCCHHH
```

```
Q ss_pred              HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCC-------CCCchhHhccccEEEE
Q Klein_Draft   245    RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT-------LRGSSAYEGGVDTVYF
Q Consensus     245    ~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~---------~~Gs~~~~~~~d~vi~
                       .....+...+..|..++++++++++++|..+....       ..|+..+...++..+.
T Consensus     490    ~~~~~~~~~l~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 3CMT_D        490    LAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLD
T ss_dssp              HHHHHHHHHHHHHHHHHHHHHTCEEEEEECEEECSSCCSSCCEEESSCSHHHHHEEEEEE
T ss_pred              HHHHHHHHHHHHHHHHHHHcCeEEEEEcCccccCCCcCCCCcccCCchHHheeEEEEE

Q ss_pred              -----cEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft   302    -----GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus     302    -----~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                            .+.+...|++..+.....+.+....+
T Consensus     560    ~~~~~~~~~~i~k~~~~~~~~~~~~~~~~~~~  591 (1706)
T 3CMT_D        560    NVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  591 (1706)
T ss_dssp              EEEEEEEEEEEEEESSSCSCCEEEEEEETTTE
T ss_pred              ceeceEEEEEEEeCCCCCCccEEEEEEecCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3bs4)

87. **3BS4_A (http://pdb.rcsb.org/pdb/explore.do?structureId=3BS4) Uncharacterized protein PH0321, Unkn GENOMICS, UNKNOWN FUNCTION, PSI-2; 1.6A {Pyrococcus horikoshii}**

Probability: 98.62 E-value: 1.1E-8 Score: 94.95 Aligned Cols: 195 Identities: 9% Similarity:

```
Q ss_pred              CCCcccccCcccCCCEEEEE-cCCCCCHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLY-GRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~-G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                       +.++.++. ++++|..++|. |++|+|||+|+..++.....         .+.+++|++
T Consensus     8      ~~LD~~L~-gi~~g~~vli~~g~~gsgk~~l~~~~~~~~l~~~~~~~~~~~~~vl~is
T 3BS4_A        8      EELDREIG-KIKKHSLILIHEEDASSRGKDILFYILSRKLK---------SDNLVGMFS
T ss_dssp              HHHHHHHC-CBCTTCEEEEEECSGGGCHHHHHHHHHHHHH---------TTCEEEEEE
T ss_pred              HHHHHHhC-CcccCCcEEEEEECCCCCCHHHHHHHHHHHHh---------cCCeEEEEe

Q ss_pred              HHHHHHHHcCcCcccCCEEEEecCcc------------------cCcHHHHHHHHHHH-
Q Klein_Draft   182    INAWETAWRQTLEEGSITFLPVPVN-----------------LMSQDVGALVEDIKD-
Q Consensus     182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-
                       +..+.........+.+.++.....                  ........+.+.++.
T Consensus     68     ~~~~~~~~~~~~~~~~l~i~d~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 3BS4_A        68     LSRFGVDVIKYLENHRLAIVDTFGSFHGIKATMPGVWYLEGMLSSETLPIKYAKAVEDH
T ss_dssp              HHHTTCCHHHHHHHTTSEEEECHHHHHHTC---CTTEECCCSCCCTTTHHHHHHHHHHHH
T ss_pred              HHHcCCCHHHHHHhCCEEEEECCccccCCCCCCCCeEEeccCCCccchhHHHHHHHHHH

Q ss_pred              Cc--EEEEeChHHHcCCCccCCHHHHHHHHHHHHHHHHcCC-------CCeEEEEEcc
Q Klein_Draft   224    FE--FIVLDTIARCTVGAEENSARDVGIVIDSMTRLMDATPD-------HRGCVLGIHH
Q Consensus     224    ~~--lviiD~l~~~~~~~~~n~~~~~~~~~~~l~~L~~~~~~-------~~~~vl~v~H
                       ..  ++|||+++.++.....      ..+.+.+..+...+++       .+++++++ |
T Consensus     138    ~~~~~vviD~l~~l~~~~~~-----~~~~~~l~~l~~~l~~~~~~~~~~~~~~i~~-~
T 3BS4_A        138    GRELYGFAISMSGYLEVFTP------EETLRYLETSAEVRYGHPAYKKYPRGTNFWL-W
T ss_dssp              TCCEEEEEETGGGGGGTSCH------HHHHHHHHHHHHHHHHCHHHHSSCCCEEEEE-E
T ss_pred              CCceEEEEEecchHHHhcCH------HHHHHHHHHHHHHHhcCccccCCCCcEEEEE-e

Q ss_pred              hhHhccccEEEEEEeCC-----cEEEEEeeecCCCCC-CCeeEEEEEec
Q Klein_Draft   285    SAYEGGVDTVYFVERGN-----GITLTCKKQKDAPEG-DRHTLRLQPID  327 (416
Q Consensus     285    ~~~~~~~d~vi~l~~~~-----~~~l~~~K~r~~~~~-~~~~~~~~~~~  327 (416
                       ..+...+|.++.+....     .+.+...|.+..... ..+.|.+...+
T Consensus     199    ~~l~~~ad~vi~l~~~~~~~~~~~l~v~K~~~~~~~~~~~~~~i~~~G  247 (260
T 3BS4_A        199    LSVYRRADYVLKTRSSLGENGIKRELLVIKTPKPIEELVRFEYEFKGNE  247 (260
T ss_dssp              HHHHHHCSEEEEEEEEEETTEEEEEEEEEECCC-----CEEEEEEETTE
T ss_pred              HHHHHhCCEEEEEeeeeccCceEEEEEEEecCCCcccccceEEEEEeCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmw)

88. **3CMW_C (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMW) PROTEIN recA/DNA Complex; homo recombination-DNA COMPLEX; HET: ALF, ADP, MG; 2.8A {Escherichia coli}**

Probability: 98.61 E-value: 7.4E-9 Score: 120.58 Aligned Cols: 196 Identities: 15% Similarit

```
Q ss_pred                CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft     114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus       114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                         +.++.++. +++++|.+++|+|+||+|||+|+..++..+..         .+.+|+|++
T Consensus       1068   ~~lD~~l~~gG~~~g~~~li~G~~G~GKT~l~~~~a~~~~~---------~~~~v~~i~
T 3CMW_C          1068   LSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFID
T ss_dssp                HHHHHHTSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHHH---------TTCCEEEEC
T ss_pred                HHHHHHhccCCccCCcEEEEECCCcCCHHHHHHHHHHHHHH---------CCCeEEEEe

Q ss_pred                HHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCc
Q Klein_Draft     182    INAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAE
Q Consensus       182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~
                         ....          ....+.............+...+...++++||||+++.+.....
T Consensus       1129   ~~~~----------~~~~i~~~~~~~~~~~~~~~~~~~~~~~lvviDsl~~l~~~~~
T 3CMW_C          1129   KLGV----------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAE
T ss_dssp                HTTC----------CGGGCEEECCSSHHHHHHHHHHHHHHTCCSEEEESCGGGCCCHHH
T ss_pred                HcCC----------CcccEEEEeCCCCHHHHHHHHHHHHcCCceEEEEeChhhcCCHHH

Q ss_pred                HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCC-------CCCchhHhccccEEEE
Q Klein_Draft     245    RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT-------LRGSSAYEGGVDTVYF
Q Consensus       245    ~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~-------~~Gs~~~~~~~d~vi~
                         .....+...+..|..++++++++|++++|..+....       ..|+..+...++..+.
T Consensus       1189   ~~~~~~~~~l~~L~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 3CMW_C          1189   LAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLD
T ss_dssp                HHHHHHHHHHHHHHHHHHHHTTCEEEEEECEEECTTCCSBCCEEESSCSHHHHHEEEEEE
T ss_pred                HHHHHHHHHHHHHHHHHHHHcCeEEEEEcCccccCCCcCCCCcccCCchHHheeEEEEEE

Q ss_pred                -----cEEEEEeeecCCCCCCCeeEEEEEecC
Q Klein_Draft     302    -----GITLTCKKQKDAPEGDRHTLRLQPIDG  328 (416)
Q Consensus       302    -----~~~l~~~K~r~~~~~~~~~~~~~~~~~  328 (416)
                              .+.+...|++..+.....+.+....+
T Consensus       1259   ~~~~~~~~~~i~k~~~~~~~~~~~~~~~~~g  1290 (1706)
T 3CMW_C          1259   NVVGSETRVKVVKNKIAAPFKQAEFQILYGEG  1290 (1706)
T ss_dssp                EEEEEEEEEEEEEESSSCSCCEEEEEEETTTE
T ss_pred                ceeeeEEEEEEEeCCCCCCceEEEEEEecCCc
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3cmv)

89. **3CMV_F (http://pdb.rcsb.org/pdb/explore.do?structureId=3CMV) PROTEIN recA; homologous recombir MG; 4.3A {Escherichia coli}**

Probability: 98.6 E-value: 9.4E-9 Score: 117.11 Aligned Cols: 192 Identities: 15% Similarity

```
Q ss_pred                CCCccccc-CcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEE
Q Klein_Draft     114    PKPEPLIE-GVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVV
Q Consensus       114    ~~~~~l~~-~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~
                         +.+++++. +.+++|..++|+|+||+|||+|+..++..+..         .+.+|+|++
T Consensus       718    ~~ld~~l~~gg~~~g~~~ll~G~~G~GKT~l~~~la~~~~~---------~~~~v~~i~
T 3CMV_F          718    LSLDIALGAGGLPMGRIVEIYGPESSGKTTLTLQVIAAAQR---------EGKTCAFID
T ss_dssp                HHHHHHHSSSSEETTSEEEEECSTTSSHHHHHHHHHHHHHT---------SSCCEEEEE
T ss_pred                HHHHHHHcCCCccCceEEEEECCCCCCHHHHHHHHHHHHH---------cCCeEEEEe
```

```
Q ss_pred              HHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCc
Q Klein_Draft   182    INAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAE
Q Consensus     182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~
                       ....          ....+.............+.+.++..++++||||+++.+.....
T Consensus     779    ~~~~----------~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~lviiD~i~~l~~~~~
T 3CMV_F        779    KLGV----------DIDNLLCSQPDTGEQALEICDALARSGAVDVIVVDSVAALTPKAE
T ss_dssp              HHTC----------CGGGCEEECCSCHHHHHHHHHHHHTTSCCCEEEEECGGGCCCHHH
T ss_pred              HhCC----------CCceEEEeCCCCHHHHHHHHHHHHHcCCcEEEEEeChHHhCCHHH

Q ss_pred              HHHHHHHHHHHHHHHHcCCCCeEEEEEccCCCCCCC-------CCCchhHhccccEEEE
Q Klein_Draft   245    RDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKT-------LRGSSAYEGGVDTVYF
Q Consensus     245    ~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~--------~~Gs~~~~~~~d~vi~
                       .....+...+..|...+..++++|++++|.++....       ..|+..+...++..+.
T Consensus     839    ~~~~~~~~~l~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T 3CMV_F        839    LAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETTTGGNALKFYASVRLD
T ss_dssp              CCCHHHHHTHHHHHHHTTTTTCEEEEEEC----------------CCTTHHHHEEEEEE
T ss_pred              HHHHHHHHHHHHHHHHHhcCEEEEEEecccccCCccCCCCccCCCCcccceeeEEEEEE

Q ss_pred              ----CcEEEEEeeecCCCCCCCeeEEEE
Q Klein_Draft   301    ----NGITLTCKKQKDAPEGDRHTLRLQ  324 (416)
Q Consensus     301    ----~~~~l~~~K~r~~~~~~~~~~~~~  324 (416)
                           ..+.+...|+|..+......|.+.
T Consensus     909    ~~~~~~~~~~~k~~~~~~~~~~~~~~~  936 (1357)
T 3CMV_F        909    NVVGSETRVKVVKNKIAAPFKQAEFQIL  936 (1357)
T ss_dssp              SEEEEEEEEEEEEESSSCCSCEEEEEEE
T ss_pred              eEeeeeEEEEEEecCCCCCccEEEEEEe
```

Template alignment

90. **TIGR02655 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR02655) circ_KaiC; circadia**
this family are the circadian clock protein KaiC, part of the kaiABC operon that controls circadian rhytl

Probability: 98.28 E-value: 5.4E-7 Score: 90.91 Aligned Cols: 196 Identities: 13% Similarity

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHcCCCCCCCCCC-CCcEEEEE
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETE-KVKVLYVV
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~-~~~Vl~i~
                       +.++.+..+.+++|+.++|+|++|+|||+|+..++.....         . ...++|++
T Consensus     8      ~~l~~~~~g~i~~g~~~~i~G~~gsGKt~l~~~~~~~~~~---------~~~~~~~~i~
T TIGR02655     8      EGFDDISHGGLPIGRSTLVSGTSGTGKTLFSIQFLYNGII---------HFDEPGVFVT
T ss_pred              ccccccccCCCCCCCEEEEEeCCCCCHHHHHHHHHHhhcc---------cCCCCeEEEe

Q ss_pred              HHHHHHHHcCcCccCCEEEEecCcc----------cCcHHHHHHHHHHHHhCCcEEEEe
Q Klein_Draft   182    INAWETAWRQTLEEGSITFLPVPVN----------LMSQDVGALVEDIKDYGFEFIVLD
Q Consensus     182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                       +...............++.......          .+......+...+....+.+++||
T Consensus     69     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T TIGR02655     69     ARSFGWDLQKLVDEGKLFILDASPDPEGQDVVGGFDLSALIERINYAIRKYKAKRVSID
T ss_pred              HHhcCCcHHHHhhcCCeeEeeCCCCcccccccccCCHHHHHHHHHHHHHhcCCcEEEEe

Q ss_pred              CCHHHHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeC
Q Klein_Draft   242    NSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERG
Q Consensus     242    n~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~
                           ........+..+...++..++++++++|.........+...+...+|.++.+...
T Consensus     138    ----~~~~~~~~~l~~l~~~~~~~~~~vi~~~~~~~~~~~~~~~~~~~~~d~~~~l~~~
T TIGR02655     138    ----AVSVVRREIFRLVARLKQIGVTTVMTTERIEEYGPIARYGVEEFVSDNVVILRNV
T ss_pred              ----chHHHHHHHHHHHHHHHHcCCEEEEEcCChhhcccccccCcchhheeEEEEEecc

Q ss_pred              EeeecCCCCC-CCeeEEE
```

```
Q Klein_Draft   307    CKKQKDAPEG-DRHTLRL  323 (416)
Q Consensus     307    ~~K~r~~~~~-~~~~~~~  323 (416)
                       ..|.+..... ....|.+
T Consensus     204    v~k~~~~~~~~~~~~~~i  221 (484)
T TIGR02655     204    ILKLRGTSHMKGEYPFTI  221 (484)
T ss_pred              EEeecCCCCCCceeEEEE
```

Template alignment

91. **TIGR00623 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR00623) sula; cell division i family for which the functions are known are cell division inhibitors.**

Probability: 98.26 E-value: 2.3E-7 Score: 80.14 Aligned Cols: 146 Identities: 8% Similarity:

```
Q ss_pred              CCCcccccCcccCCCEEEEEcCCC--CCHHHHHHHHHHHHHcCCCCCCCCCCCCcEEEE
Q Klein_Draft   114    PKPEPLIEGVFNRGSTALLYGRWG--TSKSFIALDWACSLATGRNWQGRETEKVKVLYV
Q Consensus     114    ~~~~~l~~~~l~~g~~~~i~G~~G--~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i
                       +.++.++.++++.|.++.|+|++|  +|||+|+..++..+..         .++.++|+
T Consensus     17     ~~~d~~l~gg~~~G~i~ei~G~~~~~~Gkt~l~l~l~~~~~~---------~~~~v~~I
T TIGR00623     17     RNVARNTTENKAAGLISEVVYREDQPMMAQLLLLPLLQQLGQ---------QSRWQLWL
T ss_pred              cchhhcCCCccCCeEEEEEecCCCccHHHHHHHHHHHHHcc---------CCCcEEEE

Q ss_pred              HHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHHHhCCcEEEEeChHHHcCCCc
Q Klein_Draft   182    INAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKDYGFEFIVLDTIARCTVGAE
Q Consensus     182    l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~lviiD~l~~~~~~~~
                       ..         .....-.+.............+.+.++...+.+||+|....+.
T Consensus     78     ~~---------~g~~~~ri~~v~~~~~~~~~~~~~~~l~~~~~~lVIid~~~~l~----
T TIGR00623     78     QS---------SGLPLTKVMQISQLSPCNTVESMIRALRTGNYSVVIGWLTDELT----
T ss_pred              HH---------cCCCHHhEEEEeCCCHHHHHHHHHHHHHHhCCceEEEEeCchHcC----

Q ss_pred              HHHHHHHHhcCCCCeEEEEEccCCCCCCCCCCchhHhccc
Q Klein_Draft   252    DSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGV  291 (416)
Q Consensus     252    ~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~  291 (416)
                       +.+++|...+++.+++++++.|..+.....|...+.-.+
T Consensus     125    ~~~rrL~~~a~~~~~~viiin~~~~~~~~~~~~~~~~~~~  164 (168)
T TIGR00623     125    EEHAKLVRAAEEGNAMGFIMRPVRAISPPHRQLSGLKIHS  164 (168)
T ss_pred              HHHHHHHHHHHHhcCcEEEEecCCCcCCCCcccCCccEEEe
```

Template alignment

92. **TIGR01194 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR01194) cyc_pep_trnsptr; c model describes cyclic peptide transporter in bacteria.**

Probability: 98.2 E-value: 1.5E-7 Score: 96.71 Aligned Cols: 196 Identities: 11% Similarity:

```
Q ss_pred              cccCCCCcCCCChH-----hhcccchhhhccccHHHhcCCCCcccccCc---ccCCC
Q Klein_Draft   78     AAVEAPVVVMPDPE-----TLRGVDSQFRSRFLSVSDIQNMPKPEPLIEGV---FNRGS
Q Consensus     78     ~~~~~~~~~~p~~~-----~l~~~~~~~~~~~~~~~~~~~~~~l~~~~---l~~g~
                       .....+....+...     ........+.++.++|.|........+.+.+.   +++|+
T Consensus     311    ~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~v~f~y~~~~~~~~~vL~~isl~i~~G~
T TIGR01194     311    FNEPEPELELSDADNVLLLAHDKSVDSIELKDVHMNPKAPEGSEGFALGPIDLRIAQGD
T ss_pred              cCCCCcccccCcchhhhhhccCCCCceeEEEeeEecCCCCCCCCcccccceEEEeCCc

Q ss_pred              HHHHHHHHHHHHHcCCCCCCCCCCCcEEEEECC------------------------
Q Klein_Draft   140    KSFIALDWACSLATGRNWQGRETEKVKVLYVVAE------------------------
Q Consensus     140    KStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~e------------------------
                       ||||+..+.+.+..         ..+.+.+-...
T Consensus     381    KstLl~~l~g~~~~~~~~~~~~G~i~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T TIGR01194     381    KSTLAKLFCGLYIP---------QEGEILLDGAAVSADSRDDYRDLFSAIFADFHLFDD
T ss_pred              HHHHHHHHhhccCC---------ccCceecCCCccCCCCHHHHHHHHHHHHccchhhcc
```

```
Q ss_pred             HHHHHHHHHHHcCcCccCCEEEEecCcccCcHHHHHHHHHHH--hCCcEEEEeChHHH
Q Klein_Draft   179   SSRINAWETAWRQTLEEGSITFLPVPVNLMSQDVGALVEDIKD--YGFEFIVLDTIARC
Q Consensus     179   ~~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~--~~~~lviiD~l~~~
                      ...+.......+..........-......++.++++++.+++.  .+++++++|++...
T Consensus     442   ~~~~~~~l~~~~~~~~~~~~~~~~~~~~lS~gq~~rl~laral~~~~~~~~lDe~~~~
T TIGR01194     442   LDNAQQYLQRLEIADKVKIEDGGFSTTTALSTGQQKRLALICAWLEDRPILLFDEWAAD
T ss_pred             HHHHHHHHHHcCccccceeecCCCCccccCCCHHHHHHHHHHHHHHhCCCEEEecccccC

Q ss_pred             HHHHHHHHHHHHHhcCCCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeCC
Q Klein_Draft   247   VGIVIDSMTRLMDATPDHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERGN  30
Q Consensus     247   ~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~~  30
                      .......+..+.+...+.++|+++++|...          ....+|.++.+..++
T Consensus     503   ~~~~~~~~~~~~~~~~~~~~~~i~~~h~~~~~~~~~~~~~~~~~d~~~~~~~g~  54
T TIGR01194     503   PAFKRFFYEELLPDLKRQGKTIIIISHDDQ----------YFELADQIIKLAAGC  54
T ss_pred             HHHHHHHHHHHHHHHHHhCCCEEEEEeCCHH----------HHHhcceEEEecCCc
```

Template alignment | CDD (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam05625)

93. **PF05625.10 (http://pfam.xfam.org/family/PF05625.10#tabview=tab0) ; PAXNEB ; PAXNEB protein**

Probability: 98.06 E-value: 6.2E-7 Score: 87.7 Aligned Cols: 192 Identities: 11% Similarity:

```
Q ss_pred             CCCcccccC--cccCCCEEEEEcCCCCC--HHHHHHHHHHHHHcCCCCCCCCCCCcEE
Q Klein_Draft   114   PKPEPLIEG--VFNRGSTALLYGRWGTS--KSFIALDWACSLATGRNWQGRETEKVKVL
Q Consensus     114   ~~~~~l~~~--~l~~g~~~~i~G~~G~G--KStl~~~la~~~~~g~~~~g~~~~~~~Vl
                      +.++.++.+  +++.|.+++|.| +|+|  ||+|++.++...+.         .+.+|+
T Consensus     24    ~~LD~ll~G~~Gi~~G~i~lI~~-~g~g~~Kt~l~~~~~~~~~~~~~~~~~~~~~~v~
T PF05625.10    24    ASLDALLAGHSGLALGCSILIEE-SGTTDYAGALLRFSAAEGLL---------QGHHVH
T ss_pred             HHHHHHHCCCCCccCCeEEEEeC-CCCChHHHHHHHHHHHHHh---------cCCeEE

Q ss_pred             HHHHHHHHHHc-------------------CcCcc------------------------
Q Klein_Draft   180   SRINAWETAWR-------------------QTLEE------------------------
Q Consensus     180   ~rl~~~~~~~~--------------------~~~~~------------------------
                       .+...+....                    +.+..
T Consensus     79    -~~~~~~~~~~~~~~~~~~~~~~~~~~ia~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T PF05625.10    79    -HWGRELPGAGGESEMKEKPAASMEKMKIAWRYESLGQFGASTNTRERPQAISTQPASS
T ss_pred             -HHHHhCCCCCCcchhccCcchhhccceEehHHHHccccCCcccCCCccccCCCCCCC

Q ss_pred             EEEEecC---------------------cccCcHHHHHHHHHHH---hCCcEEEEEeCh
Q Klein_Draft   198   ITFLPVP---------------------VNLMSQDVGALVEDIKD---YGFEFIVLDTI
Q Consensus     198   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~---~~~~lviiD~l
                      ...+...                     ...+...+..+...+..   .++.+||||++
T Consensus     148   ~~~~dl~~~~~~~~~~~~~~~~~~~~~~~l~~ll~~i~~~l~~~~~~~~~~vVIDsl
T PF05625.10    148   CHTFDLTKRLVHPASSRMDFIQLGMNPTQSPFAPVLEHLKNSLSKSAPNTVHRVVIPSM
T ss_pred             cccccCCCCCChhhhhcCeEEecCCCCCCCCHHHHHHHHHHHHHcCCCCCeEEEEECCC

Q ss_pred             HHHHHHHHHHHHHHHHHcC--CCCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeC
Q Klein_Draft   244   ARDVGIVIDSMTRLMDATP--DHRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERG
Q Consensus     244   ~~~~~~~~~~l~~L~~~~~--~~~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~
                      ......+...+..|+.+++  +++++++++.|..+......+...+...+|.++.|...
T Consensus     216   ~~~~~~~~~fl~~L~~~~~~~~~~~~vi~~~~~~~~~~~~~~~~~l~~~aD~vi~L~~~
T PF05625.10    216   SSQPQCVLQFLHGLRAIFAAYPNRVTAIMSLPLSLYPRSSGLVRWMELLNDGVFELAPF
T ss_pred             cCCHHHHHHHHHHHHHHHHhCCCcEEEEEEcCHHHCCCCCChHHHHHHHHCCEEEEEeeC

Q ss_pred             -------------EEEEeeecCC--------CCCCCeeEEE
Q Klein_Draft   304   -------------TLTCKKQKDA--------PEGDRHTLRL  323 (416)
Q Consensus     304   --------------~l~~~K~r~~---------~~~~~~~~~  323 (416)
                                   .+.+.|.+..        +....+.|++
T Consensus     286   ~~~~~~~~~~~~g~l~v~k~~~~~~r~~~~~~~~~~~~f~i  326 (364)
```

```
T PF05625.10    286    RGPAGTAEEPPQGLLQVHRLPILQDRGIGTGTSENDWTFTL  326 (364)
T ss_pred              CCCCCCCCCCCceEEEEEECCCccccCCCCCCcccEEEEE
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4myc)

94. **4MYC_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4MYC) Iron-sulfur clusters transporter ATM' transporter, Membrane transport, Mitochondrial; 3.06A {Saccharomyces cerevisiae}**

Probability: 98.05 E-value: 2.6E-7 Score: 96.06 Aligned Cols: 175 Identities: 11% Similarity

```
Q ss_pred              chhhhcccccHHHhcCCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHcCC
Q Klein_Draft   97     DSQFRSRFLSVSDIQNMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGR
Q Consensus     97     ~~~~~~~~~~~~~~~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~
                       ...+.++.++|.|....+.+..+ +..+++|+.++|+|++|+|||||+..+++.+..
T Consensus     336    ~~~I~~~nv~f~y~~~~~~l~~~-~~~i~~G~~~~i~G~~GsGKstll~~l~g~~~~--
T 4MYC_A        336    PYDITFENVTFGYHPDRKILKNA-SFTIPAGWKTAIVGSSGSGKSTILKLVFRFYDP--
T ss_dssp              CCCEEEEEEEECSSTTSCSEEEE-EEEECTTCEEEEECSTTSSGGGHHHHHTTSSCC--
T ss_pred              CCceEEEEEEEEeCCCCceeeeE-EEEECCCCEEEEEcCCCCCHHHHHHHHhcccCC--

Q ss_pred              EEEEECCCcccHHHHHHHHHHHcC---------------------------------
Q Klein_Draft   167    VLYVVAEGVAGFSSRINAWETAWRQ---------------------------------
Q Consensus     167    Vl~i~~e~~~~~~~rl~~~~~~~~~---------------------------------
                       |.+-+.....--...++....-...
T Consensus     396    i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~tv~eni~~~~~~~~~~~~~~~~~~~~
T 4MYC_A        396    ILINGRDIKEYDIDALRKVIGVVPQDTPLFNDTIWENVKFGRIDATDEEVITVVEKAQL
T ss_dssp              EEETTEEGGGBCHHHHHHTEEEECSSCCCCSEEHHHHHGGGCTTCCHHHHHHHHHHTTC
T ss_pred              EEECCeecccCCHHHHHHheEecCCCCCccCccHHHHhhhcCCCCCCchHHHHHHHhch

Q ss_pred              EEEEecCcccCcHHHHHHHHHHHH--hCCcEEEEeChHHHcCCCccCCHHHHHHHHHH
Q Klein_Draft   198    ITFLPVPVNLMSQDVGALVEDIKD--YGFEFIVLDTIARCTVGAEENSARDVGIVIDSM
Q Consensus     198    ~~~~~~~~~~~~~~~~l~~~~~~--~~~~lviiD~l~~~~~~~~~n~~~~~~~~~~~l
                       ..........++.+..+.+.+++.  .+++++++|++...+         +.......+
T Consensus     466    ~~~~~~~~~~~s~g~~~~~~~~~~~~~~~~~~lde~~~~l---------d~~~~~~~~
T 4MYC_A        466    DTIVGERGLMISGGEKQRLAIARVLLKNARIMFFDEATSAL---------DTHTEQALL
T ss_dssp              GCEESTTSCCCCHHHHHHHHHHHHHHHHTCSEEEEESTTCCS---------SHHHHHHHH
T ss_pred              ccccCCCCCCCCHHHHHHHHHHHHHHhCCcEEEeeccccCC---------CHHHHHHHH

Q ss_pred              eEEEEEccCCCCCCCCCCchhHhccccEEEEEEeC
Q Klein_Draft   266    GCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERG  300 (416)
Q Consensus     266    ~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~  300 (416)
                       +++++++|....         +.. +|.++.+..+
T Consensus     527    ~~vi~~th~~~~~~~~~~~~~~d~~~~l~~g  551 (598)
T 4MYC_A        527    RTSVYIAHRLRT---------IAD-ADKIIVLDNG  551 (598)
T ss_dssp              CEEEEEESCGGG---------GTT-CSEEEEEETT
T ss_pred              ceEEEEcCCHHH---------HHc-CCEEEEEeCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4huq)

95. **4HUQ_B (http://pdb.rcsb.org/pdb/explore.do?structureId=4HUQ) Energy-coupling factor transporter A HYDROLASE; 2.998A {Lactobacillus brevis}**

Probability: 98.03 E-value: 5.1E-7 Score: 84.28 Aligned Cols: 167 Identities: 15% Similarity

```
Q ss_pred              hhcccccHHHhcCCCCCcccccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHcCCCCC
Q Klein_Draft   100    FRSRFLSVSDIQNMPKPEPLIEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQ
Q Consensus     100    ~~~~~~~~~~~~~~~~~~l~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~
                       +.+..+++.+.......-.-++..+.+|++++|+|++|+|||+|+..++.....
T Consensus     6      i~~~~~~~~~~~~~~~l~~~~~~~~~g~~~~i~G~~gsGKs~ll~~l~g~~~~-----
T 4HUQ_B        6      ISVDHLTYQYDENQAPALTDVSFTVHAGEWLAIVGHNGSGKSTLAKSLDGLLPF-----
T ss_dssp              EEEEEECCSSSSCSSCCEEEEEEEECTTCEEEEEECTTSTHHHHHHHTSSSSCC-----
T ss_pred              EEEEEeEEEcCCCCCcceEEEEEEcCCCEEEEECCCCCCHHHHHHHHccCCCC-----
```

```
Q ss_pred                ---------------cEEEEECCC-----------------------cccHHHHHHHH
Q Klein_Draft   166      ---------------KVLYVVAEG-----------------------VAGFSSRINAWE
Q Consensus     166      ---------------~Vl~i~~e~------------------------~~~~~~rl~~~~
                                        .+.|+..+.                        ......++..++
T Consensus     67       ~~~~~~~~~~~~~~~~i~~i~~~~~~~~~~~tv~~~l~~~~~~~~~~~~~~~~~~~~~l
T 4HUQ_B        67       GGITLTPETVWQVREQIGMIFQNPDNQFVGATVEDDVAFGLENRQISRDEMVPRVQAAL
T ss_dssp                TTEECCSSSHHHHHTTEEEECSCTTSSCCCSSHHHHHHHHHHHTTCCGGGHHHHHHHH
T ss_pred                CCEECCcccHHHHHheeeeeCChhhccCCCCHHHHHHHhHhccCCCHHHHHHHHHHHH

Q ss_pred                EEEEecCcccCcHHHHHHHHHHH--hCCcEEEEeChHHHcCCCccCCHHHHHHHHHH
Q Klein_Draft   198      ITFLPVPVNLMSQDVGALVEDIKD--YGFEFIVLDTIARCTVGAEENSARDVGIVIDSM
Q Consensus     198      ~~~~~~~~~~~~~~~~l~~~~~~--~~~~lviiD~l~~~~~~~~~n~~~~~~~~~~~l
                         ..........++...++++.++..  .+++++++|++...+         +.......+
T Consensus     131      ~~~~~~~~~~ls~g~~~rl~la~~l~~~p~ililDep~~~l---------d~~~~~~l~
T 4HUQ_B        131      TSFAQREPSSLSGGQKQRVALAGIVAIAPKILILDEATSML---------DPQGRIEML
T ss_dssp                GGGTTCCGGGSCSHHHHHHHHHHHHHHHCCSEEEEESCGGGS---------CHHHHHHHH
T ss_pred                CchhcCChhhCCHHHHHHHHHHHHHHhCCCEEEEeccccCC---------CHHHHHHHH

Q ss_pred                eEEEEEccCCCCCCCCCCchhHhccccEEEEEEeC
Q Klein_Draft   266      GCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERG  300 (416)
Q Consensus     266      ~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~  300 (416)
                         +++++++|....         +.. +|.++.+..+
T Consensus     192      ~~vi~~th~~~~----------~~~-~d~i~~l~~g  216 (279)
T 4HUQ_B        192      LTVISITHDIDE---------AAS-ADRVLVIDDG  216 (279)
T ss_dssp                CEEEEEECCHHH---------HHT-CSEEEEEETT
T ss_pred                cEEEEEeCCHHH---------HHh-CCEEEEEeCC
```

Template alignment

96. **TIGR01618 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR01618) phage_P_loop; pha**

This model represents an uncharacterized family of proteins from a number of phage of Gram-positive

Probability: 98.0 E-value: 2.1E-6 Score: 77.05 Aligned Cols: 171 Identities: 12% Similarity:

```
Q ss_pred                cCcccCCCEEEEEcCCCCCHHHHHHHHHHHHcCCCCCCCCCCCCcEEEEECCCcccHH
Q Klein_Draft   121      EGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLYVVAEGVAGFS
Q Consensus     121      ~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~i~~e~~~~~~
                         .....++..++|+|++|+|||+++..+.                .+++|++.+......
T Consensus     6        ~~~~~~~~~~~i~G~~G~GKT~l~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
T TIGR01618     6        GNIKRIPNMYLIYGKPGTGKTSTIKYLP----------------GKTLVLSFDMSSKVL
T ss_pred                ccCCCCCcEEEEEcCCCCCHHHHHHHcC----------------CCeEEEEcCCCchhe

Q ss_pred                CcCccCCEEEEecCcccCcHHHHHHHHHHH-hCCcEEEEeChHHHcCC----------
Q Klein_Draft   191      QTLEEGSITFLPVPVNLMSQDVGALVEDIKD-YGFEFIVLDTIARCTVG----------
Q Consensus     191      ~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~-~~~~lviiD~l~~~~~~----------
                              ............+....+.+...... ..+++||||+++.++..
T Consensus     53       -----~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~iviD~~~~~~~~~~~~~~~~
T TIGR01618     53       -----NVDIADHDDMPPIQAMVEFYVMQNIQAVKYDNIVIDNISALQNLWLENIGRAAK
T ss_pred                -----ccccccCCCChhHHHHHHHHHHhchHhcCCCEEEEcChhHHHhhHHHhhhHHHh

Q ss_pred                HHHHHHHHHHhcCCCCeEEEEEccCCCCC---------------CCCCCchhHhccccE
Q Klein_Draft   250      VIDSMTRLMDATPDHRGCVLGIHHTGKDE---------------KTLRGSSAYEGGVDT
Q Consensus     250      ~~~~l~~L~~~~~~~~~~vl~v~H~~k~~~~~~~~~~~~~~~~~~~~Gs~~~~~~~d~
                         ....+..+.+.+...+++|++++|.....                -..+....+...+|.
T Consensus     118      ~~~~~~~~l~~~~~~~~~vi~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~d~
T TIGR01618     118      LDLWFLDLLTVLKESNKNIYATAWELTNQSSGESGQIYNRYQPDIREKVLNAFLGLTDV
T ss_pred                HHHHHHHHHHHHHHHcCCEEEEEEEccCcccccCCCCcccccccccccHHHHHHHHhCCE
```

```
Q ss_pred              cEEEEEeeecCCCCCCCe
Q Klein_Draft   302    GITLTCKKQKDAPEGDRH  319 (416)
Q Consensus     302    ~~~l~~~K~r~~~~~~~~  319 (416)
                       .+.+...+....+....+
T Consensus     188    ~r~~~~~~~~~~~~~~r~  205 (220)
T TIGR01618     188    ERGFILDPSKGNYAKNRL  205 (220)
T ss_pred              eEEEEEeCCCCCccCCCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/5u1d)

97. **5U1D_A (http://pdb.rcsb.org/pdb/explore.do?structureId=5U1D) Antigen peptide transporter 1, Antige transporter, antigen; 3.97A {Homo sapiens}**

Probability: 97.98 E-value: 7.3E-7 Score: 95.76 Aligned Cols: 210 Identities: 14% Similarity

```
Q ss_pred              HHHHHHhhhhhcCCCccCCCCCccCCccccCCCCcCCCChHhhccchhhhcccccHHH
Q Klein_Draft   51     ATIESAFSKADRDGPRMIPERPASLVPAAVEAPVVVMPDPETLRGVDSQFRSRFLSVSD
Q Consensus     51     ~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~p~~~~l~~~~~~~~~~~~~~~~
                       ..+.+.....++         ..+++...+..+......+...   ...+.++.++|.|
T Consensus     466    ~~~~~~~~s~~r---------I~~~l~~~~~~~~~~~~~~~~~---~~~I~~~nvsf~y
T 5U1D_A        466    PRVQKAVGSSEK---------IFEYLDRTPRCPPSGLLTPLHL---EGLVQFQDVSFAY
T ss_dssp              HHHHHHHHHHHH---------HHHHHCC-------CCBCCSSC---CCCEEEEEEEECC
T ss_pred              HHHHHHHhhHHH---------HHHHhhcCCCCCCCCCCCCCCc---ceeEEEEeeEEeC

Q ss_pred              ccCcccCCCEEEEEcCCCCCHHHHHHHHHHHHHcCCCCCCCCCCCcEEE---------
Q Klein_Draft   120    IEGVFNRGSTALLYGRWGTSKSFIALDWACSLATGRNWQGRETEKVKVLY---------
Q Consensus     120    ~~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~~~~g~~~~~~~Vl~---------
                       ++..+++|+.++|+|++|+|||||+..+...+..         ..+.+.+
T Consensus     524    lsl~i~~Ge~v~I~G~~GsGKSTLL~~L~g~~~~----------~~G~i~i~~~~~~~~~
T 5U1D_A        524    LTFTLRPGEVTALVGPNGSGKSTVAALLQNLYQP---------TGGQLLLDGKPLPQYE
T ss_dssp              EEEECCSSCEEECBCCTTSSHHHHHHHHHTSSCC---------SBSCCEESSSBGGGBC
T ss_pred              eEEEECCCCEEEEEcCCCCcHHHHHHHHccccCC---------CCcEEEECCeeccccC

Q ss_pred              -----------------EECCCcc---cHHHHHHHHHHHHcCcCccCCEEEEecCcccC
Q Klein_Draft   170    -----------------VVAEGVA---GFSSRINAWETAWRQTLEEGSITFLPVPVNLM
Q Consensus     170    -----------------i~~e~~~---~~~~rl~~~~~~~~~~~~~~~~~~~~~~~~
                                   ...+...   ........-....-.....+...........+
T Consensus     585    ~q~~~l~~~tl~enl~~~~~~~~~~~~~~~~~~~~l~~~~~~l~~~l~~~~~~~~~~l
T 5U1D_A        585    GQEPQVFGRSLQENIAYGLTQKPTMEEITAAAVKSGAHSFISGLPQGYDTEVDEAGSQL
T ss_dssp              CSSCCCCSSBHHHHHTCSCSSCCCHHHHHHHHHHHHTCHHHHHHSTTGGGSBCCTTSSSS
T ss_pred              CCCchhcCCCHHHHHhccccCCCCHHHHHHHHHHHhCChhHhcCCCCCCcccccccccC

Q ss_pred              HH--hCCcEEEEeChHHHcCCCccCCHHHHHHHHHHHHHHHHcCCCCeEEEEEccCCC
Q Klein_Draft   220    KD--YGFEFIVLDTIARCTVGAEENSARDVGIVIDSMTRLMDATPDHRGCVLGIHHTGK
Q Consensus     220    ~~--~~~~lviiD~l~~~~~~~~~n~~~~~~~~~~~~l~~L~~~~~~~~~~vl~v~H~~k
                       +.  .+++++++|++...+         +.......++.+.+.+++.+.++++++|...
T Consensus     655    ral~~~~~illlDE~~~~l---------d~~~~~~i~~~l~~~~~~~~~tvi~vth~~~
T 5U1D_A        655    RALIRKPCVLILDDATSAL---------DANSQLQVEQLLYESPERYSRSVLLITQHLS
T ss_dssp              HHHHHCCSEEEEBSCSTTC---------CHHHHHHHHCCCCCCGGGGGCEEEEBCSSHH
T ss_pred              HHHhcCCcEEEEEeCccCCC---------CHHHHHHHHHHHHHChhhcCcEEEEEeCCHH

Q ss_pred              hccccEEEEEEeC
Q Klein_Draft   288    EGGVDTVYFVERG  300 (416)
Q Consensus     288    ~~~~d~vi~l~~~  300 (416)
                       ...+|.++.++.+
T Consensus     706    ~~~~d~v~~l~~g  718 (748)
T 5U1D_A        706    VEQADHILFLEGG  718 (748)
T ss_dssp              HHTCSCCCEEETT
T ss_pred              HhcCCEEEEEeCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4huq)

98. **4HUQ_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4HUQ) Energy-coupling factor transporter A HYDROLASE; 2.998A {Lactobacillus brevis}**

Probability: 97.97 E-value: 3.7E-7 Score: 85.65 Aligned Cols: 174 Identities: 10% Similarity

```
Q ss_pred              hhcccccHHHhcCCCCCcccc---cCcccCCCEEEEEcCCCCCHHHHHHHHHHHHcCC
Q Klein_Draft   100    FRSRFLSVSDIQNMPKPEPLI---EGVFNRGSTALLYGRWGTSKSFIALDWACSLATGR
Q Consensus     100    ~~~~~~~~~~~~~~~~~~~l~---~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~
                       +.++.+++.|....|....++   +..+.+|++++|+|++|+|||+|+..++..+..
T Consensus     3      i~~~~v~~~~~~~~~~~~~~l~~i~~~i~~g~~~~i~G~~gsGKstll~~lag~~~~--
T 4HUQ_A        3      IAFEHVTYTYQAGTPMAHTALTDVSLTVPDRGYLAIIGHTGSGKSTLIQQLNALLKP--
T ss_dssp              EEEEEEEEEESTTSSSCEEEEEEECCEECTTCEEEEECSTTSSHHHHHHHTTTSSCC--
T ss_pred              eEEEEeEEEecCCCCcccccceeeeEEEEcCCcEEEEECCCCCCHHHHHHHHhcCCCC--

Q ss_pred              EEEEECCCcc-cHHHHHHHHHHHHcCcCccCCEEEE-----------------------
Q Klein_Draft   167    VLYVVAEGVA-GFSSRINAWETAWRQTLEEGSITFL-----------------------
Q Consensus     167    Vl~i~~e~~~-~~~~rl~~~~~~~~~~~~~~~~~~~~-----------------------
                       +.+....... .............+........+.
T Consensus     64     i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~tv~~~l~~~~~~~~~~~~~~~
T 4HUQ_A        64     IKIDEFTITPETTNAALKPLRQHVGMVFQFPENQLFEETVRQDIAFGPKNFGMADADAL
T ss_dssp              EEETTEEECTTCCGGGGTTHHHHEEEECSSGGGGCCSSSHHHHHTHHHHHTSCCHHHHH
T ss_pred              EEECCEecCcccchhhHHHHHceEEEecCcccccccccHHHHHHhCccccCCChHHHH

Q ss_pred              ------ecCcccCcHHHHHHHHHHHH--hCCcEEEEeChHHHcCCCccCCHHHHHHHH
Q Klein_Draft   202    ------PVPVNLMSQDVGALVEDIKD--YGFEFIVLDTIARCTVGAEENSARDVGIVID
Q Consensus     202    ------~~~~~~~~~~~~~~l~~~~~~--~~~~lviiD~l~~~~~~~~~n~~~~~~~~~
                             ......++....+++.++..  .+++++++|++...+         +......
T Consensus     134    l~~~~~~~~~~~ls~ge~~~~~la~~l~~~~~ililDep~~~l---------d~~~~~
T 4HUQ_A        134    LDQSYAERSPFELSGGQMRRVAIAGVLAMQPKVLVLDEPTAGL---------DPQGRQE
T ss_dssp              CCGGGTTSCGGGSCHHHHHHHHHHHHHHTTCCSEEEEESTTTTC---------CHHHHHH
T ss_pred              CCHHHhcCCcccCCHHHHHHHHHHHHHHhcCCCEEEEeCCCCCC---------CHHHHHH

Q ss_pred              CCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeC
Q Klein_Draft   264    HRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERG  300 (416)
Q Consensus     264    ~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~  300 (416)
                       .+++++++.|....         +...+|.++.+..+
T Consensus     195    ~~~tvi~~t~~~~~~~~~~~~~~~~d~v~~l~~G  222 (290)
T 4HUQ_A        195    QGLTIVLVTHQMED---------VAQYAEQVAVMHEG  222 (290)
T ss_dssp              TTCEEEEEESCHHH---------HHHHCSEEEEEETT
T ss_pred              cCCEEEEEECCHHH---------HHhhCCEEEEEeCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4rfs)

99. **4RFS_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4RFS) Energy-coupling factor transporter ATI ECF, HYDROLASE, TRANSPORT PROTEIN; 3.232A {Lactobacillus brevis}**

Probability: 97.97 E-value: 3.7E-7 Score: 85.65 Aligned Cols: 174 Identities: 10% Similarity

```
Q ss_pred              hhcccccHHHhcCCCCCcccc---cCcccCCCEEEEEcCCCCCHHHHHHHHHHHHcCC
Q Klein_Draft   100    FRSRFLSVSDIQNMPKPEPLI---EGVFNRGSTALLYGRWGTSKSFIALDWACSLATGR
Q Consensus     100    ~~~~~~~~~~~~~~~~~~~l~---~~~l~~g~~~~i~G~~G~GKStl~~~la~~~~~g~
                       +.++.+++.|....|....++   +..+.+|++++|+|++|+|||+|+..++..+..
T Consensus     3      i~~~~v~~~~~~~~~~~~~~l~~i~~~i~~g~~~~i~G~~gsGKstll~~lag~~~~--
T 4RFS_A        3      IAFEHVTYTYQAGTPMAHTALTDVSLTVPDRGYLAIIGHTGSGKSTLIQQLNALLKP--
T ss_dssp              EEEEEEEEEEETTTSSSCEEEEEEEEEEECTTCEEEEECSTTSSTTTTHHHHHTSSCC--
T ss_pred              eEEEEeEEEecCCCCcccccceeeeEEEEcCCcEEEEECCCCCCHHHHHHHHhcCCCC--

Q ss_pred              EEEEECCCcc-cHHHHHHHHHHHHcCcCccCCEEEE-----------------------
```

```
Q Klein_Draft   167    VLYVVAEGVA-GFSSRINAWETAWRQTLEEGSITFL-----------------------
Q Consensus     167    Vl~i~~e~~~-~~~~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                       +.+....... .............+........+.
T Consensus     64     i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~tv~~~l~~~~~~~~~~~~~~
T 4RFS_A        64     IKIDEFTITPETTNAALKPLRQHVGMVFQFPENQLFEETVRQDIAFGPKNFGMADADAL
T ss_dssp              EEETTEEECTTCCTTSCTTHHHHEEEECSSGGGGCCCSSSHHHHHHHHHTTTCCHHHHH
T ss_pred              EEECCEecCcccchhhhHHHHhceEEEecCcccccccccHHHHHHhCccccCCChHHHH

Q ss_pred              ------ecCcccCcHHHHHHHHHHHH--hCCcEEEEeChHHHcCCCccCCHHHHHHHH
Q Klein_Draft   202    ------PVPVNLMSQDVGALVEDIKD--YGFEFIVLDTIARCTVGAEENSARDVGIVID
Q Consensus     202    ------~~~~~~~~~~~~~~l~~~~~~--~~~~lviiD~l~~~~~~~~~n~~~~~~~~~~
                             ......++....+++.++..  .+++++++|++...+         +......
T Consensus     134    l~~~~~~~~~~~ls~ge~~~~~la~~l~~~~~ililDep~~~l---------d~~~~~~
T 4RFS_A        134    LDQSYAERSPFELSGGQMRRVAIAGVLAMQPKVLVLDEPTAGL---------DPQGRQE
T ss_dssp              CCGGGGGSCTTTSCHHHHHHHHHHHHHHTTCCSEEEESCTTTTC---------CHHHHHH
T ss_pred              CCHHHhcCCcccCCHHHHHHHHHHHHHhcCCCEEEEeCCCCCC---------CHHHHHH

Q ss_pred              CCeEEEEEccCCCCCCCCCCchhHhccccEEEEEEeC
Q Klein_Draft   264    HRGCVLGIHHTGKDEKTLRGSSAYEGGVDTVYFVERG  300 (416)
Q Consensus     264    ~~~~vl~v~H~~k~~~~~~Gs~~~~~~~d~vi~l~~~  300 (416)
                       .+++++++.|....         +...+|.++.+..+
T Consensus     195    ~~~tvi~~t~~~~~~~~~~~~~~~~d~v~~l~~G  222 (290)
T 4RFS_A        195    QGLTIVLVTHQMED---------VAQYAEQVAVMHEG  222 (290)
T ss_dssp              SCCEEEEECSCHHH---------HHHHCSEEEEEETT
T ss_pred              cCCEEEEEECCHHH---------HHhhCCEEEEEeCC
```

Template alignment | Template 3D structure | PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4a8j)

100. **4A8J_D (http://pdb.rcsb.org/pdb/explore.do?structureId=4A8J) ELONGATOR COMPLEX PROTEIN 4, ELON {SACCHAROMYCES CEREVISIAE}**

Probability: 97.95 E-value: 2.7E-6 Score: 82.96 Aligned Cols: 194 Identities: 10% Similarity

```
Q ss_pred              CCCccccc-CcccCCCEEEEEc-CCCCCHHHHHHHHHHHHHcCCCCCCCCCCCC-----
Q Klein_Draft   114    PKPEPLIE-GVFNRGSTALLYG-RWGTSKSFIALDWACSLATGRNWQGRETEKV-----
Q Consensus     114    ~~~~~l~~-~~l~~g~~~~i~G-~~G~GKStl~~~la~~~~~g~~~~g~~~~~~-----
                       +.++.++. ++++.|.+++|.| ++|+|||+|+++++...+.         .+.
T Consensus     26     ~~LD~llg~gGlp~Gs~~li~gd~~~~gk~~l~~~f~a~g~~---------~g~~~~~~
T 4A8J_D        26     ADLDSILGHMGLPLGNSVLVEEQSTTEFHSILGKLFAAQGIV---------HNRISDSS
T ss_dssp              HHHHHHTTSSSEETTCEEEEEECSSCCTHHHHHHHHHHHHH---------HHTC----
T ss_pred              HHHHHHhcCCCcccCcEEEEEcCCCCchHHHHHHHHHHHHH---------cCCCcCCC

Q ss_pred              EEEECCCc-----c-cHHHHHHHHHHHH-------------------cCcCccCCEEEE
Q Klein_Draft   168    LYVVAEGV-----A-GFSSRINAWETAW-------------------RQTLEEGSITFL
Q Consensus     168    l~i~~e~~-----~-~~~~rl~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~
                       +|++.+..     . .+..+.......                    ...........+
T Consensus     87     l~is~~~~~~~~lp~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~lkIa~
T 4A8J_D        87     IVLSLNQMFAKELPGIYKGSRKQMKKNLISEEESKVTVQNLNETQRSTPSRYKDLKIAW
T ss_dssp              EEECSCGGGGGGCCEEC-----------------------------------------
T ss_pred              EEEechHHHHHhCCcccccccHHHHHhhccchhhhccchhcccccccCCCcccccccEEEE

Q ss_pred              ---------------------------------------CcccCcHHHHHHHHHHH--H
Q Klein_Draft   204    ---------------------------------------PVNLMSQDVGALVEDIK--D
Q Consensus     204    ---------------------------------------~~~~~~~~~~~l~~~~~---~
                                                                ....+...+..+...++  .
T Consensus     157    ~~~~~~~~~~~~~~~~~~fDl~~~~~~~~~~~~~~~~~~~~~~ll~~i~~~l~~~~
T 4A8J_D        157    SPDRDDIQQNSEYKDYNHQFDITTRLMPAPIASELTFIAPTQPVSTILSQIEQTIKRND
T ss_dssp              ------------CTTSSCCEETTSCCSSCCCTTTEEEECTTSCHHHHHHHHHHHHHHTT
T ss_pred              CCCcccccccccccccccccccCCcCCCcccccccEEeCCCCcHHHHHHHHHHHHHcCC
```

```
Q ss_pred             HHHcCCCccCCHHH---HHHHHHHHHHHHHcCCCCe--EEEEEccCCCCCCCCCCchh
Q Klein_Draft   233   ARCTVGAEENSARD---VGIVIDSMTRLMDATPDHRG--CVLGIHHTGKDEKTLRGSSA
Q Consensus     233   ~~~~~~~~~n~~~~---~~~~~~~~l~~L~~~~~~~~~~--~vl~v~H~~k~~~~~~Gs~~
                      +.++....     .   ...+.+.+..|+.+++.+++  +++++.|....  ...+...
T Consensus     227   s~l~~~~~-----~~~~~~~~i~~fl~~L~~~~r~~~~~~t~llt~~~~~~--~~~~~~~~
T 4A8J_D        227   LHPAMYPP-----KMFESSEIIGLMHGVRSLVKKYYERVVLFASISIDII--TPPLLVL
T ss_dssp             TCTTTSCG-----GGGBHHHHHHHHHHHHHHHHHHTTTTEEEEEEEECTTS--CHHHHHH
T ss_pred             CChhhCCc-----cccCHHHHHHHHHHHHHHHHhCCcEEEEEEEehhhc--ChhHHHH

Q ss_pred             EeCCc------------------EEEEEeeecC-------CCCCCCeeEEE
Q Klein_Draft   298   ERGNG------------------ITLTCKKQKD-------APEGDRHTLRL  323 (
Q Consensus     298   ~~~~~--------------------~~l~~~K~r~-------~~~~~~~~~~~  323 (
                      +....                   ..|++.|.+.       .+....+.|++
T Consensus     290   ~~~~~~~~~~~~~~~~~~~~~~~g~L~V~K~~~~~~~~~~~~~~~~~fki  341 (
T 4A8J_D        290   EPFNQEMTEFLERVYKSQPGKIQHGLVHILKLPVFTDRGEMRVLKSEWAFKN  341 (
T ss_dssp             EECCHHHHHHHHHHTTTCGGGCCCEEEEEEECTTHHHHTCCCCEEEEEEEEE
T ss_pred             EecChhhhHHHHHhhcCCCCcceeEeEEEEEeCCCccCCCcccccceEEEEe
```

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