MPI
Bioinformatics
Toolkit

HHpred

JobID: 7621124_2 Created: May 8, 2019 5:27 PM

Results

Visualization

Number of hits: **250**

1GPP_A
2VS7_G
3CPE_A
4LX3_A
d1jva
d1jvaa3
4BIJ_D
d1gppa1
3HYJ_D
Terminase_1 Pha
5OL1_A
LAGLIDADG_2 LAG
5OE8_A
d1oa8a_
2DCH_X
4IDH_A
Hom_end_hint Ho
3C6A_A
1DQ3_A
5TGE_A
1DFA_A
5M1P_B
2CW8_A
Terminase_6C Ter
Intein_splicing
5C12_A
5OL7_A
d1b24a1
d1dq3a4
2O0J_A
Terminase_3C Ter
Hint Hint
3C0W_A
Terminase_GpA P
6BS8_A
d1dq3a3
Hom_end
Terminase_6 Ter
4IOX_B
d3nzma_
d1b24a2
d1b24a2
4ZNK_A
3N4P_D
d1at0a_
LAGLIDAD
Terminase_3 Pha
4DKW_D
2IMZ_B
2WBN_A
d1am2a_
3HYI_A
4LX3
DNA_pack_C Prob
d3qvea1
LAGLIDAD
Podovirus_Gp16
d1kcfa2
cd00081
1MOW_G
6AIB_A
5E6F_B
3NZM_A
2QOJ_Z
ResIII Type III
1KCF_A
d4kl5a1
2AB5_B
DNA_pack_N
Pox_A22 Poxviru
d1mi8a_
d1b24a1
PhoH PhoH-like
d1h jra_
4O1S_B
4EFJ_B
d1rifa_
cd00529
Vint N
d1dq3a3
d5gjua_
1HJR_B
2JMZ_A
6BCE_A
5GJU_A
4EP4_B
1AM2_A
d1jvaa
1RIF_A
1IV0_A
d4o1ra1
d2ab5a1
3B85_A
d4ep4a_
Hint_2
3FD2_A
5ZBZ_A
RuvC Crossover
d1dq3a1
6BD0_A
d1w36d1
d1iv0a_
6DSL_B
d3eh8a2
5HD9_A
DUF3882 Lactoco
2LCJ_A
d3eh8a1
1QDE_A
1NU0_A
5O9J_B
4LQ0_A
3FE2_A
4KTW_B
4O1R_A
1MOW_G
3BER_A
d1nu0a_
2LWY_A
4YIT_A
d1hv8a1
RuvX Hollida
1AT0_A
d1m5xa_
Helicase_RecD
1VHX_B
3QVE_B
d2ab
cd00046
Tex_YqgF
6FRE_A
d1r7ma2
cd00268
d1vhxa1
4E2U_A
5ESP_B
3LY5_B
d3bzca5
4KL5_B
2AB5_B
d1am2
YqgF Hol
1OA8_D
2FLD_B
d2g9na1
Ydc2-catalyt Mi
5K08_A
WhiA_N
d3mwja_
5OLA_A
AXH At
1AF5
d3fe2a_
PT-HIN
2QOJ_Z
d2j0sa1
5NBB_A
4LOX_A
d1wp9a1
ProQ
3HYJ_D
d2eyqa3
YajC
5A77_A
SWI2_SNF2 SWI2/S
d4uc4
2EX5_A
2GXQ_A
d1t9i
d1gm5a3
3E54_B
5JPQ_j
LA
d3bera_
1T9I
Flavi_DEAD Flav
d2pl3a1
1AM2
1WP9_B
5OL1
d3ly5a_
d2v6ia1
d1qdea_
3IUY_A
d2p6ra3
d3dkpa1
3B6E_A
5WWP_A
2FZ4_A
2PL3_A
d1s2ma1
3NZM
2OXC_A
1W36_G
1HV8_A
DEAD DEAD/DEAH
4A2P_A
d1q0ua_
d1mi8
1WRB_B
d1a1va1
5ANR_B
d2gk6a1
3LLM_A
1VEC_A

3FHC_B
3TBK_A
d3nz
3FHT_B
d2oxca_
d1t6na_
d3kx2a1
3E1S_A
3DKP_A
6DSL
5ZC9_A
1FUU_B
5OF4_A
4LJY_A
5M59_C
d3iuya1
6C90_A
2OCA_A
d4ct4b1
5IY9_V
4U4C_A
3I5X_A
5SUP_C
d3fhta1
2XZL_A
5MZN_A
1Q0U_A
6EM3_D
d1wrba1
d4kl5
6NMI_A
d2z0ma1
3FMP_B
4CBH_A
5Y4Z_A
6IEH_B
2KBE_A
2L8B_A
6ICZ_D
1Z63_A
2V6I_A
5FMF_1
Herpes_ori_bp
3FMO_B

Hitlist

Show 25 entries

Search:

Nr	Hit	Name	Probability	E-value	SS	Cols	Target Length
1	3CPE_A	DNA packaging protein Gp17; large terminase, Alternative initiation, ATP-binding; HET: PO4; 2.8A {Bacteriophage T4}	99.89	5.1e-24	32.5	377	592
2	4BIJ_D	DNA MATURASE B; HYDROLASE, ATPASE, DNA TRANSLOCATION, SINGLE-PARTICLE; 16.0A {ENTEROBACTERIA PHAGE T7}	99.89	2.4e-23	35.2	362	476
3	PF03354.15	; Terminase_1 ; Phage Terminase	99.85	6.3e-22	32.2	377	467
4	5OE8_A	Large subunit terminase; large terminase, VIRAL PROTEIN; 2.2A {Deep-sea thermophilic phage D6E}	99.84	2.1e-21	30.8	364	430
5	4IDH_A	Gene 2 protein; DNA packaging, terminase, ATPase, nuclease; 1.69A {Shigella phage Sf6}	99.81	2.9e-20	32.9	372	490
6	PF05203.16	; Hom_end_hint ; Hom_end-associated Hint	99.8	1.1e-20	26.3	313	475
7	1DQ3_A	CRYSTAL STRUCTURE OF AN ARCHAEAL; Endonuclease, PI-PfuI, Intein-encoded, HYDROLASE; 2.1A {Pyrococcus furiosus} SCOP: d.50.3.1, d.95.2.2, b.86.1.2	99.79	1.5e-20	25.3	302	454
8	1DFA_A	PI-SCEI ENDONUCLEASE (E.C.3.6.1.34); INTEIN, HOMING ENDONUCLEASE, HYDROLASE; 2.0A {Saccharomyces cerevisiae} SCOP: d.95.2.2, b.86.1.2	99.77	1.1e-19	26.4	323	454
9	2CW8_A	Endonuclease PI-PkoII (E.C.3.1.-.-); hydrolase; HET: GOL, SO4, MSE; 2.5A {Thermococcus kodakarensis}	99.74	8.2e-19	28	304	537
10	3C6A_A	Terminase large subunit; terminase nuclease, VIRAL PROTEIN; 1.16A {Enterobacteria phage RB49}	99.35	1.1e-13	16.9	186	232
11	5TGE_A	Phage terminase large subunit; nuclease, VIRAL PROTEIN; 2.6A {Thermus phage P7426}	99.3	5.2e-13	17.9	183	248
12	5M1P_B	Terminase large subunit; large terminase, nuclease domain, Hydrolase; 1.1A {Thermus phage G20c}	99.13	9.2e-12	15.8	164	191
13	PF17289.2	; Terminase_6C ; Terminase RNaseH-like domain	98.89	1.5e-10	12.9	138	161
14	5C12_A	Gene 2 protein; nuclease domain, metal binding site; 1.517A {Enterobacteria phage Sf6}	98.79	1.1e-9	15.9	188	278
15	PF14890.6	; Intein_splicing ; Intein splicing domain	98.66	2.5e-9	13.6	243	296
16	2O0J_A	DNA packaging protein Gp17; nucleotide-binding fold, HYDROLASE; HET: ADP; 1.8A {Enterobacteria phage T4}	98.64	5.5e-9	15.8	199	385
17	PF05876.12	; Terminase_GpA ; Phage terminase large subunit (GpA)	98.49	2.1e-7	24.3	407	541
18	PF03237.15	; Terminase_6 ; Terminase-like family	98.47	8.6e-8	18	222	232
19	2VS7_G	HOMING ENDONUCLEASE I-DMOI (E.C.3.1.-.-); PROTEIN/NUCLEIC ACID CRYSTALLOGRAPHY, ENDONUCLEASE, MEGANUCLEASE; 2.05A {DESULFUROCOCCUS MOBILIS}	98.37	8.9e-8	14.5	148	199
20	4ZNK_A	Phage terminase large subunit; DNA Translocation, VIRAL PROTEIN; HET: SO4; 1.931A {Thermus phage P7426}	98.37	1.5e-7	17.1	201	274
21	d1jvaa3	d.95.2.2 (A:582-698) VMA1-derived endonuclease (VDE) PI-SceI {Baker's yeast (Saccharomyces cerevisiae) [TaxId: 4932]}	98.36	4.1e-8	10.7	94	117
22	3HYJ_D	Protein DUF199/WhiA; LAGLIDADG, homing endonuclease, helix-turn-helix, HTH; HET: GOL; 2.6A {Thermotoga maritima}	98.27	4.1e-8	9	141	198
23	1GPP_A	ENDONUCLEASE PI-SCEI (E.C.3.6.3.14); ENDONUCLEASE, HOMING, PROTEIN SPLICING; 1.35A {SACCHAROMYCES CEREVISIAE} SCOP: l.1.1.1, b.86.1.2	98.18	1.2e-7	9.8	72	237

Nr	Hit	Name	Probability	E-value	SS	Cols	Target Length
24	PF03161.13	; LAGLIDADG_2 ; LAGLIDADG DNA endonuclease family	98.13	1.8e-7	9.8	142	174
25	2DCH_X	putative homing endonuclease; alpha/beta fold, HYDROLASE; HET: SO4; 2.06A {Thermoproteus}	98.11	4.6e-7	12.5	155	216

Showing 1 to 25 of 250 entries

Previous 1 2 3 4 5 … 10 Next

Alignments

Template alignment | Template 3D structure | PDBe

1. **3CPE_A DNA packaging protein Gp17; large terminase, Alternative initiation, ATP-binding; HET: PO4; 2.8A {Bacteriophage T4}; Related PDB entries: 3EZK_D 3EZK_E 3EZK_C 3EZK_B 3EZK_A**

Probability: 99.89 E-value: 5.1E-24 Score: 252.82 Aligned Cols: 377 Identities: 10% Similarity: 0.065

```
Q ss_pred              CCeEEEcCCccccCCChhHHhhHHHHHHccCCCCeEEEeehhHHHHHHcHHHHHHHHHHHchHhCccccCC
Q Q_7621124_2     402  DGLYLVGEHMTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARRNGAAVRELVREYGPEFGLNLSP  471 (881)
Q Consensus       402  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ili~s~~~~~a~~~~~~i~~~~~~~~~~~~~~~~~  471 (881)
                      ....++  .+++.+++|++.....+|.++..+...+++++++.++|+.++..++.+++.++....  ...
T Consensus       178  ~~~~~i--~~~R~~GKT~~~~~~~~~~~~~~p~~~i~i~s~t~~~a~~~~~~ik~~~~~~p~~~~--~~~  243 (592)
T 3CPE_A          178  KRMTVC--NLSRQLGKTTVVAIFLAHFVCFNKDKAVGILAHKGSMSAEVLDRTKQAIELLPDFLQ--PGI  243 (592)
T ss_dssp              CSEEEE--EECSSSCHHHHHHHHHHHHHHTSSSCEEEEEEESSHHHHHHHHHHHHHHHTTSCTTTS--CCE
T ss_pred              CCeEEE--eccccCHHHHHHHHHHHHHHHhCCCCcEEEEeCChhHHHHHHHHHHHHHHHhCcHHhc--CCc

Q ss_pred              CCccccCceEeecCceEEEEccCC-CcccCCCcEEEEeCCCCCHHHHcCHHHHHHHHHHHHHhhhcccC-C
Q Q_7621124_2     472  DESSKTDWSIRAGGTMRSRGLRG-NFTGQPMDLGIIDDPITNRAQAESLVVRDFVWDWYSSVWSQRKA-P  539 (881)
Q Consensus       472  ~~~~~~~~~~~~~~~i~~~g~~~-s~rG~~~~~ii~DE~~~~~~~~~~~s~~~~~~~~~~~~~~~~~~~-~  539 (881)
                      ..++...+.+.+|+.|.+.+... +++|.+++++++||+.......         +++......+.. +
T Consensus       244  ~~~~~~~i~~~nGs~i~~~~~~~~~~irG~~~~~iiiDE~~~~~~~~~----------~~~~~i~~~l~~~~  303 (592)
T 3CPE_A          244  VEWNKGSIELDNGSSIGAYASSPDAVRGNSFAMIYIEDCAFIPNFH----------DSWLAIQPVISSGR  303 (592)
T ss_dssp              EEECSSEEEETTSCEEEEEECCHHHHHHSCCSEEEEETGGGCTTHH----------HHHHHHHHHHSSSS
T ss_pred              eeccCCeEEeCCCCEEEEEeCCCCcccccceeEEEEeeHhhCCChH----------HHHHHHHhHhhcCC

Q ss_pred              CCeEEEEccccCcccHHHHHHhccCCCCcCCCeEEEEEeceEeCCccccccCCCCCCCCCCCccCCCCCCCC
Q Q_7621124_2     540  TYREVLVMTRWHQDDLAGRLLARDGRVEEGGVWRVVHLPAIAMPVDEKRGVYPDPLGREPGEPLTHPLIV  609 (881)
Q Consensus       540  ~~~~i~i~T~~~~~d~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~  609 (881)
                      ++++++++||++.++++..+.+..    ....+|..+..++...+
T Consensus       304  ~~~ii~~sTp~~~~~~~~~~~~~~~~~--~~~~~~~~~~~~~~~~~~~~~~~~~--------------------------  344 (592)
T 3CPE_A          304  RSKIIITTTPNGLNHFYDIWTAAV---EGKSGFEPYTAIWNSVK--------------------------  344 (592)
T ss_dssp              CCEEEEEECCCTTSHHHHHHHHHH---TTCSSCEEEEECGGGSG--------------------------
T ss_pred              CeEEEEEeCCCcCcHHHHHHHHHH---cCCCCcccceeeeceecC--------------------------

Q ss_pred              CCChhhcccChhHHHHHHHHHHHHHHhccccHHHHHhcCCCCcccccccHHHHHhhcCC----------
Q Q_7621124_2     610  PDDPATWSQAPTHREALTNWWAAKRKMSTARDWSSMSQGLPSSAENALLTDADIRAATAP----------  669 (881)
Q Consensus       610  ~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~f~~ey~~~~~~~~~~~~~~f~~~~i~~~~~~----------  669 (881)
                          ..+-..+...+.-..+..+.+..+++..|++||+|+|...++.+|+.+++..+...
T Consensus       345  ----~~~~~~~~~~~~~l~~e~~~~~~~~~~~~~~~~f~~e~~~~~~~~~~g~~f~~~~l~~~~~~~~~~~~~~~~~~~~  410 (592)
T 3CPE_A          345  ----ERLYNDEDIFDDGWQWSIQTINGSSLAQFRQEHTAAFEGTSGTLISGMKLAVMDFIEVTPDDHGFH  410 (592)
T ss_dssp              ----GGGBCTTSBBCTTHHHHHHHHTTSCHHHHHHHHSCCCTTSCSBSSCHHHHTTCCCCCCCCCSSSEE
T ss_pred              ----CcccCccccCCcchHHHHHHhCCCHHHHHHHhHHccccCCCCccCHHHHhhcccccccCCCCCee

Q ss_pred              ---CCccceEEEEEEeCCCCCCCcCCcEEEEEEEECCCCcEEEEecccccCcchHHHHHHHHHHHHhCCC
Q Q_7621124_2     670  ---VPDELTRVVVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTAVLTPLEWPRAVCLLAYERDAS  736 (881)
Q Consensus       670  ---~~~~~~~~~~~~~~~~iD~a~~~~~~~~~D~tai~v~~~~~~~g~~~v~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~  736 (881)
                         .+.....+++|+|+|.+.+  +|+||++++..+.+...+|......+.++.++.+.|.+++.+|++.
T Consensus       411  ~~~~~~~~~~~~~~~~~gvD~A~g~~--~D~tai~v~~~~~~~~~~~~~~v~~~~~~~~~~~~~~~~~~~~~~i~~l~~~y~~~  478 (592)
T 3CPE_A          411  QFKKPEPDRKYIATLDCSEGRG--QDYHALHIIDVTDDVWEQVGVLHSNTISHLILPDIVMRYLVEYNEC  478 (592)
T ss_dssp              ESSCCCTTCCEEEEEEECCSSBT--TBCEEEEEEECSSSSEEEEEEEEESSSCTTTHHHHHHHHHHHHTTSC
T ss_pred              EeeCCCCCCcEEEEEECccCCC--CCceEEEEEEcCCCCceEEEEEEeCCCCCcchHHHHHHHHHHHHHhCCC

Q ss_pred              EEEEEcccCchHHHHHHHHHHHHHHhccCCCCCCCCccccCcccCCCCce-----eecc-CCCCHHHhHHHHHH
Q Q_7621124_2     737  MIVYEKNYGGGMASALITQAWAALQNEPINADTDETMIPKSANCPYV-----KGVS-AKISKVLRAEPIA  800 (881)
Q Consensus       737  ~i~iE~~~~g~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i-----~~~~-~~~~K~~ri~~l~  800 (881)
                      .+++|.++.|..+...+..   .+...               ++. +     .++. .+.+|..++..|.
T Consensus       479  ~i~iE~~~~G~~v~~~l~~---~l~~~---------------~i~-~~~~~~~~~g~~~~~~~~~K~~~~~~~~l~  529 (592)
T 3CPE_A          479  PVYIELNSTGVSVAKSLYM---DLEYE---------------GVI-CDSYTDLGMKQTKRTKAVGCSTLK  529 (592)
T ss_dssp              CEEEEESHHHHHHHCCCC---CSCCS---------------CEE-CSSSSCSSEECCHHHHHHHHHHHH
T ss_pred              cEEEEecCchHHHHHHHHHh---hcCcC---------------Cee-ccccCCccccCCcccHHHHHHHHH
```

```
Q ss_pred                HHHHcCCeEEcccCccHHHHHHHhccCC-------CCCCCCcHHHHHHHHHHHhcCC
Q Q_7621124_2       801  QAVKTGRAKFAQLGNLGSLTNEFTLWQP-------GSTWSPGALDAAVYGATEVLPP  850 (881)
Q Consensus         801  ~~~~~g~i~~~~~~~~~~l~~el~~~~~-------~~~~~dD~~Dal~~~~~~~~~~  850 (881)
                         .++++|+|.++.    ..++.||..|..       ..+.|||++||++++++.+...
T Consensus         530  ~~i~~g~i~i~~-----~~li~El~~~~~~~~~~~~~~~hdD~vDAl~~a~~~~~~~  582 (592)
T 3CPE_A            530  DLIEKDKLIIHH----RATIQEFRTFSEKGVSWAAEEGYHDDLVMSLVIFGWLSTQS  582 (592)
T ss_dssp                HHHHTTSEECCC----HHHHHHHTSEEEETTEEEECTTCCCHHHHHHHHHHHHHHSG
T ss_pred                HHHHcCCceeCC----HHHHHHHHhhhhcCCcccccCCCCHHHHHHHHHHHHHhcc
```

Template alignment | Template 3D structure | PDBe

2. **4BIJ_D DNA MATURASE B; HYDROLASE, ATPASE, DNA TRANSLOCATION, SINGLE-PARTICLE; 16.0A {ENTEROBACTERIA PHAGE T7}; Related PDB entries: 4BIL_C 4BIL_B 4BIL_A 4BIJ_E 4BIJ_C 4BIJ_B 4BIJ_A 4BIL_D 4BIL_E**

Probability: 99.89 E-value: 2.4E-23 Score: 241.16 Aligned Cols: 362 Identities: 17% Similarity: 0.231

```
Q ss_pred                cCCCCeEEEcCCccccCCChhHHhhHHHHHHcccCCCCeEEEeehhHHHHHHcHHHHHHHHHHHchHhCcc
Q Q_7621124_2       399  DSPDGLYLVGEHMTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARRNGAAVRELVREYGPEFGLN  468 (881)
Q Consensus         399  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ili~s~~~~~a~~~~~~i~~~~~~~~~~~~~~  468 (881)
                         +......++  ..++.+++|+++....+|.+...+...+++++++.++|..++..++.+++..+.+...
T Consensus          48  ~~~~~~~~i--~~~R~~GKS~~~~~~~~~~~~~~~~~i~~~s~t~~~a~~~~~~i~~~~~~~~~~~~~-  114 (476)
T 4BIJ_D             48  NGDNKKFIL--QAFRGIGKSFITCAFVVWSLWRDPQLKILIVSASKERADANSIFIKNIIDLLPFLSEL-  114 (476)
T ss_dssp                SSSCSEEEE--ECCSSSCHHHHHHHHHHHHHHHTSSSCCEEEEECSSTHHHHHHHHHHHHHHTTSCTTTCC-
T ss_pred                cCCCCeEEE--EecCCCCChHHHHHHHHHHHHHHhCCCcEEEEEeCCHHHHHHHHHHHHHHHHhcHHHHHh-

Q ss_pred                cCCCCcccCCeEeecC-------ceEEEEccCCCcccCCCcEEEEeCCCCCHHHHcCHHHHHHHHHHHHH
Q Q_7621124_2       469  LSPDESSKTDWSIRAG-------GTMRSRGLRGNFTGQPMDLGIIDDPITNRAQAESLVVRDFVWDWYSS  531 (881)
Q Consensus         469  ~~~~~~~~~~~~~~~~~~-------~~i~~~g~~~s~rG~~~~~ii~DE~~~~~~~~~s~~~~~~~~~~~~~  531 (881)
                         +.....+...+.+.++       +.+.+.+..++.+|.+++++++|| ....++..+++.++.+++++.+
T Consensus         115  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~G~~~~~~~~DE-~~~~~~~~~~~~~~~~~~~~~~  183 (476)
T 4BIJ_D            115  KPRPGQRDSVISFDVGPANPDHSPSVKSVGITGQLTGSRADIIIADD-VEIPSNSATMGAREKLWTLVQE  183 (476)
T ss_dssp                CCSCBSTTSCSCBSCSSSSCEEEEECTTTTTHHHHHCSSEEEEEEET-TTSCTTHHHHHHHHHHHSSSH
T ss_pred                CCCCCCcccceeEEEeCCCCCCCCCeEEEEccCCcccccCCCCEEEEcC-CCCCccCCCHHHHHHHHHHHHH

Q ss_pred                hhhcccCC--CCeEEEEccccCcccHHHHHHhccCCCcCCCeEEEEEeceEeCCccccccCCCCCCCCCC-
Q Q_7621124_2       532  VWSQRKAP--TYREVLVMTRWHQDDLAGRLLARDGRVEEGGVWRVVHLPAIAMPVDEKRGVYPDPLGRE-  598 (881)
Q Consensus         532  ~~~~~~~~--~~~~i~i~T~~~~~d~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-  598 (881)
                          +.+++..  +++++++|||++.++++..+++.       ..|.++.+++...........|.......
T Consensus         184  -~~~~~~~~~~~~~i~~sTp~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  245 (476)
T 4BIJ_D            184  -FAALLKPLPSSRVIYLGTPQTEMTLYKELEDN-------RGYTTIIWPALYPRTREENLYYSQRLAPML  245 (476)
T ss_dssp                -HHHHHTTCCCCCEEEEECCCTTSHHHHHHHHH-------HTTCCCCCCCSTTSGGGGBCTTSCBCC-CH
T ss_pred                -HHHhcCCCCCCeEEEEeCCCCCCCHHHHHHHC-------CCceeeEEecccCCchhhceeeccchhHHH

Q ss_pred                -----------CCccCCCCCCCCCCChhhcccChhHHHHHHHHHHHHHHhcccchHHHHhcCCCCccccccc
Q Q_7621124_2       599  -----------PGEPLTHPLIVPDDPATWSQAPTHREALTNWWAAKRKMSTARDWSSMSQGLPSSAENAL  657 (881)
Q Consensus         599  -------------~~~~l~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~f~~ey~~~~~~~~~~~  657 (881)
                                   .+.++|+        +.++.     +.+    ++++..+++..|.+||+|.|.+.++.+
T Consensus         246  ~~~~~~~~~~~~~~~~~~~--------~~~~~-----~~l----~~~~~~~~~~~~f~~e~~~~~~~~~~~  298 (476)
T 4BIJ_D            246  RAEYDENPEALAGTPTDP--------VRFDR-----DDL----RERELEYGKAGFTLQFMLNPNLSDAEK  298 (476)
T ss_dssp                HHHHHHTTSCTTHHHHTT--------TCCCT-----TSC----SBSSCHHHHTTCCCCCCCCCSSSEEES
T ss_pred                HHHHhcCHHHHCCCCCCh--------hhCCH-----HHH----HHHHHHHhCHHHHHHHHHcCCCchhhhh

Q ss_pred                ccHHHHHhh-----------------------------------------cCCCCccceEEEEEEeCCC
Q Q_7621124_2       658  LTDADIRAA-----------------------------------------TAPVPDELTRVVVGVDPSG  685 (881)
Q Consensus         658  f~~~~i~~~-----------------------------------------~~~~~~~~~~~~~iD~a~  685 (881)
                         |+.++++.+                                         .. .+.....+++|+|+|.
T Consensus         299  f~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~p~~~~~~~~~~~~~~~~-~~~~~~~~~~g~D~a~  367 (476)
T 4BIJ_D            299  YPLRLRDAIVAALDLEKAPMHYQWLPNRQNIIEDLPNVGLKGDDLHTYHDCSN-NSGQYQQKILVIDPSG  367 (476)
T ss_dssp                SCCCTTCCEEEEEBCCCC-CCCEEEEEEECSSSSEEEEEEEESCCCSSSSHH-HHHHHHHHHTTSCCEE
T ss_pred                CcHHHHHHHHHhcCHhhCccceeccCCcccccCCCcCCCCCcccccccCCC-CCcCceeEEEEECCCC

Q ss_pred                CCCCcCCCcEEEEEEEECCCCcEEEEecccccC-cchHHHHHHHHHHHhCCCEEEEEcccCchHHHHHHH
Q Q_7621124_2       686  GEGARHDTAGISAVGLDEHQHAWFLEDRTAVLT-PLEWPRAVCLLAYERDASMIVYEKNYGGGMASALIT  754 (881)
Q Consensus         686  ~~~~~~D~tai~v~~~~~~g~~~v~~~~~~~~~-~~~~~~~i~~~~~~~~~~i~iE~~~~g~~~~~~l~  754 (881)
                         ++   +|.++++++... ++.++|++.+..+.. ++++++.|.+++++|++..+++|.++.|......+.
T Consensus         368  ~~~~~d~~~~~v~~~~-~~~~~v~~~~~~~~~~~~~~~~i~~~~~~~~~~i~~d~~~~~~~~~~~~~~~~  433 (476)
T 4BIJ_D            368  RG---KDETGYAVLYTL-NGYIYLMEAGGFRDGYSDKTLELLAKKAKQWGVQTVVYESNFGDGMFGKVFS  433 (476)
T ss_dssp                EE---ESHHHHHHHHHT-SSSSSSCCSCEECSSSSCSSEECCSTHHHHHHHHHHHHHHHHTTSEECCCSHH
T ss_pred                CC---CcceEEEEEEEe-CCeEEEEeeCCCCCCchHHHHHHHHHHHHHHhCCCEEEEEeeccccchHHHHH

Q ss_pred                HHHHHhccCCCCCCCccccCcccCCCCceeeccCCCCHHHhH-HHHHHHHHcCCeEEcc
Q Q_7621124_2       755  QAWAALQNEPINADTDETMIPKSANCPYVKGVSAKISKVLRA-EPIAQAVKTGRAKFAQ  812 (881)
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```
Q Consensus         755    ~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~K~~ri-~~l~~~~~~g~i~~~~  812 (881)
                           +   .+.+.              .+++ +.+++.+.+|..++ ..|..++++|+|.+++
T Consensus         434    ~~~~l~~~~~~~~~~~~~~~~~~~~~~-v~~~~~~~~k~~~i~~~l~~~~~~g~i~~~~  474 (476)
T 4BIJ_D            434    P---ILLKH--------------HNCA-MEEIRARGMKEMRICDTLEPVMQTHRLVIRD  474 (476)
T ss_dssp                  H---HHHTS--------------EEEE-TTEEEECTTCCCHHHHHHHHHHHHHHHSGGGT
T ss_pred                  H---HHHHh--------------cCCc-ceeccccCchhhHHHhhhhHHhhcCcEEEEec
```

Template alignment | CDD

3. **PF03354.15 ; Terminase_1 ; Phage Terminase**

Probability: 99.85 E-value: 6.3E-22 Score: 228.72 Aligned Cols: 377 Identities: 10% Similarity: -0.014

```
Q ss_pred                  CeEEEcCCccccCCChhHHHhHHHHHHccC--CCCeEEEeehhHHHHHHcHHHHHHHHHHchHhCcccC
Q Q_7621124_2       403    GLYLVGEHMTPTHNSTRVSQWFPFWWLTIR--PFDRILMASAEATLARRNGAAVRELVREYGPEFGLNLS  470 (881)
Q Consensus         403    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~--~~~~ili~s~~~~~a~~~~~~i~~~~~~~~~~~~~~~  470 (881)
                           ...++  .+++.+++|.......+|.+...  +...+++++++..+++.++..++.+++..+.+....
T Consensus          24    ~~~~~--~~~r~~GKT~~~~~~~~~~~~~~~~~~~~~~~t~~~a~~~~~~~~~~~~~~~~~~~~--  89 (467)
T PF03354.15         24    RSTYH--QVGKKNGKTTDTAVPMLFTQLLDGEAAPQGFCAATTRDQAGLLFKEVGRIVKRSPVLCRMM--  89 (467)
T ss_pred                  EEEEE--EecCCCChhHHHHHHHHHHHHCcccCCcEEEEeCCHHHHHHHHHHHHHHHhCHHHHHHh--

Q ss_pred                  CCCcccCceEee-cCceEEEEccCC-CcccCCCcEEEEeCCCCHHHHcCHHHHHHHHHHHHHhhcccC
Q Q_7621124_2       471    PDESSKTDWSIR-AGGTMRSRGLRG-NFTGQPMDLGIIDDPITNRAQAESLVVRDFVWDWYSSVWSQRKA  538 (881)
Q Consensus         471    ~~~~~~~~~~~~-~~~~i~~~g~~~-s~rG~~~~~ii~DE~~~~~~~~~s~~~~~~~~~~~~~~~~~~  538 (881)
                             ..+...+.+. +++.|.+.+.+. +++|.+++++++||+.....+           +.+......+..
T Consensus          90    ~~~~~~~~i~~~~~g~~i~~~~~~~~~~G~~~~~i~~DE~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  146 (467)
T PF03354.15         90    --QTMRHEIVTPRVDGVIKCLSRDGDSSDGINPSFLARDEMHRWTDR-----------ELAETIVESMIA  146 (467)
T ss_pred                  --heecceeEecCCCCEEEEeeCCCCcccCccccEEEEechHHCCCH-----------HHHHHHHHHccc

Q ss_pred                  -CCCeEEEEccccCcc-cHHHHHHc------cCCCcCCCCeEEEEEeceEeCCcccccCCCCCCCCCCCC
Q Q_7621124_2       539    -PTYREVLVMTRWHQD-DLAGRLLAR------DGRVEEGGVWRVVHLPAIAMPVDEKRGVYPDPLGREPG  600 (881)
Q Consensus         539    -~~~~~i~i~T~~~~~-d~~~~l~~~~------~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  600 (881)
                            +.+++++++||++.. +.++.+++.      ..  .....|....+.............|......-..
T Consensus         147    ~~~~~~~~~sTp~~~~~~~~~~~~~~~~~~~~~--~~~~~~~~~~~~~~~~~~~~~~~~~~~~np~~~~  214 (467)
T PF03354.15        147    RAQPIDWVITTAGHDRHSLCGELRGYAEGVLRGA--ITDDAFFGFVAEPPADCDPLDPAFWPMGNPNLGV  214 (467)
T ss_pred                  ccCCcEEEEEcCCCCCCCchHHHHHHHHHHcCC--CCCCceeeEEecCCCCCCCCChhHHHhcCCCCCC

Q ss_pred                  ccCCCCCCCCCChhhcccChhHHHHHHHHHHHHHH-hcccchHHHHhcCCCCccccccccHHHHHhhcCC
Q Q_7621124_2       601    EPLTHPLIVPDDPATWSQAPTHREALTNWWAAKRK-MSTARDWSSMSQGLPSSAENALLTDADIRAATAP  669 (881)
Q Consensus         601    ~~l~~~~~~~~~~~~~~~~~~~l~~~~~~~~~-~~~~~~f~~ey~~~~~~~~~~f~~~~i~~~~~~  669 (881)
                           ...+                  +.+++..+..+. .+++..|.++|+|+|.+.++.+|+.+++..+...
T Consensus         215    ~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~f~~~~~~~~~~~~~~~~~~~~~~~~~~~~  265 (467)
T PF03354.15        215    SKPI-------------------GKMHEAASKAAAIAASMPNFKRFHCNLWTEGEQMWIARESWDQGAAD  265 (467)
T ss_pred                  CCCH-------------------HHHHHHHHHHHHhHhhhhhhhhhccCeEeccccccCHHHHhcccCC

Q ss_pred                  -----CCcccceEEEEEEeCCCCCCCcCCcEEEEEEEECCCCcEEEEecccccc------------------
Q Q_7621124_2       670    -----VPDELTRVVVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTAV------------------  716 (881)
Q Consensus         670    -----~~~~~~~~~~~~iD~a~~~~~~~D~tai~v~~~~~~g~~~v~~~~~~~------------------  716 (881)
                                .+.....+++|+|+|.+    +|+++++++... +++++|++.+...
T Consensus         266    ~~~~~~~~~~~~~~~g~D~a~~~~~~d~~~i~~~~~~~~~~~v~~~~~~~~~~~~~~~~~~~~~~~~~  330 (467)
T PF03354.15        266    APFDPRMLYGRDAWVGVDLSNK----IDTTAIVVAVPL-DGLIYLIAYTFLPAGPKGFIVRAQKEKREYV  330 (467)
T ss_pred                  CCCCHHHHCCCeEEEEEeCCCC----CcceEEEEEEEc-CCEEEEEEEEEcCCCchhhhhHhHhccccHH

Q ss_pred                  ---------------cCcchHHHHHHHHHHHhCCCEEEEEcccCchHHHHHHHHHHHhccCCCCCCCcc
Q Q_7621124_2       717    ---------------LTPLEWPRAVCLLAYERDASMIVYEKNYGGGMASALITQAWAALQNEPINADTDE  771 (881)
Q Consensus         717    ---------------~~~~~~~~~i~~~~~~~~~~~i~iE~~~~g~~~~~~l~~~~~~~~~~~~~~~~  771 (881)
                                                  .+++++.+.|.++++.|++..+++|.++ +..+...++.
T Consensus         331    ~~~~~g~~~~~~~~~~~~~~~~~i~~~~~~~~~~~v~~D~~~-~~~~~~~l~~-----------------  383 (467)
T PF03354.15        331    AWRDQGWLEVHTGGAIDEAQIEARIGWIAKTFAVQEIAYDPWG-MKYMADRLAK----------------  383 (467)
T ss_pred                  HHHHcCCeEecCCCccCHHHHHHHHHHHHHcCCCEEEECCCC-HHHHHHHHHH----------------

Q ss_pred                  ccCcccCCCCceeecc-CCCCHHHhHHHHHHHHHcCCeEEcccCccHHHHHHHccCCCC----------
Q Q_7621124_2       772    TMIPKSANCPYVKGVS-AKISKVLRAEPIAQAVKTGRAKFAQLGNLGSLTNEFTLWQPGS----------  830 (881)
Q Consensus         772    ~~~~~~~~~~~i~~~~-~~~~K~~ri~~l~~~~~~g~i~~~~~~~~~~l~~el~~~~~~~~~~~~~~~~  830 (881)
                                 .+++ +.++. ...+|..++..+..++++|+|.++.   ++.|.+||..+....
T Consensus         384    ------g~~-~~~~~~~~~~~k~~~~~~l~~~~~~g~i~~~~~~~~~~l~~~l~~~~~~~~~~g~~~~~  443 (467)
T PF03354.15        384    ------RRLP-MVEHRQGFASMSNPMKRVEELVAQNRLRHGG---NPVLAWQVGNVHRDEDAAENIKPNK  443 (467)
T ss_pred                  ------CCCC-eEEecCCcccCCHHHHHHHHHHHcCCeeeCC---CHHHHHHHhceEEeeCCCCCcccCC

Q ss_pred                  ---CCCCcHHHHHHHHHHHcC
Q Q_7621124_2       831    ---TWSPGALDAAVYGATEVLP  849 (881)
Q Consensus         831    ---~~~dD~~Dal~~~~~~~~  849 (881)
                              +.|||.+||+++|+..+..
```

```
T Consensus         444    ~~~~~~~D~~da~~~a~~~~~~  465 (467)
T PF03354.15        444    KRSTGRIDAAVAMIMAVGRAAA  465 (467)
T ss_pred                  CCCCCCCCHHHHHHHHHHHHHc
```

Template alignment | Template 3D structure | PDBe

4. **5OE8_A Large subunit terminase; large terminase, VIRAL PROTEIN; 2.2A {Deep-sea thermophilic phage D6E}; Related PDB entries: 5OE8_C 5OE8_B 5OE9_C 5OE9_B 5OE9_A 5OEE_E 5OEE_F 5OEE_A 5OEE_D 5OEE_B 5OEE_C 5OEA_E 5OEA_F 5OEA_A 5OEA_D 5OEA_B 5OEA_C 5OEB_E 5OEB_F 5OEB_A 5OEB_D 5OEB_B 5OEB_C**

Probability: 99.84 E-value: 2.1E-21 Score: 221.86 Aligned Cols: 364 Identities: 12% Similarity: 0.027

```
Q ss_pred                  CCCCeEEEcCCccccCCCHHHHHHHHHHHc-cCCCCeEEEeehhHHHHHH-cHHHHHHHHHHHchHhCc
Q Q_7621124_2       400    SPDGLYLVGEHMTPTHNSTRVSQWFPFWWLT-IRPFDRILMASAEATLARR-NGAAVRELVREYGPEFGL  467 (881)
Q Consensus         400    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-~~~~~~ili~s~~~~~a~~-~~~~i~~~~~~~~~~~~~  467 (881)
                           ......++  .+++++++|.......++.++ ..+...+++++++.++|.. +...++.+++..+.....
T Consensus         35     ~~~~~~~i--~~~r~~GKT~~~~~~~~~~~~~~~~~~~~~~~~~a~~~~~~~~~~~~~~~~~~~~  102 (430)
T 5OE8_A            35     SDKDGIIC--DGSIRAGKTIVMSFSYVMWAMDTFNEQNFGMAGKTIGALRRNVITPLKRMLKSRGYRVKD  102 (430)
T ss_dssp                  TTSSEEEE--EECSSSSCHHHHHHHHHHHHHHHCSSCEEEEEESSHHHHCCCCCHHHHHHHHHTTCEEEE
T ss_pred                  CCCceEEE--ecCccCCHHHHHHHHHHHHHHHHhCCCCcEEEEeCcHHHHHHHHHHHHHHHHHhcCeeeee

Q ss_pred                  ccCCCCcccCceEeecC-ceEEEEcc-----CCCcccCCCcEEEEeCCCCHHHHcCHHHHHHHHHHHHH
Q Q_7621124_2       468    NLSPDESSKTDWSIRAG-GTMRSRGL-----RGNFTGQPMDLGIIDDPITNRAQAESLVVRDFVWDWYSS  531 (881)
Q Consensus         468    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  531 (881)
                           ..   ..+...+.+.++ +.+...+.     ..+.+|.+++++++||+.....+.            +..
T Consensus         103    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  157 (430)
T 5OE8_A            103    HR---ADNYLTITFKGKTNYFYLFGGKDESSQDLIQGITLAGMFFDEVALMPESF------------VNQ  157 (430)
T ss_dssp                  ET---TTTEEEEEEETTEEEEEEEEECCSTTGGGGSSSCCCSEEEEESGGGSCHHH------------HHH
T ss_pred                  ec---CCCcEEEEEcCCeeEEEEEeCCCcccchhhccceEeEEEEecHHHCCHHH------------HHH

Q ss_pred                  hhhcccCCCCeEEEEcccccCcccHHHHHHHccCCCcCCCeEEEEEeceEeCCcccccCCCCCCCCCCCc
Q Q_7621124_2       532    VWSQRKAPTYREVLVMTRWHQDDLAGRLLARDGRVEEGGVWRVVHLPAIAMPVDEKRGVYPDPLGREPGE  601 (881)
Q Consensus         532    ~~~~~~~~~~~~i~i~T~~~~~d~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  601 (881)
                           ....+..+++++++++||.+..+.++.++...   ...+.|..+.+++..+
T Consensus         158    ~~~~l~~~~~~~i~~~tp~~~~~~~~~~~~~---~~~~~~~~~~~~~~~~n-------------------  205 (430)
T 5OE8_A            158    ATARCSVDGAKLWFNCNPAGPYHWFKVEYLDK---LDEKNLLHLHFTMDDN-------------------  205 (430)
T ss_dssp                  HHHTCCSTTCEEEEECCCCCTTSHHHHHTGGG---HHHHTEEEEEECGGGC-------------------
T ss_pred                  HHHHccCCCCeEEEEeCCCCCCcchhhhcccc---cccCCeEEEEeeHhhc-------------------

Q ss_pred                  cCCCCCCCCCChhhcccChhHHHHHHHHHHHHHHhcccchHHHHhcCCCCccccccccHHHHHhhcCC-C
Q Q_7621124_2       602    PLTHPLIVPDDPATWSQAPTHREALTNWWAAKRKMSTARDWSSMSQGLPSSAENALLTDADIRAATAP-V  670 (881)
Q Consensus         602    ~l~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~f~~ey~~~~~~~~~~f~~~~i~~~~~~-~  670 (881)
                                     +.++.     +.+    +++++.+++..|+++|++.|.+.++.+|+.....+... .
T Consensus         206    ------------p~~~~-------~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  254 (430)
T 5OE8_A            206    ------------LSLSK-----QVK----ERYQRMYKGVFYQRYILGLWVLAEGIIYDMFDQDEHVVPTV  254 (430)
T ss_dssp                  ------------TTSCH-----HHH----HHHHHTCCTHHHHHHTTCCCCCCCSBSCTTCCTTTSEECCC
T ss_pred                  ------------cCCCH-----HHH----HHHHHHcCchHHHHHHHheeeccCcccccCcccceeCCC

Q ss_pred                  CcccceEEEEEEeCCCCCCCcCCcEEEEEEEECCCCcEEEEecccc-------ccCcchHHHHHHHHHH-
Q Q_7621124_2       671    PDELTRVVVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTA-------VLTPLEWPRAVCLLAYE-  732 (881)
Q Consensus         671    ~~~~~~~~~~iD~a~~~~~~D~tai~v~~~~~~g~~~v~~~~~~-------~~~~~~~~~~~~i~~~~~-  732 (881)
                           +.....+++|+|+|.     +|+++++++..+ ++.+++++.+..       +.+++++++.|.+++++
T Consensus         255    ~~~~~~~~~g~D~~~-----~d~~~~~~~~~~-~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  318 (430)
T 5OE8_A            255    PRPYEKYYVSCDYGT-----QNPTTFGLWGLY-NGVWYKVKEYHYDGRKENKQKTDQEYYEDLMKFIEDI  318 (430)
T ss_dssp                  CCCCSCEEEEEECCS-----SSCEEEEEEEEE-TTEEEEEEEEECHHHHTCCCCHHHHHHHHHHHTTTS
T ss_pred                  CCCCcEEEEEEecCC-----CCCcEEEEEEEE-CCEEEEEEEEEecCCcccccCChHHHHHHHHHHHHHH

Q ss_pred                  --hCCCEEEEEcccCchHHHHHHHHHHHHhccCCCCCCcccccCcccCCCCceeeccCCCCHHHhHHHHH
Q Q_7621124_2       733    --RDASMIVYEKNYGGGMASALITQAWAALQNEPINADTDETMIPKSANCPYVKGVSAKISKVLRAEPIA  800 (881)
Q Consensus         733    --~~~~~~i~iE~~~~g~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~K~~ri~~l~  800 (881)
                             |++..+++|.++..          ..+.+.+.+                  +.......+|..++..+.
T Consensus         319    ~~~~~~~i~~D~~g~~~~~~~~~~~~~l~~~g-------------------~~~~~~~~~~~~~~~~~~  361 (430)
T 5OE8_A            319    EKHKFKGVIVDPSAAS---------FIALLRQKG-----------------IKVIKAKNDVLDGIRNVA  361 (430)
T ss_dssp                  CGGGEEEEEECTTCHH---------HHHHHHHTT-----------------CCEEECCCCHHHHHHHHH
T ss_pred                  HhcCCCEEEeCCchHH---------HHHHHHHcC-----------------CEEEeCCCchHHHHHHHH

Q ss_pred                  HHHHcCCeEEcccCccHHHHHHHccCCCC-----------CCCCcHHHHHHHHHHHcCCCCCccccc
Q Q_7621124_2       801    QAVKTGRAKFAQLGNLGSLTNEFTLWQPGS-----------TWSPGALDAAVYGATEVLPPVGSTTELE  858 (881)
Q Consensus         801    ~~~~~g~i~~~~~~~~~~l~~el~~~~~~~~~~~~~~~~~dD~~Dal~~~~~~~~~~~~~~~~~~~  858 (881)
                           .++++|+|.++.  .+..|++||..+....           +.|||.+||+++++..+..........+
T Consensus         362    ~~~~~~~i~i~~~~~~~~l~~~l~~~~~~~~~~~~~~~~~~~~dd~~Da~~~~~~~~~~~~~~~~~~~  428 (430)
T 5OE8_A            362    TALNKKMILYND--CCKETFREYSSYVWDEKAAERGEDKPVKQNDHQLDADRYFVNTILFGNKLRAVPS  428 (430)
T ss_dssp                  HHHHTTSEEEET--TCHHHHHHHTTCBBCHHHHHTTCCCBCCSSCHHHHHHHHHCCCCCCC--------
T ss_pred                  HHhhCCCEEECC--CCHHHHHHHHhcccChhhhCCCCCCCCCCcHHHHHHHHHHHHhcccceecCCC
```

Template alignment | Template 3D structure | PDBe

5. **4IDH_A Gene 2 protein; DNA packaging, terminase, ATPase, nuclease; 1.69A {Shigella phage Sf6}; Related PDB entries: 4IEI_A 4IFE_A 4IEE_A**

Probability: 99.81   E-value: 2.9E-20   Score: 216.39   Aligned Cols: 372   Identities: 12%   Similarity: 0.019

```
Q ss_pred                 CCCeEEEcCCccccCCChhHHhhHHHHHHccCCCCeEEEeehhHHHHHH-cHHHHHHHHHHHchHhCccc
Q Q_7621124_2       401   PDGLYLVGEHMTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARR-NGAAVRELVREYGPEFGLNL  469 (881)
Q Consensus         401   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ili~s~~~~~a~~-~~~~i~~~~~~~~~~~~~~~  469 (881)
                          .....++  ..++.+++|+......+|.++..+ .++++++++.+++.. ++..++.+++..+......
T Consensus         34    ~~~~~~i--~~~~R~~GKT~~~~~~~~~~~~~~~-~~~~~~~s~~~~~a~~~~~~~~~~~~~~~~~~~~~-  99 (490)
T 4IDH_A          34    AHRYKVA--KGGRGSGKSWAIARLLVEAARRQP-VRILCARELQNSISDSVIRLLEDTIEREGYSAEFE-  99 (490)
T ss_dssp               CCSEEEE--ECCTTCCHHHHHHHHHHHHHTTSC-CEEEEEESCCSSGGGSSHHHHHHHHHHTCGGGEE-
T ss_pred               cCCEEEE--EeCCCCCCHHHHHHHHHHHHhcCC-cEEEEEeCChHhHHHHHHHHHHHHHHHHhCCccee-

Q ss_pred                 CCCCcccCceEeecCceEEEEccC---CCcccCC-CcEEEEeCCCCCHHHHcCHHHHHHHHHHHHHhhhc
Q Q_7621124_2       470   SPDESSKTDWSIRAGGTMRSRGLR---GNFTGQP-MDLGIIDDPITNRAQAESLVVRDFVWDWYSSVWSQ  535 (881)
Q Consensus         470   ~~~~~~~~~~~~~~~~i~~~g~~~---~s~rG~~-~~~ii~DE~~~~~~~~~~s~~~~~~~~~~~~~~~~  535 (881)
                             ......+.+.+|+.+...+.+   .+.+|.+ ++++++||+....++.            +......
T Consensus         100   ---~~~~~~~~~~gs~i~~~~~~~~~~~~~G~~~~~iiiDE~~~~~~~~~-----------~~~~~~~  154 (490)
T 4IDH_A          100   ---IQRSMIRHLGTNAEFMFYGIKNNPTKIKSLEGIDICWVEEAEAVTKES-----------WDILIPT  154 (490)
T ss_dssp               ---EETTEEEETTTCCEEEEEETTTCHHHHHHCCCCCEEEECSGGGCCHHH-----------HHHHGGG
T ss_pred               ---ecCCeEEEcCCCCEEEEEecCChhhhccccCCCEEEEEccccCCHHH-----------HHHHHHH

Q ss_pred                 ccCCCCeEEEEccccCcccHHHHHHhccCCCcCCCCeEEEEEeceEeCCccccccCCCCCCCCCCCccCCC
Q Q_7621124_2       536   RKAPTYREVLVMTRWHQDDLAGRLLARDGRVEEGGVWRVVHLPAIAMPVDEKRGVYPDPLGREPGEPLTH  605 (881)
Q Consensus         536   ~~~~~~~~i~i~T~~~~~d~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~  605 (881)
                      +..+++.+++++||.+..+.++..+..    .....|..+.+++..+
T Consensus         155   l~~~~~~~~~~~Tp~~~~~~~~~~~~~~~~~----~~~~~~~~~~~~~~~n----------------------  197 (490)
T 4IDH_A          155   IRKPFSEIWVSFNPKNILDDTYQRFVV----NPPDDICLLTVNYTDN----------------------  197 (490)
T ss_dssp               CCSTTCEEEEEECCCBTTSHHHCCCCC----SCCSSEEEEECCGGGC----------------------
T ss_pred               hcCCCceEEEEeCCCCCChHHHHhcc----CCCCCeEEEEcccccC----------------------

Q ss_pred                 CCCCCCChhhcccChhHHHHHHHHHHHHHHhccccchHHHHhcCCCCcccc-ccccHHHHHHhcCC----C
Q Q_7621124_2       606   PLIVPDDPATWSQAPTHREALTNWWAAKRKMSTARDWSSMSQGLPSSAEN-ALLTDADIRAATAP----V  670 (881)
Q Consensus         606   ~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~f~~ey~~~~~~~~~-~~f~~~~i~~~~~----~  670 (881)
                              +.+++     +.++.  .+.....+++..|+++|+|+|...++ .+|+.+++..+...    .
T Consensus         198   --------p~~~~-----~~~~~--~~~~~~~~~~~~~f~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~  252 (490)
T 4IDH_A          198   --------PHFPE-----VLRLE--MEECKRRNPTLYRHIWLGEPVSASDMAIIKREWLEAATDAHKKLG  252 (490)
T ss_dssp               --------TTCCH-----HHHHH--HHHHHHHHCHHHHHHHHSCCCBCCCTTBSSCHHHHHHHBTHHHHHT  
T ss_pred               --------CCCCH-----HHHHH--HHHHHhhChHHHHHHHhCCCCcccccccCCHHHHHHHHHHHHHcC

Q ss_pred                 CccceEEEEEEeCCCCCCCcCCcEEEEEEEEECCCCcEEEEecccccCcchHHHHHHHHHHHHhCCCEEEE
Q Q_7621124_2       671   PDELTRVVVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTAVLTPLEWPRAVCLLAYERDASMIVY  740 (881)
Q Consensus         671   ~~~~~~~~~~~iD~a~~~~~~~~D~tai~v~~~~~~~g~~~v~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~i~i  740 (881)
                            +.....+++|+|+|.++   +|++++++..    ++.+++++.+.+.. .++.++++.|.+++++|++..+++
T Consensus         253   ~~~~~~~~gvD~a~~~~~----d~svi~~~~~~----~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~i~~  315 (490)
T 4IDH_A          253   WKAKGAVVSAHDPSDTG---PDAKGYASRH---GSVVKRIAEGLL-MDINEGADWATSLAIEDGADHYLW  315 (490)
T ss_dssp               CCCCSCEEEEEECCCSS---SCCEEEEEEE---TTEEEEEEEECS-CCHHHHHHHHHHHHHHTTCSEEEE
T ss_pred               CCCCCcEEEEECCccCC---CCCcEEEEee---CCEEEEEeeecc-CCHhHHHHHHHHHHHHhCCCeEEE

Q ss_pred                 EcccCChHHHHHHHHHHHHHhccCCCCCCCCccccCcccCCCCceeeccCCC--------------------
Q Q_7621124_2       741   EKNYGGGMASALITQAWAALQNEPINADTDETMIPKSANCPYVKGVSAKI--------------------  790 (881)
Q Consensus         741   E~~~~g~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~--------------------  790 (881)
                      |.++.|..+...+......+.-.                    +.++..+.
T Consensus         316   D~~g~g~~~~~~~l~~~~~~~~~~~~~~~~~~--------------------~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  366 (490)
T 4IDH_A          316   DGDGVGAGLRRQTTEAFSGKKIT-------------------ATMFKGSESPFDEDAPYQAGAWADEVVQ  366 (490)
T ss_dssp               ECSSGGGGCHHHHHHHTTTSCCE-------------------EEEECTTSCCTTTTSBCCC---------
T ss_pred               cCCCcchhHHHHHHHHhcCCCCcE-------------------EEeeCCCCCCCCCCCccCCCCccchhcc

Q ss_pred                 -------------CHHHhHHHHHHHHHHc-------CCeEEcccCcc--------------HHHHHHHhcc
Q Q_7621124_2       791   -------------SKVLRAEPIAQAVKT-------GRAKFAQLGNL--------------GSLTNEFTLW  826 (881)
Q Consensus         791   -------------~K~~ri~~l~~~~~~~~~-------g~i~~~~~~~~~~~--------------~~~l~~el~~~  826 (881)
                                   .|..++..+...+++        |++.++.    .                +.|.+||..+
T Consensus         367   ~~~~~~~~~~~~~~~~k~~~~~~l~~~~~~~~~~~~~~g~i~~~~~~---~~~~~~~~~~~~~~~~~~~~~~~~~l~~el~~~  433 (490)
T 4IDH_A          367   GDNVRTIGDVFRNKRAQFYYALADRLYLTYRAVVHGEYADPD---DMLSFDKEAIGEKMLEKLFAELTQI  433 (490)
T ss_dssp               ---CCBHHHHBSSHHHHHHHHHHHHHHHHHHHHHHCCCCCGG---GCCEECHHHHCHHHHHHHHHHHTTC
T ss_pred               CCcccchhHhhccHHHHHHHHHHHHHHHHHHHHHHHHcCCcCCHH---HccccCHHHhCHHHHHHHHHHHHhhc

Q ss_pred                 CCC------------------CC-CCCcHHHHHHHHHHHHhcCCCCCCcccccCCC
Q Q_7621124_2       827   QPG------------------ST-WSPGALDAAVYGATEVLPPVGSTTELERPEG  862 (881)
Q Consensus         827   ~~~-------------------~~-~~dD~~Dal~~~~~~~~~~~~~~~~~~~~~~~~  862 (881)
```

```
                                ...                  .+ .|||.+||+++++.............+.+.
T Consensus         434         ~~~~~~~g~~~~~~k~~~~~~~g~~~~D~~dAl~~a~~~~~~~~~~~~~~~~~~  488 (490)
T 4IDH_A            434         QRKFNNNGKLELMTKVEMKQKLGIPSPNLADALMMCMHCPALVREETEIYVPSSS  488 (490)
T ss_dssp                       BBCCCTTSCBCBCCHHHHHHHHCCCCCHHHHHHHHTTCCCCBCCTTSCCBCC---
T ss_pred                       ceeeCCCCCEEEeeHHHHHHHhCCCCCcHHHHHHHHhcCchhcccccccccCCCC
```

Template alignment | CDD

6. **PF05203.16 ; Hom_end_hint ; Hom_end-associated Hint**

Probability: 99.8 E-value: 1.1E-20 Score: 217.44 Aligned Cols: 313 Identities: 19% Similarity: 0.24

```
Q ss_pred                       cccCCCCcEECCCc-cEEHHHcCCCCEEECCCCCEEEEEEEecCCCCeEEEEeCC---------CCeEEEC
Q Q_7621124_2       90          LVAHDTPVPTPTG-WTTHGELRPGDEVYHPSGKVVTVRAISADAHASIRVSTSD---------GGSIVVH  149 (881)
Q Consensus         90          C~~~dt~Vlt~~G-~~~i~~i~~gd~v~~~~g~~~~v~~~~~~~~~~~~i~t~~---------G~~i~~T  149 (881)
                                |++++|+|+|.+| +++|+++..|+.+++.++.+..+..+....+++|+|.+.+         |..+++|
T Consensus         1           C~~~dt~v~t~~G~~~~i~ei~~g~~v~~~~~~~~~v~~~~~~~~~~~~i~~~~~~~~~~~~~g~~i~~T  70 (475)
T PF05203.16        1           CFAKGTEVLMANGADKKIEDVVIGDKVMGKDGRPRDVVALPRGFDTMYTVSQKISRKGAKSSNNLSYTCN  70 (475)
T ss_pred                       CCCCCCEEEECCCCCEEEHHhcCCCCEEEeCCCCeEEEEEEccCccccEEEEeccccCCCccCCCceEEEC

Q ss_pred                       CCCeEEEEeCCC-------------CeEEEcchhHHhhhe-------eecCCCCccccccCCCCCCCCC-
Q Q_7621124_2       150         PRHEWTVWDRNR-------------KRWSTMETGDMMRRA-------YVDRSGRPAFMLPHRDPLEGVD-  198 (881)
Q Consensus         150         ~~H~~~~~~~~~-------------~~~~~~~~~~l~~~~-------~~~~~~~~~~~ip~~~~~~~~-  198 (881)
                                ++|+|++.+...              .......+.++..++       .        ..++......+..
T Consensus         71          ~~H~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  132 (475)
T PF05203.16        71          ATHKLVLKTPQQISLVEQVVRGKKQSSVSFLRLADVVVGSSRGGDRRR--------IQIVKKVTKSFQHE  132 (475)
T ss_pred                       CCCEEEecCccceEeeEeeeCCceeEEEEEEEeeEeeecCCCCCceee--------eEEEEEEeeccCCC

Q ss_pred                       ------------------------------------------------------------------C
Q Q_7621124_2       199         ------------------------------------------------------------------D  199 (881)
Q Consensus         199         ------------------------------------------------------------------~  199 (881)
                                                                                                    .
T Consensus         133         ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  202 (475)
T PF05203.16        133         PRGVEKARELAMEFLSTIGDDDIYWTIEARDYTLVSQEVRELTQQMISPVLFEKADLQNRLVKRGISAKY  202 (475)
T ss_pred                       cccHHHHHHHHHHHHHccCCCceeEEEEhhHHHHcCHHHHHHHHHHhhcceeeccChhHHHHHHHCCCChhh

Q ss_pred                       cccchHHHHHHHhcccccCCCCeEEecCChHHhhhchhh--------cCeEEecCCc--------------
Q Q_7621124_2       200         TLLIDPYTLGVWLGDGSSTKAAITHHADDEYVLPYPKS--------ADCVHQTTGV--------------  247 (881)
Q Consensus         200         ~~~~~~~llG~~l~dG~~~~~~i~~~~~~~~~~~~~~~~--------~~~~~~~~~~~~--------------  247 (881)
                                . +.+++++|+++|||++....+.+...+..+.+.+..        ..........
T Consensus         203         l-~~~~~llG~~~~dG~~~~~~~~~~~~~~~~~~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~  271 (475)
T PF05203.16        203         A-SEAAYLLGVWVGAGFSRSSAFSLYEEDSELVSRIISFGKALGLKAVTAEHNPRTVKIVRGELGVDGTF  271 (475)
T ss_pred                       H-HHHHHHHHHHhCCCCCCcceeeCChhhHHHHHHHHHHHHHcCCeeeeccCCCceeeeeeccccCCCc

Q ss_pred                       EEEE-------------------------------eCChHHHHHHHcCCCC-CCcCCHHHHHCCHHHHHH
Q Q_7621124_2       248         VTSY-------------------------------YRGGLHTALKTLGVHA-NKHIPVQYLRASESSRRA  285 (881)
Q Consensus         248         ~~~~-----------------------------------~~~~l~~~l~~~g~~~-~k~iP~~i~~~~~~~~~  285 (881)
                                ...+                                 .+..+..++..++... .+.+|.+++.++.+.+.+
T Consensus         272         ~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~k~ip~~i~~~~~~~~~  341 (475)
T PF05203.16        272         TSEVEDLVEVVDFQEGSEIPAWEQRGNLSVSFEGNTDNVFWKLISDLGFSGAVKSIPSHFAYESFPVREA  341 (475)
T ss_pred                       cceeeeceeeeeeecCCCCCcccccCccccCCCccccHHHHHHHHcCCCCCCccCCChHHHhCCHHHHHH

Q ss_pred                       HHHHHHHcCCeeCCCC--eEEEEeCCHHHHHHHHHHHHHCCCcEEEEEecCCCCCCCCCccCeeeEEEEEE
Q Q_7621124_2       286         LLAGLIDSDGTIAKSG--QVSFINTNRRLYDGVVELIRTLGYRATIHAPLQPSTSSSGVAGTRVLYRVSF  353 (881)
Q Consensus         286         fL~Gl~dgDG~~~~~~~--~i~~~t~s~~l~~~l~~Ll~~lGi~~~i~~~~~~~~~~~~~~~~~~y~~~i  353 (881)
                                ||+||+++||++....  .+.+++.++.++++++.+|.++||.+++.......   .+.......|++.+
T Consensus         342         fl~Gl~~~dG~~~~~~~~~~~~~~~~~l~~~i~~ll~~~Gi~~~~~~~~~~~---~~~~~~~~~~~l~~i  408 (475)
T PF05203.16        342         FLAGLIDADGSVKHGDLSSAHLSTTSPKVRDGTVRIARSLGISAYVSTKSEQI---VDGVYYPETYTIEL  408 (475)
T ss_pred                       HHHHHccCCCceecCCCCeEEEEeCCHHHHHHHHHHHHHCCCeEEEEeeeccc---cCCcccCCeEEEEE

Q ss_pred                       ecCCCCCCceEEeeccccccc-----CCCCceeEEEEEEEeCCeeeeeEEE-cCCCCeEEEcCCccccC
Q Q_7621124_2       354         TPHDGIPPARLSRKVAMSHC-----HGQRRRTSIIGIEPVDPRPGRCVEV-DSPDGLYLVGEHMTPTH  415 (881)
Q Consensus         354         ~~~~~~~~f~~~~k~~~~~~-----~~~~~~~~~I~~Ie~~~~~~vy~~~v-~~~~~~~~~~~~~~~~  415 (881)
                                .+.+.+..|....+......     ........|..|++.+.+.|||++| ++++|+|+++ ++..+|
T Consensus         409         ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~vy~itv~~~~~h~f~~~-g~~v~h  475 (475)
T PF05203.16        409         EGNEALQSVLSKSALSSNVAPAPGSFERKAVPMYFDLGITTPANYYGVTLAEDSDHQFLLS-NLTLVH  475 (475)
T ss_pred                       eCcHHHHHHHHhcCCCCCCCCCCCCccCceeeEEEeEEcCCCcEEEEEEccCCCceEEec-CeEEeC
```

Template alignment | Template 3D structure | PDBe

7. **1DQ3_A CRYSTAL STRUCTURE OF AN ARCHAEAL; Endonuclease, PI-PfuI, Intein-encoded, HYDROLASE; 2.1A {Pyrococcus furiosus} SCOP: d.50.3.1, d.95.2.2, b.86.1.2**

Probability: 99.79 E-value: 1.5E-20 Score: 216.68 Aligned Cols: 302 Identities: 16% Similarity: 0.145

```
Q ss_pred                        cccCCCcEECCCc----cEEHHHc-----CCCC------------------EEECCCCC-----EEEEEE
Q Q_7621124_2         90         LVAHDTPVPTPTG----WTTHGEL-----RPGD------------------EVYHPSGK-----VVTVRA  127 (881)
Q Consensus           90         C~~~dt~Vlt~~G----~~~i~~i-----~~gd------------------~v~~~~g~-----~~~v~~  127 (881)
                                 |++++|.|++.+|    +.+|+++     ..|+                  .|++.+..     +.++..
T Consensus           1          c~~~~t~v~~~~g~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~~~~~~~~~~~~~i~~  70 (454)
T 1DQ3_A              1          CIDGKAKIIFENEGEEHLTTMEEMYERYKHLGEFYDEEYNRWGIDVSNVPIYVKSFDPESKRVVKGKVNV  70 (454)
T ss_dssp                          CEETTCEEEEESSSCEEEEEHHHHHHHHGGGCEEEETTTTEEEEECTTSCCEEEEEETTTTEEEEEEEEE
T ss_pred                          CCCCCCeEEeecCCceEEEeHHHHHHHHhhcCCeeeccccceeeeeccCCCcEEEEECCCCCeEeeeeccE

Q ss_pred                        EecC--CCC--eEEEEeCCCCeEEECCCCeEEEEe-CCCCeEEEcchhHHhhheeecCCCCccccccCCC
Q Q_7621124_2         128        ISAD--AHA--SIRVSTSDGGSIVVHPRHEWTVWD-RNRKRWSTMETGDMMRRAYVDRSGRPAFMLPHRD  192 (881)
Q Consensus           128        ~~~~--~~~--~~~i~t~~G~~i~~T~~H~~~~~~~-~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~ip~~~  192 (881)
                                 +++.  ..+  +|+|++.+|..++||++|+|++.+ +....|+.  +.++..+++        ...+...
T Consensus           71         ~~~~~~~~~~~~~~~~i~~~~G~~i~~T~~H~~~~~~~~~~~~~~~~~~~~~~--~~~l~~gd~--------l~~~~~~~  130 (454)
T 1DQ3_A              71         IWKYELGKDVTKYEIITNKGTKILTSPWHPFFVLTPDFKIVEKR--ADELKEGDI--------LIGGMPD  130 (454)
T ss_dssp                          EEEEEECTTSCEEEEEEETTCCEEEECTTCEEEEECTTSCEEEEE--TTTCCTTCE--------ECBCCCC
T ss_pred                          EEEeecCCCceeEEEEECCCCEEEeCCCceeEEECCCCcEEEEE--HHHcCCCCE--------EeecCCC

Q ss_pred                        CCCCCCCccccchHHHHHHhcccccCCCCe------------EEecCChHHhhhchhh---------cCeE
Q Q_7621124_2         193        PLEGVDDTLLIDPYTLGVWLGDGSSTKAA------------ITHHADDEYVLPYPKS---------ADCV  241 (881)
Q Consensus           193        ~~~~~~~~~~~~~~~~llG~~l~dG~~~~~~~~------------i~~~~~~~~~~~~~~~~~~~~~~~---------~~~~  241 (881)
                                 ......   +..++++|++++||++....             +.+...+....+.+..          ....
T Consensus           131        ~~~~~~---~~~~~l~G~~~~dG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  197 (454)
T 1DQ3_A              131        GEDYKF---IFDYWLAGFIAGDGCFDKYHSHVKGHEYIYDRLRIYDYRIETFEIINDYLEKTFGRKYSIQ  197 (454)
T ss_dssp                          CCCCCC---CHHHHHHHHHHHHEEEEEEECCBTTBCCEEEEEEEEESCHHHHHHHHHHHHHHHSCCCCCE
T ss_pred                          Cccccc---chHHHHHHHHhcCceecccccccCCcceeeEEEEEecCCHHHHHHHHHHHHHHHHHCCCcEEe

Q ss_pred                        EecCCcEEEEeCChHHHHHHHHcCCCCCCcCCHHHHHCCHHHHHHHHHHHHHHcCCeeCCCCeEEEEeCCHH
Q Q_7621124_2         242        HQTTGVVTSYYRGGLHTALKTLGVHANKHIPVQYLRASESSRRALLAGLIDSDGTIAKSGQVSFINTNRR  311 (881)
Q Consensus           242        ~~~~~~~~~~~~~~~~~~l~~~l~~~g~~~~~k~iP~~i~~~~~~~~~~~~~~~~fL~Gl~dgDG~~~~~~~~~~i~~~t~s~~  311 (881)
                                 .......+.+.+..+...+..+.....+.+|.+++.++.+++.+||+|||++||++...+.+.+.+.|+.
T Consensus           198        ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ip~~i~~~~~~~~~~~~~~~fl~g~~~~~dG~v~~~~~~~~~~~~~~t~s~~  267 (454)
T 1DQ3_A              198        KDRNIYYIDIKARNITSHYLKLLEGIDNGIPPQILKEGKNAVLSFIAGLFDAEGHVSNKPGIELGMVNKR  267 (454)
T ss_dssp                          ESSSCEEEEECCHHHHHHHHHHHTTGGGSSCHHHHTTCHHHHHHHHHHHHHHHHCEEETTTEEEEEESCHH
T ss_pred                          cCCCEEEEEEccHHHHHHHHHHhcCcccCCCHHHHhcCHHHHHHHHHHHhhccCcccCCCcEEEEeCCHH

Q ss_pred                        HHHHHHHHHHHCCCcEEEEecCCCCCCCCCccCeeeEEEEEEecCCCCCCceEEeeccccccCCC-----
Q Q_7621124_2         312        LYDGVVELIRTLGYRATIHAPLQPSTSSSGVAGTRVLYRVSFTPHDGIPPARLSRKVAMSHCHGQ-----  376 (881)
Q Consensus           312        l~~~l~~Ll~~lGi~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~y~~~i~~~~~~~~~~~~~f~~~~k~~~~~~~~~~~~~~-----  376 (881)
                                 ++.+++.||.++|+.+++..+..+..          ..|.+.+.+...+..|...........+.
T Consensus           268        l~~~l~~ll~~lgi~~~~~~~~~~~~~~~~~---------~~~~l~i~~~~~~~~~~~f~~~i~~~~~~~~~~~~k~~~~~~~  328 (454)
T 1DQ3_A              268        LIEDVTHYLNALGIKARIREKLRKDG---------IDYVLHVEEYSSLLRFYELIGKNLQNEEKREKLEK  328 (454)
T ss_dssp                          HHHHHHHHHHTTTCCCEEEEEEECSSS---------EEEEEEECCHHHHHHHHHHTGGGCSCHHHHHHHHH
T ss_pred                          HHHHHHHHHHcCCCcEEEEeecCCC---------ceEEEEechhHHHHHHHHHhCcccCCHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

8. **1DFA_A PI-SCEI ENDONUCLEASE (E.C.3.6.1.34); INTEIN, HOMING ENDONUCLEASE, HYDROLASE; 2.0A {Saccharomyces cerevisiae} SCOP: d.95.2.2, b.86.1.2; Related PDB entries: 1JVA_B 1JVA_A 1EF0_B 1EF0_A 1UM2_B 1UM2_A 1LWS_A 1LWT_A 1VDE_B 1VDE_A**

Probability: 99.77 E-value: 1.1E-19 Score: 209.24 Aligned Cols: 323 Identities: 18% Similarity: 0.212

```
Q ss_pred                        cccCCCcEECCCcc-EEHHHcCCCCEEECCCCCEEEEEEEecCCCCeEEEEeCCC---------------
Q Q_7621124_2         90         LVAHDTPVPTPTGW-TTHGELRPGDEVYHPSGKVVTVRAISADAHASIRVSTSDG---------------  143 (881)
Q Consensus           90         C~~~dt~Vlt~~G~-~~i~~i~~gd~v~~~~g~~~~v~~~~~~~~~~~~~~~~~~i~t~~G---------------  143 (881)
                                 |++++|+|+|.+|. ++|+++..|+.+++.+|++..+..+.....++|+|.+..|
T Consensus           1          c~~~~t~v~~~~g~~~~~i~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  70 (454)
T 1DFA_A              1          CFAKGTNVLMADGSIECIENIEVGNKVMGKDGRPREVIKLPRGRETMYSVVQKSQHRAHKSDSSREVPEL  70 (454)
T ss_dssp                          CBCTTCEEEBTTSCEEEGGGCCTTCCBBCTTSCBCCBCCCCCEEEEEEEEEECCSSCCCSCSCTTSCCCC
T ss_pred                          CCCCCCEEEcCCCCCEEEHHHcCCCCEEEccCCCeeEEEEeCCCeeEeEEEEecccccccCCCCCCCCCCc

Q ss_pred                        CeEEECCCCeEEEEeCCCCeEEE-----------------------------------------------
Q Q_7621124_2         144        GSIVVHPRHEWTVWDRNRKRWST-----------------------------------------------  166 (881)
Q Consensus           144        ~~i~~T~~H~~~~~~~~~~~~~~~~~~~~-----------------------------------------------  166 (881)
                                 ..+.||++|++++....+..+..
T Consensus           71         ~~~~~t~~h~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  140 (454)
T 1DFA_A              71         LKFTCNATHELVVRTPRSVRRLSRTIKGVEYFEVITFEMGQKKAPDGRIVELVKEVSKSYPISEGPERAN  140 (454)
T ss_dssp                          SEEEEETTCEEEEEEECEEESSSSSCCCSSCCCCEEEEEEEEECTTSCEEEEEEEEECSSCCSCC------
T ss_pred                          eEEEECCCCeEEEcCCCCceEeeeeeCCeeEEEEEEEEeceEECCCCCeEEEEEEeeccCCCCCChHHHH

Q ss_pred                        -----------------cchhHHhhheeecCCCCccccccCCCC-------------CCCCCCccccchHH
Q Q_7621124_2         167        -----------------METGDMMRRAYVDRSGRPAFMLPHRDP-------------LEGVDDTLLIDPY  206 (881)
Q Consensus           167        -----------------~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~ip~~~~~-------------~~~~~~~~~~~~~~~~~~~~~  206 (881)
```

```
                                      +...++................|....            ...+....+..++
T Consensus         141     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  210 (454)
T 1DFA_A            141     ELVESYRKASNKAYFEWTIEARDLSLLGSHVRKATYQTYAPILYENDHFFDYMQKSKFHLTIEGPKVLAY  210 (454)
T ss_dssp                   -----------CCEEEEEEEEGGGGGGSCHHHHHHCBEEECCCCCCCCTTTTCCC-----CCSSSHHHHHH
T ss_pred                   HHHHHHHHhcCCCceEEEEEhHHHHhhcHHHHHHHHhhhcchhhcChhHHHHHHhcCCCCCCCccHHHHH

Q ss_pred                   HHHHhccccCCCCeEEecCChHHhhhchhhcCeEEecCCcEEE--------------------------
Q Q_7621124_2        207     TLGVWLGDGSSTKAAITHHADDEYVLPYPKSADCVHQTTGVVTS--------------------------  250 (881)
Q Consensus         207     llG~~l~dG~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~--------------------------  250 (881)
                            ++|++++||++....+.+...+..+.+.+...............
T Consensus         211     llG~~~~dG~~~~~~i~~~~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  280 (454)
T 1DFA_A            211     LLGLWIGDGLSDRATFSVDSRDTSLMERVTEYAEKLNLCAEYKDRKEPQVAKTVNLYSKVVRGNGIRNNL  280 (454)
T ss_dssp                   HHHHHHHHCBTTBSCCCCCTTCHHHHHHHHHHHHHHTSCCSSCC--------------------------
T ss_pred                   HHHHHhCCCCCCCCeEEeeCCCHHHHHHHHHHHHHHcCCeeEEeecCcccccceeEeeEEeecCCCccccc

Q ss_pred                   EeCChHHHHHHHcCCC--CCCcCCHHHHHCCHHHHHHHHHHHHHcCCeeCCCCe--EEEEeCCHHHHHHH
Q Q_7621124_2        251     YYRGGLHTALKTLGVH--ANKHIPVQYLRASESSRRALLAGLIDSDGTIAKSGQ--VSFINTNRRLYDGV  316 (881)
Q Consensus         251     ~~~~~l~~~l~~~g~~--~~k~iP~~i~~~~~~~~~~~~fL~Gl~dgDG~~~~~~~~--i~~~t~s~~l~~~l  316 (881)
                            ..+..+..++..++..  ..+.+|.+++.++.+...+||+||+++||++...+.  +.+.+.++.++.++
T Consensus         281     ~~~~~l~~~l~~~~~~~~~~~~k~~p~~i~~~~~~~~~~~~fl~g~~~~dG~~~~~~~~~~~~~~~t~s~~l~~~l  350 (454)
T 1DFA_A            281     NTENPLWDAIVGLGFLKDGVKNIPSFLSTDNIGTRETFLAGLIDSDGYVTDEHGIKATIKTIHTSVRDGL  350 (454)
T ss_dssp                   CCSCTTHHHHHHTTCBSSSSBCCCGGGGTSCHHHHHHHHHHHHHHHHCCEECTTSCEEEEEEESCHHHHHHH
T ss_pred                   cCCCHHHHHHHHHcCCccccCCccccCHHHhcCCHHHHHHHHHHHHhcCCCeEecCCceEEEEEeCCHHHHHHH

Q ss_pred                   HHHHHHCCCcEEEEecCCCCCCCCCccCeeeEEEEEEecCCCCCCceEEeecccccc------CCCCcee
Q Q_7621124_2        317     VELIRTLGYRATIHAPLQPSTSSSGVAGTRVLYRVSFTPHDGIPPARLSRKVAMSHC------HGQRRRT  380 (881)
Q Consensus         317     ~~Ll~~lGi~~~i~~~~~~~~~~~~~~~~~~~~~~~~y~~~i~~~~~~~~~~~f~~~k~~~~~~------~~~~~~~  380 (881)
                            +.+|.++|+.+.+...+.........  ...+|.+.+.+...+..+.......+...      .....+.
T Consensus         351     ~~ll~~~Gi~~~~~~~~~~~~~~~~~~~~~~~--~~~~~~l~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  418 (454)
T 1DFA_A            351     VSLARSLGLVVSVNAEPAKVDMNGTK--HKISYAIYMSGGDVLLNVLSKCAGSKKFRPAPAAAFARECRG  418 (454)
T ss_dssp                   HHHHHHTTCEEEEEEEECCCGGGTSS--CSEEEEEEEECTHHHHHHHTTCCSTTTCCCCCSSCCCCCCEE
T ss_pred                   HHHHHHcCCEEEEEecccccCCCCCe--eeeEEEEEEechHHHHHHHhhccccCCcCCCCchHHhhhccc

Q ss_pred                   EEEEEEEeCCeeeeeEEEc-CCCCeEE-EcCCccccCC
Q Q_7621124_2        381     SIIGIEPVDPRPGRCVEVD-SPDGLYL-VGEHMTPTHN  416 (881)
Q Consensus         381     ~I~~Ie~~~~~~vy~~~v~-~~~~~~~~-~~~~~~~~~~~~  416 (881)
                            .|.+|+..+.+.|||++|+ +++|+|+ .  ++..+||
T Consensus         419     ~v~~i~~~~~~~~Vydl~V~~~~~~~~f~~~--ngiv~HN  454 (454)
T 1DFA_A            419     FYFELQELKEDDYYGITLSDDSDHQFLLA--NQVVVHN  454 (454)
T ss_dssp                   ECEEEEEEEEEEECCCCBCTTSCSEEEBT--TCBEEEC
T ss_pred                   eeEEEEEcccCcEEEeEEcCCCCCCEEec--CcEEEcC
```

Template alignment | Template 3D structure | PDBe

9. **2CW8_A Endonuclease PI-PkoII (E.C.3.1.-.-); hydrolase; HET: GOL, SO4, MSE; 2.5A {Thermococcus kodakarensis}; Related PDB entries: 2CW7_A**

Probability: 99.74 E-value: 8.2E-19 Score: 206.63 Aligned Cols: 304 Identities: 15% Similarity: 0.124

```
Q ss_pred                   cccCCCcEECCCCc----cEEHHHc----------------------CCCCEEE-----CCCCCEEEEEEE
Q Q_7621124_2        90      LVAHDTPVPTPTG----WTTHGEL----------------------RPGDEVY-----HPSGKVVTVRAI  128 (881)
Q Consensus         90      C~~~dt~Vlt~~G----~~~i~~i----------------------~~gd~v~-----~~~g~~~~v~~~  128 (881)
                            |++++|.|++.+|    +.+|+++                      ..|+.|+     +....+.+|..+
T Consensus         1       ~~~~~t~v~~~~~g~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~g~~v~s~~~~~~~~~~~~~~~~v~~~  70 (537)
T 2CW8_A            1       SILPEEWLPVLEEGEVHFVRIGELIDRMMEENAGKVKREGETEVLEVSGLEVPSFNRRTNKAELKRVKAL  70 (537)
T ss_dssp                   CBCTTCEEEEEEETTEEEEEEHHHHHHHHHHHTTGGGCEEETTEEEEECCSEEEEEECTTTCCEEEEEEEEE
T ss_pred                   CCCCCceeEEeeCCEEEEEEhHHHHHHHHHHHcccceeecCceEEEecCCceEEEEeCCCCeEEEEecEEE

Q ss_pred                   ecCC--CCeEEEEeCCCCeEEECCCCeEEEEeCCCCeEEEcchhHHhhheeecCCCCccccccCCC----
Q Q_7621124_2        129     SADA--HASIRVSTSDGGSIVVHPRHEWTVWDRNRKRWSTMETGDMMRRAYVDRSGRPAFMLPHRD----  192 (881)
Q Consensus         129     ~~~~--~~~~~i~t~~G~~i~~T~~H~~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~ip~~~----  192 (881)
                            +...  +++++|++.+|..+.|||+|++++..+....|..  +.++..+++        ..+|...
T Consensus         71      ~~~~~~~~~~~~~i~~~~g~~i~~T~~H~~~~~~~~~~~~~~~~~--a~~l~~g~~--------l~~~~~~~~~~~~~  130 (537)
T 2CW8_A            71      IRHDYSGKVYTIRLKSGRRIKITSGHSLFSVRNGELVEVT--GDELKPGDL--------VAVPRRLELPE  130 (537)
T ss_dssp                   EEEEEEEEEEEEEEETTSCEEEEETTCEEEEEETTEEEEEE--TTTCCTTCE--------EEEESCCCCC
T ss_pred                   EEecCCCCEEEEEeCCCCEEEECCCCceEEEECCEEEEEe--hhhCCCCCE--------EEeecCCCCCC
```

Template alignment | Template 3D structure | PDBe

10. **3C6A_A Terminase large subunit; terminase nuclease, VIRAL PROTEIN; 1.16A {Enterobacteria phage RB49}; Related PDB entries: 3C6H_B 3C6H_A**

Probability: 99.35 E-value: 1.1E-13 Score: 143.76 Aligned Cols: 186 Identities: 12% Similarity: 0.095

```
Q ss_pred                   ccchHHHHhcCCCCccccccccHHHHHhhcC------------CCCccceEEEEEEeCCCCCCCCcCCCcEE
Q Q_7621124_2        638     TARDWSSMSQGLPSSAENALLTDADIRAATA------------PVPDELTRVVVGVDPSGGEGARHDTAG  695 (881)
Q Consensus         638     ~~~~f~~ey~~~~~~~~~~~~~~~f~~~~i~~~~~~------------~~~~~~~~~~~~~~~~~~iD~a~~~~~~~~D~ta  695 (881)
```

```
                                +...|.++..+ |..+++.+|+++.+..+..            ..|.....+++++|+|.+.+  +|+||
T Consensus          11         ~~~~~~~~~~~-f~~~~~~~~~~~l~~~~~~~p~~~~~~~~~~~~~~~~~v~gvD~A~g~~---~D~ta  77 (232)
T 3C6A_A             11         SSGLVPRGSHM-LEDPMGTLIRATTLSRLSFIDVVNDNGFYQFEKPKEGRKYVATLDCSEGRG--QDYHA  77 (232)
T ss_dssp                       -----------------CBSSCHHHHHHCCCCCCCCCBTTEEESSCCCTTCCEEEEEECCCSSS--SCCEE
T ss_pred                       cCCCCCCcccc-ccCCCCCeeCHHHHHhcccccccccCCCeEEEEeCCCCCCeEEEEEECCCCCC--CCCce

Q ss_pred                       EEEEEECCCCcEEEEecccccc-cCcchHHHHHHHHHHHhCCCEEEEEcccCchHHHHHHHHHHHHhccCC
Q Q_7621124_2        696        ISAVGLDEHQHAWFLEDRTAV-LTPLEWPRAVCLLAYERDASMIVYEKNYGGGMASALITQAWAALQNEP  764 (881)
Q Consensus          696        i~v~~~~~~g~~~v~~~~~~~-~~~~~~~~~i~~~~~~~~~~~i~iE~~~~g~~~~~~l~~~~~~~~~~  764 (881)
                                ++|+... .+..++++.+..+ .+++++++.|..++++|++..|++|.++.|..+...++.   ++...
T Consensus          78         i~v~~~~~~~~~~~v~~~~~~~~~~~~~~~~i~~~~~~y~~~~i~iE~~g~G~~~~~~l~~~~~~~~~~  142 (232)
T 3C6A_A             78         LQIIDIT-EFPYKQVAVYHSNTTSHFILPDIVFKYLMMYNECPVYIELNSTGVSIAKSLAM---DLEYD-  142 (232)
T ss_dssp                       EEEEECS-SSSEEEEEEEEESCCCTTTHHHHHHHHHHHHTTSCCEEEBCSHHHHHHHHHHHH---TSCCC-
T ss_pred                       EEEEEcC-CCCcEEEEEEEcCCCCHhHHHHHHHHHHHHhCCCcEEEecCchHHHHHHHHHH---HcCCC-

Q ss_pred                       CCCCCccccCcccCCCCcee-----ecc-CCCCHHHhHHHHHHHHHcCCeEEcccCcchHHHHHHHccCC
Q Q_7621124_2        765        INADTDETMIPKSANCPYVK-----GVS-AKISKVLRAEPIAQAVKTGRAKFAQLGNLGSLTNEFTLWQP  828 (881)
Q Consensus          765        ~~~~~~~~~~~~~~~~~~i~-----~~~-~~~~K~~ri~~l~~~~~~g~i~~~~~~~~~~l~~el~~~~~  828 (881)
                                                   +++ +.     ++. .+.+|..++..+..++++|+|.|+.    .+|++||..|+.
T Consensus          143        ---------------~~~-~~~~~~~~~~~~~~~K~~~~~~l~~~~e~g~l~i~~-----~~l~~ql~~f~~  193 (232)
T 3C6A_A             143        --------------NII-CDSFIDLGMKQSKRSKAMGCSALKDLIEKDKLIINH----KGTIQELRTFSE  193 (232)
T ss_dssp                       --------------CBC-CSBTTBSSBCCCHHHHHHHHHHHHHHHHTTCEECCC----HHHHHHHHHCBS
T ss_pred                       --------------Cce-eccccccCCCCCChHHHHHHHHHHHHHHHHcCCeeeCC----HHHHHHHHhcEe

Q ss_pred                       C-------CCCCCcHHHHHHHHHHHcCC
Q Q_7621124_2        829        G-------STWSPGALDAAVYGATEVLPP  850 (881)
Q Consensus          829        ~-------~~~~dD~~Dal~~~~~~~~~~  850 (881)
                                .       .+.|||++||+++|+..+...
T Consensus          194        ~~~~~~~~~g~hdD~vdAla~a~~~~~~~  222 (232)
T 3C6A_A             194        KGVSWAAEEGFHDDLVMSLVIFGWLTTQE  222 (232)
T ss_dssp                       CC--------CCCHHHHHHHHHHHHHTSG
T ss_pred                       cCCcccccCCCCHHHHHHHHHHHHHcch
```

Template alignment | Template 3D structure | PDBe

11. **5TGE_A Phage terminase large subunit; nuclease, VIRAL PROTEIN; 2.6A {Thermus phage P7426}**

Probability: 99.3 E-value: 5.2E-13 Score: 140.21 Aligned Cols: 183 Identities: 12% Similarity: 0.041

```
Q ss_pred                       CCcccccccccHHHHHhcCC----------CCcccceEEEEEEeCCCCCCCcCCcEEEEEEEECCCCcEEE
Q Q_7621124_2        650        PSSAENALLTDADIRAATAP----------VPDELTRVVVGVDPSGGEGARHDTAGISAVGLDEHQHAWF  709 (881)
Q Consensus          650        ~~~~~~~~f~~~~i~~~~~~----------~~~~~~~~~~~iD~a~~~~~~~D~tai~v~~~~~~g~~~v  709 (881)
                                |.++++.+|+++++..+...           .+.....+++++|+|.+    +|+||++|+... .+.+++
T Consensus          2          p~~s~~~~f~~~~l~~~~~~~~~~~~~~~~~~~~~ig~D~A~~~~~~D~tai~v~~~~~~~~~v~  66 (248)
T 5TGE_A             2          PGGSMNSVFSGLDMLILLPYERRGTRLVVEDYRPDHIYCIGADFGKN----QDYSVFSVLDLD-TGAIVC  66 (248)
T ss_dssp                       -----CBSCGGGGGCEEECCEEETTEEESCCCCTTSCEEEEEECCSS----CSEEEEEEEETT-TTEEEE
T ss_pred                       CCCcccccccchHHHHhcccccccCceeeeccCCCCceEEEEEEcCCC----CCCceEEEEEcC-CCeEEE

Q ss_pred                       EecccccCcchHHHHHHHHHHHhCCCEEEEEcccCchHHHHHHHHHHHhccCCCCCCCccccCcccCC
Q Q_7621124_2        710        LEDRTAVLTPLEWPRAVCLLAYERDASMIVYEKNYGGGMASALITQAWAALQNEPINADTDETMIPKSAN  779 (881)
Q Consensus          710        ~~~~~~~~~~~~~~~~i~~~~~~~~~~~i~iE~~~~g~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~  779 (881)
                                ++.+ .+.+++++++.|.+++.+|++..+++|.++.|..+...+.+                      .+
T Consensus          67         ~~~~~~~~~~~~~~~~i~~~~~~~~~~~i~iE~~g~G~~~~~~L~~-----------------------~g  113 (248)
T 5TGE_A             67         LERM-NGATWSDQVARLKALSEDYGHAYVVADTWGVGDAIAEELDA----------------------QG  113 (248)
T ss_dssp                       EEEE-ESCCHHHHHHHHHHHHTTTSCEEEECCC---CCSTTHHHH----------------------HT
T ss_pred                       EEEc-CCCCHHHHHHHHHHHHHhCCCEEEECCCCCCCHHHHHHHHH----------------------CC

Q ss_pred                       CCceeecc--CCCCHHHhHHHHHHHHHcCCeEEcccCcchHHHHHHHccCCCC------------CCCCc
Q Q_7621124_2        780        CPYVKGVS--AKISKVLRAEPIAQAVKTGRAKFAQLGNLGSLTNEFTLWQPGS------------TWSPG  835 (881)
Q Consensus          780        ~~~i~~~~~~~~~~K~~ri~~l~~~~~~g~i~~~~~~~~~~l~~el~~~~~~~~~~~~~~~~~~~dD  835 (881)
                                ++ +.++.  ...+|..++..++.++++|+|.++.   ...|++||..|+...            +.|||
T Consensus          114        ~~~~~~~~~~~~~K~~~~~~~~~~~~g~i~i~~~~~~~l~~El~~~~~~~~~g~~~~~~~~~~hdD  179 (248)
T 5TGE_A             114        IN-YTPLPVKSSSVKEQLISNLALLMEKGQVAVPN---DKTILDELRNFRYYRTASGNQVMRAYGRGHDD  179 (248)
T ss_dssp                       CC-EEECCCCSHHHHHHHHHHHHHHHHHTTCCEEEC---CHHHHHHHHHEEEEECSSSCEEEEECTTCCCH
T ss_pred                       CC-ccccCCCChhHHHHHHHHHHHHHHHcCCccCCC---CHHHHHHHHcCeEEECCCCCeeeecCCCCChH

Q ss_pred                       HHHHHHHHHHHhcCCCCcccccccCCCCC
Q Q_7621124_2        836        ALDAAVYGATEVLPPVGSTTELERPEGRR  864 (881)
Q Consensus          836        ~~Dal~~~~~~~~~~~~~~~~~~~~~~~  864 (881)
                                .+||+++|+..+.................
T Consensus          180        ~vDAl~~a~~~~~~~~~~~~~~~~~~~~  208 (248)
T 5TGE_A             180        IVMSLALAYSQYEGKDGYKFELAEERPSK  208 (248)
T ss_dssp                       HHHHHHHHHTTCCSSSCCCC---------
```

```
T ss_pred                HHHHHHHHHHHHhcCCCCCCccccccCCcc
```

Template alignment | Template 3D structure | PDBe

12. **5M1P_B Terminase large subunit; large terminase, nuclease domain, Hydrolase; 1.1A {Thermus phage G20c}; Related PDB entries: 5M1F_A 5M1K_B 5M1K_A 5M1N_B 5M1N_A 5M1O_B 5M1O_A 5M1P_A 5M1Q_A**

Probability: 99.13 E-value: 9.2E-12 Score: 125.43 Aligned Cols: 164 Identities: 11% Similarity: 0.016

```
Q ss_pred                     ccccccccHHHHHhhcC------------CCCccceEEEEEEeCCCCCCCcCCcEEEEEEEEECCCCcEEE
Q Q_7621124_2        652     SAENALLTDADIRAATA------------PVPDELTRVVVGVDPSGGEGARHDTAGISAVGLDEHQHAWF  709 (881)
Q Consensus          652     ~~~~~~f~~~~i~~~~~------------~~~~~~~~~~~~iD~a~~~~~~~D~tai~v~~~~~~g~~~v  709 (881)
                              +.++++|+  .+..+..            ..+.....+++++|+|.+    +|+|||++++... ++.+++
T Consensus          2       ~~~~~~f~--~~~~~~~~~p~~~~g~~~~~~~~~~~~~~~~~~~~D~a~~----~D~tai~v~~~~-~~~~~~~  64 (191)
T 5M1P_B             2       PAMNSVFS--GLDMLILLPYERRGTRLVVEDYRPDHIYCIGADFGKN----QDYSVFSVLDLD-TGAIAC  64 (191)
T ss_dssp                   CCTTBSCT--TGGGCEEECCEEETTEEESCCCCTTSCEEEEEECCST----TSCEEEEEEETT-TTEEEE
T ss_pred                   chhhcccc--chHHheecccccCceeeeeccCCCceEEEEEEeccC----CCceEEEEEECC-CCeEEE


Q ss_pred                     EeccccccCcchHHHHHHHHHHHHhCCCEEEEEcccCchHHHHHHHHHHHHhccCCCCCCCccccCccccCC
Q Q_7621124_2        710     LEDRTAVLTPLEWPRAVCLLAYERDASMIVYEKNYGGGMASALITQAWAALQNEPINADTDETMIPKSAN  779 (881)
Q Consensus          710     ~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~i~iE~~~~~g~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  779 (881)
                              ++.+ .+.+++++.+.|.+++.+|++..+++|.++.|..+...+.+                       .+
T Consensus          65      ~~~~-~~~~~~~~~~~~~~i~~~~~~~~~~~i~~e~~~~g~~~~~~~l~~----------------------~~  111 (191)
T 5M1P_B             65      LERM-NGATWSDQVARLKALSEDYGHAYVVADTWGVGDAIAEELDA----------------------QG  111 (191)
T ss_dssp                   EEEE-CSCCHHHHHHHHHHHHHHTTSCEEEECCCSSSSHHHHHHHHH----------------------TT
T ss_pred                   EEEe-CCCCHHHHHHHHHHHHHHhCCCEEEEcCCCCcHHHHHHHHH----------------------CC


Q ss_pred                     CCceeecc--CCCCHHHhHHHHHHHHHHcCCeEEcccCccHHHHHHHhccCCC------------CCCCCc
Q Q_7621124_2        780     CPYVKGVS--AKISKVLRAEPIAQAVKTGRAKFAQLGNLGSLTNEFTLWQPG------------STWSPG  835 (881)
Q Consensus          780     ~~~i~~~~~--~~~~K~~ri~~l~~~~~~~g~i~~~~~~~~~~~~~l~~el~~~~~~~------------~~~~dD  835 (881)
                              ++ +.++.  +..+|..++..+...+++|+|+++.   ...|++||..+...              .+.|||
T Consensus          112     ~~-~~~~~~~~~~~~~k~~~~~~~l~~~~~~g~i~~~~---~~~l~~el~~~~~~~~~~~~~g~~~~~~~~~~~dD  177 (191)
T 5M1P_B             112     IN-YTPLPVKSSSVKEQLISNLALLMEKGQVAVPN---DKTILDELRNFRYYRTASGNQVMRAYGRGHDD  177 (191)
T ss_dssp                   CC-EEECCCCSHHHHHHHHHHHHHHHHTTCCEEEC---CHHHHHHHHTEEEEECTTCCEEEEESTTCCCH
T ss_pred                   CC-CCCcccCCchHHHHHHHHHHHHHHHcCCccCCC---CHHHHHHHhccEEEECCCCCeEEecCCCCChH


Q ss_pred                     HHHHHHHHHHHhcC
Q Q_7621124_2        836     ALDAAVYGATEVLP  849 (881)
Q Consensus          836     ~~Dal~~~~~~~~~~~~  849 (881)
                              .+||+++++++..+..
T Consensus          178     ~~da~~~a~~~~~~~~  191 (191)
T 5M1P_B             178     IVMSLALAYSQYEG  191 (191)
T ss_dssp                   HHHHHHHHHTTCC-
T ss_pred                   HHHHHHHHHHHHhhC
```

Template alignment | CDD

13. **PF17289.2 ; Terminase_6C ; Terminase RNaseH-like domain**

Probability: 98.89 E-value: 1.5E-10 Score: 112.85 Aligned Cols: 138 Identities: 12% Similarity: 0.067

```
Q ss_pred                     EEEeCCCCCCCcCCcEEEEEEEEECCCCcEEEEecccc-ccCcchHHHHHHHHHHHHhCCCEEEEEccc---
Q Q_7621124_2        679     VGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTA-VLTPLEWPRAVCLLAYERDASMIVYEKNY---  744 (881)
Q Consensus          679     ~~iD~a~~~~~~~~~D~tai~v~~~~~~~~g~~~v~~~~~~~~-~~~~~~~~~~~~~~i~~~~~~~~~~~~~~~~i~iE~~~~---  744 (881)
                              +++|+|.+    +|+++++++....++.++|++.+.. ..+++++++.|.++..+|++..+.+|+++
T Consensus          1       ig~D~g~~----~d~~~i~~~~~~~~~~~~~~~v~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~~d~~~~~~  66 (161)
T PF17289.2          1       IGIDLGFD----HPNAIACVAWDPEKDKYYLYDERSESGETLGMHADAIYLKGGHQIPVVVPHDAFKHDG  66 (161)
T ss_pred                   CceeccCC----CCCEEEEEEeCCCCEEEEEEeecccCCCHHHHHHHHHhCcCCCeeEeCCcccCCC


Q ss_pred                     --CchHHHHHHHHHHHHHhccCCCCCCCccccCccccCC-CCceeeccCC--------CCHHHhHHHHHHHHH
Q Q_7621124_2        745     --GGGMASALITQAWAALQNEPINADTDETMIPKSAN-CPYVKGVSAK--------ISKVLRAEPIAQAV  803 (881)
Q Consensus          745     --~g~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~-~~~i~~~~~~~--------~~K~~ri~~l~~~~  803 (881)
                                .|..+...++.                         .+ ++ +.+....         .+|..|+..+..++
T Consensus          67      ~~~g~~~~~~l~~------------------------~~~~~-~~~~~~~~~~~~~~~~~~~k~~~i~~l~~~~  113 (161)
T PF17289.2          67      ATSGRRFVDLLKD----------------------DHNLN-VVYEPFSNPPGPDGKHGGNSVEFGVNWML  113 (161)
T ss_pred                   CCCCCCHHHHHHH----------------------cCCce-EEeccCCCCCCCCCCcccchHHHHHHHH


Q ss_pred                     ---HcCCeEEcccCccHHHHHHHhccCCCCC----CCCcHHHHHHHHHHH
Q Q_7621124_2        804     ---KTGRAKFAQLGNLGSLTNEFTLWQPGST----WSPGALDAAVYGAT  845 (881)
Q Consensus          804     ---~~g~i~~~~~~~~~~~~~l~~el~~~~~~~~----~~dD~~Dal~~~~~  845 (881)
                                ++|++.|+.  .+..+++||..|+....     .|||++||+++++.
T Consensus          114     ~~~~~~~~i~i~~--~~~~~~~~el~~~~~~~~~~~~~~~~dd~~Dal~~~~~  160 (161)
T PF17289.2          114     TRMENGDLKVFN--TCTNFLKEMKMYHRKDGKIIDRNDDMISATRYALL  160 (161)
T ss_pred                   HHhhcCCEEEcC--CCHHHHHHHhhhccCCCCCCCchHHHHHHHHHHh
```

Template alignment | Template 3D structure | PDBe

14. **5C12_A Gene 2 protein; nuclease domain, metal binding site; 1.517A {Enterobacteria phage Sf6}; Related PDB entries: 5C2D_A 5C15_A 5C2F_A 5C10_A**

Probability: 98.79 E-value: 1.1E-9 Score: 116.49 Aligned Cols: 188 Identities: 18% Similarity: 0.051

```
Q ss_pred                 hcCCCCcccccccccHHHHHhhcCC----CCccceEEEEEEeCCCCCCCcCCcEEEEEEEECCCCcEEEEe
Q Q_7621124_2       646   SQGLPSSAENALLTDADIRAATAP----VPDELTRVVVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLE  711 (881)
Q Consensus         646   y~~~~~~~~~~f~~~~i~~~~~~~----~~~~~~~~~~~iD~a~~~~~~~D~tai~v~~~~~~g~~~v~~  711 (881)
                          |.|.|.++++.+|+.+++..+...    .+.....+++|+|+|..+   .|+|++++    ..|..++.-
T Consensus         12    ~~~~~~~~~~~i~~~~i~~a~~~~~~~~~~~~~~~iGvDvA~~G---~D~svi~v-----~~g~~v~~v  74 (278)
T 5C12_A            12    SGLVPRGSHMAIIKREWLEAATDAHKKLGWKAKGAVVSAHDPSDTG---PDAKGYAS----RHGSVVKRI  74 (278)
T ss_dssp                 ---------CBSSCHHHHHHHBTHHHHHTCCCCSCEEEEEECCSSS---SSCEEEEE----EETTEEEEE
T ss_pred                 CCcCCCCCCCCceecHHHHHHHHHHHHHhCCCCCCCeEEEEecccCC---CCCEEEEE----EeCCEEEEE

Q ss_pred                 ccccccCcchHHHHHHHHHHHhCCCEEEEEcccCchHHHHHHHHHHHHhccCCCCCCCccccCcccCCCC
Q Q_7621124_2       712   DRTAVLTPLEWPRAVCLLAYERDASMIVYEKNYGGGMASALITQAWAALQNEPINADTDETMIPKSANCP  781 (881)
Q Consensus         712   ~~~~~~~~~~~~~i~~~~~~~~~~~i~iE~~~~g~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~  781 (881)
                          ......++.+++..|.+++.+|++..|+||.+|.|..+...+..   .....               ++.
T Consensus         75    ~~~~~~~~~~~a~~i~~~~~~~~~~~i~vD~~GvG~gv~~~L~~~---~~~~~~~~~~~~~~~~~~~~~~  126 (278)
T 5C12_A            75    AEGLLMDINEGADWATSLAIEDGADHYLWDGDGVGAGLRRQTTE---AFSGK---------------KIT  126 (278)
T ss_dssp                 EEECSCCHHHHHHHHHHHHHHHTTCSEEEEECSSTTTTCHHHHHH---HTTTS---------------CCE
T ss_pred                 EEecCCCHHHHHHHHHHHHHHhCCCEEEEeCCCCChhHHHHHHH---HhcCC---------------CcE

Q ss_pred                 ceeeccCCC--------------------------------CHHHhHHHHHHHHHc-------CCeEEc
Q Q_7621124_2       782   YVKGVSAKI--------------------------------SKVLRAEPIAQAVKT-------GRAKFA  811 (881)
Q Consensus         782   ~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~K~~ri~~l~~~~~~~~~~~~~~~g~i~~~  811 (881)
                           +..+..+.                                .|.+.+..++.++++       |++.++
T Consensus         127   -~v~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~n~kae~~~~l~~~l~~~~~~~~~~g~i~ip  195 (278)
T 5C12_A            127   -ATMFKGSESPFDEDAPYQAGAWADEVVQGDNVRTIGDVFRNKRAQFYYALADRLYLTYRAVVHGEYADP  195 (278)
T ss_dssp                 -EEEECTTSCCTTTTSBCCC------------CCBHHHHBSSHHHHHHHHHHHHHHHHHHHHHHCCCCCG
T ss_pred                 -EEEeecCCCCCCCCCcccCCcccccccCCCCccchhHhcccHHHHHHHHHHHHHHHhhchhccCCcCCH

Q ss_pred                 ccCcc--------------HHHHHHHhccCCC------------------CC-CCCcHHHHHHHHHHHc
Q Q_7621124_2       812   QLGNL--------------GSLTNEFTLWQPG------------------ST-WSPGALDAAVYGATEVL  848 (881)
Q Consensus         812   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  848 (881)
                          .   .               .+|++||..+...                  .+ .|||.+||++++++...
T Consensus         196   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  262 (278)
T 5C12_A            196   D---DMLSFDKEAIGEKMLEKLFAELTQIQRKFNNNGKLELMTAVEMKQKLGIPSPNLADALMMCMHCPA  262 (278)
T ss_dssp                 G---GCCEECHHHHCHHHHHHHHHHHHTTCBBCCCTTSCBCBCCHHHHHHHHCCCCCHHHHHHHHTTCCCC
T ss_pred                 H---hccccChhHhCHHHHHHHHHHHHhCeEeeCCCCCEEEeeHHHHHHHHCCCCCHHHHHHHHHHcCch

Q ss_pred                 CCCCCcccccccCCC
Q Q_7621124_2       849   PPVGSTTELERPEG  862 (881)
Q Consensus         849   ~~~~~~~~~~~~~~  862 (881)
                          .......-..+++.
T Consensus         263   ~~~~~~~~~~~~~~  276 (278)
T 5C12_A            263   LVREETEIYVPSSS  276 (278)
T ss_dssp                 --------------
T ss_pred                 hccCcCcccccCCcC
```

Template alignment | CDD

15. **PF14890.6 ; Intein_splicing ; Intein splicing domain**

Probability: 98.66 E-value: 2.5E-9 Score: 116.41 Aligned Cols: 243 Identities: 19% Similarity: 0.166

```
Q ss_pred                 EECCCccE-EHHHcCC-CCEEE---CCCCCEEEEEEEecCC-C---CeEEEEeCCCCeEEECCCCeEEEE
Q Q_7621124_2       97    VPTPTGWT-THGELRP-GDEVY---HPSGKVVTVRAISADA-H---ASIRVSTSDGGSIVVHPRHEWTVW  157 (881)
Q Consensus         97    Vlt~~G~~-~i~~i~~-gd~v~~~~~~g~~~~v~~~~~~~~~~~~~~~~i~t~~G~~i~~T~~H~~~~~  157 (881)
                          |++.+|.. +|+++.. |+.++   ...+.......++... .   .+++|++..|..+.+|++|++++.
T Consensus         1     v~~~~g~~~~i~~~~~~~~v~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~g~~~~~t~~h~~~~~  70 (296)
T PF14890.6         1     VPLLDGHQKTLREMTEEGGTHWVYSLDSERKIVPGRAVGLKTREDAELMRVTVSGGEEIICTPDHEFMLN  70 (296)
T ss_pred                 CCCCCCceeeHHHHHhCCEEEEEECCCCeEEEcCeEEecCCCCCCccEEEEECCCCEEEECCCCeeeec

Q ss_pred                 eCCCCeEEEcchhHHhhheeecCCCCcccccccCCCCCCCCCcccchHHHHHHc---ccccCCCCeEEe
Q Q_7621124_2       158   DRNRKRWSTMETGDMMRRAYVDRSGRPAFMLPHRDPLEGVDDTLLIDPYTLGVWL---GDGSSTKAAITH  224 (881)
Q Consensus         158   ~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~ip~~~~~~~~~~~~~~~~~llG~~l~~~~dG~~~~~~i~~  224 (881)
                              .+|. .++.++..++.+......                   +.+++|+++   ++|+........
T Consensus         71    ----~~~~~-~~~~~l~~g~~l~~~~~~~~~~~~~~~~~~~~~~~~~g~~~~~~~~g~~~~~~~~~  116 (296)
T PF14890.6         71    ----DGTY-REARDLQFNDSLMPLYRK-------------------WQTRDGYESASTGKGSARQTHVMV  116 (296)
T ss_pred                 ----CCcE-EeHHHCCCCCeecchhce-------------------eccccCceeecCCCcccccceeeh

Q ss_pred                 cCChHHhhhchhhcCeEEecCCcEEEEeCChHHHHHHcCCCCCCcCCHHHHHCCHHHHHHHHHHHHcC
```

```
Q Q_7621124_2       225    HADDEYVLPYPKSADCVHQTTGVVTSYYRGGLHTALKTLGVHANKHIPVQYLRASESSRRALLAGLIDSD  294 (881)
Q Consensus         225    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~l~~~g~~~~k~iP~~i~~~~~~~~~~fL~Gl~dgD  294 (881)
                           .   ................                   ....+.+|.+++.++.+.+.+|
T Consensus         117    ~---~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ip~~~~~~~~~~~~~~~~--------  156 (296)
T PF14890.6         117    Y---EALHGAVPDDHVVHHKN-------------------HIHFDNRPENLEIMEKGEHSRY--------  156 (296)
T ss_pred                  H---HHHhCCCCCCCccccCC-------------------ccchhcCCHHHHhCChhHHHHH--------

Q ss_pred                  CeeCCCCeEEEEeCCHHHHHHHHHHHHCCCcEEEEecCCCCCCCCCcccCeeeEEEEEecCCCCCCceE
Q Q_7621124_2       295    GTIAKSGQVSFINTNRRLYDGVVELIRTLGYRATIHAPLQPSTSSSGVAGTRVLYRVSFTPHDGIPPARL  364 (881)
Q Consensus         295    G~~~~~~~i~~~t~s~~l~~~l~~Ll~~lGi~~~i~~~~~~~~~~~~~~~~~y~~~i~~~~~~~~f~~  364 (881)
                              .....+.+.+.|+.|++     |.++|+..++...             ...|.+.+.+...+..|..
T Consensus         157    ---~~~~~~~~~~~~s~~l~~~~~~l~~~gi~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  205 (296)
T PF14890.6         157    ---HRRVGHSFDNTSPEFQE-----LRMAGIRRRAEDP-------------AKRERMVEVGTKNITAYME  205 (296)
T ss_pred                  ---HhhcccceeecCCHHHHH-----HHHcCcchhhcCc-------------CcceEEEEecchHHHHHHh

Q ss_pred                  Eeec----------------------------------------cccccCCC-CceeEEEEEEeC-Ceee
Q Q_7621124_2       365    SRKV-------------------------------------AMSHCHGQ-RRRTSIIGIEPVD-PRPG  393 (881)
Q Consensus         365    ~~k~----------------------------------------~~~~~~~~-~~~~~I~~Ie~~~-~~~v  393 (881)
                           .+..                                        .......+ ..+.+|.+|+..+ .++|
T Consensus         206    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v  275 (296)
T PF14890.6         206    GKPEHFKEAVADNGKRGAPYLTNFNTSPRACDECGEVSENPAALRWHKNREHGTNHKVIRIEHLDERADV  275 (296)
T ss_pred                  cCHHHHHHHHHchhcCCCCCCCcccCCcccCcCCCCCCCChHHHHHHHccCCCceeEEEEEcCCCcce

Q ss_pred                  eeEEEcCCCCeEEEcCCccccCC
Q Q_7621124_2       394    RCVEVDSPDGLYLVGEHMTPTHN  416 (881)
Q Consensus         394    y~~~v~~~~~~~~~~~~~~~~~  416 (881)
                           ||++| +++|+|+++ ++..+||
T Consensus         276    Ydl~v-~~~~~fia~-ngiv~hN  296 (296)
T PF14890.6         276    YCLQV-EEHNNFALA-AGVFVHN  296 (296)
T ss_pred                  eeEEc-CCCCceecc-cceEEeC
```

Template alignment | Template 3D structure | PDBe

16. **2O0J_A DNA packaging protein Gp17; nucleotide-binding fold, HYDROLASE; HET: ADP; 1.8A {Enterobacteria phage T4}; Related PDB entries: 2O0H_A 2O0K_A**

Probability: 98.64 E-value: 5.5E-9 Score: 117.66 Aligned Cols: 199 Identities: 7% Similarity: 0.012

```
Q ss_pred                  CCeEEEcCCccccCCChhHHhhhHHHHHHcccCCCCeEEEeehhHHHHHHcHHHHHHHHHHHchHhCcccCC
Q Q_7621124_2       402    DGLYLVGEHMTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARRNGAAVRELVREYGPEFGLNLSP  471 (881)
Q Consensus         402    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ili~s~~~~~a~~~~~~i~~~~~~~~~~~~~~~~~  471 (881)
                           ....++  ..++++++|.++..+..|.+...+...+++++++.++++..+..++.+++..+....  ...
T Consensus         178    ~r~~vl--~~~rgsGKT~~~~~~i~~~~~~~~~~~vl~la~s~e~a~q~~~~i~~~~~~~p~~~~--~~~~  243 (385)
T 2O0J_A            178    KRMTVC--NLSRQLGKTTVVAIFLAHFVCFNKDKAVGILAHKGSMSAEVLDRTKQAIELLPDFLQ--PGI  243 (385)
T ss_dssp                  SSEEEE--EECSSSCHHHHHHHHHHHHHHSSSSCEEEEEESSHHHHHHHHHHHHHHHHHSCTTTS--CCE
T ss_pred                  CCeEEE--EeCcccChHHHHHHHHHHHHHHhCCCceEEEEeCCHHHHHHHHHHHHHHHHhCHHHhC--CCe

Q ss_pred                  CCcccCceEeecCceEEEEccCC-CcccCCCCcEEEEeCCCCCH--HHHcCHHHHHHHHHHHHHhhhcccC
Q Q_7621124_2       472    DESSKTDWSIRAGGTMRSRGLRG-NFTGQPMDLGIIDDPITNR--AQAESLVVRDFVWDWYSSVWSQRKA  538 (881)
Q Consensus         472    ~~~~~~~~~~~~~~~i~~~g~~~-s~rG~~~~~ii~DE~~~~~--~~~~~s~~~~~~~~~~~~~~~~~~  538 (881)
                           ..++...+.+.+|+.+.+.+.+. +.+|.+++++++||+....  ...             ...+.+++.
T Consensus         244    ~~~~~~~i~~~nG~~i~~~~~~~~~~G~~~~lviiDEa~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~l~  300 (385)
T 2O0J_A            244    VEWNKGSIELDNGSSIGAYASSPDAVRGNSFAMIYIEDCAFIPNFHDS-------------WLAIQPVIS  300 (385)
T ss_dssp                  EEECSSEEEEETTSCEEEEEECSHHHHHTSCCSEEEEESGGGSTTHHHHH-------------HHHHHHHHH
T ss_pred                  eecCCCEEEEECCCCEEEEEeCCCcccccCCccEEEEccHHHCCChHHH-------------HHHHHHHhh

Q ss_pred                  C--CCeEEEEccccCcccHHHHHHccCCCcCCCeEEEEEeceEeCCcccccCCCCCCCCCCCCcccCCCC
Q Q_7621124_2       539    P--TYREVLVMTRWHQDDLAGRLLARDGRVEEGGVWRVVHLPAIAMPVDEKRGVYPDPLGREPGEPLTHP  606 (881)
Q Consensus         539    ~--~~~~~i~i~T~~~~~d~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~  606 (881)
                           .  .+++++++||.+. +.+++++....  .....|....+++...+.
T Consensus         301    ~~~~~~liltsTP~~~-~~~~~l~~~~~--~~~~~~~~~~~~~~~~~~~~----------------------  345 (385)
T 2O0J_A            301    SGRRSKIIITTTPNGL-NHFYDIWTAAV--EGKSGFEPYTAIWNSVKE----------------------  345 (385)
T ss_dssp                  STTCCEEEEEECCCSS-SHHHHHHHHHH--TTCSSCEEEEECGGGSGG----------------------
T ss_pred                  cCCCcEEEEEECCCCC-CHHHHHHHHHH--cCCCCceeEEeehhhcCC----------------------

Q ss_pred                  CCCCCChhhcccChhHHHHHH----HHHHHHHHhcccchHHHHhcCCCCccc
Q Q_7621124_2       607    LIVPDDPATWSQAPTHREALT----NWWAAKRKMSTARDWSSMSQGLPSSAE  654 (881)
Q Consensus         607    ~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~f~~ey~~~~~~~~  654 (881)
                                  ..++.     +.++    +|.+++++.+++..|.+||+|+|.+.+
T Consensus         346    -------~~~~~~-----e~l~~~~~~~~~~~~~~~~~f~qEy~g~f~~~~  385 (385)
T 2O0J_A            346    -------RLYND-----EDIFDDGWQWSIQTINGSSLAQFRQEHTAAFEGTS  385 (385)
T ss_dssp                  -------GGBCT-----TSBBCTTHHHHHHHHHHTSCHHHHHHHHSCCCSSCC
T ss_pred                  -------ccCCc-----cccccccchHHHHHHHHhCCCHHHHHHHcccccccCC
```

Template alignment | CDD

17. **PF05876.12 ; Terminase_GpA ; Phage terminase large subunit (GpA)**

Probability: 98.49 E-value: 2.1E-7 Score: 111.05 Aligned Cols: 407 Identities: 12% Similarity: 0.005

```
Q ss_pred                    CCCeEEEcCCccccCCChhHHhhHHHHHHccCCCCeEEEeehhHHHHHHcH-HHHHHHHHHHchHhCccc
Q Q_7621124_2       401     PDGLYLVGEHMTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARRNG-AAVRELVREYGPEFGLNL  469 (881)
Q Consensus         401     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ili~s~~~~~a~~~~-~~i~~~~~~~~~~~~~~~~  469 (881)
                             ..+..++  ..++..++|.+.....+|.+...+ ..+++++++.++|+.++ ..+..+++..+.+-...
T Consensus         32      ~~~~v~i--~~~~rq~GKT~~~~~~~~~~~~~~~~-~~i~~~~pt~~~a~~~~~~~~i~~~i~~~p~l~~~~-  97 (541)
T PF05876.12        32      ETEEIIF--VKPTQVGGTETLQNCLGYVVTQDP-SPSMVVYPTDTLAESISENRLQPMFRNSPGLKQRF-  97 (541)
T ss_pred                    CccEEEE--EeCCcCcHHHHHHHHHHHHHHHhCC-CCEEEEEeCHHHHHHHHHhhhHHHHHhCHHHHHHH-

Q ss_pred                    CCCCcccCceEeecCceEEEEccCC-CcccCCCcEEEEeCCCCCHHH-------HcCHHHHHHHHHHHHH
Q Q_7621124_2       470     SPDESSKTDWSIRAGGTMRSRGLRG-NFTGQPMDLGIIDDPITNRAQ-------AESLVVRDFVWDWYSS  531 (881)
Q Consensus         470     ~~~~~~~~~~~~~~~~i~~~g~~~-s~rG~~~~~ii~DE~~~~~~~~-------~~s~~~~~~~~~~~~~  531 (881)
                             .....+...+.+.++..+...+.+. +.+|.+++++|+||+.....+        .          +.+..
T Consensus         98      ~~~~~~~~~~~~~~~g~~~~a~s~~~~~g~~~~~~i~DE~~~~~~~~~eg~~~---------~~~~~  157 (541)
T PF05876.12        98      RERESSKLELQCDGMYISLNGANSPSSLSSKPIRFLFLDEVDKYPGASKKEADPI----------KLARE  157 (541)
T ss_pred                    ccCCCCcEEEEeCCcEEEEeeCCChHHhccCcccEEEEeCHhhCCccCCCCCHH----------HHHHH

Q ss_pred                    hhhcccCCCCeEEEEccccCcccHHHHHHhccCCCcCCCeEEEEEeceEeCCccccccCCCCCCC------
Q Q_7621124_2       532     VWSQRKAPTYREVLVMTRWHQDDLAGRLLARDGRVEEGGVWRVVHLPAIAMPVDEKRGVYPDPL------  595 (881)
Q Consensus         532     ~~~~~~~~~~~~i~i~T~~~~~d~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~------  595 (881)
                             .+...  ..++++++|||...++.++.+++.         .-....|...+....+....-+...
T Consensus         158     r~~~~-~~~~~~~~sTp~~~~~~i~~~~~~~--------~~~~~~~~~~~~Cp~Cg~~~~l~~~~~~~~~~  217 (541)
T PF05876.12        158     RTKTF--PNRKIFITSTPTLKTGHIWKAKES--------ADVVKHYKVPCPHCGEYIEFRFKNIIWPKED  217 (541)
T ss_pred                    HHHhC--CCCeEEEEcCCccCCCHHHHHHHh--------CCEEEEEEccCCCCCCEEEEeehhceeccCcc

Q ss_pred                    ------CCCCCccCCCCCCCCCCh---------hhcccChh--------------------HHHHHHHH
Q Q_7621124_2       596     ------GREPGEPLTHPLIVPDDP---------ATWSQAPT--------------------HREALTNW  629 (881)
Q Consensus         596     ------~~~~~~~l~~~~~~~~~~~---------~~~~~~~~~--------------------~~~~l~~~  629 (881)
                                  ......+.++.+...-+.          ..|-..++                       +.+-..++
T Consensus         218     ~~~~~~~~~~~~~C~~C~~~i~~~~~~~~~~~~~g~W~~~~p~~~~~~~~g~~i~~l~sp~~~~~~l~~~~  287 (541)
T PF05876.12        218     GMSSADRAEFAHYVCQECGSIITDQNKHQMLRFGRWEVVEKRTQFPRKVCYWMNTLYSPFVRFGEIAKEF  287 (541)
T ss_pred                    CCCccchhhcEEECCCCCCeecHHHHHHHHHhCeEEECCcCCCCCCEEEEEecchhccCCHHHHHHHH

Q ss_pred                    HHHHHHhccchHHHHhcCCCCccccccccHHHHHhhcCC-----CCccceEEEEEeCCCCCCCcCCcE
Q Q_7621124_2       630     WAAKRKMSTARDWSSMSQGLPSSAENALLTDADIRAATAP-----VPDELTRVVVGVDPSGGEGARHDTA  694 (881)
Q Consensus         630     ~~~~~~~~~~~~~f~~ey~~~~~~~~~~~~~~~~f~~~~i~~~~~~~-----~~~~~~~~~~~~~iD~a~~~~~~~D~t  694 (881)
                             ++..........|....++.|....+..++.+.+..+...      .|.....+++|||++..       ..
T Consensus         288     ~~a~~~~~~~~~~~F~n~~lg~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~p~~~~~~~~~GvD~~~~~------~~  351 (541)
T PF05876.12        288     LATKDDPEAFQNFVNSWLAEPWEDTKLKTNADLVMERQTTYEEFTVPDWTVFLTGGVDVQET------SL  351 (541)
T ss_pred                    HhcCCCHHHHHHHhhcccccCccccccCCCHHHHHHHHHhcCCcCCCCCCCeeEEEEEEEeCCC------eE

Q ss_pred                    EEEEEEECCCCcEEEEecccccCcchHHHHHHHHHH---------HhCCCEEEEEcccCchHHHHHHHH
Q Q_7621124_2       695     GISAVGLDEHQHAWFLEDRTAVLTPLEWPRAVCLLAY---------ERDASMIVYEKNYGGGMASALITQ  755 (881)
Q Consensus         695     ai~v~~~~~~g~~~v~~~~~~~~~~~~~~~~~~~~i~~~~~~~---------~~~~~~~i~iE~~~~~g~~~~~~~l~~  755 (881)
                             .++|++...     ++++...-.-++. ..+.+.+++.          .+++..++||..+....+..+...
T Consensus         352     ~~~v~~~~~~----~~i~~~~~~~g~~~~~~l~~~~~~~~~~~~~~~~~g~~~~i~~~~iD~g~~t~~v~~~~~~  416 (541)
T PF05876.12        352     YWTIRAFGP----YLTSQNIAHGQAV-SFREIENIMNAEYKKLNGEAHMVNLCGIDSGDQTDDVYDFCAD  416 (541)
T ss_pred                    EEEEEEEee----EEEEEEEEcCChh-HHHHHHHHHhCeeEcCCCCEEEEEEEEecCCCHHHHHHHHh

Q ss_pred                    HHHHhccCCCCCCCcccCcccC-----------CCCceeeccCCCCHHHHHHHHHHHHHHcCCeEEccC
Q Q_7621124_2       756     AWAALQNEPINADTDETMIPKSA-----------NCPYVKGVSAKISKVLRAEPIAQAVKTGRAKFAQLG  814 (881)
Q Consensus         756     ~~~~~~~~~~~~~~~~~~~~~~~~-----------~~~~i~~~~~~~~~~K~~ri~~l~~~~~~g~i~~~~~~  814 (881)
                             ....+..-.....   +..+...                +.. +..+....-|......|...-..|.++++. .
T Consensus         417     ~~~~v~~~kG~~---~~~~~~~~~~~~~~~~~~~~~~~~~~-~~~~~~~~~~~kd~l~~~l~~~~~~g~~~~p~~~  481 (541)
T PF05876.12        417     NSEWAIPVKGVPS---GYSHFKISTINKTSSRAHGSR-LLLVDGGKYKDMIASRMAKPNGQGSWMVYK-G  481 (541)
T ss_pred                    cCCcEEEEccCCC---CccceeccCCCceecccCCCe-EEEEehHHHHHHHHHHHhcCCCCCCCeEEecC-C

Q ss_pred                    ccHHHHHHHHc----------------cCCCCC-CCCcHHHHHHHHHHHHh
Q Q_7621124_2       815     NLGSLTNEFTL----------------WQPGST-WSPGALDAAVYGATEV  847 (881)
Q Consensus         815     ~~~~l~~el~~~~~~~----------------~~~~~~-~~dD~~Dal~~~~~~~~~  847 (881)
                             ...++.+||.+                 |....+ ..+|..|++.|+....
T Consensus         482     ~~~~~~~~ql~~e~~~~~~~~~~~~G~~~~~~w~~~~~~~~nh~~D~~~y~~~a~  531 (541)
T PF05876.12        482     CDREYAEQVTAEHKVNSKGSGGKVTQVWQPKTSHADNHFLDAEVYCMAAA  531 (541)
T ss_pred                    CCHHHHHhheeEEEeeccccCCeeeEEEEeCCCCCChHHHHHHHHHHHHH
```

Template alignment | CDD

18. PF03237.15 ; **Terminase_6 ; Terminase-like family**

Probability: 98.47 E-value: 8.6E-8 Score: 100.05 Aligned Cols: 222 Identities: 27% Similarity: 0.343

```
Q ss_pred                  ccccCCChhHHHHHHHHHccCCCCeEEEEeehhHHHHHHcHHHHHHHHHHHchHhCcccCCCCcccCceE
Q Q_7621124_2       411    MTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARRNGAAVRELVREYGPEFGLNLSPDESSKTDWS  480 (881)
Q Consensus         411    ~~~~~~~~~~~~~~~~~~~~~~~~ili~s~~~~~a~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~  480 (881)
                           +++.+++|.......++.+...+...+++++++.+++...+......+..+...-.......   ...+.
T Consensus         4      ~~rg~GKT~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~---~~~~~~  70 (232)
T PF03237.15        4      IPPQHGKSTVITETFPAYYLMRHPDSLVMVVSYSKELFQKFGRKNREKFRLFSDQLFGLQIS---SETSS  70 (232)
T ss_pred                  cCCCCCChhHHHHHHHHHHHhhCCCceEEEEeCCHHHHHHhhHHHHHHHHHhhChhhHhhcC---ceeee


Q ss_pred                  eecCce-EEEEccC-----CCcccCCCcEEEEeCCCCCHHHHcCHHHHHHHHHHHHhhhcccCCCCeEE
Q Q_7621124_2       481    IRAGGT-MRSRGLR-----GNFTGQPMDLGIIDDPITNRAQAESLVVRDFVWDWYSSVWSQRKAPTYREV  544 (881)
Q Consensus         481    ~~~~~~-i~~g~~------~s~rG~~~~~ii~DE~~~~~~~~~s~~~~~~~~~~~~~~~~~~~~~~~i  544 (881)
                           +.+++. +...+..     .+.+|.+++++++||+.....+..+...+.....+....+.+...+.+.+.
T Consensus         71     ~~ng~~~i~~~~~~~~~~~~~~G~~~~~i~iDE~~~~~~~~~~~~~~~~~~~~~~~~st~~~~~~~~  140 (232)
T PF03237.15        71     VSEWGVEGHLGSLYSTSILGGATGRGARLLIIDDPIKNRAEAESKTIRDKIYNEWQDTFYSRLTADASVI  140 (232)
T ss_pred                  ccccccccccceeeEEecCCCcccccCCCEEEEEeCCCCChHHhcCHHHHHHHHHHHHHhhcccCCCCeEE


Q ss_pred                  EEccccCcccHHHHHHhccCCCcCCCeEEEEEeceEeCCcccccCCCCCCCCCCCcCCCCCCCCCCCCCCh
Q Q_7621124_2       545    LVMTRWHQDDLAGRLLARDGRVEEGGVWRVVHLPAIAMPVDEKRGVYPDPLGREPGEPLTHPLIVPDDPA  614 (881)
Q Consensus         545    ~i~T~~~~~d~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  614 (881)
                           .+.+++...+++..+.....     ..|....+++....+...........-.......-+
T Consensus         141    ~~~~~~~~~~~~~~~~~~~~-----~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  196 (232)
T PF03237.15        141    VIMTRWHEDDLAGRLLKEQT-----LPWEEIKIPAIAEDDDLLGRKPGEALAPEIGKDEEW---------  196 (232)
T ss_pred                  EEeeccCcccHHHHHHhcCC-----CCcEEEEeeEEecCccccCCCCCCCCCcccCCHHHH---------


Q ss_pred                  hcccChhHHHHHHHHHHH-HHHhcccchHHHHhcCCCCcccccccCHHHHHh
Q Q_7621124_2       615    TWSQAPTHREALTNWWAA-KRKMSTARDWSSMSQGLPSSAENALLTDADIRA  665 (881)
Q Consensus         615    ~~~~~~~~~~~l~~~~~~-~~~~~~~~~~f~~ey~~~~~~~~~~~f~~~~i~~  665 (881)
                                                  .. .+...+.-.|.+||||.|.+.++.+|+.+++++
T Consensus         197    ----------------~~~~~~~~~g~~~~~~~~~~~p~~~~~~~f~~~~i~~  232 (232)
T PF03237.15        197    ----------------AAKTKAVTGSRGWAALYQQRPTPAGGNIFKRSWIKF  232 (232)
T ss_pred                  ----------------HHHHHHHHhCchhHHHHHcCCCCCCCCCcccHHHcCC
```

Template alignment | Template 3D structure | PDBe

19. 2VS7_G **HOMING ENDONUCLEASE I-DMOI (E.C.3.1.-.-); PROTEIN/NUCLEIC ACID CRYSTALLOGRAPHY, ENDONUCLEASE, MEGANUCLEASE; 2.05A {DESULFUROCOCCUS MOBILIS}; Related PDB entries: 5O6G_G 5O6G_D 5O6G_A 5O6I_F 5O6I_A 5O6I_K 2VS8_F 2VS8_A 2VS8_K 4D6O_G 4UNB_G 4D6O_D 4UNB_D 4D6O_A 4UNB_A 5AK9_E 5AK9_J 5AK9_A 5A0W_G 5A0W_D 5A0W_A 5AKM_F 2VS7_D 5AKM_A 2VS7_A 5AKM_K 5AKN_F 4UNC_G 5AKN_A 4UNC_D 5AKF_E 5AKN_K 4UNC_A 4UN7_G 5AKF_I 4UN7_D 5AKF_A 4UN7_A 4UN8_G 4UN8_D 4UN8_A 4UN9_G 4UN9_D 4D6N_F 4UN9_A 4UT0_F 4D6N_A 4UNA_G 4UT0_A 4D6N_K 4UNA_D 4UT0_K 4UNA_A 1B24_A**

Probability: 98.37 E-value: 8.9E-8 Score: 97.53 Aligned Cols: 148 Identities: 20% Similarity: 0.225

```
Q ss_pred                  CCCCCcccchHHHHHHhcccccCCCC---------eEEecCChHHhhhchhh---------------cCe
Q Q_7621124_2       195    EGVDDTLLIDPYTLGVWLGDGSSTKA---------AITHHADDEYVLPYPKS---------------ADC  240 (881)
Q Consensus         195    ~~~~~~~~~~~llG~~l~dG~~~~~----------i~~~~~~~~~~~~~~~~----------------~~~  240 (881)
                           ..+....+..++++|+++|||++...          .+.+...+....+.+..                ...
T Consensus         2      ~~~~~~~~~~~l~G~~~gdG~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  71 (199)
T 2VS7_G            2      HNNENVSGISAYLLGLIIGDGGLYKLKYKGNRSEYRVVITQKSENLIKQHIAPLMQFLIDELNVKSKIQI  71 (199)
T ss_dssp                  ---CTHHHHHC-CHHHHHHHCBC-CCC-CCSCCC-CEEC-CCCSTTCCCCCHHHHHHHHHHHTCCCCEEE
T ss_pred                  CCCCCCCHHHHHHHHHHHcccceeeeccCCCceeEEEEEEeCCHHHHHHHHHHHHHHHHHcCCceeeEE


Q ss_pred                  EEecCCcEEEEeCChHHHHHHHcCCCCCCcCCHHHHHCCHHHHHHHHHHHHHcCCeeCCCCeEEEEeCCH
Q Q_7621124_2       241    VHQTTGVVTSYYRGGLHTALKTLGVHANKHIPVQYLRASESSRRALLAGLIDSDGTIAKSGQVSFINTNR  310 (881)
Q Consensus         241    ~~~~~~~~~~~~~~~l~~~l~~~g~~~~k~iP~~i~~~~~~~~~~fL~Gl~dgDG~~~~~~~i~~~t~s~  310 (881)
                           ........+.+.+..+..++..+        |..+..++.+...+||+|+|++||++... .+.+.+.|+
T Consensus         72     ~~~~~~~~~~~~~~~~~~~l~~~-------~~~~~~~~~~~~~~~fl~g~~~~dG~~~~~~~i~~~~~~~  132 (199)
T 2VS7_G            72     VKGDTRYELRVSSKKLYYYFANM--------LERIRLFNMREQIAFIKGLYVAEGDKTLK-RLRIWNKNK  132 (199)
T ss_dssp                  CCCC-C-CEEECCSCC---CHHH--------HHTGGGCCHHHHHHHHHHC-CCSSCC-CC-SEEC-CCCH
T ss_pred                  EcCCcEEEEEEccCHHHHHHHHHh--------HHHHhhcCHHHHHHHHHHHHhhCCCeecc-eEEEEeCCH


Q ss_pred                  HHHHHHHHHHHHCCCcEEEEecCCCCCCCCCcCceeeEEEEEEecCCCCCCc
Q Q_7621124_2       311    RLYDGVVELIRTLGYRATIHAPLQPSTSSSGVAGTRVLYRVSFTPHDGIPPA  362 (881)
Q Consensus         311    ~l~~~l~~Ll~~lGi~~~i~~~~~~~~~~~~~~~~~~y~~~i~~~~~~~~f  362 (881)
                           +++++|+.+|.++||.+++..++...          ..|.+.+.+.+.. .|
T Consensus         133    ~~~~~l~~ll~~~gi~~~~~~~~~~~~~~~~~~~~~~~~l~i~~~~~~-~~  173 (199)
T 2VS7_G            133    ALLEIVSRWLNNLGVRNTIHLDDHRH----------GVYVLNISLRDRI-KF  173 (199)
T ss_dssp                  HHHHHHHC-CTTTTCCC-CCCCCTTT----------TC-CCEECGGGHH-HH
T ss_pred                  HHHHHHHHHHHHcCCcceEEeCCCCc----------eEEEEEEecchhE-Eh
```

Template alignment | Template 3D structure | PDBe

20. 4ZNK_A **Phage terminase large subunit; DNA Translocation, VIRAL PROTEIN; HET: SO4; 1.931A {Thermus phage P7426}; Related PDB entries: 4ZNI_A 4ZNJ_A 4ZNL_C 4ZNL_B 4ZNL_A**

Probability: 98.37 E-value: 1.5E-7 Score: 101.26 Aligned Cols: 201 Identities: 10% Similarity: 0.032

```
Q ss_pred                 CCeEEEcCCccccCCChhHHhhHHHHHHHccCCCCeEEEeehhHHHHHHcHHHHHHHHHHHchHhCcccCC
Q Q_7621124_2       402   DGLYLVGEHMTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARRNGAAVRELVREYGPEFGLNLSP  471 (881)
Q Consensus         402   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ili~s~~~~~a~~~~~~i~~~~~~~~~~~~~~~~~  471 (881)
                          ....++  .++++.++|.......++.+...+...+++++++..+++.++..+...+.....++.....
T Consensus         35    ~~~~~i--~~~~~gsGKT~~~~~~~~~~~~~~~~~~~i~~~~~~~a~~~~~~~~~~~~~~~~~~~~~~  102 (274)
T 4ZNK_A            35    AKRRVA--CLGRQSGKSEAASVEAVFELFARPGSQGWIIAPTYDQAEIIFGRVVEKVERLAEVFPATEVQ  102 (274)
T ss_dssp                 CSEEEE--EECTTSSHHHHHHHHHHHHHHHSTTCEEEEEEESSHHHHHHHHHHHHHHHHHHHTTCTTEEEE
T ss_pred                 CCeEEE--EeCCCCCHHHHHHHHHHHHHHHhCCCCEEEEEeCCHHHHHHHHHHHHHHHHHHHHhCCcccee

Q ss_pred                 CCcccCceEeec--------------CceEEEEccCC--CcccCCCcEEEEeCCCCHHHHcCHHHHHHH
Q Q_7621124_2       472   DESSKTDWSIRA--------------GGTMRSRGLRG--NFTGQPMDLGIIDDPITNRAQAESLVVRDFV  525 (881)
Q Consensus         472   ~~~~~~~~~~~~--------------~~~i~~~g~~~--s~rG~~~~~ii~DE~~~~~~~~~s~~~~~~~  525 (881)
                          .........+..              ++.+...+...  +.+|.+++++++||+....++.
T Consensus         103   ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~g~~~~~ii~DE~~~~~~~~~~~~~~~  163 (274)
T 4ZNK_A            103   LQRRRLRLLVHHYDRPVNAPGAKRVATSEFRGKSADRPDNLRGATLDFVILDEAAMIPFSV---------  163 (274)
T ss_dssp                 EETTTTEEEEEEESSCTTSTTCCEEEEEEEEEEETTCGGGCCSCCCSEEEEETGGGSCHHC---------
T ss_pred                 ccccccceeeeccCCCcCCCCCceeeccEEEEEeCCCccccCCCCCCEEEEeCHhhCCHHH---------

Q ss_pred                 HHHHHHhhhcccCC-CCeEEEEccccCcccHHHHHHhccCCCcC-------------CCeEEEEEeceEe
Q Q_7621124_2       526   WDWYSSVWSQRKAP-TYREVLVMTRWHQDDLAGRLLARDGRVEE-------------GGVWRVVHLPAIA  581 (881)
Q Consensus         526   ~~~~~~~~~~~~~~~~~~i~i~T~~~~~d~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  581 (881)
                             +...+.+++.. ++++++++||.+.++++..+.+..+  ..             .+.|.+++++...
T Consensus         164   ---~~~~~~~~~~~~~~~~~~~~Tp~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  228 (274)
T 4ZNK_A            164   ---WSEAIEPTLSVRDGWALIISTPKGLNWFYEFFLMGWR--GGLKEGIPNSGINQTHPDFESFHAASWD  228 (274)
T ss_dssp                 ---CCCCCGGGGTTTTCEEEEEECCCSSSHHHHHHHHHCC--SCSBTTBTTTTSCCCCTTEEEEEECHHH
T ss_pred                 ---HHHhHHHhhcccCcEEEEEeCCCcccHHHHHHHHhhc--CCcccCCCCCCCCCCCCceeeeecccc

Q ss_pred                 CCccccccCCCCCCCCCCCccCCCCCCCCCChhhcccChhHHHHHHHHHHHHHHHhcccchHHHHhcCCCC
Q Q_7621124_2       582   MPVDEKRGVYPDPLGREPGEPLTHPLIVPDDPATWSQAPTHREALTNWWAAKRKMSTARDWSSMSQGLPS  651 (881)
Q Consensus         582   ~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~f~~ey~~~~~  651 (881)
                          ++                                      ..-.++++++++.+++..|+++|+|++.
T Consensus         229   n~-------------------------------------~~~~~~~~~~~~~~~~~~~~~~~~~~~g~~~  258 (274)
T 4ZNK_A            229   VW--------------------------------------PERREWYMERRLYIPDLEFRQEYGAEFV  258 (274)
T ss_dssp                 HC--------------------------------------GGGHHHHHGGGGTSCHHHHHHHTTCCCC
T ss_pred                 CC--------------------------------------cchHHHHHHHHhCCHHHHHHHhccEEE

Q ss_pred                 ccccccc
Q Q_7621124_2       652   SAENALL  658 (881)
Q Consensus         652   ~~~~~~f  658 (881)
                          ..++.+|
T Consensus         259   ~~~~~~~  265 (274)
T 4ZNK_A            259   SHSGLEH  265 (274)
T ss_dssp                 CHHHHTC
T ss_pred                 ecCCCcc
```

Template alignment | Template 3D structure | PDB | NCBI

21. d1jvaa3 **d.95.2.2 (A:582-698) VMA1-derived endonuclease (VDE) PI-SceI {Baker's yeast (Saccharomyces cerevisiae) [TaxId: 4932]}**

Probability: 98.36 E-value: 4.1E-8 Score: 90.11 Aligned Cols: 94 Identities: 24% Similarity: 0.377

```
Q ss_pred                 CCCcCCHHHHHCCHHHHHHHHHHHHHcCCeeCCCC--eEEEEeCCHHHHHHHHHHHHHCCCcEEEEecCC
Q Q_7621124_2       267   ANKHIPVQYLRASESSRRALLAGLIDSDGTIAKSG--QVSFINTNRRLYDGVVELIRTLGYRATIHAPLQ  334 (881)
Q Consensus         267   ~~k~iP~~i~~~~~~~~~~fL~Gl~dgDG~~~~~~~~~i~~~t~s~~l~~~l~~Ll~~lGi~~~i~~~~~  334 (881)
                          .+|.||++++.++.+.+.+||+|||++||++...+  .+.+++.|+.|+++++.||.++||.+++.....
T Consensus         1     ~~k~iP~~~~~~~~~~~~~fL~G~~d~dG~~~~~~~~~i~~~t~s~~l~~~i~~ll~~lGi~~~~~~~~  70 (117)
T d1jvaa3           1     GVKNIPSFLSTDNIGTRETFLAGLIDSDGYVTDEHGIKATIKTIHTSVRDGLVSLARSLGLVVSVNAEPA  70 (117)
T ss_dssp                 TEECCCGGGGGSCHHHHHHHHHHHHHHHHEEEECTTSCEEEEEESCHHHHHHHHHHHHHHTCEEEEEEEC-
T ss_pred                 CCCCCCHHHhhCCHHHHHHHHHHHHHcCCeEecCCccEEEEEECCHHHHHHHHHHHHHCCCeEEEEecC

Q ss_pred                 CCCCCCCcccCeeeEEEEEEecCCCCCCc
Q Q_7621124_2       335   PSTSSSGVAGTRVLYRVSFTPHDGIPPA  362 (881)
Q Consensus         335   ~~~~~~~~~~~~~y~~~i~~~~~~~~f  362 (881)
                          +.  ..........|.+.+.+.+.+..|
T Consensus         71    ~~-~~~~~~~~~~~~l~i~~~~~~~~~  96 (117)
T d1jvaa3           71    KV--DMNGTKHKISYAIYMSGGDVLLNV  96 (117)
T ss_dssp                 -----------CCEEEEEEECTHHHHH
T ss_pred                 cc--CCCCceeceEEEEEEcCchHHHHH
```

Template alignment | Template 3D structure | PDBe

22. **3HYJ_D Protein DUF199/WhiA; LAGLIDADG, homing endonuclease, helix-turn-helix, HTH; HET: GOL; 2.6A {Thermotoga maritima}; Related PDB entries: 3HYJ_A**

Probability: 98.27 E-value: 4.1E-8 Score: 99.76 Aligned Cols: 141 Identities: 9% Similarity: -0.076

```
Q ss_pred                    CCCcccchHHHHHHhcccccCCC--CeEEecCChHhhhhchhh-----------cCeEEecC--CcEEEE
Q Q_7621124_2        197     VDDTLLIDPYTLGVWLGDGSSTK--AAITHHADDEYVLPYPKS-----------ADCVHQTT--GVVTSY  251 (881)
Q Consensus          197     ~~~~~~~~~~llG~~l~dG~~~~--~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  251 (881)
                             +....+.+++++|++++||++..  ..+.+...+..+.+.+..           ........  ...+.+
T Consensus          22      ~~~~~~~~a~llG~~~~dG~i~~~~~~i~~~~~~~~~~~~~i~~l~~~~f~~~~~i~~~~~~~~~~~~~~i  91 (198)
T 3HYJ_D             22      FGSREEVISELLGFIKARGDLDVKSRHIVFSLHSFAASRRLLNLMKYLSKPVSEIIVEKSHNIKKRYIKI  91 (198)
T ss_dssp                    CCCHHHHHHHHHHHHHHHEESSSSTTEEEEEESCHHHHHHHHHHHHTTCCEEEEEEEECSSSBEEEEEE
T ss_pred                    CCChHHHHHHHHHHHHhceEEEEcCCEEEEEECCHHHHHHHHHHHHHhCCceEEEEEeCCCCCCcEEEE

Q ss_pred                    eCChHHHHHHHcCCCCCcCCHHHHHCCHHHHHHHHHHHHHcCCeeCC---CCeEEEEeCCHHHHHHHHH
Q Q_7621124_2        252     YRGGLHTALKTLGVHANKHIPVQYLRASESSRRALLAGLIDSDGTIAK---SGQVSFINTNRRLYDGVVE  318 (881)
Q Consensus          252     ~~~~l~~~l~~~g~~~~k~iP~~i~~~~~~~~~~fL~Gl~dgDG~~~~~---~~~i~~~t~s~~l~~~l~~  318 (881)
                             .+..+          ....+|.  ...+.+..++||+|+|++||++..   +..++|.+.|+.++++++.
T Consensus          92      ~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~aflrGlfd~dG~i~~~~~~~~i~~~~~s~~l~~~l~~  149 (198)
T 3HYJ_D             92      TAEYS----------ESFMVIE--PFFDVALFVSFLRGLFLSGGSMTNPRYHYHLEINLFEEETLALTRK  149 (198)
T ss_dssp                    EEECC----------TTTTSCC--CSSSHHHHHHHHHHHHHHHEEECCTTTCCCEEEECCCHHHHHHHHH
T ss_pred                    cccch----------hhccccc--ccCCHHHHHHHHHHHHhcccceecCCCCceeEEEEcCCHHHHHHHHH

Q ss_pred                    HHH-HCCCcEEEEecCCCCCCCCCcCeeeEEEEEEecCCCCCCc
Q Q_7621124_2        319     LIR-TLGYRATIHAPLQPSTSSSGVAGTRVLYRVSFTPHDGIPPA  362 (881)
Q Consensus          319     Ll~~lGi~~~i~~~~~~~~~~~~~~~~~~y~~~i~~~~~~~~f  362 (881)
                             +|. .+||.+++..+             +..|.+.+.+.+++..|
T Consensus          150     lL~~~~gi~~~~~~~~~~~~~~~~~~~~~l~i~~~~~i~~f  181 (198)
T 3HYJ_D             150     SLKDFFNINAGIIEL-------------RNTRKLYIKSIKDILVF  181 (198)
T ss_dssp                    HHHHHHCCCCEEEEC-------------SSCEEEEECCHHHHHH
T ss_pred                    HHHHHcCCCceEEEe-------------CCeEEEEEcCHHHHHH
```

Template alignment | Template 3D structure | PDBe

23. **1GPP_A ENDONUCLEASE PI-SCEI (E.C.3.6.3.14); ENDONUCLEASE, HOMING, PROTEIN SPLICING; 1.35A {SACCHAROMYCES CEREVISIAE} SCOP: l.1.1.1, b.86.1.2**

Probability: 98.18 E-value: 1.2E-7 Score: 95.96 Aligned Cols: 72 Identities: 17% Similarity: 0.17

```
Q ss_pred                    cccCCCcEECCCcc-EEHHHcCCCCEEECCCCCEEEEEEEecCCCCeEEEEeCCC---------------
Q Q_7621124_2        90      LVAHDTPVPTPTGW-TTHGELRPGDEVYHPSGKVVTVRAISADAHASIRVSTSDG---------------  143 (881)
Q Consensus          90      C~~~dt~Vlt~~G~-~~i~~i~~gd~v~~~~g~~~~v~~~~~~~~~~~i~t~~G---------------  143 (881)
                             |++.+|+|++++|+ ++|++|++||.|++.||++++|..+.+..+++|+|+..+|
T Consensus          11      ~~a~gT~VlmadG~~k~IedI~vGD~Vmg~DG~pr~V~~~~~g~~~mY~V~~~~ghra~~~d~~~~~~g~  80 (237)
T 1GPP_A             11      CFAKGTNVLMADGSIECIENIEVGNKVMGKDGRPREVIKLPRGSETMYSVVQKSQHRAHKSDSSREMPEL  80 (237)
T ss_dssp                    EECTTCEEEBTTSCEEEGGGCCTTCEEEBTTSSEEEEEECCEEEEEEEEEEECC------------CCCC
T ss_pred                    cccCCCCEEEcCCCCEEEHHHcccCCEEEcCCCCeEeEEEEcCCceEEEEEEECCCccccCCCCCCCCCc

Q ss_pred                    CeEEECCCCeEEEEeCCC
Q Q_7621124_2        144     GSIVVHPRHEWTVWDRNR  161 (881)
Q Consensus          144     ~~i~~T~~H~~~~~~~~~  161 (881)
                             ..++||.+|.|.+.....
T Consensus          81      ~~~~c~~~H~l~l~t~~~  98 (237)
T 1GPP_A             81      LKFTCNATHELVVRTPRS  98 (237)
T ss_dssp                    CEEEEETTCEEEEEEECC
T ss_pred                    eEEEeCCCCEEEEecCCc
```

Template alignment | CDD

24. **PF03161.13 ; LAGLIDADG_2 ; LAGLIDADG DNA endonuclease family**

Probability: 98.13 E-value: 1.8E-7 Score: 92.93 Aligned Cols: 142 Identities: 13% Similarity: 0.095

```
Q ss_pred                    HHHHHHHcccccCCCC------eEEe--cCChHhhhhchhh-----------cCeEE--------ecCCc
Q Q_7621124_2        205     PYTLGVWLGDGSSTKA------AITH--HADDEYVLPYPKS-----------ADCVH--------QTTGV  247 (881)
Q Consensus          205     ~~llG~~l~dG~~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  247 (881)
                             ++++|+++|||++...       .+.+  ...+....+.+..            .....        .....
T Consensus          2       a~l~G~l~gDG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  71 (174)
T PF03161.13         2       SILFGSLLGDSHAERRAIGNGTRISFTQEAIHKEYLIWLHNLIFNLGYSTPNLPKIQTRLGLGGKLRYVL  71 (174)
T ss_pred                    ceeeeeeeecEEEEecCCCCceEEEEEEchhcHHHHHHHHHHHHHhcCCCCCCeeeccCCCCceEEEE

Q ss_pred                    EEEEeCChHHHHHHHcCCC-CCCcCCHHHHHCCHHHHHHHHHHHHHcCCeeCCCCeEEEEeC--CHHHHH
Q Q_7621124_2        248     VTSYYRGGLHTALKTLGVH-ANKHIPVQYLRASESSRRALLAGLIDSDGTIAKSGQVSFINT--NRRLYD  314 (881)
Q Consensus          248     ~~~~~~~~l~~~l~~~g~~-~~k~iP~~i~~~~~~~~~~fL~Gl~dgDG~~~~~~~i~~~t~--s~~l~~  314 (881)
                             .+...+..+..++..++.. ..|.||.+++..   ...+||+|+|++||++... .+++.+.  |++++.
T Consensus          72      ~~~~~~~~~~~~l~~~~~~~~~k~ip~~i~~~~~~~~~~L~g~~~~DG~~~~~~-~i~~~~~~~s~~~~~  137 (174)
T PF03161.13         72      RFHTFTYSSLNWIHDLWYVNGVKCVPKNIGEF---ITPLALAIWIMDDGGRVGK-GLKFATNSFSYEDCL  137 (174)
T ss_pred                    EEEEeecchhHHHHHhhccCCcccCcccHHHh---cCHHHHHHHhccCCcccCC-cEEEECCCCCHHHHH
```

```
Q ss_pred                HHHHHHHH-CCCcEEEEecCCCCCCCCCccCeeeEEEEEEecCCCCCCc
Q Q_7621124_2       315  GVVELIRT-LGYRATIHAPLQPSTSSSGVAGTRVLYRVSFTPHDGIPPA  362 (881)
Q Consensus         315  ~l~~Ll~~-lGi~~~i~~~~~~~~~~~~~~~~~~y~~~i~~~~~~~~f  362 (881)
                         +++.+|.+ +||.+++.....+.           .|.+.|++ .+...|
T Consensus         138  ~~~~~L~~~~gi~~~~~~~~~~~~~~~~~~~~~~~~~~l~i~~~~~~~f  174 (174)
T PF03161.13        138  LLSNVLFDKYNLRTSVQSAGIEN-----------QYIIYVFK-ESMPAL  174 (174)
T ss_pred                HHHHHHHHhcCeEEEEEEcCCCC-----------eEEEEEEH-hhcCCC
```

Template alignment | Template 3D structure | PDBe

25. **2DCH_X putative homing endonuclease; alpha/beta fold, HYDROLASE; HET: SO4; 2.06A {Thermoproteus}**

Probability: 98.11 E-value: 4.6E-7 Score: 93.76 Aligned Cols: 155 Identities: 18% Similarity: 0.145

```
Q ss_pred                CCCCCCCCCCcccchHHHHHHcccccCCC-CeEEecCChHHhhhchhh-----------cCeEEecCCc
Q Q_7621124_2       190  HRDPLEGVDDTLLIDPYTLGVWLGDGSSTK-AAITHHADDEYVLPYPKS-----------ADCVHQTTGV  247 (881)
Q Consensus         190  ~~~~~~~~~~~~~~~~llG~~l~dG~~~~-~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  247 (881)
                         ...+........+.+++++|++++||++.. ..+.+...+..+.+.+..           ..........
T Consensus          10  ~~~~~~~~~~~~~~~a~llG~~~~dG~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  79 (216)
T 2DCH_X             10  HSSGLVPRGSHMKVWDYLCGLIAADGHLDEEGYITILQKDRRFIDKIVALLKSAEIKISSLFYDKGAGVW  79 (216)
T ss_dssp                CCCSSCCCGGGCCHHHHHHHHHHHHHEEECTTSEEEEEESCHHHHHHHHHHHHHTCCEEEEEEEETTTTEE
T ss_pred                CCCCCCCCcccchHHHHHHHHHcccCCcccCCCCcEEEEeCCHHHHHHHHHHHHHcCCCCceEEEECCCCEE

Q ss_pred                EEEEeCChHHHHHHHHcCCCCCC-----cCCHHHHHCCHHHHHHHHHHHHHcCCeeCC-----------CC
Q Q_7621124_2       248  VTSYYRGGLHTALKTLGVHANK-----HIPVQYLRASESSRRALLAGLIDSDGTIAK-----------SG  301 (881)
Q Consensus         248  ~~~~~~~~l~~~l~~~g~~~~k------iP~~i~~~~~~~~~~fL~Gl~dgDG~~~~~~~~~~~~~~~~~~  301 (881)
                         .+.+.+..+..++..++....+     .+|.+++.     ..+||+||+++||++..           ..
T Consensus          80  ~~~~~~~~~~~~l~~~g~~~~~~~~~~~ip~~~~~~~~~~~~fL~G~~d~dG~i~~~~~~~~~~~~~~~~~  144 (216)
T 2DCH_X             80  KIKVKDERLYRYLVNNGVIPGKKAHVLRPPSSAVD-----PLWYIIGFIDGDGWVEQVVKRAGDKSYYYI  144 (216)
T ss_dssp                EEEEECHHHHHHHHTTTCCSCC---CCCCCCTTSC-----HHHHHHHHHHHHCEEEEEEEEETTEEEEEE
T ss_pred                EEEECCHHHHHHHHHCCCCCCCCCCcccCCCcccCC-----hHHHHHhhccCCCceEEeeecCCCCceeEE

Q ss_pred                eEEEEeCCHHHHHHHHHHHHHCCCcEEEEecCCCCCCCCCccCeeeEEEEEEecCCCCCCc
Q Q_7621124_2       302  QVSFINTNRRLYDGVVELIRTLGYRATIHAPLQPSTSSSGVAGTRVLYRVSFTPHDGIPPA  362 (881)
Q Consensus         302  ~i~~~t~s~~l~~~l~~Ll~~~lGi~~~i~~~~~~~~~~~~~~~~~~y~~~i~~~~~~~~f  362 (881)
                         .+.+.+.+++++.+|+.+|..+||.+.+.++             ...|.+.|.+.+++..+
T Consensus         145  ~i~~~~~~~~l~~~i~~lL~~~gi~~~i~~~~-------------~~~~~l~i~~~~~~~~~  192 (216)
T 2DCH_X            145  RIGIKTKSKELRDWIAQTLNDLGIRASRADK-------------SDGYEVHIDGVEAWRLV  192 (216)
T ss_dssp                EEEEEESCHHHHHHHHHHHHHHTCCCEEEEE-------------TTEEEEEEETHHHHTTG
T ss_pred                EEEEEeCCHHHHHHHHHHHHHcCCccEEecC-------------CCeEEEEEcCCcceeEe
```

Template alignment | CDD

26. **PF04466.13 ; Terminase_3 ; Phage terminase large subunit**

Probability: 98.08 E-value: 1.6E-6 Score: 88.31 Aligned Cols: 190 Identities: 5% Similarity: -0.051

```
Q ss_pred                CCeEEEcCCccccCCChhHHhhHHHHHHccC---CCCeEEEeehhHHHHHH-cHHHHHHHHHHHchHHCc
Q Q_7621124_2       402  DGLYLVGEHMTPTHNSTRVSQWFPFWWLTIR---PFDRILMASAEATLARR-NGAAVRELVREYGPEFGL  467 (881)
Q Consensus         402  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  467 (881)
                         ....++  .+++++++|.......++.+...   +...++ ++++.+++.. +...++.++...+   -.
T Consensus          1   ~~~~~~~~~~~~rg~GKT~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  64 (202)
T PF04466.13         1   HLTEVW--YGGASSGKSHGVVQKVVLKSLQHWNVPRKVLW-LRKVDRTVKNSIFTDVTECLSGWN---IL  64 (202)
T ss_pred                CcEEEE--EcCCCCChHHHHHHHHHHHHHHccCCCceEEE-EEecCHHHHHHHHHHHHHHcCC---CC

Q ss_pred                ccCCCCcccCceEeecCceEEEEccCC--CcccC-CCcEEEEeCCCCCHHHHcCHHHHHHHHHHHHhhh
Q Q_7621124_2       468  NLSPDESSKTDWSIRAGGTMRSRGLRG--NFTGQ-PMDLGIIDDPITNRAQAESLVVRDFVWDWYSSVWS  534 (881)
Q Consensus         468  ~~~~~~~~~~~~~~~~~~~i~~~g~~~~--s~rG~~~~~ii~DE~~~~~~~~~s~~~~~~~~~~~~~~~~  534 (881)
                         ...........+.+.+++.+...+...  +.+|. +++++|+||+.......            +...+.
T Consensus          65  ~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~g~~~~~~~i~DE~~~~~~~~~~~~~~~~~~~~~~~~~~~~  122 (202)
T PF04466.13         65  QYCHVNRSDKTIVLPNGAIFLFQGMDDPEKIKSIKGLSDVVMEEASEFNHND------------YTQLTL  122 (202)
T ss_pred                cccceeecccCEEEcCCCCEEEEEeCCCHHHhccccCCCEEEEechhhCCHHH------------HHHHHH

Q ss_pred                ccc---CCCCeEEEEccccCcccHHHHHHhccCCCCcCCCeEEEEEeceEeCCcccccCCCCCCCCCCCc
Q Q_7621124_2       535  QRK---APTYREVLVMTRWHQDDLAGRLLARDGRVEEGGVWRVVHLPAIAMPVDEKRGVYPDPLGREPGE  601 (881)
Q Consensus         535  ~~~~---~~~~~~~i~i~T~~~~~d~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  601 (881)
                         .+.   .+.+++++++||....+.++.++...........|..+.+++..+
T Consensus         123  ~l~~~~~~~~~~~~~~tp~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~n-------------------  173 (202)
T PF04466.13        123  RLREPKHKQRQIFCMFNPVSKLNWTYQTWFDPSADYDRSRVAIHQSTYKDN-------------------  173 (202)
T ss_pred                HhcCCCcCCCEEEEEeCCCcccchHHHhccCCCcCCcCCeEEEEcccccC-------------------

Q ss_pred                cCCCCCCCCCChhhcccChhHHHHHHHHHHHHHH--hcccchHHHHhcCC
Q Q_7621124_2       602  PLTHPLIVPDDPATWSQAPTHREALTNWWAAKRK--MSTARDWSSMSQGL  649 (881)
```

```
Q Consensus         602    ~l~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~--~~~~~~f~~ey~~~  649 (881)
                                   +.++.     +.+    ++++.  .+++..|+++|+|+
T Consensus         174    ------------p~~~~-----~~~-----~~~~~~~~~~~~~~~~~~~g~  202 (202)
T PF04466.13        174    ------------RFLDE-----DNI----RTIEELKNTNPAYYKIYTLGE  202 (202)
T ss_pred                  ------------CCCCH-----HHH----HHHHHHHhCHHHHHhccCC
```

Template alignment | Template 3D structure | PDBe

27. **4DKW_D Large terminase protein; DNA-packaging, Large terminase, Small terminase; HET: SO4; 2.02A {Enterobacteria phage P22}; Related PDB entries: 4DKW_C 4DKW_B 4DKW_A**

Probability: 98.08 E-value: 1.7E-6 Score: 89.24 Aligned Cols: 172 Identities: 13% Similarity: 0.031

```
Q ss_pred                  CccccccccHHHHHhcC-CCccceEEEEEEeCCCCCCCcCCcEEEEEEECCC-CcEEEEeccc-ccc
Q Q_7621124_2       651    SSAENALLTDADIRAATAP-VPDELTRVVVGVDPSGGEGARHDTAGISAVGLDEH-QHAWFLEDRT-AVL  717 (881)
Q Consensus         651    ~~~~~~~f~~~~i~~~~~~-~~~~~~~~~~~iD~a~~~~~~~D~tai~v~~~~~~-g~~~v~~~~~-~~~  717 (881)
                           +..+|.+|+...-..... .....+++|+|+|.     ++++|++++..+.+ +.+|+++.+. ...
T Consensus         1      ~~~~G~iy~~~~~~~~v~~~~~~~~~~~~~g~D~G~------~~p~a~~~~~~~~~~~~~v~dE~~~~~~  65 (211)
T 4DKW_D            1      TMGSGRIFQIPEETIKCQPFECPDHFYVIDAQDFGW-----NHPQAHIQLWWDKDADVFYLARVWKKSEN  65 (211)
T ss_dssp                  CCBTEESCCSCHHHHEECCCCCCTTSEEEEEEECCS-----SSCEEEEEEEEETTTTEEEEEEEEEESSC
T ss_pred                  CCCcceeccCCHHheecCCCCCCCCCeEEEEEeCCC-----CCCcEEEEEEEeCCCCEEEEEEEEEecCCC

Q ss_pred                  CcchHHHHHHHHHHHhCCCEEEEEcc----cCchHHHHHHHHHHHHhcCCCCCCCccccCcccCCCCce
Q Q_7621124_2       718    TPLEWPRAVCLLAYERDASMIVYEKN----YGGGMASALITQAWAALQNEPINADTDETMIPKSANCPYV  783 (881)
Q Consensus         718    ~~~~~~~~i~~~~~~~~~~~i~iE~~-----~~g~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~i  783 (881)
                           ++.++++.|.++...+++. +++|..    ..+..+...+++                     .+++ +
T Consensus         66     ~~~~~~~~i~~~~~~~~~~-~~~D~~~~~~~~~~~~~~l~~-----------------------~G~~-~  111 (211)
T 4DKW_D            66     TAVQAWGAVKSWANKIPVA-WPHDGHQHEKGGGEQLKTQYAD----------------------AGFS-M  111 (211)
T ss_dssp                  CHHHHHHHHHHHHTTCEEE-CCCSSCSSSSSCHHHHHHHHHH----------------------HTCE-E
T ss_pred                  CHHHHHHHHHHHHcCCCcc-cCCCcccccCCCchhHHHHHHH----------------------CCCc-c

Q ss_pred                  eec-----cCCCCHHHhHHHHHHHHHHcCCeEEcccCccHHHHHHHhccCCCC-----CCCCcHHHHHHHH
Q Q_7621124_2       784    KGV-----SAKISKVLRAEPIAQAVKTGRAKFAQLGNLGSLTNEFTLWQPGS-----TWSPGALDAAVYG  843 (881)
Q Consensus         784    ~~~-----~~~~~~K~~ri~~l~~~~~~g~i~~~~~~~~~~l~~el~~~~~~~~-----~~~dD~~Dal~~~  843 (881)
                           .+.     ....++..+++.+..++.+++++|..  .+..|++||..|....     ..+||.+||+.++
T Consensus         112    ~~~~~~~~~~~~~~~~~i~~v~~~l~~~~l~i~~---c~~li~el~~y~~~~~g~p~k~~dh~~Da~rY~  179 (211)
T 4DKW_D            112    LPDHATFPDGGNSVESGISELRDLMLEGRFKVFN--TCEPFFEEFRLYHRDENGKIVKTNDDVLDATRYG  179 (211)
T ss_dssp                  CSSCCCCTTSCCCHHHHHHHHHHHHHTTCEEEET--TCHHHHHHHHCEECTTSCBCCSSCHHHHHHHHH
T ss_pred                  ccCccCCCCCCCchHHHHHHHHHHHHcCCEEEeC--CCHHHHHHHHcccCCCCCCCCCchHHHHHHHH

Q ss_pred                  HHHhcCCCCC
Q Q_7621124_2       844    ATEVLPPVGS  853 (881)
Q Consensus         844    ~~~~~~~~~~  853 (881)
                           +.........
T Consensus         180    ~~~~~~~~~~  189 (211)
T 4DKW_D            180    YMMRRFARMM  189 (211)
T ss_dssp                  HHTGGGCEEH
T ss_pred                  HHhhhccccc
```

Template alignment | Template 3D structure | PDBe

28. **2WBN_A TERMINASE LARGE SUBUNIT; LARGE TERMINASE, NUCLEASE, VIRAL PROTEIN; 1.9A {BACILLUS PHAGE SPP1}; Related PDB entries: 2WC9_A**

Probability: 98.0 E-value: 1.0E-6 Score: 90.93 Aligned Cols: 182 Identities: 10% Similarity: 0.043

```
Q ss_pred                  cchHHHHhcCCCCccccccccHHHHHhhcC--CCccceEEEEEEeCCCCCCCcCCcEEEEEEEECC-CC
Q Q_7621124_2       639    ARDWSSMSQGLPSSAENALLTDADIRAATAP--VPDELTRVVVGVDPSGGEGARHDTAGISAVGLDE-HQ  705 (881)
Q Consensus         639    ~~~f~~ey~~~~~~~~~~f~~~~i~~~~~~-~~~~~~~~~~~iD~a~~~~~~~D~tai~v~~~~~-~g  705 (881)
                           ...|+++++++|...++.+|+...-.....  .....+++++|+|..    .|+++++++.+++ ++
T Consensus         11     ~~~~~~~~~G~~~~~~g~vy~~f~~~~h~~~~~~~~~~~~~giD~G~~-~~~~p~~~~~~~~~~~~  76 (212)
T 2WBN_A            11     SSGLVPRGSHMALGSGVVPFENLQIEEGIITDAEVARFDNIRQGLDFGYG----PDPLAFVRWHYDKRKN  76 (212)
T ss_dssp                  ----------------CCSCTTEEECTTCSCHHHHHHCCCEEEEEECCBT----TBCEEEEEEEETTTT
T ss_pred                  cCCCcccccceeeeecCCccccCCcEEeecCCCHHHHhccCceEEEEEcCCC----CCCCEEEEEEEECCCC

Q ss_pred                  cEEEEecccccc-cCcchHHHHHHHHHHHhCCCEEEEEcccCchHHHHHHHHHHHHhccCCCCCCCccccC
Q Q_7621124_2       706    HAWFLEDRTAV-LTPLEWPRAVCLLAYERDASMIVYEKNYGGGMASALITQAWAALQNEPINADTDETMI  774 (881)
Q Consensus         706    ~~~v~~~~~~~-~~~~~~~~~~i~~~~~~~~~~~i~iE~~~~g~~~~~~l~~~~~~~~~~~~~~~~~~~  774 (881)
                           .+||++.+... .+++++++.|.++.  ++...+++|+.+..         ...++.+.
T Consensus         77     ~~~v~~e~~~~~~~~~~~~~~~~i~~~~--~~~~~~~~~D~a~~~---------~~~~l~~~~~~~~~~  124 (212)
T 2WBN_A            77     RIYAIDELVDHKVSLKRTADFVRKNK--YESARIIADSSEPR---------SIDALKLE-----------  124 (212)
T ss_dssp                  EEEEEEEEEESSCCHHHHHHHHHHTT--CTTSCEEECTTCHH---------HHHCCCCC-----------
T ss_pred                  EEEEEEEEeCCCCCHHHHHHHHHHCC--CCCCeEEEcCCCch---------hHHHHHHH-----------

Q ss_pred                  cccCCCC-ceeeccCCCCHHHhHHHHHHHHHHcCCeEEcccC-ccHHHHHHHHccCCCC-----------C
Q Q_7621124_2       775    PKSANCP-YVKGVSAKISKVLRAEPIAQAVKTGRAKFAQLG-NLGSLTNEFTLWQPGS-----------T  831 (881)
```

```
Q Consensus         775     ~~~~~~~-~i~~~~~~~~K~~ri~~l~~~~~~g~i~~~~~~-~~~~l~~el~~~~~~~-----------~  831 (881)
                               .+++ .....+.+.++..+++.+.   ...++.|.  + .+..|++||..|....          +
T Consensus         125     ---~G~~~~~~~~~~~~~~~~~~i~~~~---~~~~~~i~--~~~c~~li~el~~y~~~~~~~g~~~~~p~~  186 (212)
T 2WBN_A            125     ---HGINRIEGAKKGPDSVEHGERWLD---ELDAIVID--PLRTPNIAREFENIDYQTDKNGDPIPRLED  186 (212)
T ss_dssp                  ---TCCTTEEECCSCGGGHHHHHHHHH---TSSEEEEC--TTTCHHHHHHHHHCCEEECTTCCEEEEECS
T ss_pred                  ---hCCCeeeecCCCCCcHHHHHHHHH---hCCcEEEC--CCCCHHHHHHHHhCccccCCCCCCCCCCCC


Q ss_pred                  CCCcHHHHHHHHHHHhcCCCCCc
Q Q_7621124_2        832     WSPGALDAAVYGATEVLPPVGST  854 (881)
Q Consensus         832     ~~dD~~Dal~~~~~~~~~~~~~~  854 (881)
                            .+||.+||+.+++.......+++
T Consensus         187     ~~dH~~Da~rY~~~~~~~~~~~~  209 (212)
T 2WBN_A            187     KDNHTIDATRYAFERDMKKGGVS  209 (212)
T ss_dssp                  SSCHHHHHHHHHTGGGCC-----
T ss_pred                  CCCHHHHHHHHHHhhccccCCcc
```

Template alignment | Template 3D structure | PDBe

29. **4LX3_A DNA polymerase III, alpha subunit; trans-structure, naturally occurring, TRANSFERASE; HET: MSE; 1.5A {Nostoc punctiforme}; Related PDB entries: 4QFQ_A**

Probability: 97.7   E-value: 3.8E-6   Score: 75.83   Aligned Cols: 81   Identities: 14%   Similarity: 0.131

```
Q ss_pred                  cCCCcEECCCccEEHHHcCCC---CEEECCCC----CEEEEEEEecCC-CCeEEEEeCCCCeEEECCCe
Q Q_7621124_2        92      AHDTPVPTPTGWTTHGELRPG---DEVYHPSG----KVVTVRAISADA-HASIRVSTSDGGSIVVHPRHE  153 (881)
Q Consensus         92      ~~dt~Vlt~~G~~~i~~i~~g---d~v~~~~g----~~~~v~~~~~~~~-~~~~~i~t~~G~~i~~T~~H~  153 (881)
                            .++|+|+|.+|+++|+++..+   ..|++.+.    .+.++..++... +++|+|++++|+.+.||++|+
T Consensus         10      ~~~t~vlt~~G~~~I~dl~~~~~~~~~v~s~d~~g~~~~~~v~~~~~~~~~~~~~~i~~~~G~~i~~T~~H~  79 (108)
T 4LX3_A            10      YETEILTVEYGLLPIGKIVEKRIECTVYSVDNNGNIYTQPVAQWHDRGEQEVFEYCLEDGSLIRATKDHK  79 (108)
T ss_dssp                  TTCEEEETTTEEEEHHHHHHTTCCCEEEEECTTSCEEEEECCEEEEEEEEEEEEEETTSCEEEECTTCE
T ss_pred                  CCCcEEEeCCceEEHHHHHhccCCcEEEEECCCCCEEEEeceEeEeCCCceEEEEEECCCCEEEEcCCCe


Q ss_pred                  EEEEeCCCCeEE-EcchhHH-hhheee
Q Q_7621124_2        154     WTVWDRNRKRWS-TMETGDM-MRRAYV  178 (881)
Q Consensus         154     ~~~~~~~~~~~~~-~~~~~~l-~~~~~~  178 (881)
                            |++.++    |. .  ++++ ..++++
T Consensus         80      ~lt~~g----w~~~--~~~L~~~gd~l  100 (108)
T 4LX3_A            80      FMTVDG----QMLP--IDEIFERELDL  100 (108)
T ss_dssp                  EEBTTS----CEEE--HHHHHHTTCCB
T ss_pred                  eEeeCC----eEEE--HHHhccCCCee
```

Template alignment | Template 3D structure | PDB | NCBI

30. **d1dq3a4 d.95.2.2 (A:227-335) PI-Pfui intein {Pyrococcus furiosus [TaxId: 2261]}**

Probability: 97.68   E-value: 5.1E-6   Score: 75.29   Aligned Cols: 83   Identities: 23%   Similarity: 0.417

```
Q ss_pred                  CCHHHHHCCHHHHHHHHHHHHHHcCCeeCCCCeEEEEeCCHHHHHHHHHHHHHHCCCcEEEEecCCCCCCCC
Q Q_7621124_2        271     IPVQYLRASESSRRALLAGLIDSDGTIAKSGQVSFINTNRRLYDGVVELIRTLGYRATIHAPLQPSTSSS  340 (881)
Q Consensus         271     iP~~i~~~~~~~~~~~~fL~Gl~dgDG~~~~~~~~i~~~t~s~~l~~~l~~Ll~~lGi~~~i~~~~~~~~~~~~~  340 (881)
                            +|++++..+.+...+||+|+||+||++.....+.+.+.++.++++++.+|.++|+...+........
T Consensus         1       ip~~~~~~~~~~~~~~~fl~G~~dgdG~i~~~~~~~~~~~~~~~~~~~~i~~~l~~~gi~~~~~~~~~~~~~~---  67 (109)
T d1dq3a4           1       IPPQILKEGKNAVLSFIAGLFDAEGHVSNKPGIELGMVNKRLIEDVTHYLNALGIKARIREKLRKDG---  67 (109)
T ss_dssp                  SCHHHHTTCHHHHHHHHHHHHHHHHHHCEEETTTEEEEEEESCHHHHHHHHHHHHHTTTCCCEEEEEEECSSS---
T ss_pred                  CChHHHhcCHHHHHHHHHHHHHHhcCCccCCCCEEEEEcCHHHHHHHHHHHHHHCCCCcEEEEEecCCC---


Q ss_pred                  CccCeeeEEEEEEecCCCCCCc
Q Q_7621124_2        341     GVAGTRVLYRVSFTPHDGIPPA  362 (881)
Q Consensus         341     ~~~~~~~~y~~~i~~~~~~~~~f  362 (881)
                                  ..|.+.+.+..++..|
T Consensus         68      ------~~~~l~~~~~~~~~~~~~  83 (109)
T d1dq3a4           68      ------IDYVLHVEEYSSLLRF  83 (109)
T ss_dssp                  ------EEEEEEECCHHHHHHH
T ss_pred                  ------cEEEEEEechhHHHHH
```

Template alignment | Template 3D structure | PDBe

31. **3C0W_A Intron-encoded endonuclease I-SceI (E.C.3.1.-.-)/DNA Complex; endonuclease, homing, LADLIDADG, catalytic mechanism; 2.2A {Saccharomyces cerevisiae}; Related PDB entries: 3OOL_A 3OOR_A 1R7M_B 1R7M_A 3C0X_A 5A0M_B 5A0M_A**

Probability: 97.66   E-value: 6.0E-6   Score: 86.67   Aligned Cols: 139   Identities: 11%   Similarity: 0.04

```
Q ss_pred                  cchHHHHHHhccccCCCC------eEEecCChHHhhhchhh---------cCeEEecC-------CcEE
Q Q_7621124_2        202     LIDPYTLGVWLGDGSSTKA------AITHHADDEYVLPYPKS---------ADCVHQTT-------GVVT  249 (881)
Q Consensus         202     ~~~~~llG~~l~dG~~~~~~------~i~~~~~~~~~~~~~~~~~~~---------~~~~~~~~~~-------~~~~  249 (881)
                            +..++++|+++|||++...      .+++...+....+.+..          ........       ...+
T Consensus         32      ~~~a~l~G~llGDG~i~~~~~~~~~~~~i~~~~~~~~~~~l~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~g~~~~~~~~~~  101 (235)
T 3C0W_A            32      EQFEAGIGLILGDAYIRSRDEGKTYCMQFEWKNKAYMDHVCLLYDQWVLSPPHKKERVNHLGNLVITWGA  101 (235)
```

```
T ss_dssp                HHHHHHHHHHHHTTCEEECSSTTSCBEEEEEESCHHHHHHHHHHTGGGCCSCCEEEEEECTTSCEEEEEEE
T ss_pred                HHHHHHHHHHHcCeEEEECCCCCcEEEEEEEcCHHHHHHHHHHHHHHcccCCCeeeeeeCCCCCEEEEEEE

Q ss_pred                EEeCChHHHHHHHcCCC-CCCcCCHHHHHCCHHHHHHHHHHHHHcCCeeCC------CCeEEEEeCC--H
Q Q_7621124_2       250  SYYRGGLHTALKTLGVH-ANKHIPVQYLRASESSRRALLAGLIDSDGTIAK------SGQVSFINTN--R  310 (881)
Q Consensus         250  ~~~~~~l~~~l~~~g~~-~~~k~iP~~i~~~~~~~~~~fL~Gl~dgDG~~~~-------~~~i~~~t~s--~  310 (881)
                         ...+..+...+..+... ..|.||.+++.  ......||+|+|++||++..      ...+.+++.|  +
T Consensus         102  ~s~~~~~~~~l~~~~~~~~~K~iP~~il~--~~~~~~~L~g~~~~DG~v~~~~~~~~~~~i~i~~~~~s~  169 (235)
T 3C0W_A            102  QTFKHQAFNKLANLFIVNNKKTIPNNLVE--NYLTPMSLAYWFMDDGGKWDYNKNSTNKSIVLNTQSFTF  169 (235)
T ss_dssp                ECCCBGGGHHHHHTTBSSSSBCCCTTHHH--HHCCHHHHHHHHHHHEEESCCSTTCCCCCEEECCTTSCH
T ss_pred                EeeecHHHHHHHHHHccCCeeCCCChhHHH--HhcCHhhheEeeccCCcccccccccCCCeEEEEcCCCCH

Q ss_pred                HHHHHHHHHHH-HCCCcEEEEecCCCCCCCCCcccCeeeEEEEEEec
Q Q_7621124_2       311  RLYDGVVELIR-TLGYRATIHAPLQPSTSSSGVAGTRVLYRVSFTP  355 (881)
Q Consensus         311  ~l~~~l~~Ll~-~lGi~~~i~~~~~~~~~~~~~~~~~~y~~~i~~  355 (881)
                         +.+..++.+|. ++||.+++.+.             +..|++.|+.
T Consensus         170  ~~l~~l~~~L~~~~gi~~~i~~~~~~~~~~~~~~~~~~l~i~~  202 (235)
T 3C0W_A            170  EEVEYLVKGLRNKFQLNCYVKIN-------------KNKPIIYIDS  202 (235)
T ss_dssp                HHHHHHHHHHHHHHCCCEEEEEE-------------TTEEEEEECG
T ss_pred                HHHHHHHHHHHHHHcCceeEEEec-------------CCeEEEEEEH
```

Template alignment | CDD

32. **PF05204.14 ; Hom_end ; Homing endonuclease**

Probability: 97.62 E-value: 1.0E-5 Score: 71.19 Aligned Cols: 72 Identities: 25% Similarity: 0.394

```
Q ss_pred                cCCHHHHHCCHHHHHHHHHHHHHcCCeeCCC--CeEEEEeCCHHHHHHHHHHHHHCCCcEEEEecCCCCC
Q Q_7621124_2       270  HIPVQYLRASESSRRALLAGLIDSDGTIAKS--GQVSFINTNRRLYDGVVELIRTLGYRATIHAPLQPST  337 (881)
Q Consensus         270  ~iP~~i~~~~~~~~~~fL~Gl~dgDG~~~~~~--~~~i~~~t~s~~l~~~l~~Ll~~lGi~~~i~~~~~~~~  337 (881)
                         .+|++++..+.+.+.+||+|++++||++...  ..+.+++.++.++.+++.+|.++|+.+.+...
T Consensus         1    ~ip~~i~~~~~~~~~~fl~g~~d~dG~~~~~~~~~~~~~~~~~~l~~~l~~ll~~~gi~~~~~~~~-----  65 (95)
T PF05204.14        1    VIPSSIAVENIEVRESFLAGFVDASQTELKQDSAIINIGASNKSIIANIVKLARSLGIKAACKDD-----  65 (95)
T ss_pred                CCChHHhcCCHHHHHHHHHHHcccCCcEEeCCccCEEEEEeCCHHHHHHHHHHHHHCCCeEEEEeeC-----

Q ss_pred                CCCCccCeeeEEEEEEec
Q Q_7621124_2       338  SSSGVAGTRVLYRVSFTP  355 (881)
Q Consensus         338  ~~~~~~~~~~~y~~~i~~  355 (881)
                                  ..|.+.+.+
T Consensus         66   ---------~~~~~~i~~  74 (95)
T PF05204.14        66   ---------GLNRITLEG  74 (95)
T ss_pred                ---------CceEEEEEc
```

Template alignment | Template 3D structure | PDB | NCBI

33. **d1gppa1 b.86.1.2 (A:-1-453) VMA1-derived endonuclease (VDE) PI-Scei intein {Baker's yeast (Saccharomyces cerevisiae) [TaxId: 4932]}**

Probability: 97.55 E-value: 8.9E-6 Score: 84.23 Aligned Cols: 73 Identities: 16% Similarity: 0.172

```
Q ss_pred                ccccCCCcEECCCc-cEEHHHcCCCCEEECCCCCEEEEEEEecCCCCeEEEEeCCC--------------
Q Q_7621124_2        89  KLVAHDTPVPTPTG-WTTHGELRPGDEVYHPSGKVVTVRAISADAHASIRVSTSDG--------------  143 (881)
Q Consensus          89  kC~~~dt~Vlt~~G-~~~i~~i~~gd~v~~~~g~~~~v~~~~~~~~~~~i~t~~G--------------  143 (881)
                         +|+.++|.|++++| .++|++|.+||.|++.+|.+.+|..+.+....+|+|+...+
T Consensus          1   gCF~~gT~V~madG~~k~IedI~~Gd~V~~~dg~~~~V~~l~~~~~~~y~I~~~~~~~~~~~~~~~~~~  70 (228)
T d1gppa1            1   ACFAKGTNVLMADGSIECIENIEVGNKVMGKDGRPREVIKLPRGSETMYSVVQKSQHRAHKSDSSREMPE  70 (228)
T ss_dssp                EEECTTCEEEBTTSCEEEGGGCCTTCEEEBTTSSEEEEEECCEEEEEEEEEECC------------CCC
T ss_pred                CCccCCCEEECCCCCEEEHHHcCCCCEEEeeCCCeeEEEEeCCCcceeEEEEecccCcccCCCCCCCCCC

Q ss_pred                -CeEEECCCCeEEEEeCCC
Q Q_7621124_2       144  -GSIVVHPRHEWTVWDRNR  161 (881)
Q Consensus         144  -~~i~~T~~H~~~~~~~~~  161 (881)
                          ..+.||++|++++.....
T Consensus         71   ~~~~~~t~~H~l~l~t~~~  89 (228)
T d1gppa1           71   LLKFTCNATHELVVRTPRS  89 (228)
T ss_dssp                CCEEEEETTCEEEEEEECC
T ss_pred                ceEEEECCCCEEEeCCccc
```

Template alignment | Template 3D structure | PDB | NCBI

34. **d1b24a2 d.95.2.1 (A:100-179) DNA endonuclease I-dmoI {Desulfurococcus mobilis [TaxId: 2274]}**

Probability: 97.54 E-value: 1.9E-5 Score: 66.96 Aligned Cols: 67 Identities: 22% Similarity: 0.334

```
Q ss_pred                CCHHHHHHHHHHHHHcCCeeCCCCeEEEEeCCHHHHHHHHHHHHHCCCcEEEEecCCCCCCCCCcccCeee
Q Q_7621124_2       278  ASESSRRALLAGLIDSDGTIAKSGQVSFINTNRRLYDGVVELIRTLGYRATIHAPLQPSTSSSGVAGTRV  347 (881)
Q Consensus         278  ~~~~~~~~fL~Gl~dgDG~~~~~~~i~~~t~s~~l~~~l~~Ll~~lGi~~~i~~~~~~~~~~~~~~~~~  347 (881)
```

```
                                .|.+...+||+||||+||++...  .+.+++.|+.++++++.+|.++|+.+.+..+          .....
T Consensus          2          ~~~~~~~~flrG~~d~dG~v~~~-~i~~~~~~~~~~~~~~~~~l~~~gi~~~~~~~----------~~~~~  60 (80)
T d1b24a2            2          FNMREQIAFIKGLYVAEGDKTLK-RLRIWNKNKALLEIVSRWLNNLGVRNTIHLD----------DHRHG  60 (80)
T ss_dssp                         CCHHHHHHHHHHHHHHHSCTTCS-SCEEEESCHHHHHHHHHHHHHTTCCEEEEEE----------ETTTT
T ss_pred                         CCHHHHHHHHHHHHHhcCCceeec-eEEEEeCCHHHHHHHHHHHHHcCCceEEEeC----------CCCCc


Q ss_pred                         EEEEEEec
Q Q_7621124_2        348      LYRVSFTP  355 (881)
Q Consensus          348      ~y~~~i~~  355 (881)
                                .|++.+.+
T Consensus          61       ~~~l~i~~  68 (80)
T d1b24a2            61       VYVLNISL  68 (80)
T ss_dssp                         EEEEEECG
T ss_pred                         EEEEEEEe
```

Template alignment | Template 3D structure | PDBe

35. **5OL1_A DNA polymerase III subunit alpha,DNA; intein, extein, SICLOPPS, cyclic peptide; HET: CSO, PGE, SO4; 1.751A {Synechocystis sp. (strain PCC 6803 / Kazusa)}; Related PDB entries: 5OL5_D 5OL5_C 5OL5_B 5OL5_A**

Probability: 97.51   E-value: 1.8E-5   Score: 77.63   Aligned Cols: 97   Identities: 12%   Similarity: 0.13

```
Q ss_pred                       CeEEEEeCCCCCccccCCCcEECCC-ccEEHHHc---CCCCEEECCCC----CEEEEEEEecCC-CCeEE
Q Q_7621124_2        77       ARVMIFTPSQVGKLVAHDTPVPTPT-GWTTHGEL---RPGDEVYHPSG----KVVTVRAISADA-HASIR  137 (881)
Q Consensus          77       ~~~~~~g~~g~gkC~~~dt~Vlt~~-G~~~i~~i---~~gd~v~~~~g----~~~~v~~~~~~~-~~~~~  137 (881)
                               ..+++......+.|+.++|.|++.+ |..+|++|    ..++.+++.+.    ....+..++..+ +++|+
T Consensus          30       ~gi~~~~~~~~~~~~C~~~~T~v~~~~g~~~~I~~i~~~~~~~~~~v~~~~~~~~~~~~~~~~~~~~~~~g~~~v~~  99 (162)
T 5OL1_A             30       NGAIAHACAFHPQALSFGTEILTVEYGPLPIGKIVSEEINCSVYSVDPEGRVYTQAIAQWHDRGEQEVLE  99 (162)
T ss_dssp                         TSBEEECCCSSSCCEETTCEEEETTTEEEEHHHHHHHTCCCEEEEECTTSCEEEEECCEEEEEEEEEEE
T ss_pred                         ccEEecCCCCCcccccccceEEeecccceEeHHHcccCCCCceEEEEcCCCCEEEEeeeEEEecCCCCcEEE


Q ss_pred                         EEeCCCCeEEECCCCeEEEEeCCCCeEEEcchhHH-hhheee
Q Q_7621124_2        138      VSTSDGGSIVVHPRHEWTVWDRNRKRWSTMETGDM-MRRAYV  178 (881)
Q Consensus          138      i~t~~G~~i~~T~~H~~~~~~~~~~~~~~~~~~~~~~l-~~~~~~~  178 (881)
                                |++.+|+.|.||+||++++.++   .|+.  +.++ ..++.+
T Consensus          100      I~t~~G~~i~~T~dH~~lt~~G---~w~~--~~~l~~~gd~l  136 (162)
T 5OL1_A             100      YELEDGSVIRATSDHRFLTTDY---QLLA--IEEIFARQLDL  136 (162)
T ss_dssp                         EEETTSCEEEECTTCEEEBTTS---CEEE--HHHHHHHTCEE
T ss_pred                         EEeCCCCEEEEcCCCeeEcCCC---cEEE--HHHHhCCCcE
```

Template alignment | Template 3D structure | PDBe

36. **2IMZ_B Endonuclease PI-MtuI (EC 3.1.-.-); N-terminal cysteine sulfinic acid C-terminal; HET: CSD, SNN; 1.7A {Mycobacterium tuberculosis}; Related PDB entries: 2IMZ_A**

Probability: 97.45   E-value: 1.3E-4   Score: 71.87   Aligned Cols: 158   Identities: 16%   Similarity: 0.131

```
Q ss_pred                       cccCCCcEECC-Cc-cEEHHHcCCCC---EEECCCC----CEEEEEEEecCC-CCeEEEEeCCCCeEEEC
Q Q_7621124_2        90       LVAHDTPVPTP-TG-WTTHGELRPGD---EVYHPSG----KVVTVRAISADA-HASIRVSTSDGGSIVVH  149 (881)
Q Consensus          90       C~~~dt~Vlt~-~G-~~~i~~i~~gd---~v~~~~g----~~~~v~~~~~~~-~~~~~i~t~~G~~i~~T  149 (881)
                                |+..++.|.++ +| ...|+++..|+   .++..+.     ...++..+.... ..++++.+..|..+.+|
T Consensus          1        c~~~~t~v~~~~~g~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~g~~~~~t  70 (168)
T 2IMZ_B             1        ALAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVAAAKDGTLHARPVVSWFDQGTRDVIGLRIAGGAILWAT  70 (168)
T ss_dssp                         CEETTCEEEETTTTEEEEHHHHHHTTCCCEEEEECTTSCEEEEEEEEEEEEEEEEEEEEEEETTSCEEEEC
T ss_pred                         CCCCCcEEEeCCCCCEEEHHHhccCCCCeEEEEECCCCCEEEEeceEEEeCCCccEEEEEeCCCCEEEEC


Q ss_pred                         CCCeEEEEeCCCCeEEEcchhHHhhheeecCCCCccccccCCCCCCCCCCccccchHHHHHHhccccCCC
Q Q_7621124_2        150      PRHEWTVWDRNRKRWSTMETGDMMRRAYVDRSGRPAFMLPHRDPLEGVDDTLLIDPYTLGVWLGDGSSTK  219 (881)
Q Consensus          150      ~~H~~~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~ip~~~~~~~~~~~~~~~~~~~~~llG~~l~dG~~~~~  219 (881)
                                ++|++++.    ..|..  +.++..+++         ...+...+........+...+++|++++|++..
T Consensus          71       ~~h~~~~~~----~~~~~~~~--~~~~~~g~~--------l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~g~~~~~  126 (168)
T 2IMZ_B             71       PDHKVLTE----YGWRA--AGELRKGDR--------VAQPRRFDGFGDSAPIPARVQALADALDDKFLHD  126 (168)
T ss_dssp                         TTCEEEET----TEEEE--GGGCCTTCE--------EEEECCTTCC----------------------
T ss_pred                         CCCceeec----cccEE--hhhcCCCCE--------EEccccCCCCCCCCChHHHHHHHHHhcccccHh


Q ss_pred                         CeEEecCChHHhhhchhhcCeEEecCCCcEEEEeCChHHHHHHHcCCCCCCCcCCHHHHHCCHHHHHHHHHH
Q Q_7621124_2        220      AAITHHADDEYVLPYPKSADCVHQTTGVVTSYYRGGLHTALKTLGVHANKHIPVQYLRASESSRRALLAG  289 (881)
Q Consensus          220      ~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~~l~~~g~~~~k~iP~~i~~~~~~~~~~~~~~fL~G  289 (881)
                                .
T Consensus          127      ~---------------------------------------------------------------------  127 (168)
T 2IMZ_B             127      M---------------------------------------------------------------------  127 (168)
T ss_dssp                         ----------------------------------------------------------------------
T ss_pred                         h---------------------------------------------------------------------


Q ss_pred                         HHHcCCeeCCCCeEEEEeCCHHHHHHHHHHHHHHCCCcEEEEecCCCCCCCCCCccCeeeEEEEEEecCCCC
Q Q_7621124_2        290      LIDSDGTIAKSGQVSFINTNRRLYDGVVELIRTLGYRATIHAPLQPSTSSSGVAGTRVLYRVSFTPHDGI  359 (881)
```

```
Q Consensus         290    l~dgDG~~~~~~~i~~~t~s~~l~~~l~~Ll~~lGi~~~i~~~~~~~~~~~~~~~~~~y~~~i~~~~~~  359 (881)
                              ..+...+..|.+|+..+...+||++| ++.|+|++  ++..+||
T Consensus         128    ------------------------------------------------------------------  127 (168)
T 2IMZ_B            128    ------------------------------------------------------------------  127 (168)
T ss_dssp                  ------------------------------------------------------------------
T ss_pred                  ------------------------------------------------------------------
```

Template alignment | Template 3D structure | PDB | NCBI

37. **d1oa8a_ b.145.1.1 (A:) Ataxin-1 {Human (Homo sapiens) [TaxId: 9606]}**

Probability: 97.43 E-value: 1.4E-5 Score: 75.1 Aligned Cols: 88 Identities: 16% Similarity: 0.185

```
Q ss_pred                  CCCCCccccCCCcEECCCc-cEEHHHcCCCCEEECCCCCEE------EEEEEecCC-CCeEEEEeCCCC-
Q Q_7621124_2       84     PSQVGKLVAHDTPVPTPTG-WTTHGELRPGDEVYHPSGKVV------TVRAISADA-HASIRVSTSDGG-  144 (881)
Q Consensus         84     ~~g~gkC~~~dt~Vlt~~G-~~~i~~i~~gd~v~~~~g~~~------~v~~~~~~~-~~~~~i~t~~G~-  144 (881)
                           ....+.|+.++|.|.+.+| +++|++|..||.|++.+....      +|..++... ..+++|++..|.
T Consensus         7      ~~~~~~cf~~gT~i~~~~G~~~~Ie~l~~Gd~v~~~~~~~~~~~~~~~v~~~~~~~~~~~~~i~~~~g~~  76 (128)
T d1oa8a_           7      PPTLPPYFMKGSIIQLANGELKKVEDLKTEDFIQSAEISNDLKIDSSTVERIEDSHSPGVAVIQFAVGEH  76 (128)
T ss_dssp                  CSSCCGGGSTTCEEECTTSCEEEGGGCCHHHHHHHHHHCSSEEEEEEEEEEEEECSSTTEEEEEEEETTT
T ss_pred                  CCCCCccccCCCEEEeCCCCEEEHHHcccccccecccccCCcccceeEEEEEecCCCCCeEEEEEEeCCC

Q ss_pred                  ----eEEECCCCeEEEEeCCCC-------------eEEEcchhH
Q Q_7621124_2       145    ----SIVVHPRHEWTVWDRNRK-------------RWSTMETGD  171 (881)
Q Consensus         145    ----~i~~T~~H~~~~~~~~~~-------------~~~~~~~~~  171 (881)
                               .+.+|++|+|++.+.++.             ....++.+|
T Consensus         77     ~~~~~l~~t~~Hp~~~~~~gw~~~~~~~~~~~~~~~a~~L~~GD  120 (128)
T d1oa8a_           77     RAQVSVEVLVEYPFFVFGQGWSSCCPERTSQLFDLPCSKLSVGD  120 (128)
T ss_dssp                  TEEEEEEEETTCCEEETTTEEEESCHHHHHHHHCCCCEECCTTC
T ss_pred                  CcEEEEEEcccccEEecCCcccCCCHhHHHHHHCCCCcccCCCC
```

Template alignment | CDD

38. **PF14527.6 ; LAGLIDADG_WhiA ; WhiA LAGLIDADG-like domain**

Probability: 97.25 E-value: 1.0E-5 Score: 70.83 Aligned Cols: 67 Identities: 16% Similarity: 0.114

```
Q ss_pred                  HHHHHHHHHHcCCeeCCCC---eEEEEeCCHHHHHHHHHHHHCCCcEEEEecCCCCCCCCcccCeeeEE
Q Q_7621124_2       283    RRALLAGLIDSDGTIAKSG---QVSFINTNRRLYDGVVELIRTLGYRATIHAPLQPSTSSSGVAGTRVLY  349 (881)
Q Consensus         283    ~~~fL~Gl~dgDG~~~~~~~---~i~~~t~s~~l~~~l~~Ll~~lGi~~~i~~~~~~~~~~~~~~~~~y  349 (881)
                           ..+||+|+||+||++....   .+++++.|++++.+++.+|.++||.+++..+             ...|
T Consensus         1      ~~~flrG~fd~dG~i~~~~~~~~i~~~~~s~~l~~~i~~~L~~~gi~~~~~~~~~~~~~~~~~~~~~~  57 (93)
T PF14527.6         1      CSNFLIGAMLSGGSIAHPLENYHLEIRCDSNNYIPLLTKALARYGLEYKIIYR-------------NKKT  57 (93)
T ss_pred                  CchhhhheEeeceEEEcCCCCeEEEEEeCChhHHHHHHHHHHCCCCcEEEEE-------------CCEE

Q ss_pred                  EEEEecCCCCCCc
Q Q_7621124_2       350    RVSFTPHDGIPPA  362 (881)
Q Consensus         350    ~~~i~~~~~~~~f  362 (881)
                           .+.+.+.+++..|
T Consensus         58     ~l~i~~~~~i~~f  70 (93)
T PF14527.6         58     IVYFKKSEIISDF  70 (93)
T ss_pred                  EEEEeCHHHHHHH
```

Template alignment | CDD

39. **PF02499.15 ; DNA_pack_C ; Probable DNA packing protein, C-terminus**

Probability: 97.23 E-value: 0.0022 Score: 69.9 Aligned Cols: 290 Identities: 12% Similarity: -0.005

```
Q ss_pred                  ccCCCCeEEEEccccCcccHHHHHHccCCCcCCCeEEEEEeceEeCCccccc---CCCCCCCCCCCCcc
Q Q_7621124_2       536    RKAPTYREVLVMTRWHQDDLAGRLLARDGRVEEGGVWRVVHLPAIAMPVDEKR---GVYPDPLGREPGEP  602 (881)
Q Consensus         536    ~~~~~~~~i~i~T~~~~d~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~---~~~~~~~~~~~~~~  602 (881)
                           ++..++++|+|+++...++....+.+-..  ....-+.++  .......-+..   .-.....-+....|
T Consensus         1      m~q~~~KiIfISS~ns~~~stSfl~~Lk~-~~e~llnVV-~~YvC~~H~~~~~~~~~tsCpCy~l~~P  66 (347)
T PF02499.15        1      MLQKDAKLIFISSVNSSDRSTSFLLNLRN--AQEKMLNVV--SYVCADHREDFHLQDALVSCPCYRLHIP  66 (347)
T ss_pred                  CCcCCcEEEEEeccCCCCcceehhhhhhc--ccccceEEE--EEEeHHHHHHchhcCCCccCCchhhcCC

Q ss_pred                  CCCCCCCCCChhhcccChhHHHHHHHHHHHHHHhcccchHHHHhcCCCCc----ccccccHHHHHhhcC
Q Q_7621124_2       603    LTHPLIVPDDPATWSQAPTHREALTNWWAAKRKMSTARDWSSMSQGLPSS----AENALLTDADIRAATA  668 (881)
Q Consensus         603    l~~~~~~~~~~~~~~~~~~~~l~~~~~~~~~~~~~~~f~~ey~~~~~~----~~~~~~f~~~~i~~~~~  668 (881)
                           .|                     -.+.+-+++.....-+..|.+|.++.-..    ....+|+...++....
T Consensus         67     ~~-------------------Itid~~vr~t~nlfl~gsF~~EimGg~~~~~~~~~~~~fte~~~~~F~~  117 (347)
T PF02499.15        67     TY-------------------ITIDESIKTTTNLFMEGAFDTELMGEGAASSNATLYRVVGDAALTQFDM  117 (347)
T ss_pred                  ce-------------------eccCHHHHHHHHHHcCCcchhcccCCcccCcccccccccccHHHHHHHhc

Q ss_pred                  CCCcc---------ceEEEEEEeCCCCCCCcCCcEEEEEEEECCC--CcEEEEecccc-----ccCcchH
```

```
Q Q_7621124_2       669    PVPDE---------LTRVVVGVDPSGGEGARHDTAGISAVGLDEH--QHAWFLEDRTA-----VLTPLEW  722 (881)
Q Consensus         669    ~~~~~~~~~~~~~~~~~~~iD~a~~~~~~~D~tai~v~~~~~~--g~~~v~~~~~~~-----~~~~~~~  722 (881)
                           ..+..         ....|++|||+++.+.....+++++++...+  ++++|+....-     .......
T Consensus         118    ~r~~t~~~~~~~~~~~~lyvyiDPa~t~nt~aSgtGI~~v~~~~~~~~~~IVlGlEhffl~~lt~~s~~~  187 (347)
T PF02499.15        118    CRVDTTAQQVQKCLGKQLFVYIDPAYTNNTEASGTGVGAVVTSTQTPTRSLILGMEHFFLRDLTGAAAYE  187 (347)
T ss_pred                  ccccCCcHHHHHhhCCEEEEEECCCCCCCccccCeEEEEEEecCCCCcEEEEEEeeecHHhccccHHHH

Q ss_pred                  HHH--------HHHHHHHhCCCEEEEEcccCchHHHHHHHHHHHHhccCCCCCCCccccCcccCCCCcee
Q Q_7621124_2       723    PRA--------VCLLAYERDASMIVYEKNYGGGMASALITQAWAALQNEPINADTDETMIPKSANCPYVK  784 (881)
Q Consensus         723    ~~~--------i~~~~~~~~~~~i~iE~~~~g~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~i~  784 (881)
                           +..        |..+...+..-.+++|.|.+++....+..    .+......+..--+-..++.++. -.
T Consensus         188    i~~ca~~~i~~I~~lhp~~~~v~~v~vEgNs~qdsaV~Ia~~~~~i~~~~~~~v~fyh~~~~~~~~~~-~p  252 (347)
T PF02499.15        188    IASCACTMIKAIAVLHPTIERVNAAVEGNSSQDSGVAIAT----VLNEICPLPIHFLHYTDKSSALQ-WP  252 (347)
T ss_pred                  HHHHHHHHHHHHHHHCccccceeEEEEecCCCChHHHHHHHH----HHHHhCCCCEEEEEEcCCCCccc-ce

Q ss_pred                  eccCCCCHHHhHHHHHHHHHcCCeEEcc----------cCccHHHHHHHhccCCC-------------CC
Q Q_7621124_2       785    GVSAKISKVLRAEPIAQAVKTGRAKFAQ----------LGNLGSLTNEFTLWQPG-------------ST  831 (881)
Q Consensus         785    ~~~~~~~K~~ri~~l~~~~~~g~i~~~~----------~~~~~~l~~el~~~~~~~-------------~~  831 (881)
                           .+.-++.|....+.+..++.+|.|....          .+..+-|++||.++...              ++
T Consensus         253    ~y~l~~~K~~af~~fi~~fnsg~i~asq~lvS~ti~l~~dpv~yl~~Ql~~~~~~~~~~~~~~~ysgK~~~  322 (347)
T PF02499.15        253    IYMLGGEKSSAFETFIYALNSGTLSASQTVVSNTIKISFDPVTYLVEQVRAIKCVPLRDGGQSYSAKQKH  322 (347)
T ss_pred                  EecccccHHHHHHHHHHHHHcCCeEEeeEEEcccccccCCChHHHHHHHHcCEEEEcCCCCeEEecCCCC

Q ss_pred                  CCCcHHHHHHHHHHHcCCCCC
Q Q_7621124_2       832    WSPGALDAAVYGATEVLPPVGS  853 (881)
Q Consensus         832    ~~dD~~Dal~~~~~~~~~~~~~  853 (881)
                           ..||++.|+.||..........
T Consensus         323    ~sDDl~va~vMa~y~~~~~~~~  344 (347)
T PF02499.15        323    MSDDLLVAVVMAHFMATDDRHM  344 (347)
T ss_pred                  CCHHHHHHHHHHHHHcCCccc
```

Template alignment | Template 3D structure | PDBe

40. **5OL7_A DNA-directed DNA polymerase,DNA-directed DNA polymerase; intein, extein, SICLOPPS, cyclic peptide; 1.6A {Nostoc punctiforme (strain ATCC 29133 / PCC 73102)}; Related PDB entries: 5OL6_B 5OL6_A**

Probability: 97.22 E-value: 9.4E-5 Score: 71.75 Aligned Cols: 94 Identities: 14% Similarity: 0.082

```
Q ss_pred                  CCccccCCCcEECCCcc-EEHHHc---CCCCEEECCCC----CEEEEEEEecCC-CCeEEEEeCCCCeEE
Q Q_7621124_2       87     VGKLVAHDTPVPTPTGW-TTHGEL---RPGDEVYHPSG----KVVTVRAISADA-HASIRVSTSDGGSIV  147 (881)
Q Consensus         87     ~gkC~~~dt~Vlt~~G~-~~i~~i---~~gd~v~~~~g----~~~~v~~~~~~~-~~~~~i~t~~G~~i~  147 (881)
                           .++|++++|.|++.+|. .+|+++   ..++.+++.+.    ...++..++... .++++|.+.+|..+.
T Consensus         40     ~~~C~~~~t~vl~~~g~~~~i~~l~~~~~~~~v~~~~~~~~~~~~~v~~~~~~~~~~~~i~~~~g~~i~  109 (150)
T 5OL7_A            40     HPQALSYETEILTVEYGLLPIGKIVEKRIECTVYSVDNNGNIYTQPVAQWHDRGEQEVFEYCLEDGSLIR  109 (150)
T ss_dssp                  SSCCEETTCEEEETTTEEEEHHHHHHTTCCCEEEEECTTSCEEEEEEEEEEEEEEEEEEEEETTSCEEE
T ss_pred                  CCCcccCCCEEEeccCCeEEHHHHHhcCCceEEEEECCCCCEEEEEeeEEEEcCCCCeEEEEeCCCCEEE

Q ss_pred                  ECCCCeEEEEeCCCCeEE-EcchhHH-hhheeecCCCCccc
Q Q_7621124_2       148    VHPRHEWTVWDRNRKRWS-TMETGDM-MRRAYVDRSGRPAF  186 (881)
Q Consensus         148    ~T~~H~~~~~~~~~~~~~-~~~~~~l-~~~~~~~~~~~~~~  186 (881)
                           +|++|++++.    .+|. .  ++++ ..++.+.......+
T Consensus         110    ~T~~H~~lt~-----~gw~~~-~~~~l~~~g~~l~~~~~~~~  144 (150)
T 5OL7_A            110    ATKDHKFMTV----DGQMLP--IDEIFERELDLMRVDNLPN  144 (150)
T ss_dssp                  ECTTCEEEBT----TSCEEE--HHHHHHTTCEECBCCCCC-
T ss_pred                  ECCCCeEEee----CCeEEE--HHHHccCCceeEEecCCCC
```

Template alignment | CDD

41. **PF01079.20 ; Hint ; Hint module**

Probability: 97.01 E-value: 2.6E-4 Score: 75.58 Aligned Cols: 94 Identities: 17% Similarity: 0.217

```
Q ss_pred                  eCCCCCccccCCCcEECCCc-cEEHHHcCCCCEEECCCC----CEEEEEEEecCCC----------CeEE
Q Q_7621124_2       83     TPSQVGKLVAHDTPVPTPTG-WTTHGELRPGDEVYHPSG----KVVTVRAISADAH----------ASIR  137 (881)
Q Consensus         83     g~~g~gkC~~~dt~Vlt~~G-~~~i~~i~~gd~v~~~~g----~~~~~v~~~~~~~~~~~~~~~~~~~~~  137 (881)
                           ...+.+.|+++++.|.+++| .++|++|++||.|++.++    .+.+|..+.....          ..++
T Consensus         5      ~~~~~~~Cf~~~t~V~~~~G~~~~i~~L~~GD~Vls~~~g~~~~~~v~~~~~~~~~~~~~~~~~~~~v~  74 (256)
T PF01079.20        5      DAAKYGGCFPGESTVIVPGEGHVPISSLQPGDQVLAIDKSGAVITDTFLSFMDARSDIVSGHQAYRQMVE  74 (256)
T ss_pred                  ccccCCCCccCCCEEEcCCCCEEEHHHCCCCCEEEEECCCCCEEEEEEEEEEeCCccccccccceeeeEEE

Q ss_pred                  EEeCCCCeEEECCCCeEEEEeCCCC----------------------------eEEEcchhHHhhheee
Q Q_7621124_2       138    VSTSDGGSIVVHPRHEWTVWDRNRK----------------------------RWSTMETGDMMRRAYV  178 (881)
Q Consensus         138    i~t~~G~~i~~T~~H~~~~~~~~~~----------------------------~~~~~~~~~l~~~~~~  178 (881)
                           |++.+|..+.+|++|++++.+....                           .|..  +.++..++.+
T Consensus         75     i~~~~g~~l~lT~~H~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~--A~~l~~Gd~l  139 (256)
```

```
T PF01079.20        75     ITTENGFSVTLTRNHLIYVSKPTYDASLLTATSNATQQNNERLGLQDFTSPHSSF--AAKVRQGDYI  139 (256)
T ss_pred                  EEeCCCcEEEEcccEEEEecCCCChhhhhhcccchhhhhhcCCCCCCCCeeee--HhhCCCCCEE
```

Template alignment | Template 3D structure | PDBe

42. 6BS8_A Replicative DNA helicase (E.C.3.6.4.12); class 3 intein, DnaB, HYDROLASE; 1.95A {Mycobacterium smegmatis}; Related PDB entries: 6BS8_C 6BS8_B

Probability: 96.84 E-value: 5.8E-4 Score: 64.89 Aligned Cols: 67 Identities: 39% Similarity: 0.687

```
Q ss_pred                  cccCCCcEECCCccEEHHHcCCCCEEECCCCCEEEEEEEec-CC-CCeEEEEeCCCCeEEECCCCeEEE
Q Q_7621124_2       90     LVAHDTPVPTPTGWTTHGELRPGDEVYHPSGKVVTVRAISA-DA-HASIRVSTSDGGSIVVHPRHEWTV  156 (881)
Q Consensus         90     C~~~dt~Vlt~~G~~~i~~i~~gd~v~~~~g~~~~v~~~~~-~~-~~~~~~i~t~~G~~i~~T~~H~~~~  156 (881)
                           |+..+|.|++.+|+++|+++..|+.+++.++...+|..++. .. ..++++.+.+|..+.+|++|++++
T Consensus         1      c~~~~t~v~~~~g~~~i~~~~~gd~v~~~~~~~~~v~~~~~~~~~~~~~~~~~~g~~~~~t~~h~~~~  69 (139)
T 6BS8_A            1      ALALDTPLPTPSGWTTMGDVAVGDHLLGPDGEPTRVVADTDVMLGRPCYVVEFSDGTAIVADAQHQWPT  69 (139)
T ss_dssp                  CEETTCEEEETTEEEETTTCCTTCEEECTTSSEEEEEEECCCBCSCCEEEEEETTSCEEEEETTCEEEE
T ss_pred                  CCCCCCceeCCCceEEHHHcCCCCEEECCCCCeEEEEEEeeccCCccEEEEEeCCCCEEEEcCCCEEEc
```

Template alignment | Template 3D structure | PDBe

43. 3HYI_A Protein DUF199/WhiA; LAGLIDADG, homing endonuclease, helix-turn-helix, HTH; HET: GOL; 2.34A {Thermotoga maritima}

Probability: 96.77 E-value: 1.4E-4 Score: 79.39 Aligned Cols: 144 Identities: 10% Similarity: -0.09

```
Q ss_pred                  hHHHHHHHhcccccCCC--CeEEecCChHHhhhchhhcCeEEecCCcEEEEeCCh---HHHHHHHcCCCCC
Q Q_7621124_2       204    DPYTLGVWLGDGSSTK--AAITHHADDEYVLPYPKSADCVHQTTGVVTSYYRGG---LHTALKTLGVHAN  268 (881)
Q Consensus         204    ~~~llG~~l~dG~~~~-~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~---l~~~l~~~g~~~~  268 (881)
                           .+.++|++.++|++..  ..+.+...+..+.+.+...-.........+......   ...+.........
T Consensus         29     ~aeL~G~i~~~G~i~~~~~~i~i~~~~~~~ar~i~~l~~~~~~~~~~i~~~~~~~~~~~~i~i~~~~~~~  98 (295)
T 3HYI_A            29     ISELLGFIKARGDLDVKSRHIVFSLHSFAASRRLLNLMKYLSKPVSEIIVEKSHNIKKRYIKITAEYSES  98 (295)
T ss_dssp                  HHHHHHHHHHHHEEEETTTTEEEEEESCHHHHHHHHHHHHHTTCCEEEEEEEC----CCCEEEEEEECCGG
T ss_pred                  HHHHHHHHHhcCeEEeCCCEEEEEEeCCHHHHHHHHHHHHHHhCCCcEEEEEeCCCCCceEEEEeccccccc

Q ss_pred                  CcCCHHHHHCCHHHHHHHHHHHHHcCCeeCCC---CeEEEEeCCHHHHHHHHHHHH-HCCCcEEEEecCC
Q Q_7621124_2       269    KHIPVQYLRASESSRRALLAGLIDSDGTIAKS---GQVSFINTNRRLYDGVVELIR-TLGYRATIHAPLQ  334 (881)
Q Consensus         269    k~iP~~i~~~~~~~~~~fL~Gl~dgDG~~~~~---~~i~~~t~s~~l~~~l~~Ll~-~lGi~~~i~~~~~  334 (881)
                           -.+|.  ...+.....+||+|+|++||++...   -.++|.+.+++++.+++.+|. ++||.+.+..+
T Consensus         99     l~~~~--~~~~~~~~~~afLRG~Fl~~Gsi~~p~~~yhLEi~~~~~~~a~~l~~~L~~~~gi~~~~~~r--  164 (295)
T 3HYI_A            99     FMVIE--PFFDVALFVSFLRGLFLSGGSMTNPRYHYHLEINLFEEETLALTRKSLKDFFNINAGIIEL--  164 (295)
T ss_dssp                  GGSCC--TTSSHHHHHHHHHHHHHHHEEECCTTTCCCEEEEESCHHHHHHHHHHHHHHCCCCEEEEC--
T ss_pred                  ccccC--cCCCHHHHHHHHHHHHhhCcccCCCCcceEEEEeCCHHHHHHHHHHHHhHhccCcEEEEe--

Q ss_pred                  CCCCCCCcccCeeeEEEEEEecCCCCCCc
Q Q_7621124_2       335    PSTSSSGVAGTRVLYRVSFTPHDGIPPA  362 (881)
Q Consensus         335    ~~~~~~~~~~~~~~y~~~i~~~~~~~~f  362 (881)
                                     ...|.|.+.+.+.+..|
T Consensus         165    ------------~~~~~vyiK~~~~I~~f  181 (295)
T 3HYI_A            165    -----------RNTRKLYIKSIKDILVF  181 (295)
T ss_dssp                  -----------SSCEEEEECCHHHHHHH
T ss_pred                  -----------CCeEEEEEeCHHHHHHH
```

Template alignment | Template 3D structure | PDB | NCBI

44. d3nzma_ b.86.1.0 (A:) automated matches {Synechocystis sp. [TaxId: 1148]}

Probability: 96.72 E-value: 8.2E-4 Score: 66.39 Aligned Cols: 75 Identities: 15% Similarity: 0.139

```
Q ss_pred                  CCCCccccCCCcEECCCc-cEEHHHcCCC-----CEEECCCCCEE--EEEEEecCC-CCeEEEEeCCCCe
Q Q_7621124_2       85     SQVGKLVAHDTPVPTPTG-WTTHGELRPG-----DEVYHPSGKVV--TVRAISADA-HASIRVSTSDGGS  145 (881)
Q Consensus         85     ~g~gkC~~~dt~Vlt~~G-~~~i~~i~~g-----d~v~~~~g~~~--~v~~~~~~~-~~~~~i~t~~G~~  145 (881)
                           |-.+.|+.++|.|.+.+| ..+|+++..+     ....+.+|+..  .+..++... .++|+|++.+|+.
T Consensus         1      ~~~~~C~~~~t~i~~~~~~~~~i~~l~~~~~~~~~~~~~~~~~~~~~v~~~~~~~~~~~~~i~~~~g~~  70 (164)
T d3nzma_           1      PFCPGCLSFGTEILTVEYGPLPIGKIVSEEINCSVYSVDPEGRVYTQAIAQWHDRGEQEVLEYELEDGSV  70 (164)
T ss_dssp                  CCCSSCEETTCEEEETTTEEEEHHHHHHTTCCCEEEEECTTSEEEEEECCEEEEEEEEEEEEEEETTSCE
T ss_pred                  CCCCCccCCCCEEEcCCCcEEEHHHHcccccCCceEEEECCCCCEEEEeeeEEEecCcceEEEEEeCCCCE

Q ss_pred                  EEECCCCeEEEEeC
Q Q_7621124_2       146    IVVHPRHEWTVWDR  159 (881)
Q Consensus         146    i~~T~~H~~~~~~~  159 (881)
                           +.+|++|++++.++
T Consensus         71     i~~T~~H~~~~~~g  84 (164)
T d3nzma_           71     IRATSDHRFLTTDY  84 (164)
T ss_dssp                  EEECTTCEEEBTTS
T ss_pred                  EEECCCCeEEEeCCC
```

Template alignment | CDD

45. **PF14528.6 ; LAGLIDADG_3 ; LAGLIDADG-like domain**

Probability: 96.62 E-value: 3.9E-4 Score: 59.34 Aligned Cols: 74 Identities: 16% Similarity: 0.249

```
Q ss_pred                  HHHHHHHHHHHHcCCeeCCCCe-----EEEEeCCHHHHHHHHHHHHCCCcEEEEecCCCCCCCCCcccCe
Q Q_7621124_2       281    SSRRALLAGLIDSDGTIAKSGQ-----VSFINTNRRLYDGVVELIRTLGYRATIHAPLQPSTSSSGVAGT  345 (881)
Q Consensus         281    ~~~~~fL~Gl~dgDG~~~~~~~~-----i~~~t~s~~l~~~l~~Ll~~lGi~~~i~~~~~~~~~~~~~~~  345 (881)
                           +...+||+|+|++||++.....     +.+.+.++.++.+++.+|.++|+.+++.....+.        .
T Consensus         1      ~~~~~~l~G~~d~dG~i~~~~~~~~~~i~~~~~~~~~~~~~~~~l~~~g~~~~i~~~~~~~--------~  62 (84)
T PF14528.6         1      DLLAKVLQGYFSGDGSFYLKNHKRSAFIEAVTTSRQLANELLVALQRFGIVANLKVRRNRC--------G  62 (84)
T ss_pred                  ChhHHHHHHHHcCceeEEEecCCcCCeEEEEEcCHHHHHHHHHHHHCCcccEEEEeecCC--------C

Q ss_pred                  eeEEEEEEecCCCCCCc
Q Q_7621124_2       346    RVLYRVSFTPHDGIPPA  362 (881)
Q Consensus         346    ~~~y~~~i~~~~~~~~f  362 (881)
                           ...|.+.+.+..++..|
T Consensus         63     ~~~~~~~~~~~~~~~~  79 (84)
T PF14528.6         63     NYEYRILIGRTEFIRIF  79 (84)
T ss_pred                  CceEEEEEeCHHHHHHH
```

Template alignment | Template 3D structure | PDB | NCBI

46. **d1at0a_ b.86.1.1 (A:) Hedgehog {Fruit fly (Drosophila melanogaster) [TaxId: 7227]}**

Probability: 96.61 E-value: 0.0017 Score: 62.53 Aligned Cols: 89 Identities: 18% Similarity: 0.288

```
Q ss_pred                  cccCCCCcEECCCCc-cEEHHHcCCCCEEECCCC----CEEEEEEEecCC----CCeEEEEeCCCCeEEECC
Q Q_7621124_2       90     LVAHDTPVPTPTG-WTTHGELRPGDEVYHPSG----KVVTVRAISADA----HASIRVSTSDGGSIVVHP  150 (881)
Q Consensus         90     C~~~dt~Vlt~~G-~~~i~~i~~gd~v~~~~g----~~~~~v~~~~~~~~~----~~~~~i~t~~G~~i~~T~  150 (881)
                           |+.+++.|.+.+| .++|+++..||.+++.++    .+.++.......    ..++++.+.+|..+.+|+
T Consensus         1      c~~~~t~i~~~~G~~~~i~~l~~gd~v~~~~~~g~~~~~~v~~~~~~~~~~~~~~~~i~~~~~~~~~~t~  70 (145)
T d1at0a_           1      CFTPESTALLESGVRKPLGELSIGDRVLSMTANGQAVYSEVILFMDRNLEQMQNFVQLHTDGGAVLTVTP  70 (145)
T ss_dssp                  CBCTTCEEEBTTSCEEEGGGCCTTCEEEEECTTSCEEEEEEEEEEEEEEEEEEEEEEEEETTSCEEEECT
T ss_pred                  CCCCCCEEEeCCCCEEEHHHCCCCCEEEEECCCCCEEEEEEEEEECCcccceeEEEEEECCCCEEEECC

Q ss_pred                  CCeEEEEeCCCCeEEEcchhHHhhheee
Q Q_7621124_2       151    RHEWTVWDRNRKRWSTMETGDMMRRAYV  178 (881)
Q Consensus         151    ~H~~~~~~~~~~~~~~~~~~l~~~~~~  178 (881)
                           +|++++.+........+.+.++..++.+
T Consensus         71     ~h~~~~~~~~~~~~~~~~~~l~~gd~l  98 (145)
T d1at0a_           71     AHLVSVWQPESQKLTFVFADRIEEKNQV  98 (145)
T ss_dssp                  TCEEEEEETTTTEEEEEEGGGCCTTCEE
T ss_pred                  CcEEEEecCCcCceEEEEHHHcCCCCEE
```

Template alignment | Template 3D structure | PDB | NCBI

47. **d1am2a_ b.86.1.2 (A:) GyrA intein {Mycobacterium xenopi [TaxId: 1789]}**

Probability: 96.59 E-value: 0.0021 Score: 65.99 Aligned Cols: 87 Identities: 18% Similarity: 0.276

```
Q ss_pred                  cccCCCCcEECCCcc-EEHHHcCCCC----------EEECCCCCEEEEEEEecCC-CCeEEEEeCCCCeEE
Q Q_7621124_2       90     LVAHDTPVPTPTGW-TTHGELRPGD----------EVYHPSGKVVTVRAISADA-HASIRVSTSDGGSIV  147 (881)
Q Consensus         90     C~~~dt~Vlt~~G~-~~i~~i~~gd----------~v~~~~g~~~~v~~~~~~~-~~~~~i~t~~G~~i~  147 (881)
                           |+.++|.|.+.+|. ++|+++..|+          .+++..+...++..+.... +.+++|.+.+|..+.
T Consensus         2      C~~~~t~i~~~~g~~~~i~~l~~g~~~~~~~~~~~~~~~~~~~v~~~~~~~~~~~~~i~~~~g~~l~  71 (199)
T d1am2a_           2      SITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDRHGNPVLADRLFHSGEHPVYAVRTVEGLRVT  71 (199)
T ss_dssp                  CEETTCEEECSTTCEEEGGGSSTTCCTTEEEEEEEEEECTTSCEEEEEEEEEEEEEEEEEEEETTSCEEE
T ss_pred                  cccCCCEEECCCCCEEEHHHcCCCCCCCCCceEEEEECCCCCEEEccEEEecCCCCEEEEEeCCCCEEE

Q ss_pred                  ECCCCeEEEEeC----CCCeEEEcchhHHhhheee
Q Q_7621124_2       148    VHPRHEWTVWDR----NRKRWSTMETGDMMRRAYV  178 (881)
Q Consensus         148    ~T~~H~~~~~~~----~~~~~~~~~~~~~l~~~~~  178 (881)
                           +|++|++++.+.    ....|..  +.++..++++
T Consensus         72     ~T~~H~i~~~~~~~~~~~~w~~--~~~~l~~g~~l  104 (199)
T d1am2a_           72     GTANHPLLCLVDVAGVPTLLWKL--IDEIKPGDYA  104 (199)
T ss_dssp                  ECTTCEEEEEEEETTEEEEEEE--GGGCCTTCEE
T ss_pred                  ecCCceeEEEecCCCCccEEEEE--HHHCCCCCEE
```

Template alignment | Template 3D structure | PDBe

48. **1MOW_G chimera of homing endonuclease I-DmoI; LAGLIDADG, homing, engineering, design, endonuclease; HET: SO4, GOL; 2.4A {Desulfurococcus mobilis} SCOP: d.95.2.1; Related PDB entries: 1MOW_A 1MOW_J 1MOW_D**

Probability: 96.55 E-value: 5.2E-4 Score: 73.81 Aligned Cols: 119 Identities: 19% Similarity: 0.21

```
Q ss_pred                  CCCCCCcccchHHHHHHhcccccCCC---------CeEEecCC-hHHhhhchhhcC--------------
Q Q_7621124_2       194    LEGVDDTLLIDPYTLGVWLGDGSSTK---------AAITHHAD-DEYVLPYPKSAD--------------  239 (881)
Q Consensus         194    ~~~~~~~~~~~~llG~~l~dG~~~~----------~~i~~~~~-~~~~~~~~~~~~~--------------  239 (881)
```

```
                                ...+....+.++|++|++.|||++..         ..+.+... +..++..+...-
T Consensus         1           ~~~~~~~~~~~yl~G~i~gDG~i~~~~~~~~~~~~~i~i~~~~~~~~l~~i~~~~~~~~~~~~~~~~~~  70 (260)
T 1MOW_G            1           MHNNENVSGISAYLLGLIWGDGGLYKLKYKGNRSEYRVVITQKSENLIKQFIAPRMQFLIDELNVKSKIQ  70 (260)
T ss_dssp                       ----CCHHHHHHHHHHHHHHEEEEEEEETTTEEEEEEEEESCHHHCCCCCHHHHHHHHHHTCCSCEE
T ss_pred                       CCCCcCcchHHHHHHHHHcccEEEEEecCCeeEEEEEEEeCcHHHHHHHHHHHHHHHHhCceeEEE

Q ss_pred                       eEEecCCcEEEEeCChHHHHHHHcCCCCCCcCCHHHHCCHHHHHHHHHHHHcCCeeCCCCe-------
Q Q_7621124_2       240         CVHQTTGVVTSYYRGGLHTALKTLGVHANKHIPVQYLRASESSRRALLAGLIDSDGTIAKSGQ-------  302 (881)
Q Consensus         240         ~~~~~~~~~~~~~~~~l~~~l~~~g~~~~k~iP~~i~~~~~~~~~~fL~Gl~dgDG~~~~~~~-------  302 (881)
                                .........+.+.+..+...+..+.       |..+ ..+.+...+||+|++||||++.....
T Consensus         71          ~~~~~~~~~~~i~sk~~~~~l~~~~-------~~~~~~~~~~~~~~l~Gf~DgdG~~~~~~~~~~~~~~  132 (260)
T 1MOW_G            71          IVKGDTRYELRVSSKKLYYYFANML-------ERIR-LFNGNRFLAYLAGIVDGDGSIIAQIKPNQSYKF  132 (260)
T ss_dssp                       EEECSSCEEEEEEECHHHHHHHHHHT-------TTGG-GCCHHHHHHHHHHHHHHHEEEEEEEEECTTSTT
T ss_pred                       EECCCcEEEEEECCHHHHHHhcccc-------ccee-ccCCCcccHHHHHHHHcCcEEEEEEEEeCCCCCc

Q ss_pred                       -------EEEEeC--CHHHHHHHHHHH
Q Q_7621124_2       303         -------VSFINT--NRRLYDGVVELI  320 (881)
Q Consensus         303         -------i~~~t~~-s~~l~~~l~~Ll  320 (881)
                                       +.++..  +..+++.++.+|
T Consensus         133         ~~~~~~~~~i~q~~~~~~ll~~i~~~l  159 (260)
T 1MOW_G            133         KHQLSLTFQVTQKTERRWFLDKLVDEI  159 (260)
T ss_dssp                       SEEEEEEEEEEEEGGGHHHHHHHHHHH
T ss_pred                       cEEEEEEEEEEeCcccHHHHHHHHHHH
```

Template alignment | CDD

49. **PF17288.2 ; Terminase_3C ; Terminase RNAseH like domain**

Probability: 96.52 E-value: 0.0055 Score: 58.91 Aligned Cols: 127 Identities: 13% Similarity: 0.045

```
Q ss_pred                       eCCCCCCCcCCcEEEEEEEECC-CCcEEEEeccc-cccCcchHHHHHHHHHHhCCCEEEEEcccCchHH
Q Q_7621124_2       682         DPSGGEGARHDTAGISAVGLDE-HQHAWFLEDRT-AVLTPLEWPRAVCLLAYERDASMIVYEKNYGGGMA  749 (881)
Q Consensus         682         D~a~~~~~~~D~tai~v~~~~~-~g~~~v~~~~~-~~~~~~~~~~~i~~~~~~~~~~~i~iE~~~~g~~~  749 (881)
                                |+|..    .|++|++.+.+++ ++.+||++.+. .+.++.++++.|.++..  +...++.|+.+..
T Consensus         1           D~G~~-----~~p~a~~~~~~~~~~~~~v~~e~~~~~~~~~~~~~~i~~~~~--~~~~~~~d~a~~~---  61 (143)
T PF17288.2         1           DFGFV----ESYNAVVRVAVDHEKKYLYIYWEYYKNGLTDDKTAEELKEFAE--TKELIKADSAEPK---  61 (143)
T ss_pred                       CCCCC----CCCcEEEEEEEeCCCCEEEEEEEEecCCCCHHHHHHHHHHhhc--ccCeEEEcCCChH---

Q ss_pred                       HHHHHHHHHHhccCCCCCCCccccCcccCCCCceeecc-CCCCHHHhHHHHHHHHHcCCeEEcccCccHH
Q Q_7621124_2       750         SALITQAWAALQNEPINADTDETMIPKSANCPYVKGVS-AKISKVLRAEPIAQAVKTGRAKFAQLGNLGS  818 (881)
Q Consensus         750         ~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~-~~~~K~~ri~~l~~~~~~g~i~~~~~~~~~~  818 (881)
                                      ..++++..               ++. +.+.. .+.+...+++.+..+.   ++.+.+  .+..
T Consensus         62          ------~~~~l~~~~~~~~~~~~~~~~g~~-~~~~~~~~~~~~~~~i~~~~~~~---~~~i~~-~~c~~  104 (143)
T PF17288.2         62          ------TIRYFQQH---------------GFN-MVGARKYQGSRLQYTKKIKRFR---KIICSD--RCEN  104 (143)
T ss_pred                       ------HHHHHHHc---------------CCe-EEEcccCCCCCHHHHHHHHHhcc---EEEeCC--CCHH

Q ss_pred                       HHHHHhccCCC-----------CCCCCcHHHHHHHHH
Q Q_7621124_2       819         LTNEFTLWQPG-----------STWSPGALDAAVYGA  844 (881)
Q Consensus         819         l~~el~~~~~~~~~~~~~~~~~~~dD~~Dal~~~~  844 (881)
                                |++||..|...           .+.+||.+||+.+++
T Consensus         105         li~el~~y~~~~~~~~~~~~~~~~~dH~~Da~rY~~  141 (143)
T PF17288.2         105         TIYELKPLAYATDKLGNIIEDEFTIDPHTLSAIWYAL  141 (143)
T ss_pred                       HHHHHHHcccccCCCCCCccCCCCCChhHHHHHHHhc
```

Template alignment | Template 3D structure | PDB | NCBI

50. **d3qvea1 b.145.1.0 (A:206-342) automated matches {Human (Homo sapiens) [TaxId: 9606]}**

Probability: 96.47 E-value: 5.0E-4 Score: 65.32 Aligned Cols: 86 Identities: 13% Similarity: 0.132

```
Q ss_pred                       CCCCCccccCCCcEECCCcc-EEHHHcCCCCEEECCCCCEE----------------EEEEEecC--C-C
Q Q_7621124_2       84          PSQVGKLVAHDTPVPTPTGW-TTHGELRPGDEVYHPSGKVV----------------TVRAISAD--A-H  133 (881)
Q Consensus         84          ~~g~gkC~~~dt~Vlt~~G~~~~i~~i~~gd~v~~~~g~~~~~~~~~~~~~~~~~v~~~~~~~~~~~  133 (881)
                                +.+.+.|+.++|.|.+.+|. ++|++|.  |.|++.+....                +|..+...  . .
T Consensus         3           ~~~~~~CF~~GT~I~~~~G~~k~Ie~i~~D~v~s~~~~~~~~~~~~~~~~~~~~~v~~i~~~~~~~~  70 (137)
T d3qvea1           3           PSTVWHCFLKGTRLCFHKGSNKEWQDVE--DFARAEGCDNEEDLQMGIHKGYGSDGLKLLSHEESVSFGE  70 (137)
T ss_dssp                       CCCSBTTBCTTCEEEEESSSSCCSCEEHH--HHHHHCC---------CTTTTTTTTCEEEEEEEEEEETTE
T ss_pred                       CCCCCCccccCCCEEEeCCCCeeeeehHH--HHHHhcCCCchhHHhhhhccccCCCCcEEEEEEccccCCC

Q ss_pred                       CeEEEEeCCCC------eEEECCCCeEEEEeCCC-------------CeEEEcchhH
Q Q_7621124_2       134         ASIRVSTSDGG------SIVVHPRHEWTVWDRNR-------------KRWSTMETGD  171 (881)
Q Consensus         134         ~~~~i~t~~G~-------i~~T~~H~~~~~~~~~~-------------~~~~~~~~~~  171 (881)
                                .+++|++..|.       .+.+|++|+|++.+.+|              .....+..+|
T Consensus         71          ~~~~i~~~~~~~~~~~~~~~t~~Hpf~v~~~Gw~s~~P~~~~~~~gl~~~~L~~GD  127 (137)
T d3qvea1           71          SVLKLTFDPGTVEDGLLTVECKLDHPFYVKNKGWSSFYPSLTVVQHGIPCCEVHIGD  127 (137)
```

```
T ss_dssp                EEEEEEEECSCGGGCCEEEEEETTCEEEETTTEEEESSHHHHHHHHCCCCEECCTTC
T ss_pred                cEEEEEEcCCCCcccceEEEEEeCCcceEecCCcccccCChhhceeecCCCCeeCCCCC
```

Template alignment | Template 3D structure | PDBe

51. **2QOJ_Z Intron-encoded DNA endonuclease I-AniI (E.C.3.1.-.-)/DNA; LAGLIDADG homing endonuclease, I-AniI, Hydrolase; HET: MSE; 2.4A {Emericella nidulans} SCOP: l.1.1.1, d.95.2.1; Related PDB entries: 3UVF_B 3UVF_A 3EH8_G 3EH8_D 3EH8_A 1P8K_Z**

Probability: 96.42 E-value: 6.6E-4 Score: 72.69 Aligned Cols: 139 Identities: 14% Similarity: 0.127

```
Q ss_pred                cchHHHHHHhcccccCCCCe----------EEecCChHHhhhchhh--------cCeEEecCCcEEEEeC
Q Q_7621124_2       202  LIDPYTLGVWLGDGSSTKAA----------ITHHADDEYVLPYPKS--------ADCVHQTTGVVTSYYR  253 (881)
Q Consensus         202  ~~~~~llG~~l~dG~~~~~~----------i~~~~~~~~~~~~~~~~--------~~~~~~~~~~~~~~~~  253 (881)
                         ...+|++|++.|||++....          +++...+..+++.+..        ...........+.+.+
T Consensus         4    ~~~~~l~Gf~~gDG~i~~~~~~~~~~~~~~I~~~~~d~~~L~~i~~~~~~g~i~~~~~~~~~~~~~~i~~  73 (254)
T 2QOJ_Z            4    LTYAYLVGLFEGDGYFSITKKGKYLTYELGIELSIKDVQLIYKIKKILGIGIVSFRKRNEIEMVALRIRD  73 (254)
T ss_dssp                THHHHHHHHHHHHEEEEEEEETTEEEEEEEEEEEGGGHHHHHHHHHHSCCEEEEECTTTSCEEEEEECC
T ss_pred                cchHHHHHheeccEEEEEEEcCcEEEEEEEEEEecCCHHHHHHHHHHhCCCEEEEecCCCccEEEEEEec

Q ss_pred                Ch-----HHHHHHHcCCCCCCcCCHH----------------------------HHHCCHHHHHHHHHH
Q Q_7621124_2       254  GG-----LHTALKTLGVHANKHIPVQ----------------------------YLRASESSRRALLAG  289 (881)
Q Consensus         254  ~~-----l~~~l~~~g~~~~k~iP~~-----------------------------i~~~~~~~~~~fL~G  289 (881)
                         ..     +..++..++....|...-.                              ....+.+...+||+|
T Consensus         74   ~~~~~~~i~~~~~~~~~~~k~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~G  143 (254)
T 2QOJ_Z            74   KNHLKSFILPIFEKYPMFSNKQYDYLRFRNALLSGIISLEDLPDYTRSDEPLNSIESIINTSYFSAWLVG  143 (254)
T ss_dssp                HHHCCCCCHHHHHHSCCCSTHHHHHHHHHHHHHHTCCSTTTSCCCCCCSSCSSCHHHHHTSTTHHHHHHH
T ss_pred                HHHHHHHHHHHHHhCCCCChhHHHHHHHHHHHHHhCCCChhhCCCCcCCCCCCcCChhHHHcccccchHHHH

Q ss_pred                HHHcCCeeCCC----------CeEEEEeCCHH-HHHHHHHHHHCCCcEEEEecCCCCCCCCCcccCeeeE
Q Q_7621124_2       290  LIDSDGTIAKS----------GQVSFINTNRR-LYDGVVELIRTLGYRATIHAPLQPSTSSSGVAGTRVL  348 (881)
Q Consensus         290  l~dgDG~~~~~~~~~~~~~~~i~~~t~s~~-l~~~l~~Ll~~lGi~~~i~~~~~~~~~~~~~~~~~~~~  348 (881)
                         ++||||++.-.          ..+.++..+.. +++.++..|..-|........               .
T Consensus         144  f~DgdGsf~~~~~~~~~~~~~~~f~i~~~~~~~ll~~i~~~l~~~~~i~~~~~~----------------~  198 (254)
T 2QOJ_Z            144  FIEAEGCFSVYKLNKDDDYLIASFDIAQRDGDILISAIRKYLSFTTKVYLDKTN---------------C  198 (254)
T ss_dssp                HHHHHEEEECCBSSTTSCCBCCEEEEEEEETCHHHHHHHHHHTTCCSCCEECSSS---------------E
T ss_pred                hheeeeeEEEEEecCCCCeEEEEEEEeecccHHHHHHHHHHcCCCCeEEECCCC---------------e

Q ss_pred                EEEEEec
Q Q_7621124_2       349  YRVSFTP  355 (881)
Q Consensus         349  y~~~i~~  355 (881)
                         |++.+++
T Consensus         199  ~~~~i~~  205 (254)
T 2QOJ_Z            199  SKLKVTS  205 (254)
T ss_dssp                EEEEECS
T ss_pred                EEEEEec
```

Template alignment

52. **cd00081 Hint; Hedgehog/Intein domain, found in Hedgehog proteins as well as proteins which contain inteins and undergo protein splicing (e.**

Probability: 96.4 E-value: 0.0026 Score: 60.06 Aligned Cols: 87 Identities: 23% Similarity: 0.29

```
Q ss_pred                cccCCCCcEECC-CccEEHHHcCC--CCEEECCCC----CEEEEEEEecC-C-CCeEEEEeCCCCeEEECC
Q Q_7621124_2        90  LVAHDTPVPTP-TGWTTHGELRP--GDEVYHPSG----KVVTVRAISAD-A-HASIRVSTSDGGSIVVHP  150 (881)
Q Consensus          90  C~~~dt~Vlt~-~G~~~i~~i~~-~gd~v~~~~g----~~~~~v~~~~~~-~~~~~~i~t~~G~~i~~T~  150 (881)
                         |+.+++.|.+. .|.++|+++..  |+.++..++    .+.++..++.. . .+++++.+.+|..+.+|+
T Consensus          1   c~~~~~~i~~~~~~~~~i~~l~~~~g~~v~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~t~  70 (136)
T cd00081            1   CFTGDTLVLLEDGGRKKIEELVEKKGDKVLALDETGKLVFSKVLKVLRRDYEKKFYKIKTESGREITLTP  70 (136)
T ss_pred                CCCCCcEEEecCCCEEEHHHheeecCCEEEEECCCCCEEEeeeeeeEEecCCCceEEEEeCCCCEEEECC

Q ss_pred                CCeEEEEeCCCCeEEEcchhHHhhheee
Q Q_7621124_2       151  RHEWTVWDRNRKRWSTMETGDMMRRAYV  178 (881)
Q Consensus         151  ~H~~~~~~~~~~~~~~~~~~l~~~~~~  178 (881)
                         +|++++.......|..  +.++..++.+
T Consensus         71   ~h~~~~~~~~~~~~~~--~~~~~~~~~i  96 (136)
T cd00081           71   DHLLFVLEDGELKWVF--ASDLKPGDYV  96 (136)
T ss_pred                CceEEEEeCCEEEEEE--HHHCCCCCEE
```

Template alignment | Template 3D structure | PDBe

53. **3NZM_A DNA polymerase III subunit alpha; disulfide bond, TRANSFERASE; HET: SO4; 1.55A {Synechocystis sp. PCC 6803} SCOP: b.86.1.0; Related PDB entries: 4GIG_A 1ZDE_A 1ZD7_B 1ZD7_A**

Probability: 96.31 E-value: 0.003 Score: 62.56 Aligned Cols: 79 Identities: 14% Similarity: 0.129

```
Q ss_pred                eCCCCCccccCCCcEECCC-ccEEHHHcC---CCCEEECCCCC----EEEEEEEecCC-CCeEEEEeCCC
Q Q_7621124_2        83  TPSQVGKLVAHDTPVPTPT-GWTTHGELR---PGDEVYHPSGK----VVTVRAISADA-HASIRVSTSDG  143 (881)
```

```
Q Consensus         83     g~~g~gkC~~~dt~Vlt~~-G~~~i~~i~~~~gd~v~~~~g~~~~~~~v~~~~~~~~~~~~~~i~t~~G  143 (881)
                           ..+..+.|+.+++.|++.+ |.++|+++.   .|+.++..+..    ...+...+... +++++|.+.+|
T Consensus         3      ~~~~~~~c~~~~t~v~~~~~g~~~i~~~~~~~~~~v~~~~~~~~~~~~~~~~~~~~~~~~v~~~~g  72 (168)
T 3NZM_A            3      PDPFCPGCLSFGTEILTVEYGPLPIGKIVSEEINCSVYSVDPEGRVYTQAIAQWHDRGEQEVLEYELEDG  72 (168)
T ss_dssp                  --CCCSSCEETTCEEEETTTEEEEHHHHHHTTCCCEEEEECTTSEEEEEECCEEEEEEEEEEEEEETTS
T ss_pred                  CCCCCCCCCCCCCEEEcCCCceEEHHHHhcccCCcEEEEECCCCCEEEeceeEEEeCCCccEEEEEeCCC

Q ss_pred                  CeEEECCCCeEEEEeCCC
Q Q_7621124_2       144    GSIVVHPRHEWTVWDRNR  161 (881)
Q Consensus         144    ~~i~~T~~H~~~~~~~~~  161 (881)
                           ..+.+|++|++++.++.+
T Consensus         73     ~~i~~T~~h~~~~~~~~~  90 (168)
T 3NZM_A            73     SVIRATSDHRFLTTDYQL  90 (168)
T ss_dssp                  CEEEECTTCEEEBTTSCE
T ss_pred                  CEEEECCCCeEEecCCcE
```

Template alignment | Template 3D structure | PDBe

54. **2AB5_B bI3 LAGLIDADG Maturase; maturase, LAGLIDADG endonuclease, group I; HET: SO4, MSE; 2.2A {Saccharomyces cerevisiae} SCOP: d.95.2.0; Related PDB entries: 2AB5_A**

Probability: 95.9 E-value: 0.0072 Score: 65.59 Aligned Cols: 153 Identities: 13% Similarity: 0.126

```
Q ss_pred                  cCCCCCCCCCCCccccHHHHHHhccccCCCCe----------EEecCChHHhhhchhh------cCeE
Q Q_7621124_2       188    LPHRDPLEGVDDTLLIDPYTLGVWLGDGSSTKAA----------ITHHADDEYVLPYPKS------ADCV  241 (881)
Q Consensus         188    ip~~~~~~~~~~~~~~~~llG~~l~dG~~~~~~----------i~~~~~~~~~~~~~~~~------~~~~  241 (881)
                           .....+..+.....+..+|++|++.|||++....          +.+...+..+++.++.      ....
T Consensus         1      ~~~~~~~~~~~~~~~~a~l~Gf~dgDG~~~~~~~~~~~~~~~~I~~~~~d~~~L~~ik~~lg~g~i~~~  70 (269)
T 2AB5_B            1      MGHHHHHHKLNTDNPIYAYIVGLFEGDGWITISKKGKYLLYELGIEMHIRDIQLLYKIKNILGIGKVTIK  70 (269)
T ss_dssp                  -------CCCCCCCTHHHHHHHHHHHHHEEEEEEEETTEEEEEEEEEEEGGGHHHHHHHHHHHSCCEEEEE
T ss_pred                  CCCCcccCCCCCCCCcHHHHHHheeccceEEEEEEcCeEEEEEEEEEEecccHHHHHHHHHHCCCeEEEc

Q ss_pred                  E-------ecCCcEEEEeC-----ChHHHHHHHcCCCCCCcCCHHHHH----------------------
Q Q_7621124_2       242    H-------QTTGVVTSYYR-----GGLHTALKTLGVHANKHIPVQYLR----------------------  277 (881)
Q Consensus         242    ~-------~~~~~~~~~~~~~~------~~l~~~l~~~g~~~~k~iP~~i~~----------------------  277 (881)
                           .       ......+.+.+     ..+..++........|..-..+.
T Consensus         71     ~~~~~~~~~~~~~~~~i~s~~~~~~~i~~~~~~~~~~~K~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  140 (269)
T 2AB5_B            71     KLKMKDGTIKEMCKFNVRNKNHLKNIIIPIFNKYPMLTNKHYDYLYFKDNLLKDIKYYNDLSYYLRPIKP  140 (269)
T ss_dssp                  EEECTTSCEEEEEEEEECCHHHCCCCCHHHHHHSCCSSTTHHHHHHHHHHHHHTTCCBGGGCCCCCCCSSC
T ss_pred                  ccccCCCCCccceEEEEEcCHHHHHHHHHHHHHhCCCCCchHHHHHHHHHHHHHhHhhcccchhccccCC

Q ss_pred                  -------CCHHHHHHHHHHHHHcCCeeCC---------CCeEEEEe-CCHHHHHHHHHHHHHCCCcEEEE
Q Q_7621124_2       278    -------ASESSRRALLAGLIDSDGTIAK---------SGQVSFIN-TNRRLYDGVVELIRTLGYRATIH  330 (881)
Q Consensus         278    -------~~~~~~~~~~fL~Gl~dgDG~~~~----------~~~i~~~t-~s~~l~~~l~~Ll~~lGi~~~i~  330 (881)
                                  .+.....+||+|++||||++.-         ...+.++. .++.+++.|+..|...+......
T Consensus         141    ~~~~~~~~~~~~~~~wl~Gf~DgdGsf~~~~~~~~~~~~~~f~i~q~~~~~lL~~i~~~l~~~~~i~~~~  210 (269)
T 2AB5_B            141    FNTTEDILNKNYFSSWLIGFFEAKSCFSIYKPMNKKMKTASFEVSMNNNMEVMLAIKSYLKINNNIYMNE  210 (269)
T ss_dssp                  SSCHHHHHTCTTHHHHHHHHHHHHHEEEEEECC-----CEEEEEEECSSCHHHHHHHHHHTTCCSCEEEES
T ss_pred                  CCCchhHhccCCCchHHHHHHhceEEEEEEecCCCCceEEEEEeecCCCHHHHHHHHHHhCCCCcEEecC

Q ss_pred                  ecCCCCCCCCCccCeeeEEEEEEec
Q Q_7621124_2       331    APLQPSTSSSGVAGTRVLYRVSFTP  355 (881)
Q Consensus         331    ~~~~~~~~~~~~~~~~~~y~~~i~~  355 (881)
                           ..               .|++.+.+
T Consensus         211    ~~----------------~~~l~i~~  220 (269)
T 2AB5_B            211    FN---------------NSKMTTKS  220 (269)
T ss_dssp                  SS---------------CEEEEECC
T ss_pred                  CC---------------ceEEEECc
```

Template alignment | Template 3D structure | PDB | NCBI

55. **d4kl5a1 b.86.1.0 (A:1-139) automated matches {Nostoc punctiforme [TaxId: 63737]}**

Probability: 95.8 E-value: 0.011 Score: 56.09 Aligned Cols: 82 Identities: 15% Similarity: 0.161

```
Q ss_pred                  cccCCCcEECCCc-cEEHHHcCCCCE---EECCCC----CEEEEEEEecCC-CCeEEEEeCCCCeEEECC
Q Q_7621124_2       90     LVAHDTPVPTPTG-WTTHGELRPGDE---VYHPSG----KVVTVRAISADA-HASIRVSTSDGGSIVVHP  150 (881)
Q Consensus         90     C~~~dt~Vlt~~G-~~~i~~i~~gd~---v~~~~g----~~~~~v~~~~~~~-~~~~~i~t~~G~~i~~T~  150 (881)
                           |+.+++.|.+.+| .++|+++..|+.   +++.+.    ....+..... ..++++++.+|..+.+|+
T Consensus         1      c~~~~t~i~~~~g~~~~i~~l~~~~~~~~~~~~~~~~~~~~v~~~~~~~~~~~~~i~~~~~~~~~~T~  70 (139)
T d4kl5a1           1      ALSYETEILTVEYGLLPIGKIVEKRIECTVYSVDNNGNIYTQPVAQWHDRGEQEVFEYCLEDGSLIRATK  70 (139)
T ss_dssp                  CEETTCEEEETTTEEEEHHHHHHTTCCCEEEEECTTSCEEEEECCEEEEEEEEEEEEEEETTSCEEEECT
T ss_pred                  CCCCCCEEEecCCcEEEHHHHHHcCCceEEEEECCCCCEEEecceEEEEcCcccEEEEEeCCCCEEEECC

Q ss_pred                  CCeEEEEeCCCCeEEEcchhHHhhhe
```

```
Q Q_7621124_2       151    RHEWTVWDRNRKRWSTMETGDMMRRA  176 (881)
Q Consensus         151    ~H~~~~~~~~~~~~~~~~~~l~~~~  176 (881)
                           +|++++..+.   |..  +.++..++
T Consensus         71     ~H~~~~~~~~-~~~~-~~~~l~~g~  91 (139)
T d4kl5a1           71     DHKFMTVDGQ---MLP--IDEIFERE  91 (139)
T ss_dssp                  TCEEEBTTSC---EEE--HHHHHHHT
T ss_pred                  CCeEEeECCc---EEE--HHHcCCCc
```

Template alignment | Template 3D structure | PDB | NCBI

56. **d1mi8a_ b.86.1.2 (A:) DnaB intein {Synechocystis sp. PCC 6803 [TaxId: 1148]}**

Probability: 95.72 E-value: 0.016 Score: 56.55 Aligned Cols: 85 Identities: 11% Similarity: 0.188

```
Q ss_pred                  CccccCCCCcEECCC--ccEEHHHc--CCCCEEECCCCC-----EEEEEEEecCC-CCeEEEEeCCCCeEE
Q Q_7621124_2       88     GKLVAHDTPVPTPT--GWTTHGEL--RPGDEVYHPSGK-----VVTVRAISADA-HASIRVSTSDGGSIV  147 (881)
Q Consensus         88     gkC~~~dt~Vlt~~~-G~~~i~~i--~~gd~v~~~~g~-----~~~v~~~~~~-~~~~~i~t~~G~~i~  147 (881)
                           +.|+.+++.|.+.+  |..+|+++  ..|+.++..+..     ..++..... ..+++|.+.+|..+.
T Consensus         1      ~gc~~~~t~i~~~~g~~~~i~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~  70 (158)
T d1mi8a_           1      SGAISGDSLISLASTGKRVSIKDLLDEKDFEIWAINEQTMKLESAKVSRVFMTGKKLVYILKTRLGRTIK  70 (158)
T ss_dssp                  CCCEETTCEEEETTTTEEEESGGGTTCCSCEEEEEETTTTEEEEEECCEEEEEEEEEEEEEETTCCEEE
T ss_pred                  CCccccCCceEEeCCCCCEEEHHHHhcCCCcEEEEEeCCCCeEEEeeccEEEecCCceEEEEeCCCCEEE

Q ss_pred                  ECCCCeEEEEeCCCCeEEEcchhHHhhheee
Q Q_7621124_2       148    VHPRHEWTVWDRNRKRWSTMETGDMMRRAYV  178 (881)
Q Consensus         148    ~T~~H~~~~~~~~~~~~~~~~~l~~~~~~  178 (881)
                           +|++|++++.    ..|+.  +.++..++++
T Consensus         71     ~t~~h~~~~~-~~~~~~-~~~~l~~g~~l  95 (158)
T d1mi8a_           71     ATANHRFLTI----DGWKR--LDELSLKEHI  95 (158)
T ss_dssp                  ECTTCEEEET----TEEEE--GGGCCTTCEE
T ss_pred                  EcCCCceeec----cccEE--HHHCCCCCeE
```

Template alignment | Template 3D structure | PDBe

57. **4O1S_B V-type ATP synthase alpha chain; splicing; HET: SO4, EPE; 2.7008A {Thermoplasma volcanium}; Related PDB entries: 4O1S_A**

Probability: 95.72 E-value: 0.029 Score: 55.63 Aligned Cols: 91 Identities: 21% Similarity: 0.239

```
Q ss_pred                  CCCccccCCCcEECCCc-cEEHHHc--------------CCCCEEE------------CCCCCEEEEEEE
Q Q_7621124_2       86     QVGKLVAHDTPVPTPTG-WTTHGEL--------------RPGDEVY------------HPSGKVVTVRAI  128 (881)
Q Consensus         86     g~gkC~~~dt~Vlt~~G-~~~i~~i--------------~~gd~v~------------~~~g~~~~v~~~  128 (881)
                           +.++|+..++.|.+.+| ..+|+++              ..|+.++            .....+.++..+
T Consensus         1      ~~~~c~~~~t~v~~~~g~~~~i~~~~~~~~~~~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~v~~~  70 (170)
T 4O1S_B            1      SGGKAVSGETPVYLADGKTIKIKDLYSSERKKEDNIVEAGSGEEIIHLKDPIQIYSYVDGTIVRSRSRLL  70 (170)
T ss_dssp                  CTTCCEETTCEEEBTTSCEEEHHHHHHHHHHCTTSEEEECSSCEEEECSSCCCEEEEETTEEEEECCCEE
T ss_pred                  CCCccccCCCeEEecCCCEEEHHHHhhHhhhccCCeEecCCCcEEEecCCCeEEEEcCCCeEEEEEceEE

Q ss_pred                  ecCC-CCeEEEEeCCCCeEEECCCCeEEEEeCCCCeEEEcchhHHhhheee
Q Q_7621124_2       129    SADA-HASIRVSTSDGGSIVVHPRHEWTVWDRNRKRWSTMETGDMMRRAYV  178 (881)
Q Consensus         129    ~~~~-~~~~~i~t~~G~~i~~T~~H~~~~~~~~~~~~~~~~~l~~~~~~  178 (881)
                           +... ..++++.+..|..+.+|++|++++.++....|..  +..+..++++
T Consensus         71     ~~~~~~~~~~i~~~~g~~~~~t~~h~~~~~~~~~~~~~--~~~~~~g~~l  119 (170)
T 4O1S_B            71     YKGKSSYLVRIETIGGRSVSVTPVHKLFVLTEKGIEEVM--ASNLKVGDMI  119 (170)
T ss_dssp                  EEEEEEEEEEEEETTSCEEEECTTCEEEEEETTEEEEEE--GGGCCTTCEE
T ss_pred                  EeCCCCceEEEEeCCCCEEEECCCceeEEEeCCeeEEEE--HHHCCCCCEE
```

Template alignment | CDD

58. **PF14623.6 ; Vint ; Hint-domain**

Probability: 95.72 E-value: 0.014 Score: 59.6 Aligned Cols: 62 Identities: 28% Similarity: 0.242

```
Q ss_pred                  cccCCCCcEECCCc--cEEHHHcCCCCEEECCCC--CEEEEEEEecCCCCeEEEEeCCCCeEEECCCCeEE
Q Q_7621124_2       90     LVAHDTPVPTPTG--WTTHGELRPGDEVYHPSG--KVVTVRAISADAHASIRVSTSDGGSIVVHPRHEWT  155 (881)
Q Consensus         90     C~~~dt~Vlt~~G-~~~~i~~i~~gd~v~~~~g-~~~~~v~~~~~~~~~~~~i~t~~G~~i~~T~~H~~~  155 (881)
                           |+.++|.|.+.+|  .++|++|++||.|++.+|  ....|.........++++    | .+.+|++|+++
T Consensus         2      Cf~~gt~V~t~~G~~~~~Ie~L~~GD~V~t~~G~~~v~~v~~~~~~~~~~v~i-----~~l~~Tp~Hp~~  66 (194)
T PF14623.6         2      CFAGATRVRLAETATTVAIRDLARGMRVHTPLGPRAVAAVLRTRVWRAAVRRV----G-GVVVTPWHPVR  66 (194)
T ss_pred                  CccCCCEEEECCCCCCEEEHHHcCCCCEEECCCCCeeEEEEEeeecCCceEEE----c-CEEECCCCcEE

Q ss_pred                  E
Q Q_7621124_2       156    V  156 (881)
Q Consensus         156    ~  156 (881)
                           +
T Consensus         67     ~  67 (194)
T PF14623.6         67     R  67 (194)
T ss_pred                  e
```

[Template alignment](#) | [Template 3D structure](#) | [PDBe](#)

59. **2JMZ_A Hypothetical protein MJ0781; protein, UNKNOWN FUNCTION; NMR {Methanocaldococcus jannaschii}; Related PDB entries: 2JNQ_A**

Probability: 95.66   E-value: 0.021   Score: 57.86   Aligned Cols: 93   Identities: 12%   Similarity: 0.071

```
Q ss_pred                  CCCCCccccCCCcEECCCc-cEEHHHcC------------------------CCCEEECCCC-----CE
Q Q_7621124_2        84    PSQVGKLVAHDTPVPTPTG-WTTHGELR------------------------PGDEVYHPSG-----KV  122 (881)
Q Consensus          84    ~~g~gkC~~~dt~Vlt~~G-~~~i~~i~------------------------~gd~v~~~~g-----~~  122 (881)
                           .+|.+.|+..++.|.+.+| ..+|+++.                         .|..++..+.     .+
T Consensus          2     ~~g~~~c~~~~t~v~~~~g~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~s~~~~~~~~~~~  71 (186)
T 2JMZ_A             2     NTGHDGALAYDEPIYLSDGNIINIGEFVDKFFKKYKNSIKKEDNGFGWIDIGNENIYIKSFNKLSLIIED  71 (186)
T ss_dssp                  CSSCCCCEETTCBCCBTTCCCCBHHHHHHHHHHHSTTTCBCCTTSCCEEECTTTCCEEECCBTTTTBCCE
T ss_pred                  CCCCCCCcCCCCcEEeeCCCEEEEHHHHHHHHHHhhcccceeeccCCceEEEccCCCcEEEEEeCCCCeEEE

Q ss_pred                  EEEEEEecCC--CCeEEEEeCCCCeEEECCCCeEEEEeCCCCeEEEcchhHHhhheee
Q Q_7621124_2        123   VTVRAISADA--HASIRVSTSDGGSIVVHPRHEWTVWDRNRKRWSTMETGDMMRRAYV  178 (881)
Q Consensus          123   ~~v~~~~~~~--~~~~~i~t~~G~~i~~T~~H~~~~~~~~~~~~~~~~~~~l~~~~~~  178 (881)
                           .++..++...  +.+++|.+..|+.+.+|++|++++.++....|..  +.++..++++
T Consensus          72    ~~i~~~~~~~~~~~~~~i~~~~g~~~~~t~~h~~~~~~~~~~~~~~~~--~~~~~~gd~l  127 (186)
T 2JMZ_A             72    KRILRVWRKKYSGKLIKITTKNRREITLTHDHPVYISKTGEVLEIN--AEMVKVGDYI  127 (186)
T ss_dssp                  EECCEEEEECCCEEEECCCCTTSCCCCBCTTCEEEEEETTEEEEEE--GGGCCTTSEE
T ss_pred                  EeeEEEEEecCCCCeEEEEeCCCCEEEeCCCCcEEEeeCCeEEEEe--HHHCCCCCEE
```

[Template alignment](#) | [Template 3D structure](#) | [PDBe](#)

60. **4IOX_B Tripartite terminase subunit UL15, unknown; nuclease, VIRAL PROTEIN; HET: PG4, PGE; 2.458A {Human herpesvirus 1}; Related PDB entries: 4IOX_C 4IOX_A**

Probability: 95.53   E-value: 0.29   Score: 50.83   Aligned Cols: 184   Identities: 14%   Similarity: 0.022

```
Q ss_pred                  ceEEEEEEeCCCCCCCCcCCcEEEEEEEEECCCCc-EEEEecccccCcchHHHHHHHHHHHHh---------
Q Q_7621124_2        674   LTRVVVGVDPSGGEGARHDTAGISAVGLDEHQH-AWFLEDRTAVLTPLEWPRAVCLLAYER---------  733 (881)
Q Consensus          674   ~~~~~~~iD~a~~~~~~~D~tai~v~~~~~~~g~-~~v~~~~~~~~~~~~~~~~~~~~~i~~~~~~---------  733 (881)
                           ....|+-||||++.+..+..|++.+++...+.. ++=++-+..+.-........|.+.+...
T Consensus          52    ~~tLYVYvDPAfT~N~~ASGTGIaavg~~~~~iI~GlEHFFL~~LTg~sa~~Ia~Ca~~~i~~v~~lHp  121 (286)
T 4IOX_B             52    APDLYVYVDPAFTANTRASGTGVAVVGRYRDDYIIFALEHFFLRALTGSAPADIARCVVHSLTQVLALHP  121 (286)
T ss_dssp                  EEEEEEEEECC--------CEEEEEEEEEETTEEEEEEEEEEECC----CCHHHHHHHHHHHHHHHHHHHST
T ss_pred                  CCeEEEEECcccccCccCCCCceeEEEEEeCCcEEEEEEEhhHHHHHhCChHHHHHHHHHHHHHHHHHHHhCC

Q ss_pred                  ---CCCEEEEEcccCchHHHHHHHHHHHHHHhcc---------CCCCCCCccccCcccCCCCceeeccCCCC
Q Q_7621124_2        734   ---DASMIVYEKNYGGGMASALITQAWAALQN---------EPINADTDETMIPKSANCPYVKGVSAKIS  791 (881)
Q Consensus          734   ---~~~~i~iE~~~~g~~~~~~l~~~~~~~~~---------~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~  791 (881)
                              +--.|.||.|..++........+.+++..          ..-.+..=-.-.+++.++.  ..-+--++.
T Consensus          122   ~~f~~v~VaVEGNSsQdSAVaIA~~i~~~l~~~~~~~~~~~~~~~~~~~v~FyH~~~~~~~~v~~~PfylL~ke  190 (286)
T 4IOX_B             122   GAFRGVRVAVEGNSSQDSAVAIATHVHTEMHRLLASEGADAGSGPELLFYHCEPPGSAVL-YPFFLLNKQ  190 (286)
T ss_dssp                  TTCSEEEEEEBCSSCHHHHHHHHHHHHHHHTCCC--------CCCEEEECCBCCTTCCSC-BSCBCCSTT
T ss_pred                  cccCeEEEEEeCCCCHHHHHHHHHHHHHHHHHHHHHHccCccCCCCCeEEEEEeCCCCCccc-cccccccccc

Q ss_pred                  HHHhHHHHHHHHHcCCeEEcc----------cCccHHHHHHHhccCCC--------------CCCCCcHH
Q Q_7621124_2        792   KVLRAEPIAQAVKTGRAKFAQ----------LGNLGSLTNEFTLWQPG--------------STWSPGAL  837 (881)
Q Consensus          792   K~~ri~~l~~~~~~~g~i~~~~~----------~~~~~~~~l~~el~~~~~~~~~~----------------~~~~dD~~  837 (881)
                           |....+.+..++++|.|....             -+..+=|++||.++...                .+-.||.+
T Consensus          191   Kt~AFe~FI~~fNSG~i~ASQelVS~TIkLs~DPVeYL~eQikni~~~~~~~~~~~~~tysgK~~~~SDDll  260 (286)
T 4IOX_B             191   KTPAFEHFIKKFNSGGVMASQEIVSATVRLQTDPVEYLLEQLNNLTETVSPNTDVRTYSGKRNGASDDLM  260 (286)
T ss_dssp                  HHHHHHHHHHHHHHTTCEEEEEEEEECSSSSSSSCHHHHHHHHHTTCC-------------------CCHHH
T ss_pred                  chHHHHHHHHHHHcCCeeEeeeEEccccccCCCCHHHHHHHHHhhCeeeeCCCCCceEEeccCCCCCCHHHH

Q ss_pred                  HHHHHHHHHHcCCCCCCccccc
Q Q_7621124_2        838   DAAVYGATEVLPPVGSTTELE  858 (881)
Q Consensus          838   Dal~~~~~~~~~~~~~~~~~~~  858 (881)
                           -|+.|++............+
T Consensus          261   VAvVMA~Yla~~~~~~~~~fk~  281 (286)
T 4IOX_B             261   VAVIMAIYLAAQAGPPHTFAP  281 (286)
T ss_dssp                  HHHHHHHHHHHTSCCCCCCCCC
T ss_pred                  HHHHHHHHHHhcCCCCCCCCcc
```

[Template alignment](#) | [Template 3D structure](#) | [PDBe](#)

61. **3N4P_D Terminase subunit UL89 protein; Terminase, Nuclease, Human cytomegalovirus, HCMV; 2.15A {Human herpesvirus 5}; Related PDB entries: 6EY7_D 6EY7_C 6EY7_B 6EY7_A 3N4P_C 3N4P_B 3N4P_A 3N4Q_D 3N4Q_C 3N4Q_B 3N4Q_A**

Probability: 95.53   E-value: 0.3   Score: 50.57   Aligned Cols: 157   Identities: 18%   Similarity: 0.086

```
Q ss_pred                  ceEEEEEEeCCCCCCCCcCCcEEEEEEEEECCCCc-EEEEecccccCcchHHHHHHHHHHHHh---------
Q Q_7621124_2        674   LTRVVVGVDPSGGEGARHDTAGISAVGLDEHQH-AWFLEDRTAVLTPLEWPRAVCLLAYER---------  733 (881)
```

```
Q Consensus         674     ~~~~~~~iD~a~~~~~~~D~tai~v~~~~~~g~-~~v~~~~~~~~~~~~~~~~i~~~~~~~---------  733 (881)
                            ....|+-||||++.+..+..|++.+++...+.. ++=++-+..+.-.......|.+.+...
T Consensus         60      ~~tLYVYvDPAfT~N~~ASGTGiaavg~~~~~~iI~GlEHfFL~~Ltg~a~~~Ia~Ca~~~i~~v~~lHp  129 (279)
T 3N4P_D            60      GKTLYVYLDPAFTTNRKASGTGVAAVGAYRHQFLIYGLEHFFLRDLSESSEVAIAECAAHMIISVLSLHP  129 (279)
T ss_dssp                   CCEEEEEEECC---------CEEEEEEEETTEEEEEEEEECC-----CHHHHHHHHHHHHHHHHHHHHHCT
T ss_pred                   cCeEEEEEcccccCCcccCCceeEEEEEeCCcEEEEEEEehHHHhhcCChHHHHHHHHHHHHHHHHHHhhCc

Q ss_pred                   --CCCEEEEEcccCchHHHHHHHHHHHHHhccCCCCCCCccccCcccCCCCceeeccCCC-----------
Q Q_7621124_2        734     --DASMIVYEKNYGGGMASALITQAWAALQNEPINADTDETMIPKSANCPYVKGVSAKI-----------  790 (881)
Q Consensus         734     --~~~~~i~iE~~~~g~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~-----------  790 (881)
                              +-..|.||.|..++........+.+.+...               ..+| +.-.+..+
T Consensus         130     ~~~~v~VaVEGNSsQdSAVaIA~~i~~~l~~~---------------~~~~-v~FyH~~~~~~i~~PfylL  184 (279)
T 3N4P_D            130     YLDELRIAVEGNTNQAAAVRIACLIRQSVQSS-------------TLIR-VLFYHTPDQNHIEQPFYLM  184 (279)
T ss_dssp                   TCCEEEEEEBCSSCHHHHHHHHHHHHHHHHHHH-------------CCCE-EEEECEEETTTEEESCBCC
T ss_pred                   ccceEEEEEeCCCcHHHHHHHHHHHHHHHHHhc-------------CCcE-EEEEEcCCcccccceEec

Q ss_pred                   --CHHHhHHHHHHHHHHcCCeEEcc----------cCccHHHHHHHhccCCC--------------CCCC
Q Q_7621124_2        791     --SKVLRAEPIAQAVKTGRAKFAQ----------LGNLGSLTNEFTLWQPG--------------STWS  833 (881)
Q Consensus         791     --~K~~ri~~l~~~~~~~g~i~~~~----------~~~~~~~l~~el~~~~~~~--------------~~~~  833 (881)
                              .|....+.+-.++++|.|....          -+..+=|++||.++..-              .+-.
T Consensus         185     ~keK~~Afe~FI~~fNSg~i~ASQelVS~TIkLs~DPVeYL~eQi~ni~~~~~~~~~~~~~~tys~K~~~~~~S  254 (279)
T 3N4P_D            185     GRDKALAVEQFISRFNSGYIKASQELVSYTIKLSHDPIEYLLEQIQNLHRVTLAEGTTARYSAKRQNRIS  254 (279)
T ss_dssp                   STHHHHHHHHHHHHHHHHTCEEEEEEEECSSSCTTSCHHHHHHHHHHTCCC-------------------
T ss_pred                   cccHHHHHHHHHHHHHhcCceEEeeeEEccceecCCCHHHHHHHHHhcCEEEecCCCceEEEcccccCCCC

Q ss_pred                   CcHHHHHHHHHH
Q Q_7621124_2        834     PGALDAAVYGAT  845 (881)
Q Consensus         834     dD~~Dal~~~~~~  845 (881)
                            ||.+-|+.|++.
T Consensus         255     DDllVAvVMA~Y  266 (279)
T 3N4P_D            255     DDLIIAVIMATY  266 (279)
T ss_dssp                   CHHHHHHHHHHH
T ss_pred                   HHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

62. **1AM2_A MXE GYRA INTEIN; INTEIN, PROTEIN SPLICING; 2.2A {Mycobacterium xenopi} SCOP: b.86.1.2; Related PDB entries: 4OZ6_A**

Probability: 95.45 E-value: 0.046 Score: 56.08 Aligned Cols: 88 Identities: 18% Similarity: 0.269

```
Q ss_pred                   ccccCCCcEECCCc-cEEHHHcCCCCE----------EECCCCCEEEEEEecCC-CCeEEEEeCCCCeE
Q Q_7621124_2        89      KLVAHDTPVPTPTG-WTTHGELRPGDE----------VYHPSGKVVTVRAISADA-HASIRVSTSDGGSI  146 (881)
Q Consensus         89      kC~~~dt~Vlt~~G-~~~~i~~i~~gd~----------v~~~~~g~~~~~v~~~~~~~~~~-~~~~~~~i~t~~G~~i  146 (881)
                            .|+.+++.|.+.+| ..+|+++..|+.           .++..+....+..++... .++++|++..|..+
T Consensus         1       ~c~~~~t~v~~~~g~~~~i~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~g~~l  70 (199)
T 1AM2_A            1       ASITGDALVALPEGESVRIADIVPGARPNSDNAIDLKVLDRHGNPVLADRLFHSGEHPVYAVRTVEGLRV  70 (199)
T ss_dssp                   CCEETTCEEECSTTCEEEGGGSSTTCCTTEEEEEEEEEECTTSCEEEEEEEEEEEEEEEEEEEEETTSCEE
T ss_pred                   CCcCCCCcEEECCCCcEEEHHHhcccCCCCCCCeEEEEEECCCCCEEecceeeeCCCCeEEEEeCCCCEE

Q ss_pred                   EECCCCeEEEEeCCCC----eEEEcchhHHhhheee
Q Q_7621124_2        147     VVHPRHEWTVWDRNRK----RWSTMETGDMMRRAYV  178 (881)
Q Consensus         147     ~~T~~H~~~~~~~~~~~~~~~~----~~~~~~~~~~~l~~~~~~~~  178 (881)
                            .+|++|++++......    .|..  +.++..++.+
T Consensus         71      ~~t~~h~~~~~~~~~~~~~~~~~~~~~~~~~--~~~~l~~g~~l  104 (199)
T 1AM2_A            71      TGTANHPLLCLVDVAGVPTLLWKL--IDEIKPGDYA  104 (199)
T ss_dssp                   EECTTCEEEEEEEETTEEEEEEE--GGGCCTTCEE
T ss_pred                   EeCCCCCceEEeecCCCCCcceEEEE--HHHCCCCCEE
```

Template alignment | Template 3D structure | PDB | NCBI

63. **d1kcfa2 c.55.3.7 (A:39-256) Mitochondrial resolvase ydc2 catalytic domain {Fission yeast (Schizosaccharomyces pombe) [TaxId: 4896]}**

Probability: 95.35 E-value: 0.36 Score: 50.7 Aligned Cols: 145 Identities: 12% Similarity: 0.03

```
Q ss_pred                   EEEEEeCCCCCCCcCCcEEEEEEEEECCCCcEEEEecccccC------------------cchHHHHHHH
Q Q_7621124_2        677     VVVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTAVLT------------------PLEWPRAVCL  728 (881)
Q Consensus         677     ~~~~iD~a~~~~~~~~~~D~tai~v~~~~~~~g~~~v~~~~~~~~~~~~------------------~~~~~~~~~i~~  728 (881)
                            .++|||+|..       ..|++++.....+.+.+++...-..+                   ...+.+.+.+
T Consensus         3       ~IlsID~Gi~------n~a~~~l~~~~~~~~~~~~l~~w~~i~l~~~~~~~~~~~~~~~~~~~~p~~l~~~i~~~i~~  66 (218)
T d1kcfa2           3       RVLGIDLGIK------NFSYCFASQNEDSKVIIHNWSVENLTEKNGLDIQWTEDFQPSSMADLSIQLFNT  66 (218)
T ss_dssp                   SEEEEEECST------TEEEEEEEECTTSCEEEEEEEEECTTSCCTTCCCCCCCCSHHHHHHHHHHHHH
T ss_pred                   eEEEEEeccc------eEEEEEEEcCCCCCeEEEEEEEEEEcchhcCCCCcCCCCCCCHHHHHHHHHHHHH

Q ss_pred                   HHHHhCCCEEEEEcc---cCc----------hHHHHHHHHHHHHHhcc-------CCCCCCCccccCccccC
Q Q_7621124_2        729     LAYERDASMIVYEKN---YGG----------GMASALITQAWAALQN-------EPINADTDETMIPKSA  778 (881)
```

```
Q Consensus         729    ~~~~~~~~~i~iE~~---~~g---------------~~~~~~l~~~~~~~~~------~~~~~~~~~~~~~~~  778 (881)
                           +...+.++.+.||..   .++          ..+..++-........       .
T Consensus         67     l~~~~~pd~v~IErQ~~r~~~~~i~e~~l~v~~~e~ml~a~l~~~~~~~~~~~~~~~---------------  121 (218)
T d1kcfa2           67     LHEKFNPHVILMERQRYRSGIATIPEWTLRVNMLESMLYALHYAEKRNSIEQKIQ--------------  121 (218)
T ss_dssp                  HHHHHCCSEEEEEECCCCTTTCCHHHHHHHHHHHHHHHHHHHHHHHHHHC---------------------
T ss_pred                  HHHhcCCCEEEEcccCCCCCCCCcCHHHHHHhHHHHHHHHHHHHHHHHHhcccccccC--------------


Q ss_pred                  CCCceeeccC---------------CCCHHHhHHHHHHHHHHcCCeEEcccCccHHHHHHHhccCCCCCC
Q Q_7621124_2       779     NCPYVKGVSA---------------KISKVLRAEPIAQAVKTGRAKFAQLGNLGSLTNEFTLWQPGSTW  832 (881)
Q Consensus         779     ~~~~i~~~~~~-----------------~~~K~~ri~~l~~~~~~g~i~~~~~~~~~~~l~~el~~~~~~~~~~  832 (881)
                           ..+ |.+..+                +..|..+++.+...+..+.+.+..    ..++.++........+
T Consensus         122    ~~~-V~~~~P~~v~~~~~~~~~~~~~~~~~~~~K~~~~~lv~~ll~~~~~~~~~~----~~~l~~~~~~~~~~~~K  186 (218)
T d1kcfa2           122    YPF-LLSLSPKSTYSYWASVLNTKASFSKKKSRVQMVKELIDGQKILFEN----EEALYKWNNGSRVEFK  186 (218)
T ss_dssp                  CCE-EEECCHHHHHHHHHHHHC-------CCCHHHHHHHHHTTSEEESS----HHHHHHHHHCCSTTTH
T ss_pred                  CCE-EEEeChHHhHHHhHhhccCcccccHHHHHHHHHHHHhCCCceeCC----HHHHHHHccCCCccCc


Q ss_pred                  CCcHHHHHHHHHHHh
Q Q_7621124_2       833     SPGALDAAVYGATEV  847 (881)
Q Consensus         833     ~dD~~Dal~~~~~~~~  847 (881)
                           .||++||++.++..+
T Consensus         187    ~DDlaDaLl~al~~~  201 (218)
T d1kcfa2           187    KDDMADSALIASGWM  201 (218)
T ss_dssp                  HHHHHHHHHHHHHHH
T ss_pred                  HHHHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

64. **5E6F_B CNPV261 Holliday junction resolvase protein; Poxvirus, Resolvase, Holliday Junction, Metal-binding; HET: TAR; 2.6A {Canarypox virus}; Related PDB entries: 5E6F_A**

Probability: 95.17 E-value: 0.17 Score: 49.63 Aligned Cols: 136 Identities: 12% Similarity: 0.063

```
Q ss_pred                  eEEEEEEeCCCCCCCcCCcEEEEEEEEECCCCcEEEEeccccccCcchHHHHHHHHHHHHhCCCEEEEEccc
Q Q_7621124_2       675     TRVVVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTAVLTPLEWPRAVCLLAYERDASMIVYEKNY  744 (881)
Q Consensus         675     ~~~~~~~iD~a~~~~~~~~~D~tai~v~~~~~~~g~~~v~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~i~iE~~~  744 (881)
                           ...++|||||..      .++++++...  .+.+.+++.-......  .+...+.+++..|+++.++||...
T Consensus         1      ~~~ilgiD~g~~-------~~G~av~~~~-~~~~~~~~~~~~~~~~~~~~~-~~~~~~l~~~l~~~~~~d~vvIE~~~  62 (152)
T 5E6F_B            1      MTIICSVDIGIK------NPAYTIFRYE-DSKVSLIAIEKSDWSD-NWEYNVTKDLTKYNPDIIVLEKQG  62 (152)
T ss_dssp                  -CEEEEEECCSS------SCEEEEEEES-SSCEEEEEEEECCCSS-SHHHHHHHHHHTTCCSEEEEECCC
T ss_pred                  CcEEEEEEecCC------ceEEEEEEeC-CCeeEEEEeecCCCCC-chHHHHHHHHHhcCCCEEEEccCC


Q ss_pred                  CchHHHHHHHHHHHHhccCCCCCCCCccccCcccCCCCceeeccCCCCHHHhHHHHHHHHHHcCCeEEcccC
Q Q_7621124_2       745     GGGMASALITQAWAALQNEPINADTDETMIPKSANCPYVKGVSAKISKVLRAEPIAQAVKTGRAKFAQLG  814 (881)
Q Consensus         745     ~g~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~K~~ri~~l~~~~~~g~i~~~~~~~~  814 (881)
                           .+.........+..-+...               ++| +..+.. .-|.            ....-....
T Consensus         63     ~~~~~~~~~~g~i~~~l~~~~---------------~i~-~~~v~p-~~k~------------~~~~~~~kk~  103 (152)
T 5E6F_B            63     YRSPNAKIIYFIKGFFYNT---------------NTS-VIVRNP-TFQG------------GSYSDRKKQ  103 (152)
T ss_dssp                  TTSTTHHHHHHHHHHTTTS---------------SCE-EEEECC-SSCS------------SCHHHHHH
T ss_pred                  CCCCchHHHHHHHHHHHcC---------------CCc-EEEeCC-ccCC------------CChhHHHH


Q ss_pred                  ccHHHHHHHhcc-------CCCCCCCCcHHHHHHHHHHHh
Q Q_7621124_2       815     NLGSLTNEFTLW-------QPGSTWSPGALDAAVYGATEV  847 (881)
Q Consensus         815     ~~~~l~~el~~~~-------~~~~~~~~dD~~Dal~~~~~~~~  847 (881)
                           ........+..+       .......||.+||+++++..+
T Consensus         104    ~v~~~~~~~~~~~~~~~~~~~~~~~~~~k~dD~aDA~~ia~~~~~  143 (152)
T 5E6F_B            104    SVITFMDKLSRYSDHIDDILSSFTKLDDIADSFNLGIAYI  143 (152)
T ss_dssp                  HHHHHHHHHC-------------CCHHHHHHHHHHHHHHH
T ss_pred                  HHHHHHHHHhhcCCchHHHHhcCCCchHHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDB | NCBI

65. **d4o1ra1 b.86.1.2 (A:0-139) automated matches {Nostoc punctiforme [TaxId: 63737]}**

Probability: 94.96 E-value: 0.056 Score: 51.08 Aligned Cols: 67 Identities: 19% Similarity: 0.214

```
Q ss_pred                  cccCCCCcEECCC-cc-EEHHHc--CCCCEEECCCC-----CEEEEEEEecCC-CCeEEEEeCCCCeEEEC
Q Q_7621124_2       90      LVAHDTPVPTPT-GW-TTHGEL--RPGDEVYHPSG-----KVVTVRAISADA-HASIRVSTSDGGSIVVH  149 (881)
Q Consensus         90      C~~~dt~Vlt~~-G~-~~i~~i--~~gd~v~~~~~g-----~~~~~v~~~~~~~~-~~~~~i~t~~G~~i~~T  149 (881)
                           |+.+++.+.+.+ |. .+|+++  ..|+.++..+.     ....+..+.... ..+++|.+..|+.+.+|
T Consensus         2      c~~~~t~~~~~~~~g~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~t  71 (140)
T d4o1ra1           2      ALAGDSLVTLVDSGLQVPIKELVGKSGFAVWALNEATMQLEKAIVSNAFSTGIKPLFTLTTRLGRKIRAT  71 (140)
T ss_dssp                  CEETTCEEECTTTCCEEEGGGGTTCCSEEEEEEETTTTEEEEEEECEEEEEEEEEEEEEEETTCCEEEEC
T ss_pred                  CccCCceEEecCCCCCEEEHHHHcccCCceEEEEeCCCCeEEEEEeeEeEeccceeeEEEEEECCCCEEEEc


Q ss_pred                  CCCeEEE
```

```
Q Q_7621124_2       150    PRHEWTV  156 (881)
Q Consensus         150    ~~H~~~~  156 (881)
                           ++|++++
T Consensus         72     ~~h~~~~  78 (140)
T d4o1ra1           72     GNHKFLT  78 (140)
T ss_dssp                  TTCEEEE
T ss_pred                  CCCeeee
```

Template alignment | Template 3D structure | PDB | NCBI

66. **d1jvaa2 d.95.2.2 (A:464-581) VMA1-derived endonuclease (VDE) PI-SceI {Baker's yeast (Saccharomyces cerevisiae) [TaxId: 4932]}**

Probability: 94.94 E-value: 0.015 Score: 53.49 Aligned Cols: 45 Identities: 22% Similarity: 0.397

```
Q ss_pred                  CCCCCCcccchHHHHHHhcccccCCCCeEEecCChHHhhhchhhc
Q Q_7621124_2       194    LEGVDDTLLIDPYTLGVWLGDGSSTKAAITHHADDEYVLPYPKSA  238 (881)
Q Consensus         194    ~~~~~~~~~~~~~llG~~l~dG~~~~~~i~~~~~~~~~~~~~~~~  238 (881)
                           +..+....+.++|+||+|+|||++....+.+++.++.+.+++..+
T Consensus         18     ~~~~~~~~~~aylLGlw~gdG~~~~~~~~i~~~D~~l~~~i~~~   62 (118)
T d1jvaa2           18     FHLTIEGPKVLAYLLGLWIGDGLSDRATFSVDSRDTSLMERVTEY  62 (118)
T ss_dssp                  SCCCTTHHHHHHHHHHHHHHHBCTTSSEEEEESSCHHHHHHHHH
T ss_pred                  CCCCCCCchHHHHHHHHHcCCCCCCceEEecCCCHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

67. **4LX3_B DNA polymerase III, alpha subunit; trans-structure, naturally occurring, TRANSFERASE; HET: MSE; 1.5A {Nostoc punctiforme}; Related PDB entries: 4QFQ_B**

Probability: 94.91 E-value: 0.035 Score: 38.68 Aligned Cols: 35 Identities: 11% Similarity: -0.056

```
Q ss_pred                  eeEEEEEEEeCCeeeeeEEEcCCCCeEE-EcCCccccCC
Q Q_7621124_2       379    RTSIIGIEPVDPRPGRCVEVDSPDGLYL-VGEHMTPTHN  416 (881)
Q Consensus         379    ~~~I~~Ie~~~~~~vy~~~v~~~~~~~~-~~~~~~~~~~  416 (881)
                           +.+|++|+..+...|||+++ ++.|.|+ +  ++..+||
T Consensus         1      ~~~v~~i~~~~~~~vyDl~v-~~~~~fi~~--ng~v~hn  36 (36)
T 4LX3_B            1      MIKIATRKYLGKQNVYDIGV-ERDHNFALK--NGFIASN  36 (36)
T ss_dssp                  CCCEEEEEEEEEEEEEEEC-STTCEEEBG--GGCEEEC
T ss_pred                  CeEEEEEEEcceEEEEEEEe-CCCCcEEee--CCEEeeC
```

Template alignment | CDD

68. **PF13403.6 ; Hint_2 ; Hint domain**

Probability: 94.87 E-value: 0.092 Score: 50.99 Aligned Cols: 67 Identities: 27% Similarity: 0.36

```
Q ss_pred                  cccCCCcEECCCcccEEHHHcCCCCEEECCCCCEEEEEEEec-----------CCCCeEEEEeCC------
Q Q_7621124_2       90     LVAHDTPVPTPTGWTTHGELRPGDEVYHPSGKVVTVRAISA-----------DAHASIRVSTSD------  142 (881)
Q Consensus         90     C~~~dt~Vlt~~G~~~i~~i~~gd~v~~~~g~~~~v~~~~~-----------~~~~~~~i~t~~------  142 (881)
                           |+.+++.|.+.+|+++|++|..|+.+++.++....+..+..           .....+.+....
T Consensus         2      c~~~~t~i~~~~G~~~i~~i~~Gd~v~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~  71 (148)
T PF13403.6         2      CFTPGTRIATPEGPKPVESLREGDRVQTRDNGAQVVQWIGARRMSGARLFVMPALRPVRIRAGALGIDRP  71 (148)
T ss_pred                  ccCCCCEEECCCcccEEHHHcCCCCEEEeCCCCeEEEEEEEEEeCcchhcCCcccCcEEEeCCcCCCCCC

Q ss_pred                  CCeEEECCCCeEEE
Q Q_7621124_2       143    GGSIVVHPRHEWTV  156 (881)
Q Consensus         143    G~~i~~T~~H~~~~  156 (881)
                           +..+.+|++|+++.
T Consensus         72     ~~~~~~t~~h~~~~  85 (148)
T PF13403.6         72     ERELLVSPEHRMLV  85 (148)
T ss_pred                  ccceEECCCCeEEE
```

Template alignment | Template 3D structure | PDBe

69. **1KCF_A HYPOTHETICAL 30.2 KD PROTEIN C25G10.02; beta-alpha-beta motif, RuvC resolvase family; HET: SO4; 2.3A {Schizosaccharomyces pombe} SCOP: a.140.2.1, c.55.3.7; Related PDB entries: 1KCF_B**

Probability: 94.41 E-value: 0.69 Score: 50.11 Aligned Cols: 164 Identities: 11% Similarity: 0.003

```
Q ss_pred                  cceEEEEEEeCCCCCCCcCCcCEEEEEEEECCCCcEEEEeccccccCcch------------------HHH
Q Q_7621124_2       673    ELTRVVVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTAVLTPLE------------------WPR  724 (881)
Q Consensus         673    ~~~~~~~~iD~a~~~~~~~D~tai~v~~~~~~g~~~v~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  724 (881)
                           .....++|||+|..      ..|++++..+......+++...-......                  ..+
T Consensus         37     ~~~~~IlsID~Gik------Nla~~~l~~~~~~~~~l~~W~~i~l~~~~~~~~~~~~~~~~p~~l~~~~~~  100 (258)
T 1KCF_A            37     YPTSRVLGIDLGIK------NFSYCFASQNEDSKVIIHNWSVENLTEKNGLDIQWTEDFQPSSMADLSIQ  100 (258)
T ss_dssp                  CCCSSEEEEEECST------TEEEEEEECTTSCEEEEEEEECTTSCCTTCCCCCCCCSHHHHHHHHHH
T ss_pred                  CCCceEEEEEeccC------eEEEEEEEcCCCCCeEEEEEEEEccchhcCCCCcCCCCCCCHHHHHHHHHH

Q ss_pred                  HHHHHHHHhCCCEEEEEcccCc-------------hHHHHHHHHHHHHHc--------cCCCCCCCcccc
Q Q_7621124_2       725    AVCLLAYERDASMIVYEKNYGG-------------GMASALITQAWAALQ--------NEPINADTDETM  773 (881)
```

```
Q Consensus         725    ~i~~~~~~~~~~~i~iE~~~~g----------~~~~~~~l~~~~~~~~-------~~~~~~~~~~~~~~  773 (881)
                           .+..+...+.++.++||..-..             ..+..++-.......        .........-..
T Consensus         101    ~v~~l~~~~~~d~vlIErQ~~r~~~~~v~~~~l~v~~le~mL~a~l~~~~~~~~~~~~~~~~V~~~~P~~  170 (258)
T 1KCF_A            101    LFNTLHEKFNPHVILMERQRYRSGIATIPEWTLRVNMLESMLYALHYAEKRNSIEQKIQYPFLLSLSPKS  170 (258)
T ss_dssp                  HHHHHHHHHCCSEEEEEECCCCTTTCCHHHHHHHHHHHHHHHHHHHHHHHHHC-------CCEEEECCHHH
T ss_pred                  HHHHHHHHcCCCEEEEccCCCCCCCCCccHHHHHHhHHHHHHHHHHHHHHhcccccccCCCEEEEeCHHH

Q ss_pred                  CcccCCCCceeeccCCCCHHHHHHHHHHHHHcCCeEEcccCccHHHHHHHHccCCCCCCCCcHHHHHHHH
Q Q_7621124_2       774    IPKSANCPYVKGVSAKISKVLRAEPIAQAVKTGRAKFAQLGNLGSLTNEFTLWQPGSTWSPGALDAAVYG  843 (881)
Q Consensus         774    ~~~~~~~~~i~~~~~~~~K~~ri~~l~~~~~~g~i~~~~~~~~~~l~~el~~~~~~~~~~dD~~Dal~~~  843 (881)
                           +.+-+... ......+..|..+++.+...++.+.+.++.    +..+..+........+.||++||++++
T Consensus         171    v~~~~~~~-~~~~~~~~~Kk~~i~lv~~ll~~~~v~~~~~---~~~l~~~~~~~~~~K~DDlaDall~a  235 (258)
T 1KCF_A            171    TYSYWASV-LNTKASFSKKKSRVQMVKELIDGQKILFEN----EEALYKWNNGSRVEFKKDDMADSALIA  235 (258)
T ss_dssp                  HHHHHHHH-HC-------CCCHHHHHHHHHHTTSEEEESS----HHHHHHHHHCCSTTTHHHHHHHHHHHH
T ss_pred                  HHHhhhhh-ccCcccccchHHHHHHHHHHHHHhCCCceecc----HHHHHHHccCCCCccchHHHHHHHHH

Q ss_pred                  HHHh
Q Q_7621124_2       844    ATEV  847 (881)
Q Consensus         844    ~~~~  847 (881)
                           +..+
T Consensus         236    la~~  239 (258)
T 1KCF_A            236    SGWM  239 (258)
T ss_dssp                  HHHH
T ss_pred                  HHHH
```

Template alignment | Template 3D structure | PDB | NCBI

70. **d1dq3a1 b.86.1.2 (A:1-128,A:415-454) PI-Pfui intein {Pyrococcus furiosus [TaxId: 2261]}**

Probability: 94.36 E-value: 0.069 Score: 53.04 Aligned Cols: 87 Identities: 15% Similarity: 0.096

```
Q ss_pred                  cccCCCCcEECCC-c---cEEHHHcCCCCE----------------------EECCCC-----CEEEEEE
Q Q_7621124_2       90     LVAHDTPVPTPT-G---WTTHGELRPGDE----------------------VYHPSG-----KVVTVRA  127 (881)
Q Consensus         90     C~~~dt~Vlt~~-G---~~~i~~i~~gd~----------------------v~~~~g-----~~~~v~~  127 (881)
                           |+.+++.|++.+ |   ..+|+++..++.                       +...+.     .+.++..
T Consensus         1      c~~~~t~i~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~~~~~~~~~~~v~~  70 (169)
T d1dq3a1           1      CIDGKAKIIFENEGEEHLTTMEEMYERYKHLGEFYDEEYNRWGIDVSNVPIYVKSFDPESKRVVKGKVNV  70 (169)
T ss_dssp                  CEETTCEEEEESSSCEEEEEHHHHHHHHGGGCEEEETTTTEEEEECTTSCCEEEEEETTTTEEEEEEEEE
T ss_pred                  CCCCCCEEEEeeCCeEEEEeHHHHHHHHHhhcCcccccccceeeEecCCCcEEEEEeCCCCeEEEEeeEE

Q ss_pred                  EecCC-CC---eEEEEeCCCCeEEECCCCeEEEEeCCC-CeEEEcchhHHhhheee
Q Q_7621124_2       128    ISADA-HA---SIRVSTSDGGSIVVHPRHEWTVWDRNR-KRWSTMETGDMMRRAYV  178 (881)
Q Consensus         128    ~~~~~-~~~---~~~i~t~~G~~i~~T~~H~~~~~~~~~-~~~~~~~~~~l~~~~~  178 (881)
                           +.... ..   +++|++.+|+.+.+|++|++++..... ..|+.  +.++..++.+
T Consensus         71     ~~~~~~~~~~~~~i~~~~~~~~~t~~h~~~~~~~~~~~~~~~~~~~~l~~gd~l  124 (169)
T d1dq3a1           71     IWKYELGKDVTKYEIITNKGTKILTSPWHPFFVLTPDFKIVEKR--ADELKEGDIL  124 (169)
T ss_dssp                  EEEEEECTTSCEEEEEETTCCEEEECTTCEEEEECTTSCEEEEE--TTTCCTTCEE
T ss_pred                  EEEeecCCCeeEEEEEECCCCEEEECCCcceEEeCCCCcEEEEE--HHHCCCCCEE
```

Template alignment | CDD

71. **PF04848.13 ; Pox_A22 ; Poxvirus A22 protein**

Probability: 93.97 E-value: 1.3 Score: 42.83 Aligned Cols: 132 Identities: 11% Similarity: 0.004

```
Q ss_pred                  EEEEEeCCCCCCCcCCcEEEEEEEECCCCcEEEEecccccCcchHHHHHHHHHHhCCCEEEEEcccCc
Q Q_7621124_2       677    VVVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTAVLTPLEWPRAVCLLAYERDASMIVYEKNYGG  746 (881)
Q Consensus         677    ~~~~iD~a~~~~~~~D~tai~v~~~~~~g~~~v~~~~~~~~~~~~~~~~i~~~~~~~~~~i~iE~~~~g  746 (881)
                           .++|||||..      .++++++... ++.+.+++.....+.+.+...+.+++. |+++.+++|.....
T Consensus         2      ~il~iDpg~~~-------~~G~av~~~~~-~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~vviE~~~~~  63 (143)
T PF04848.13        2      VVCSIDVGTR------NPARTLLEIR-GEHLRVLSVDKLDWSTDWEHRVARDVCS-VRADVVLVEKQGPR  63 (143)
T ss_pred                  eEEEEeeCcc------ceEEEEEEEc-CCceEEEEEecCCCCccHHHHHHHHHHh-cCCCEEEEecCCCC

Q ss_pred                  hHHHHHHHHHHHHHhccCCCCCCCccccCcccCCCCceeecc-------CCCCHHHhHHHHHHHHHcCCe-
Q Q_7621124_2       747    GMASALITQAWAALQNEPINADTDETMIPKSANCPYVKGVS-------AKISKVLRAEPIAQAVKTGRA-  808 (881)
Q Consensus         747    ~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~K~~ri~~l~~~~~~g~i-  808 (881)
                           ......+..+..-+.. +                ++ +..+.       .+..|...++.+...+....+
T Consensus         64     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  116 (143)
T PF04848.13        64     SPHAKFLHFMRGLLFG-Q---------------TP-VLCRNPALRGGSYRARKRRSVQLFLRRLSFFGID  116 (143)
T ss_pred                  CchHHHHHHHHHHHhC-C---------------CC-EEEecccccCCcHHHHHHHHHHHHHHHHHHhcCCC

Q ss_pred                  --EEcccCccHHHHHHHhccCCCCCCCCcHHHHHHHHHHHhcCC
Q Q_7621124_2       809    --KFAQLGNLGSLTNEFTLWQPGSTWSPGALDAAVYGATEVLPP  850 (881)
Q Consensus         809    --~~~~~~~~~~~l~~el~~~~~~~~~~dD~~Dal~~~~~~~~~  850 (881)
                             .+..                  ...+||.+||+++++..+...
```

```
T Consensus          117    ~~~~~~-------------------~~~~dd~aDA~~i~~~~~~~~  143 (143)
T PF04848.13         117    TRELRA-----------------HSKLDDVADSFHMALEYALAR  143 (143)
T ss_pred                   hHHHHh-----------------CCCchHHHHHHHHHHHHHhC
```

Template alignment | Template 3D structure | PDBe

72. **6DSL_B CatN, CatC; Intein Protein, Trans Splicing, Consensus; NMR {Enterobacteria phage T7}**

Probability: 93.89 E-value: 0.22 Score: 46.36 Aligned Cols: 58 Identities: 17% Similarity: 0.189

```
Q ss_pred                   CCEEECCCCCEEEEEEEecCC-CCeEEEEeCCCCeEEECCCCeEEEEeCCCCeEEEcchhHHhhheee
Q Q_7621124_2        112    GDEVYHPSGKVVTVRAISADA-HASIRVSTSDGGSIVVHPRHEWTVWDRNRKRWSTMETGDMMRRAYV  178 (881)
Q Consensus          112    gd~v~~~~g~~~~v~~~~~~~~-~~~~~i~t~~G~~i~~T~~H~~~~~~~~~~~~~~~~~~l~~~~~~  178 (881)
                            +-.|.+.+| +.++..++... ..+++|++.+|+.+.+|++|++++      .|..  +.++..++.+
T Consensus          16     ~~~v~~~~g-~~~v~~~~~~~~~~~~~i~~~~g~~i~~T~~H~~~~-----~~~~~--a~~l~~gd~l  74 (118)
T 6DSL_B             16     NIKVLTPSG-FKSFSGIQKVYKPFYHHIIFDDGSEIKCSDNHSFGK------DKIK--ASTIKVGDYL  74 (118)
T ss_dssp                   CCEEEETTE-EEEEEEEEEEEESCEEEEEETTSCEEEECSSCBCST------TTCB--GGGCCTTCEE
T ss_pred                   CeEEEcCCe-eEEeeEEEEccCCcEEEEEECCCCEEEeCCCCeeee------ceEE--HHHCCCCCEE
```

Template alignment | Template 3D structure | PDBe

73. **2LCJ_A Pab polC intein; HYDROLASE; NMR {Pyrococcus abyssi}**

Probability: 93.82 E-value: 0.19 Score: 50.68 Aligned Cols: 87 Identities: 20% Similarity: 0.15

```
Q ss_pred                   cccCCCCcEECC-Cc---cEEHHHcCC--------------------CCEEECCC-----CCEEEEEEEecC
Q Q_7621124_2        90     LVAHDTPVPTP-TG---WTTHGELRP--------------------GDEVYHPS-----GKVVTVRAISAD  131 (881)
Q Consensus          90     C~~~dt~Vlt~-~G---~~~~i~~i~~--------------------gd~v~~~~-----g~~~~v~~~~~~  131 (881)
                            |+.++|.|.+. +|   ..+|+++..                    |..++..+     ..+..+..++..
T Consensus          1      c~~~~t~i~~~~~g~~~~~~i~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~~~~~~  70 (185)
T 2LCJ_A             1      CFPGDTRILVQIDGVPQKITLRELYELFEDERYENMVYVRKKPKREIKVYSIDLETGKVVLTDIEDVIKA  70 (185)
T ss_dssp                   CEETTSEEEEEETTEEEEEEHHHHGGGBCCEEEETTEEEECSBSSCEEEEEEETTTTEEEEEEEEEEEE
T ss_pred                   CCCCCCEEEEeeCCEEEEEEHHHHHHHHhhcccccccceEEecccccceEEEEECCCCeEEEEeeEEEEc

Q ss_pred                   C--CCeEEEEeCCCCeEEECCCCeEEEEeCCCCeEEEcchhHHhhheee
Q Q_7621124_2        132    A--HASIRVSTSDGGSIVVHPRHEWTVWDRNRKRWSTMETGDMMRRAYV  178 (881)
Q Consensus          132    ~--~~~~~i~t~~G~~i~~T~~H~~~~~~~~~~~~~~~~~~l~~~~~~  178 (881)
                            .  ..++++.+..|..+.+|++|++++..+....|..  +.++..++++
T Consensus          71     ~~~~~~~~i~~~~g~~i~~t~~h~~~~~~~~~~~~~~--~~~~l~~g~~l  117 (185)
T 2LCJ_A             71     PATDHLIRFELEDGRSFETTVDHPVLVYENGRFIEKR--AFEVKEGDKV  117 (185)
T ss_dssp                   ECCSCEEEEEETTSCEEEECSSSEEEEEETTEEEEEE--GGGCCTTCEE
T ss_pred                   CCCCCeEEEEeCCCCEEEECCCCeEEEEECCEEEEEE--HHHCCCCCEE
```

Template alignment | Template 3D structure | PDBe

74. **5O9J_B Transcription initiation factor IIB,Transcription initiation; Transcription factor IIB, mini-intein, HINT; HET: NH4, DIO, MES, GOL; 2.0A {Methanocaldococcus jannaschii}; Related PDB entries: 5O9J_A 5O9I_A 5O9I_B**

Probability: 93.43 E-value: 0.41 Score: 48.14 Aligned Cols: 90 Identities: 17% Similarity: 0.133

```
Q ss_pred                   CCccccCCCcEECCCc----cEEHHHcC---------------------CCCEEECCCC----CEEEEEE
Q Q_7621124_2        87     VGKLVAHDTPVPTPTG----WTTHGELR---------------------PGDEVYHPSG----KVVTVRA  127 (881)
Q Consensus          87     ~gkC~~~dt~Vlt~~G----~~~i~~i~----------------------gd~v~~~~g----~~~~v~~  127 (881)
                            .|.|+.+++.|.+.+|    ..+|+++.                      .++.++..+.    .+.++..
T Consensus          1      ~~~~~~~~~~v~~~~~~~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~g~~~~~~v~~  70 (184)
T 5O9J_B             1      GGYAVDYNEPIIIKENGEIKVVKIGELIDKIIENSENIRREGILEIAKCKGIEVIAFNSNYKFKFMPVSE  70 (184)
T ss_dssp                   -CCCEETTCEEEEESSSCEEEEEHHHHHHHHHHTCSCEEEETTEEEEECSSCEEEEECTTSCEEEEECCE
T ss_pred                   CCccccCCCcEEEEECCEEEEEEhHHHHHHHHhhcccceeecCceEEeeeCCeEEEEECCCCCEEEEEceE

Q ss_pred                   EecCC-CCeEEEEeCCCCeEEECCCCeEEEEeCCCCeEEEcchhHHhhheee
Q Q_7621124_2        128    ISADA-HASIRVSTSDGGSIVVHPRHEWTVWDRNRKRWSTMETGDMMRRAYV  178 (881)
Q Consensus          128    ~~~~~-~~~~~i~t~~G~~i~~T~~H~~~~~~~~~~~~~~~~~~l~~~~~~  178 (881)
                            +.... ..++++.+..|..+.+|++|++++.......|..  +..+..+.++
T Consensus          71     ~~~~~~~~~~~~~~~g~~~~~t~~~~~~~~~~~~~~~~~--~~~~~~g~~l  120 (184)
T 5O9J_B             71     VSRHPVSEMFEIVVEGNKKVRVTRSHSVFTIRDNEVVPIR--VDELKVGDIL  120 (184)
T ss_dssp                   EEEEECCCEEEEEETTTEEEEECTTCEEEEEETTEEEEEE--GGGCCTTCEE
T ss_pred                   EEecCCCCeEEEEEcCCCEEEECCCCeEEEEeCCEEEEEE--HHHCCCCCEE
```

Template alignment | Template 3D structure | PDB | NCBI

75. **d1hjra_ c.55.3.6 (A:) RuvC resolvase {Escherichia coli [TaxId: 562]}**

Probability: 93.21 E-value: 3.1 Score: 41.21 Aligned Cols: 136 Identities: 13% Similarity: 0.08

```
Q ss_pred                   EEEEEeCCCCCCCcCCcEEEEEEEECCCCcEEEEecccccCc-------chHHHHHHHHHHhCCCEEE
Q Q_7621124_2        677    VVVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTAVLTP-------LEWPRAVCLLAYERDASMIV  739 (881)
Q Consensus          677    ~~~~iD~a~~~~~~~D~tai~v~~~~~~g~~~v~~~~~~~~~~~------~~~~~~i~~~~~~~~~~i~  739 (881)
                            .++|||||..      .++++++... ++...+++...-..+.       ..+.+.+.+++++++++.|+
```

```
T Consensus         2      ~ilgiDpg~~------~~G~Ai~~~~-~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~l~~~~~~~~vv  64 (158)
T d1hjra_           2      IILGIDPGSR------VTGYGVIRQV-GRQLSYLGSGCIRTKVDDLPSRLKLIYAGVTEIITQFQPDYFA  64 (158)
T ss_dssp                  EEEEEECCSS------EEEEEEEEEE-TTEEEEEEEEEEECCCSCHHHHHHHHHHHHHHHHHHHCCSEEE
T ss_pred                  EEEEEecCCC------ceEEEEEEEc-CCeEEEEEEEEEEcCCCCHHHHHHHHHHHHHHHHHHHHCCCEEE

Q ss_pred                  EEcccCchHHHHHHHHH-----HHHhccCCCCCCCccccCcccCCCCceeeccCCCCHHHhHHHHHHHHHH
Q Q_7621124_2       740    YEKNYGGGMASALITQA-----WAALQNEPINADTDETMIPKSANCPYVKGVSAKISKVLRAEPIAQAVK  804 (881)
Q Consensus       740    iE~~~~g~~~~~~l~~~-----~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~K~~ri~~l~~~~~  804 (881)
                           ||....+.........     ...+...               .+++ +..+....-|..-
T Consensus        65     iE~~~~~~~~~~~~~~~~~~g~i~~~~~~--------------~~i~-~~~v~p~~~k~~~---------  110 (158)
T d1hjra_          65     IEQVFMAKNADSALKLGQARGVAIVAAVN--------------QELP-VFEYAARQVKQTV---------  110 (158)
T ss_dssp                  EEECCCCCCTTTHHHHHHHHHHHHHHHHHT--------------TTCC-EEEEEHHHHHHHH---------
T ss_pred                  EeccCCCCChhHHHHHHHHHHHHHHHHHHH--------------CCCC-EEEECHHHhHHHH---------

Q ss_pred                  cCCeEEcccCccHHHHHHHhccCCCC-CCCCcHHHHHHHHHHHHh
Q Q_7621124_2       805    TGRAKFAQLGNLGSLTNEFTLWQPGS-TWSPGALDAAVYGATEV  847 (881)
Q Consensus       805    ~g~i~~~~~~~~~~~~l~~el~~~~~~~~~~-~~~dD~~Dal~~~~~~~~~  847 (881)
                           .|.=.-..    .++.+.+.......  ...+|.+||++.+....
T Consensus       111    ~g~g~~~K----~~~~~~~~~~~~~~~~~~~~~~~~~~d~aDA~~ia~~~~  150 (158)
T d1hjra_         111    VGIGSAEK----SQVQHMVRTLLKLPANPQADAADALAIAITHC  150 (158)
T ss_dssp                  TSSSSCCH----HHHHHHHHHHTTCCCCCSSCTHHHHHHHHHHH
T ss_pred                  cCCCCCCH----HHHHHHHHHHcCCCCCCCCCcHHHHHHHHHHHH
```

[Template alignment](#) | [Template 3D structure](#) | [PDBe](#)

76. **4O1R_A Replicative DNA helicase; splicing; HET: GOL; 1.4A {Nostoc punctiforme} SCOP: l.1.1.1, b.86.1.2**

Probability: 93.12 E-value: 0.51 Score: 44.54 Aligned Cols: 70 Identities: 20% Similarity: 0.219

```
Q ss_pred                  CCccccCCCcEECCC-cc-EEHHHc--CCCCEEECCCCC-----EEEEEEEecCC-CCeEEEEeCCCCeE
Q Q_7621124_2        87    VGKLVAHDTPVPTPT-GW-TTHGEL--RPGDEVYHPSGK-----VVTVRAISADA-HASIRVSTSDGGSI  146 (881)
Q Consensus         87    ~gkC~~~dt~Vlt~~-G~-~~i~~i--~~gd~v~~~~g~-----~~~v~~~~~~~-~~~~~i~t~~G~~i  146 (881)
                           ++.|+..++.+.+.+ |. .+++++  ..|+.++..++.      ...+..+.... ..++++.+..|..+
T Consensus          1     ~~~~~~~~~~~~~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  70 (142)
T 4O1R_A             1     SGGALAGDSLVTLVDSGLQVPIKELVGKSGFAVWALNEATMQLEKAIVSNAFSTGIKPLFTLTTRLGRKI  70 (142)
T ss_dssp                  CCCCEETTCEEECTTTCCEEEGGGGTTCCSEEEEEEETTTTEEEEEEEECEEEEEEEEEEEEEEEETTCCEE
T ss_pred                  CCCccccCceEEeCCCCcEEEHHHHccccCcEEEEEeCCCCeEEEEEeeeeeecccceeeEEEEECCCCEE

Q ss_pred                  EECCCCeEEE
Q Q_7621124_2       147    VVHPRHEWTV  156 (881)
Q Consensus       147    ~~T~~H~~~~  156 (881)
                           .+|++|++++
T Consensus         71    ~~t~~~~~~~~  80 (142)
T 4O1R_A            71    RATGNHKFLT  80 (142)
T ss_dssp                  EECTTCEEEE
T ss_pred                  EEcCCCceee
```

[Template alignment](#)

77. **cd00529 RuvC_resolvase; Holliday junction resolvases (HJRs) are endonucleases that specifically resolve Holliday junction DNA intermediates during homologous recombination.**

Probability: 93.0 E-value: 3.1 Score: 40.8 Aligned Cols: 134 Identities: 15% Similarity: 0.119

```
Q ss_pred                  EEEEeCCCCCCCcCCcEEEEEEEEECCCCcEEEEecccccCcc--------hHHHHHHHHHHHhCCCEEE
Q Q_7621124_2       678    VVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTAVLTPL--------EWPRAVCLLAYERDASMIV  739 (881)
Q Consensus       678    ~~~iD~a~~~~~~~~D~tai~v~~~~~~~g~~~v~~~~~~~~~~~~~~~--------~~~~~i~~~~~~~~~~~~~i~  739 (881)
                           ++|||||..      .++++++..+ .+..-+++...-..+..        .+.+.+.++++.|+++.++
T Consensus          2     ilgiD~g~~------~~g~ai~~~~-~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~i~~~~~~~~vv  64 (154)
T cd00529           2     ILGIDPGSR------NTGYGVIEQE-GRKLIYLASGVIRTSSDAPLPSRLKTIYDGLNEVIDQFQPDVVA  64 (154)
T ss_pred                  EEEEeCCCC------ceEEEEEEec-CCEEEEEEEEEEEECCCCCCHHHHHHHHHHHHHHHHHHHHCCCEEE

Q ss_pred                  EEcccCchH------HHHHHHHHHHHhccCCCCCCCccccCcccCCCCceeeccCCCCHHHhHHHHHHHHHH
Q Q_7621124_2       740    YEKNYGGGM------ASALITQAWAALQNEPINADTDETMIPKSANCPYVKGVSAKISKVLRAEPIAQAV  803 (881)
Q Consensus       740    iE~~~~g~~------~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~K~~ri~~l~~~~~  803 (881)
                           ||....+..      ...+...+...+...                 +++ +..+....-|....
T Consensus         65    iE~~~~~~~~~~~~~~~~~~g~i~~~~~~~~---------------~i~-v~~v~p~~~k~~~~-------  111 (154)
T cd00529          65    IERVFFAKNPDSALKLGQARGALILALANR---------------NLP-VFEYTPNQVKKAVT-------  111 (154)
T ss_pred                  EecCcCCCCccHHHHHHHHHHHHHHHHHHHC---------------CCC-EEEeCHHHHHHHHh-------

Q ss_pred                  HcCCeEEcccCccHHHHHHHhccCCCCC--CCCcHHHHHHHHHHHHh
Q Q_7621124_2       804    KTGRAKFAQLGNLGSLTNEFTLWQPGST--WSPGALDAAVYGATEV  847 (881)
Q Consensus       804    ~~g~i~~~~~~~~~~~~l~~el~~~~~~~~~~~~--~~dD~~Dal~~~~~~~~~  847 (881)
                             |.-.-..    .+..+.+...-....  ..+|.+||++.++...
T Consensus        112    --~~~~~~~~K---~~~~~~~~~~~~~~~~~~~~~~~~~~d~aDA~~i~~~~~~  151 (154)
```

```
T cd00529          112    --GYGKADK----DQVQHMVKRLLNLSEIPKPDDAADALAVAITHA  151 (154)
T ss_pred                 --CCCCCCH----HHHHHHHHHHcCCCcCCCCcHHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

78. **2LWY_A Bacterial Intein-Like domain; BIL, CthBIL4, Bacterial Intein-Like, HINT; NMR {Clostridium thermocellum}**

Probability: 92.94 E-value: 0.7 Score: 42.98 Aligned Cols: 74 Identities: 20% Similarity: 0.172

```
Q ss_pred                 CCccccCCCcEECCCccEEHHHcCCCCEEECCCC-----CEEEEEEEecCC-CCeEEEEeCCCCeEEECC
Q Q_7621124_2      87     VGKLVAHDTPVPTPTGWTTHGELRPGDEVYHPSG-----KVVTVRAISADA-HASIRVSTSDGGSIVVHP  150 (881)
Q Consensus        87     ~gkC~~~dt~Vlt~~G~~~i~~i~~gd~v~~~~g-----~~~~v~~~~~~~-~~~~~i~t~~G~~i~~T~  150 (881)
                          .+.|+..++.+.+..|..+++++..|+.+...+.     ....+...+... ..++++.+ .+..+.+|+
T Consensus        1      ~~~~~~~~~~~~~~g~~~i~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  69 (138)
T 2LWY_A           1      SMKAFVAGTMILTATGLVAIENIKAGDKVIATNPETFEVAEKTVLETYVRETTELLHLTI-GGEVIKTTF  69 (138)
T ss_dssp                 CCCCEETTCEEECSSSEEEGGGCCTTCEEEEECTTTCCEEEEEEEEEEEEEEEEEEEEE-TTEEEEECT
T ss_pred                 CCCccccCCCEEEcCCccEEhhhcCCCCEEEEECCCCCCeEEeEeeeEEEEcCCCcEEEEEE-CCeEEEeCC

Q ss_pred                 CCeEEEEeCCC
Q Q_7621124_2      151    RHEWTVWDRNR  161 (881)
Q Consensus        151    ~H~~~~~~~~~  161 (881)
                          +|+++.....+
T Consensus        70     ~~~~~~~~~~~  80 (138)
T 2LWY_A           70     DHPFYVKDVGF  80 (138)
T ss_dssp                 TCEEEETTTEE
T ss_pred                 CCceEecCCCe
```

Template alignment | Template 3D structure | PDBe

79. **1AT0_A 17-HEDGEHOG; DEVELOPMENTAL SIGNALING MOLECULE, CHOLESTEROL TRANSFER; HET: MSE; 1.9A {Drosophila melanogaster} SCOP: b.86.1.1**

Probability: 92.76 E-value: 1.2 Score: 42.59 Aligned Cols: 87 Identities: 21% Similarity: 0.362

```
Q ss_pred                 cccCCCcEECCCc-cEEHHHcCCCCEEECCC--CCEEEEEEEe-----cCC-CCeEEEEeCCCCeEEECC
Q Q_7621124_2      90     LVAHDTPVPTPTG-WTTHGELRPGDEVYHPS--GKVVTVRAIS-----ADA-HASIRVSTSDGGSIVVHP  150 (881)
Q Consensus        90     C~~~dt~Vlt~~G-~~~i~~i~~gd~v~~~~--g~~~~v~~~~-----~~~~-~~~~~i~t~~G~~i~~T~  150 (881)
                          |+.+++.+.+.+| ...++++..|+.+.+.+  |.........     ... ...+.+.+.+|..+.+|+
T Consensus        1      ~~~~~~~v~~~~g~~~~i~~~~~g~~~~~~~~~g~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~  70 (145)
T 1AT0_A           1      CFTPESTALLESGVRKPLGELSIGDRVLSMTANGQAVYSEVILFMDRNLEQMQNFVQLHTDGGAVLTVTP  70 (145)
T ss_dssp                 CBCTTCEEEBTTSCEEEGGGCCTTCEEEEECTTSCEEEEEEEEEEEEEEEEEEEEEEEEEETTSCEEEECT
T ss_pred                 CCCCCcEEEeeCCCeEEHHHCCCCCEEEEECCCCCCEEEeEEEEEEeCChhhceeEEEEEeCCCCEEEECC

Q ss_pred                 CCeEEEEeCC--CCeEEEcchhHHhhheee
Q Q_7621124_2      151    RHEWTVWDRN--RKRWSTMETGDMMRRAYV  178 (881)
Q Consensus        151    ~H~~~~~~~~--~~~~~~~~~~~l~~~~~~  178 (881)
                          +|+++..+..  ...|..  +..+..++.+
T Consensus        71     ~~~~~~~~~~~~~~~~~~--~~~~~~~g~~l  98 (145)
T 1AT0_A           71     AHLVSVWQPESQKLTFVF--ADRIEEKNQV  98 (145)
T ss_dssp                 TCEEEEEETTTTEEEEEE--GGGCCTTCEE
T ss_pred                 CceEEEecCccCCeEEEE--hhHCCCCCEE
```

Template alignment | CDD

80. **PF05894.12 ; Podovirus_Gp16 ; Podovirus DNA encapsidation protein (Gp16)**

Probability: 92.61 E-value: 1.6 Score: 49.28 Aligned Cols: 150 Identities: 7% Similarity: -0.086

```
Q ss_pred                 cCCCCeEEEcCCccccCCChhHHhhHHHHHHccCCCCeEEEeehhHHHHHHcHHHHHHHHHHchHhCcc
Q Q_7621124_2      399    DSPDGLYLVGEHMTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARRNGAAVRELVREYGPEFGLN  468 (881)
Q Consensus        399    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ili~s~~~~~a~~~~~~i~~~~~~~~~~~~~  468 (881)
                          ..+....+.  .+.+++++|.......+..+... +.+++++-.+....+.....+..++..++..--
T Consensus        14     ~~~~~~~~~~---GgRGsGKS~~~~~~~l~~~~~~-g~~~lilRrt~~~l~~s~~~~~~~~~~~~~~--  78 (325)
T PF05894.12       14     SKNRIMNFV--IGARGIGKTYGFKKYVINRFLKT-GKQFIYLRRYKSELAKVANFFNSLKHEFEGVDF--  78 (325)
T ss_pred                 CCCCeEEEE--EcCCCCCHHHHHHHHHHHHHHHc-CCeEEEEccChHHHHHHHHHHHHHHHHcCCeEE--

Q ss_pred                 cCCCCcccCceEeecCceE-EEEccCC--CcccCC---CcEEEEeCCCCCHH-HHcCHHHHHHHHHHHH
Q Q_7621124_2      469    LSPDESSKTDWSIRAGGTM-RSRGLRG--NFTGQP---MDLGIIDDPITNRA-QAESLVVRDFVWDWYSS  531 (881)
Q Consensus        469    ~~~~~~~~~~~~~~~~~~i-~~~g~~~--s~rG~~~~~~~ii~DE~~~~~~~~~~s~~~~~~~~~~~~  531 (881)
                              ..+...+.+ +|+.+ ...+...  ..+|..   ++.|++||+..... .-..+.+.+.+.+.+.+
T Consensus        79     ----~~~~~~~i~~-nG~~~~~~~~l~~~~k~kG~~~~~~~~I~~DEa~~~~~~~~y~~~e~~~~~~~l~s  143 (325)
T PF05894.12       79     ----KVKGRMFFI-NDKLAGWAIPLSSWQAEKSTDYPDVETILFDEFIREKDNSRYLPDEVKALLNFMDT  143 (325)
T ss_pred                 ----EEeCcEEEE-CCEEEeeccccchhHHHcCCCCCCCcEEEEECcccCCCcccCCCHHHHHHHHHHHH

Q ss_pred                 hhhcccCCCCeEEEEccccCcccHHHHHH
Q Q_7621124_2      532    VWSQRKAPTYREVLVMTRWHQDDLAGRLL  560 (881)
Q Consensus        532    ~~~~~~~~~~~~i~i~T~~~~~d~~~~l~  560 (881)
```

```
                                .+.....  .++++.++|.+..+.+...+
T Consensus         144         ~~R~~~~---~kii~t~NP~~~~~~~~~~  170 (325)
T PF05894.12        144         VIRIREG--SRLIGMSNSVSIVNPYFLYF  170 (325)
T ss_pred                       hcccCCC--CEEEEEecCCCCCCHHHHhh
```

Template alignment | Template 3D structure | PDB | NCBI

81. **d1b24a1 d.95.2.1 (A:7-99) DNA endonuclease I-dmoI {Desulfurococcus mobilis [TaxId: 2274]}**

Probability: 92.56 E-value: 0.15 Score: 44.86 Aligned Cols: 64 Identities: 19% Similarity: 0.189

```
Q ss_pred                       cccchHHHHHHhcccccCCC-------CeEEecCChHH--hh-----hchhh----------cCeEEecC
Q Q_7621124_2       200         TLLIDPYTLGVWLGDGSSTK-------AAITHHADDEY--VL-----PYPKS----------ADCVHQTT  245 (881)
Q Consensus         200         ~~~~~~~llG~~l~dG~~~~--------~~i~~~~~~~~~--~~-----~~~~~----------~~~~~~~  245 (881)
                                ..+.++|++|.++|||+++.       ..+.+...+.+  ..     +.+..          .......+
T Consensus         1           ~s~~lAyliGi~lGDG~i~~~k~~~~~~~i~l~~~Dk~~~~~~~~v~~~~~~~l~~i~~~~~i~~~~~~~  70 (93)
T d1b24a1           1           VSGISAYLLGLIIGDGGLYKLKYKGNRSEYRVVITQKSENLIKQHIAPLMQFLIDELNVKSKIQIVKGDT  70 (93)
T ss_dssp                       CHHHHHHHHHHHHHSEEEEEEECSTTCEEEEEEEEESCHHHCCCCCHHHHHHHHHHTTCCCCCEEEECSS
T ss_pred                       CCHHHHHHHHHHHcCceeeeceecCCEEEEEEEEecCChHhhhhccHHHHHHHHHHHcCCCCeEEEEcCCC

Q ss_pred                       CcEEEEeCChHHHHHHHc
Q Q_7621124_2       246         GVVTSYYRGGLHTALKTL  263 (881)
Q Consensus         246         ~~~~~~~~~~l~~~l~~~  263 (881)
                                ...+.++|+.+..+|..+
T Consensus         71          ~~~v~i~sk~l~~~L~~~  88 (93)
T d1b24a1           71          RYELRVSSKKLYYYFANM  88 (93)
T ss_dssp                       CEEEEEECHHHHHHHHHH
T ss_pred                       EEEEEECchhHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

82. **3QVE_B HMG box-containing protein 1; SGC, HMG box transcription factor; HET: SO4, EDO; 2.04A {Homo sapiens} SCOP: b.145.1.0, l.1.1.1; Related PDB entries: 3QVE_C 1V06_A 3QVE_A**

Probability: 92.55 E-value: 0.2 Score: 48.23 Aligned Cols: 91 Identities: 12% Similarity: 0.081

```
Q ss_pred                       eCCCCCccccCCCcEECCCc-cEEHHHc---CC-------CCEEECCCCCEE-------EEEEEecCCCC
Q Q_7621124_2       83          TPSQVGKLVAHDTPVPTPTG-WTTHGEL---RP-------GDEVYHPSGKVV-------TVRAISADAHA  134 (881)
Q Consensus         83          g~~g~gkC~~~dt~Vlt~~G-~~~i~~i---~~-------gd~v~~~~g~~~--------~v~~~~~~~~  134 (881)
                                .......|+..++.|.+.+| ...|+++   ..       |+.+++.+....       .|..+......
T Consensus         4           ~~~~~~~~~~~~t~v~~~g~~~~i~~i~~~~~~~~~~~g~~~~~~~~~~~~~~~~~v~~~~~~~~  73 (139)
T 3QVE_B            4           WPSTVWHCFLKGTRLCFHKGSNKEWQDVEDFARAEGCDNEEDLQMGIHKGYGSDGLKLLSHEESVSFGES  73 (139)
T ss_dssp                       CCCEEETTEETTCEEEESSSSCCSCEEHHHHHHHTC---------CTTTTTTTTCEEEEEEEEEETTEE
T ss_pred                       CCCCcccccccCCCEEEEcCCCeEEeEeHHHHHHHcCCCchhhheeeeecCcCCCccEEEEEeeeecCCc

Q ss_pred                       eEEEEeCCC------CeEEECCCCeEEEEeCCCCe-------------EEEcchhHHh
Q Q_7621124_2       135         SIRVSTSDG------GSIVVHPRHEWTVWDRNRKR-------------WSTMETGDMM  173 (881)
Q Consensus         135         ~~~i~t~~G-------~~i~~T~~H~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~  173 (881)
                                +++|++..|      ..+.+|++|++++.+..+..              ...+..++.+
T Consensus         74          ~~~i~~~~~~~~~~~~~~~~t~~h~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~gd~l  131 (139)
T 3QVE_B            74          VLKLTFDPGTVEDGLLTVECKLDHPFYVKNKGWSSFYPSLTVVQHGIPCCEVHIGDVC  131 (139)
T ss_dssp                       EEEEEEECSCGGGCCEEEEECTTCCEEETTTEEEESSHHHHHHHHCCCCEECCTTCEE
T ss_pred                       EEEEEEcCCCcccceEEEEEeCCCCEEEcCCeEEEcChHHHHHHHhCCcceeCCCCCEE
```

Template alignment | Template 3D structure | PDBe

83. **6AIB_A DEAD-box ATP-dependent RNA helicase CshA; STRUCTURAL PROTEIN; 1.5A {Staphylococcus aureus subsp. aureus MRSA252}; Related PDB entries: 6AIC_A**

Probability: 92.49 E-value: 0.35 Score: 50.21 Aligned Cols: 151 Identities: 11% Similarity: -0.018

```
Q ss_pred                       CCCeEEEcCCcccccCChhHHhhHHHHHHccCCCCeEEEeehhHHHHHHcHHHHHHHHHHHchHhCcccC
Q Q_7621124_2       401         PDGLYLVGEHMTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARRNGAAVRELVREYGPEFGLNLS  470 (881)
Q Consensus         401         ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  470 (881)
                                .....++  .++++.++|.......++.....+...+++++++...+.....+..+.............
T Consensus         38          ~~~~~~~--~~~~GsGKT~~~~~~~~~~~~~~~~~~~~~~~liv~p~~~~~~~~~~~~~~~~~~~~~~~~  105 (214)
T 6AIB_A            38          QGIDILG--QAQTGTGKTGAFGIPLIEKVVGKQGVQSLILAPTRELAMQVAEQLREFSRGQGVQVVTVFG  105 (214)
T ss_dssp                       TTCCEEE--CCCSSGGGHHHHHHHHHHHHTTCCSCCEEEECSSHHHHHHHHHHHHHHTTTSCCCEEEECT
T ss_pred                       cCCeEEE--ECCCCCcHHHHHHHHHHHHHHHcCCCceEEEEEcCHHHHHHHHHHHHHHhhcCCCeEEEEEC

Q ss_pred                       CCCcccCceEeecCceEEEEccCC-C-------cccCCCcEEEEeCCCCHHHHcCHHHHHHHHHHHHHh
Q Q_7621124_2       471         PDESSKTDWSIRAGGTMRSRGLRG-N-------FTGQPMDLGIIDDPITNRAQAESLVVRDFVWDWYSSV  532 (881)
Q Consensus         471         ~~~~~~~~~~~~~~~~i~~~g~~~-s-------~rG~~~~~ii~DE~~~~~~~~~s~~~~~~~~~~~~~  532 (881)
                                ...........++..+...+... .       ..+.+++++|+||++........        +.+...
T Consensus         106         ~~~~~~~~~~~~~~~~i~~~t~~~~~~~~~~~~~~~~~~~iivDEah~~~~~~~~~-------~~~~~~  167 (214)
T 6AIB_A            106         GMPIERQIKALKKGPQIVVGTPGRVIDHLNRRTLKTDGIHTLILDEADEMMNMGFI--------DDMRFI  167 (214)
T ss_dssp                       TSCHHHHHHHHHTCCSEEEECHHHHHHHHHHHTSSCCTTCCEEEEESHHHHHHTTCH--------HHHHHH
T ss_pred                       CCCHHHHHHHHHcCCCEEEECHHHHHHHHHHcCCCCcccccEEEEeChhHHhccchH--------HHHHHH
```

```
Q ss_pred                  hhcccCCCCeEEEEccccCc--ccHHHHHHh
Q Q_7621124_2       533    WSQRKAPTYREVLVMTRWHQ--DDLAGRLLA  561 (881)
Q Consensus         533    ~~~~~~~~~~i~i~T~~~~---~d~~~~l~~  561 (881)
                           +........++++++++...  .+++..++.
T Consensus         168    ~~~~~~~~~~~i~~sat~~~~~~~~~~~~~~  198 (214)
T 6AIB_A            168    MDKIPAVQRQTMLFSATMPKAIQALVQQFMK  198 (214)
T ss_dssp                  HHHSCCTTCEEEEECSSCCHHHHHHHHHHSC
T ss_pred                  HhcCCcccceEEEEEccCCHHHHHHHHHHHc
```

Template alignment | Template 3D structure | PDBe

84. **1HJR_B HOLLIDAY JUNCTION RESOLVASE (E.C.3.1.22.4) (RUVC); SITE-SPECIFIC RECOMBINASE; 2.5A {Escherichia coli} SCOP: c.55.3.6; Related PDB entries: 1HJR_D 1HJR_C 1HJR_A**

Probability: 92.42 E-value: 4.4 Score: 40.07 Aligned Cols: 143 Identities: 14% Similarity: 0.083

```
Q ss_pred                  EEEEEeCCCCCCCcCCcEEEEEEEECCCCcEEEEecccccCc-------chHHHHHHHHHHHhCCCEEE
Q Q_7621124_2       677    VVVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTAVLTP-------LEWPRAVCLLAYERDASMIV  739 (881)
Q Consensus         677    ~~~~iD~a~~~~~~~D~tai~v~~~~~~g~~~v~~~~~~~~~~~------~~~~~~i~~~~~~~~~~~i~  739 (881)
                           .++|||||..      .++++++... ++...+++...-..+.       ..+.+.+.++++.|+++.|+
T Consensus         2      ~ilgiDpg~~~-------~~G~av~~~~-~~~~~~~~~~~i~~~~~~~~~~~~~~~~l~~~i~~~~p~~vv  64 (158)
T 1HJR_B            2      IILGIDPGSR------VTGYGVIRQV-GRQLSYLGSGCIRTKVDDLPSRLKLIYAGVTEIITQFQPDYFA  64 (158)
T ss_dssp                  EEEEEECCSS------EEEEEEEEEE-TTEEEECCCEEEECCCSCHHHHHHHHHHHHHHHHHHHCCSEEE
T ss_pred                  EEEEEeCCCC------ceEEEEEEEe-CCeEEEEEEEEEEcCCCCHHHHHHHHHHHHHHHHHHHCCCEEE

Q ss_pred                  EEcccCchHHHH------HHHHHHHHhccCCCCCCCccccCcccCCCCceeeccCCCCHHHhHHHHHHHH
Q Q_7621124_2       740    YEKNYGGGMASA------LITQAWAALQNEPINADTDETMIPKSANCPYVKGVSAKISKVLRAEPIAQAV  803 (881)
Q Consensus         740    iE~~~~g~~~~~~------~l~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~K~~ri~~l~~~~  803 (881)
                           ||....+.....      ....+...+...               ++| +..+....-|....
T Consensus         65     iE~~~~~~~~~~~~~~~~~g~i~~~~~~~~---------------i~-~~~i~p~~~k~~~~-------  111 (158)
T 1HJR_B            65     IEQVFMAKNADSALKLGQARGVAIVAAVNQ---------------ELP-VFEYAARQVKQTVV-------  111 (158)
T ss_dssp                  EECCCCCCCSSHHHHHHHHHHHHHHHHTT---------------TCC-EEEECHHHHHHHHT-------
T ss_pred                  EeccCCCCChhHHHHHHHHHHHHHHHHHHC---------------CCC-EEEECHHHHHHHHh-------

Q ss_pred                  HcCCeEEcccCccHHHHHHHhccCCCCC-CCCcHHHHHHHHHHHHhcCCCCCcc
Q Q_7621124_2       804    KTGRAKFAQLGNLGSLTNEFTLWQPGST-WSPGALDAAVYGATEVLPPVGSTT  855 (881)
Q Consensus         804    ~~g~i~~~~~~~~~~l~~el~~~~~~~~~-~~dD~~Dal~~~~~~~~~~~~~~  855 (881)
                             |.=.-..    ..+.+.+..+..... ..+|.+||++.++..+.....+
T Consensus         112    --g~g~~~K----~~~~~~~~~~~~~~~~~~~~d~aDA~~i~~~~~~~~~~~~  158 (158)
T 1HJR_B            112    --GIGSAEK----SQVQHMVRTLLKLPANPQADAADALAIAITHCHVSQNAMQ  158 (158)
T ss_dssp                  --SCSSCCH----HHHHHHHHHHTTCCCCCSSCCHHHHHHHHHHHHHHHSCCC
T ss_pred                  --CCCCCCH----HHHHHHHHHHcCCCCCCCCChHHHHHHHHHHHHHhhhhhcC
```

Template alignment | Template 3D structure | PDBe

85. **4EP4_B Crossover junction endodeoxyribonuclease RuvC (E.C.3.1.22.4); resolvase, Hydrolase; 1.28A {Thermus thermophilus} SCOP: c.55.3.6; Related PDB entries: 4LD0_B 4LD0_A 4EP4_A 4EP5_A**

Probability: 91.73 E-value: 6.3 Score: 39.46 Aligned Cols: 136 Identities: 15% Similarity: 0.075

```
Q ss_pred                  EEEEEeCCCCCCCcCCcEEEEEEEECCC--cEEEEecccccC--------cchHHHHHHHHHHhCCC
Q Q_7621124_2       677    VVVGVDPSGGEGARHDTAGISAVGLDEHQ--HAWFLEDRTAVLT--------PLEWPRAVCLLAYERDAS  736 (881)
Q Consensus         677    ~~~~iD~a~~~~~~~D~tai~v~~~~~~g--~~~v~~~~~~~~~~--------~~~~~~i~~~~~~~~~  736 (881)
                           .++|||+|..      .++++++....+.  .+.++....-+.+        ...+.+.+.+++++|+++
T Consensus         2      ~ilgiDpg~~~--------~~G~av~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~~l~~~~~~~  65 (166)
T 4EP4_B            2      VVAGIDPGIT------HLGLGVVAVEGKGALKARLLHGEVVKTSPQEPAKERVGRIHARVLEVLHRFRPE  65 (166)
T ss_dssp                  EEEEEECCSS------EEEEEEEECSSSSCCEEEEEEEEECCTTSCHHHHHHHHHHHHHHHHHHCCS
T ss_pred                  EEEEEccCCC------ceEEEEEEecCCcceeEEEEEEEEECCCCCCHHHHHHHHHHHHHHHHHHCCC

Q ss_pred                  EEEEEcccCchH------HHHHHHHHHHHhccCCCCCCCccccCcccCCCCceeeccCCCCHHHhHHHHH
Q Q_7621124_2       737    MIVYEKNYGGGM------ASALITQAWAALQNEPINADTDETMIPKSANCPYVKGVSAKISKVLRAEPIA  800 (881)
Q Consensus         737    ~i~iE~~~~g~~------~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~K~~ri~~l~  800 (881)
                           .+++|....+..      ...+...+.......               +++ +..+....-|....
T Consensus         66     ~vviE~~~~~~~~~~~~~~~g~i~~~~~~~~---------------gi~-~~~v~p~~~k~~~~----  115 (166)
T 4EP4_B            66     AVAVEEQFFYRQNELAYKVGWALGAVLVAAFEA---------------GVP-VYAYGPMQVKQALA----  115 (166)
T ss_dssp                  EEEEECCCCSSCSSCHHHHHHHHHHHHHHHHHH---------------TCC-EEEECHHHHHHHHH----
T ss_pred                  EEEEeccccCCChHHHHHHHHHHHHHHHHHHHc---------------CCC-EEEECHHHHHHHHh----

Q ss_pred                  HHHHcCCeEEcccCccHHHHHHHhccCCCCC--CCCcHHHHHHHHHHh
Q Q_7621124_2       801    QAVKTGRAKFAQLGNLGSLTNEFTLWQPGST--WSPGALDAAVYGATEV  847 (881)
Q Consensus         801    ~~~~~g~i~~~~~~~~~~l~~el~~~~~~~~~---~~dD~~Dal~~~~~~~  847 (881)
                                 |.-.-..    ..+.+.+........  ..+|.+||++.+...+
T Consensus         116    -----g~~~~~k----~~~~~~~~~~~~~~~~~~~~d~aDA~~ia~~~~  155 (166)
T 4EP4_B            116    -----GHGHAAK----EEVALMVRGILGLKEAPRPSHLADALAIALTHA  155 (166)
```

```
T ss_dssp                  -----SSTTCCH----HHHHHHHHHHTTCSSCCSSHHHHHHHHHHHHHH
T ss_pred                  -----CCCCCCH----HHHHHHHHHHhCCCCCCCCCHHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDB | NCBI

86. **d1b24a1 d.95.2.1 (A:7-99) DNA endonuclease I-dmoI {Desulfurococcus mobilis [TaxId: 2274]}**

Probability: 91.52 E-value: 1.1 Score: 39.75 Aligned Cols: 63 Identities: 24% Similarity: 0.307

```
Q ss_pred                  HHHHHHHHHcCCeeCC----C--CeEEEEeCCHH--HH-----HHHHHHHHHCCCcEEEEecCCCCCCCC
Q Q_7621124_2       284    RALLAGLIDSDGTIAK----S--GQVSFINTNRR--LY-----DGVVELIRTLGYRATIHAPLQPSTSSS  340 (881)
Q Consensus         284    ~~fL~Gl~dgDG~~~~-----~--~~i~~~t~s~~--l~-------~~l~~Ll~~lGi~~~i~~~~~~~~~~  340 (881)
                           .|.+-|++-|||++..    .  -.+.+....++  ++     +.++.++.++|..+++.....+.
T Consensus         5      lAyliGi~lGDG~i~~~k~~~~~~~i~l~~~Dk~~~~~~~~v~~~~~~~l~~i~~~~i~~~~~~~----  70 (93)
T d1b24a1           5      SAYLLGLIIGDGGLYKLKYKGNRSEYRVVITQKSENLIKQHIAPLMQFLIDELNVKSKIQIVKGDT----  70 (93)
T ss_dssp                  HHHHHHHHHHSEEEEEEECSTTCEEEEEEEEESCHHHCCCCCHHHHHHHHHHTTCCCCCEEEECSS----
T ss_pred                  HHHHHHHHHcCceeeeceecCCEEEEEEEEecCChHhhhhccHHHHHHHHHHhCCCCeEEEEcCCC----

Q ss_pred                  CccCeeeEEEEEEecCC
Q Q_7621124_2       341    GVAGTRVLYRVSFTPHD  357 (881)
Q Consensus         341    ~~~~~~~~y~~~i~~~~  357 (881)
                                  +|.+.+.+..
T Consensus         71     --------~~~v~i~sk~  80 (93)
T d1b24a1           71     -------RYELRVSSKK  80 (93)
T ss_dssp                  -------CEEEEEECHH
T ss_pred                  -------EEEEEECchh
```

Template alignment | CDD

87. **PF04851.15 ; ResIII ; Type III restriction enzyme, res subunit**

Probability: 91.46 E-value: 1.6 Score: 41.7 Aligned Cols: 131 Identities: 9% Similarity: -0.012

```
Q ss_pred                  CCCCeEEEcCCccccCCChhHHHHHHHHHccCCCCeEEEeehhHHHHHHcHHHHHHHHHHHchhHCccc
Q Q_7621124_2       400    SPDGLYLVGEHMTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARRNGAAVRELVREYGPEFGLNL  469 (881)
Q Consensus         400    ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ili~s~~~~~a~~~~~~i~~~~~~~~~~~~~~  469 (881)
                           ...+.+++  .++.+.++|.....+........+  .+++++++...+......+.......  ......
T Consensus         21     ~~~~~~~i---g~~G~GKT~~~~~~~~~~~~~~~--~~~~~~~~~~~~~~~~~~~~~~~~~~~~--~~~~~~  84 (151)
T PF04851.15        21     RGNRRVLA--QLPTGAGKTICFAHICQKFFQKQQ--KVLVIAHRIELITQAAEKLEQIVGEP--VGIIKG  84 (151)
T ss_pred                  hCCCeEEE--ECCCCCCHHHHHHHHHHHHHHHcCC--cEEEEeChHHHHHHHHHHHHHHHhcCC--cceeec

Q ss_pred                  CCCCcccCceEeecCceEEEEccCCCcccCCCcEEEEeCCCCCHHHHcCHHHHHHHHHHHHHhhhcccCC
Q Q_7621124_2       470    SPDESSKTDWSIRAGGTMRSRGLRGNFTGQPMDLGIIDDPITNRAQAESLVVRDFVWDWYSSVWSQRKAP  539 (881)
Q Consensus         470    ~~~~~~~~~~~~~~~~~i~~~g~~~s~rG~~~~~ii~DE~~~~~~~~~s~~~~~~~~~~~~~~~~~~~~  539 (881)
                           .........+.+.....+....  ....+..+.++|+||+.....+.             ...+...+..
T Consensus         85     ~~~~~~~~~~~~~~~~~~~~~~--~~~~~~~~~~viiDE~~~~~~~~----------~~~l~~~~~~  139 (151)
T PF04851.15        85     GCAAHPERRIQVASIQTLARRD--ILELPLNIGLLLFDEAHHSSASS----------YRRLIEHYQE  139 (151)
T ss_pred                  CCCCCccccEEEEchHHHHhhc--hhhccCCeeEEEEecchhcCHHH----------HHHHHHhccC

Q ss_pred                  CCeEEEEccccC
Q Q_7621124_2       540    TYREVLVMTRWH  551 (881)
Q Consensus         540    ~~~~i~i~T~~~  551 (881)
                           ...+++.+||..
T Consensus         140    ~~~i~~~~tp~~  151 (151)
T PF04851.15        140    AQILGVTATPQR  151 (151)
T ss_pred                  cEEEEEEccCCC
```

Template alignment | Template 3D structure | PDBe

88. **1IV0_A hypothetical protein; hypothetical protein, RNaseH-like, YqgF, STRUCTURAL; NMR {Thermus thermophilus} SCOP: c.55.3.8**

Probability: 91.33 E-value: 5.7 Score: 35.64 Aligned Cols: 91 Identities: 11% Similarity: -0.043

```
Q ss_pred                  EEEEEeCCCCCCCcCCcEEEEEEEECCCCcEEEEeccccccCcchHHHHHHHHHHhCCCEEEEEc----
Q Q_7621124_2       677    VVVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTAVLTPLEWPRAVCLLAYERDASMIVYEK----  742 (881)
Q Consensus         677    ~~~~iD~a~~~~~~~D~tai~v~~~~~~g~~~v~~~~~~~~~~~~~~~~i~~~~~~~~~~~i~iE~----  742 (881)
                           .++|||||..      .+++++....  +.+..-.......+...+.+.+.+++++|+++.++++.
T Consensus         2      ~ilgID~G~~-------~~G~Av~~~~--~~~~~~~~~~~~~~~~~~~~l~~li~~~~~~~ivig~p~~~  63 (98)
T 1IV0_A            2      RVGALDVGEA------RIGLAVGEEG--VPLASGRGYLVRKTLEEDVEALLDFVRREGLGKLVVGLPLRT  63 (98)
T ss_dssp                  CEEEEEESSS------EEEEEEECSC--CSSCCCEEEEECCCHHHHHHHHHHHHHHHTCCEEEEECCCCC
T ss_pred                  eEEEEEeCCC------EEEEEEEeCC--CceeeeceeEecCChHHHHHHHHHHHHHhCCCEEEEeCccCC

Q ss_pred                  ccCchHHHHHHHHHHHhccCCCCCCCcccCcccCCCCceeeccCCCC
Q Q_7621124_2       743    NYGGGMASALITQAWAALQNEPINADTDETMIPKSANCPYVKGVSAKIS  791 (881)
Q Consensus         743    ~~~g~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~  791 (881)
                           .+........++...+.+...               ++| |..+.-..+
```

```
T Consensus          64     ~g~~~~~~~~~~~~~~~L~~~~----------------~i~-v~~vdE~~t  96 (98)
T 1IV0_A             64     DLKESAQAGKVLPLVEALRAR---------------GVE-VELWDERFT  96 (98)
T ss_dssp                   CSSSCCCSSTTHHHHHHHHHT---------------TCE-EEEECCSCC
T ss_pred                   CCCccHHHHHHHHHHHHHHc---------------CCC-EEEEcCCcc
```

Template alignment | Template 3D structure | PDB | NCBI

89. d4ep4a_ c.55.3.6 (A:) RuvC resolvase {Thermus thermophilus [TaxId: 300852]}

Probability: 91.16 E-value: 9.3 Score: 38.29 Aligned Cols: 138 Identities: 15% Similarity: 0.107

```
Q ss_pred                   EEEEEeCCCCCCCcCCcEEEEEEEECCCC--cEEEEecccccC--------cchHHHHHHHHHHhCCC
Q Q_7621124_2        677    VVVGVDPSGGEGARHDTAGISAVGLDEHQ--HAWFLEDRTAVLT--------PLEWPRAVCLLAYERDAS  736 (881)
Q Consensus          677    ~~~~iD~a~~~~~~~D~tai~v~~~~~~g-~~~~v~~~~~~~~~~--------~~~~~~~i~~~~~~~~~~  736 (881)
                            .++|||||..      .++++++..+..+  ..-+++...-...        ...+.+.+.++++.|+++
T Consensus          2      ~ilgiDpg~~~-------~tG~ai~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~~~~~~l~~~~~~~~p~  65 (166)
T d4ep4a_            2      VVAGIDPGIT------HLGLGVVAVEGKGALKARLLHGEVVKTSPQEPAKERVGRIHARVLEVLHRFRPE  65 (166)
T ss_dssp                   EEEEEECCSS------EEEEEEEEECSSSSSCEEEEEEEEEECCTTSCHHHHHHHHHHHHHHHHHHCCS
T ss_pred                   EEEEEccCCC------CEEEEEEEeCCCccccEEEEEEEEEECCCCCCHHHHHHHHHHHHHHHHHHCCC

Q ss_pred                   EEEEEcccCch------HHHHHHHHHHHHhccCCCCCCCccccCcccCCCCceeeccCCCCHHHhHHHHH
Q Q_7621124_2        737    MIVYEKNYGGG------MASALITQAWAALQNEPINADTDETMIPKSANCPYVKGVSAKISKVLRAEPIA  800 (881)
Q Consensus          737    ~i~iE~~~~g~~~~~~~~~~~l~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~K~~ri~~l~  800 (881)
                            .++||....+.      .+.....+...+...               +++ +..+....-|.....
T Consensus          66     ~vviE~~~~~~~~~~~~~l~~~~g~i~~~~~~~~~~~~~~~~~~~~i~~~~v~p~~~k~~~~g---  116 (166)
T d4ep4a_            66     AVAVEEQFFYRQNELAYKVGWALGAVLVAAFEA---------------GVP-VYAYGPMQVKQALAG---  116 (166)
T ss_dssp                   EEEEECCCCSSCSHHHHHHHHHHHHHHHHHHH---------------TCC-EEEECHHHHHHHHHS---
T ss_pred                   EEEEEeccCCCCChhHHHHHHHHHHHHHHHHHHc---------------CCC-EEEeCHHHHHHHHcC---

Q ss_pred                   HHHHcCCeEEcccCccHHHHHHHhccCCCCCCCCcHHHHHHHHHHHh
Q Q_7621124_2        801    QAVKTGRAKFAQLGNLGSLTNEFTLWQPGSTWSPGALDAAVYGATEV  847 (881)
Q Consensus          801    ~~~~~g~i~~~~~~~~~~l~~el~~~~~~~~~~dD~~Dal~~~~~~~  847 (881)
                                .|.-.=..   ..+.+.++..+..... .+|.+||++.++...
T Consensus          117    ----~g~~~K~~-~~~~~~~~~~~~~~~~~~~~~~~d~aDA~~ia~~~~  155 (166)
T d4ep4a_            117    ----HGHAAKEE---VALMVRGILGLKEAPR-PSHLADALAIALTHA  155 (166)
T ss_dssp                   ----STTCCHHH---HHHHHHHHTTCSSCCS-SHHHHHHHHHHHHH
T ss_pred                   ----CCCCCHHH---HHHHHHHHhCCCCCCC-CcHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe

90. 6FRE_A Replicative DNA helicase,Replicative DNA helicase; intein, protein splicing, Hint domain; 1.22A {Synechocystis sp. (strain PCC 6803 / Kazusa)}; Related PDB entries: 6FRH_B 6FRH_A 6FRG_A 1MI8_A

Probability: 91.06 E-value: 1.4 Score: 43.65 Aligned Cols: 71 Identities: 11% Similarity: 0.144

```
Q ss_pred                   CCCccccCCCCcEECC-Ccc-EEHHHcCCCCE--EECCCCC-----EEEEEEEecCC-CCeEEEEeCCCCe
Q Q_7621124_2        86     QVGKLVAHDTPVPTP-TGW-TTHGELRPGDE--VYHPSGK-----VVTVRAISADA-HASIRVSTSDGGS  145 (881)
Q Consensus          86     g~gkC~~~dt~Vlt~-~G~-~~i~~i~~gd~--v~~~~g~-----~~~v~~~~~~~-~~~~~i~t~G~~  145 (881)
                            ....|+..++.+.+. +|. .+++++..|+.  ++..++.     ...+..+.... ..++.+.+..|..
T Consensus          3      ~~~~~~~~~~~~~~~~g~~~~i~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~  72 (169)
T 6FRE_A             3      RESFAISGDSLISLASTGKRVPIKDLLGEKDFEIWAINEQTMKLESAKVSRVFCTGKKLVYTLKTRLGRT  72 (169)
T ss_dssp                   EECCCEETTCEEEETTTTEEEEGGGGTTCCSCEEEEEETTTTEEEEEECCEEEEEEEEEEEEEETTCCE
T ss_pred                   cccCCCccCCcEEEeCCCCCEEEHHHHcccCCcCEEEEEeCCCCeEEEeeeeEEEECCCceEEEEEeCCCCE

Q ss_pred                   EEECCCCeEEE
Q Q_7621124_2        146    IVVHPRHEWTV  156 (881)
Q Consensus          146    i~~T~~H~~~~  156 (881)
                            +.+|++|++++
T Consensus          73     ~~~t~~~~~~~  83 (169)
T 6FRE_A             73     IKATANARFLT  83 (169)
T ss_dssp                   EEECTTCEEEE
T ss_pred                   EEEcCCCeeee
```

Template alignment | Template 3D structure | PDBe

91. 4EFJ_B LAGLIDADG endonuclease/DNA Complex; DNA-cutting enzyme, HYDROLASE-DNA complex; 2.8A {Gibberella zeae}; Related PDB entries: 4EFJ_A 4Z1X_B 4Z1X_A

Probability: 90.95 E-value: 0.78 Score: 51.18 Aligned Cols: 146 Identities: 11% Similarity: 0.067

```
Q ss_pred                   CCCCcccchHHHHHHhcccccCCCC--------------eEEecCChHhhhhchhh-----cCeEEecCC
Q Q_7621124_2        196    GVDDTLLIDPYTLGVWLGDGSSTKA--------------AITHHADDEYVLPYPKS-----ADCVHQTTG  246 (881)
Q Consensus          196    ~~~~~~~~~~llG~~l~dG~~~~~~---------------i~~~~~~~~~~~~~~~~~-----~~~~~~~~~  246 (881)
                            .........+|++|++-|||+.-.               .+.+...+..+++.++.     .........
T Consensus          1      ~~~~~~~~~~~laGfidgdG~f~~~~~~~~~~~~~~~~~I~~~~~d~~~L~~i~~~l~~~g~i~~~~~~  70 (300)
T 4EFJ_B             1      MDLSTSINPWFVTGFTDAEGSFMIHLEKNKDKWRVRPTFQIKLDIRDKSLLEEIKNYFNNTGSINTSNKE  70 (300)
T ss_dssp                   -----CCCHHHHHHHHHHSCEEEEEEEECSSCEEEEEEEEEEEEGGGHHHHHHHHHHTTTCSEEEECSSE
T ss_pred                   CCCCCCCChhhHHHHcccccEEEEEEEEecCCceEEEEEEEEEEcccccHHHHHHHHHHhCCCcEEEecCCe
```

```
Q ss_pred                   cEEEEeCCh----HHHHHHHcCCCCCC-------------------------------------------
Q Q_7621124_2       247     VVTSYYRGG----LHTALKTLGVHANK-------------------------------------------  269 (881)
Q Consensus         247     ~~~~~~~~~----l~~~l~~~g~~~~k-------------------------------------------  269 (881)
                            ..+.+.+..    +..++........|
T Consensus         71      ~~~~i~~~~~~~~ii~~~~~~~~l~~~K~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~n~~~  140 (300)
T 4EFJ_B            71      CVYKVRSLKDISIIISHFDKYNLITQKKADFELFKKIINKLNSQEHLSYEVGATVLQEIISIRASMNLGL  140 (300)
T ss_dssp                    EEEEECSHHHHHHHHHHHHHHSCCCSTHHHHHHHHHHHHHHHHHHTCCEECSCTTHHHHHHHHHTTSTTCC
T ss_pred                    EEEEEecHHHHHHHHHHHHHhCCCCcccHHHHHHHHHHHHHHcCCCCCccccHHHHHHHHHHHHhccCC


Q ss_pred                   ------------cCCHHHHHCCHHHHHHHHHHHHHcCCeeCCC---------CeEEEEeC--CHHHHHHH
Q Q_7621124_2       270     ------------HIPVQYLRASESSRRALLAGLIDSDGTIAKS---------GQVSFINT--NRRLYDGV  316 (881)
Q Consensus         270     ------------~iP~~i~~~~~~~~~~~~~~fL~Gl~dgDG~~~~~---------~~i~~~t~--s~~l~~~l  316 (881)
                                        .++..+...+.....+||+|++||||++.-.         ..+.++..  +..++..+
T Consensus         141     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~l~Gf~D~dGsf~i~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~~~L~~i  210 (300)
T 4EFJ_B            141     SSSVKEDFPHIIPSNRPLIENMNIPHPEWMAGFVSGEGSFSVYTTSDDKYVSLSFRVSQHNKDKQLLKSF  210 (300)
T ss_dssp                    CHHHHHSCCCCCCCCCCCSCCCCCCHHHHHHHHHHHEEEEEEECTTSCCEEEEEEEEEESTTHHHHHHH
T ss_pred                    ChHHHHhCCCccCCCCCCcCCCCCCChhhHhHheeeeEEEEEEEeCCCCEEEEEEEEEEeCcccHHHHHHH


Q ss_pred                   HHHHHHCCCcEEEEecCCCCCCCCCccCeeeEEEEEEec
Q Q_7621124_2       317     VELIRTLGYRATIHAPLQPSTSSSGVAGTRVLYRVSFTP  355 (881)
Q Consensus         317     ~~Ll~~lGi~~~i~~~~~~~~~~~~~~~~~~~~~~~~~y~~~i~~  355 (881)
                            +..+..-++.......              ..|.+.+..
T Consensus         211     ~~~l~~~~i~~~~~~~~~--------------~~~~~~~i~~  235 (300)
T 4EFJ_B            211     VDFFGCGGFNYHNKGN--------------KAVIFVTRK  235 (300)
T ss_dssp                    CCCCCSCEEEESSTTC--------------SEEEEEECC
T ss_pred                    HHHHCCCcEEEecCCC--------------ceEEEEEec
```

92\. [Template alignment](#) | [Template 3D structure](#) | [PDBe](#)

4E2U_A Pho radA intein; HINT-fold, UNKNOWN FUNCTION; 1.582A {Pyrococcus horikoshii}; Related PDB entries: 4E2T_B 4E2T_A 2LQM_A

Probability: 90.85 E-value: 2.6 Score: 41.36 Aligned Cols: 90 Identities: 19% Similarity: 0.172

```
Q ss_pred                   CCCccccCCCcEECCCccE----EHHHc--------------------CCCCEEECCCCC-----EEEEE
Q Q_7621124_2       86      QVGKLVAHDTPVPTPTGWT----THGEL--------------------RPGDEVYHPSGK-----VVTVR  126 (881)
Q Consensus         86      g~gkC~~~dt~Vlt~~G~~----~i~~i--------------------~~gd~v~~~~g~-----~~~v~  126 (881)
                            .++.|+.++|.|.+.+|..    .|+++                    ..+..++..+..     +.++.
T Consensus         1       ~~~~c~~~~t~v~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~v~  70 (168)
T 4E2U_A            1       SQHMAFARDTEVYYENDTVPHMESIEEMYSKYASMNGELPFDNGYAVPLDNVFVYTLDIASGEIKKTRAS  70 (168)
T ss_dssp                    CCSCCEETTCEEEEEETTEEEEEEHHHHHHHHHHHHCCEEETTEEEEECSSEEEEEECTTTCCEEEEECC
T ss_pred                    CCCccccCCCCEEEEecCCcceEeeHHHHHHHHHhccCCccccCCceEEecCCeEEEEEECCCCeEEEEEce


Q ss_pred                   EEecCC-CCeEEEEeCCCCeEEECCCCeEEEEeCCCCeEEEcchHHHhhheee
Q Q_7621124_2       127     AISADA-HASIRVSTSDGGSIVVHPRHEWTVWDRNRKRWSTMETGDMMRRAYV  178 (881)
Q Consensus         127     ~~~~~~-~~~~~i~t~~G~~i~~T~~H~~~~~~~~~~~~~~~~~~~~~~~l~~~~~~  178 (881)
                            ..+...  ..++++.+..|..+.+|++|+++.....  ..|..  ..++..++++
T Consensus         71      ~~~~~~~~~~~~~~~~~~~~~~~~t~~~~~~~~~~~~~~-~~~~~--~~~~~~~~~~l  120 (168)
T 4E2U_A            71      YIYREKVEKLIEIKLSSGYSLKVTPSHPVLLFRDG-LQWVP--AAEVKPGDVV  120 (168)
T ss_dssp                    EEEEEEEEEEEEEEETTSCEEEECTTCEEEEESSS-EEEEE--GGGCCTTCEE
T ss_pred                    EEEEccCCceEEEEeCCCCEEEECCCCceEEeeCC-eEEEE--HHHCCCCCEE
```

93\. [Template alignment](#) | [CDD](#)

PF02500.15 ; DNA_pack_N ; Probable DNA packing protein, N-terminus

Probability: 90.72 E-value: 2.2 Score: 46.5 Aligned Cols: 91 Identities: 12% Similarity: 0.05

```
Q ss_pred                   CeEEEcCCccccCCChhHHhhHHHHHHccCCCCeEEEeehhHHHHHHcHHHHHHHHHHHchHhCcccCCC
Q Q_7621124_2       403     GLYLVGEHMTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARRNGAAVRELVREYGPEFGLNLSPD  472 (881)
Q Consensus         403     ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ili~s~~~~~a~~~~~~i~~~~~~~~~~~~~~~~~~~~~~~~  472 (881)
                            ...++  ..++.+++|........+.+...++..|++++++.+||...++.+...+....+......
T Consensus         176     r~~vi--~vpRr~GKT~l~a~li~~l~~~~~g~~I~~vA~~~~qA~~vF~~i~~~l~~~~p~l~~~~---  240 (272)
T PF02500.15        176     KASVF--LIPRRHGKTWIVVAIISMLLASVENINIGYVAHQKHVANSVFAEIIKTLCRWFPPKNLNI---  240 (272)
T ss_pred                    ceEEE--EecCcCCHHHHHHHHHHHHHHHhcCCCCcEEEEEEECCHHHHHHHHHHHHHHHHHHHhCCCcCcEE---


Q ss_pred                   CcccCceEee--cC--ceEEEEccC--CCccc
Q Q_7621124_2       473     ESSKTDWSIR--AG--GTMRSRGLR--GNFTG  498 (881)
Q Consensus         473     ~~~~~~~~~~~~--~~--~~i~~~g~~--~s~rG  498 (881)
                            ......|.+.  +|  +.+.+.+..  +++||
T Consensus         241     ~~~~~~I~~~~~~nG~~S~i~~aS~~n~~siRG  272 (272)
T PF02500.15        241     KKENGTIIYTRPGGRSSSLMCATCFNKNSIRG  272 (272)
T ss_pred                    ecCCCEEEEeCCCCCeEEEEEeeCCCCCCcCC
```

Template alignment | Template 3D structure | PDBe

94. **4KL5_B DNA polymerase III, alpha subunit; HINT, intein, NpuDnaE inten, UNKNOWN; HET: CIT; 1.72A {Nostoc punctiforme} SCOP: b.86.1.0, l.1.1.1; Related PDB entries: 4KL6_C 4KL6_D 4KL6_A 4KL6_B 4KL5_A 2KEQ_A**

Probability: 90.67 E-value: 2.0 Score: 40.54 Aligned Cols: 69 Identities: 16% Similarity: 0.172

```
Q ss_pred                CCccccCCCcEECCCcc-EEHHHcCCCC---EEECCCCC-----EEEEEEEecCC-CCeEEEEeCCCCeE
Q Q_7621124_2       87   VGKLVAHDTPVPTPTGW-TTHGELRPGD---EVYHPSGK-----VVTVRAISADA-HASIRVSTSDGGSI  146 (881)
Q Consensus         87   ~gkC~~~dt~Vlt~~G~-~~i~~i~~gd----v~~~~g~------~~~v~~~~~~-~~~~~i~t~~G~~i  146 (881)
                         ++.|+..++.+.+.+|. ..++++..|+   .++..+ .     ...+..++... ..++.+.+..|..+
T Consensus         1    ~~~~~~~~t~~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~  69 (144)
T 4KL5_B            1    SGGALSYETEILTVEYGLLPIGKIVEKRIECTVYSVD-NNGNIYTQPVAQWHDRGEQEVFEYCLEDGSLI  69 (144)
T ss_dssp                -CCCEETTCEEEETTTEEEEHHHHHHTTCCCEEEEEC-TTSCEEEEECCEEEEEEEEEEEEEETTSCEE
T ss_pred                CCCCcCCCCEEEeCCCcEEEHHHHhhccCCeEEEEEC-CCCCEEEEeccEeEeCCCcCEEEEEeCCCCEE

Q ss_pred                EECCCCeEEE
Q Q_7621124_2       147  VVHPRHEWTV  156 (881)
Q Consensus         147  ~~T~~H~~~~  156 (881)
                         .+|++|++++
T Consensus         70   ~~t~~~~~~~  79 (144)
T 4KL5_B            70   RATKDHKFMT  79 (144)
T ss_dssp                EECTTCEEEC
T ss_pred                EECCCCeEEe
```

Template alignment | CDD

95. **PF02562.16 ; PhoH ; PhoH-like protein**

Probability: 90.26 E-value: 1.5 Score: 44.78 Aligned Cols: 131 Identities: 10% Similarity: -0.038

```
Q ss_pred                CCCeEEEcCCccccCCChhHHHhHHHHHHccCCCCeEEEeehhHHHHHHc-------HHHHHHHHHHHch
Q Q_7621124_2       401  PDGLYLVGEHMTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARRN-------GAAVRELVREYGP  463 (881)
Q Consensus         401  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  463 (881)
                         .....++  .++++.++|........+.....+...+++++++...+..+       ...+.........
T Consensus         18   ~~~~~~i--~g~~GsGKT~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  85 (205)
T PF02562.16        18   KHDITFG--IGPAGTGKTYLAVACAVDALERELVSRVILVRPAVEAGERLGFLPGDMVQKVDPYLRPLYD  85 (205)
T ss_pred                hCCEEEE--ECCCCCCHHHHHHHHHHHHHHcCCCCeEEEEecCccccccCCCCCCChhHHHHHHHHHHH

Q ss_pred                HhCcccCCCCcccCceEeecCceEEEEccCCCcccCCCcEEEEeCCCCCHHHHcCHHHHHHHHHHHHHh
Q Q_7621124_2       464  EFGLNLSPDESSKTDWSIRAGGTMRSRGLRGNFTGQPMDLGIIDDPITNRAQAESLVVRDFVWDWYSSVW  533 (881)
Q Consensus         464  ~~~~~~~~~~~~~~~~~~~~~~i~~~g~~~s~rG~~~~~ii~DE~~~~~~~~~s~~~~~~~~~~~~~~~  533 (881)
                         ..   ...............+.............+.+.+++|+||+.......              ...+
T Consensus         86   ~~---~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~liiDE~~~~~~~~~-------------~~~~  139 (205)
T PF02562.16        86   AL---YDLMGFEKVSKHFERGIIEIAPLAFMRGRTLNQSFIILDEAQNTTAEQ-------------MKMF  139 (205)
T ss_pred                HH---HHhhCHHHHHHHHHcCCEEEeehHHHCCCCCCCcEEEEECcccCCHHH-------------HHHH

Q ss_pred                hcccCCCCeEEEEccc
Q Q_7621124_2       534  SQRKAPTYREVLVMTR  549 (881)
Q Consensus         534  ~~~~~~~~~~i~i~T~  549 (881)
                         ...+.++.+++++|||
T Consensus         140  ~~~~~~~~~~~l~g~~  155 (205)
T PF02562.16        140  LTRIGFGSKAVITGDI  155 (205)
T ss_pred                HHhccCCCEEEEECCH
```

Template alignment | Template 3D structure | PDB | NCBI

96. **d1rifa_ c.37.1.23 (A:) DNA helicase UvsW {Bacteriophage T4 [TaxId: 10665]}**

Probability: 89.95 E-value: 1.8 Score: 47.79 Aligned Cols: 141 Identities: 6% Similarity: -0.016

```
Q ss_pred                CCeEEEcCCccccCCChhHHHhHHHHHHHccCCCCeEEEeehhHHHHHHcHHHHHHHHHHHchHhCcccCC
Q Q_7621124_2       402  DGLYLVGEHMTPTHNSTRVSQWFPFWWLTIRPFDRILMASAEATLARRNGAAVRELVREYGPEFGLNLSP  471 (881)
Q Consensus         402  ~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  471 (881)
                         .+..++  .++.+.++|........+.+.. ...++++++++..++......+...........+.....
T Consensus         128  ~~~~il--~~~~tGsGKT~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  194 (282)
T d1rifa_           128  NRRRIL--NLPTSAGRSLIQALLARYYLEN-YEGKILIIVPTTALTTQMADDFVDYRLFSHAMIKKIGGG  194 (282)
T ss_dssp                HSEEEE--CCCTTSCHHHHHHHHHHHHHHHH-CSSEEEEECSSHHHHHHHHHHHHHHTSCCGGGEEECSTT
T ss_pred                cCCEEE--EcCCCCCHHHHHHHHHHHHHHh-CCCcEEEEecCHHHHHHHHHHHHHhcccccccEEEEeCC

Q ss_pred                CCcccCceEeecCceEEEEccCCCcc-----cCCCCcEEEEeCCCCCHHHHcCHHHHHHHHHHHHhhhcc
Q Q_7621124_2       472  DESSKTDWSIRAGGTMRSRGLRGNFT-----GQPMDLGIIDDPITNRAQAESLVVRDFVWDWYSSVWSQR  536 (881)
Q Consensus         472  ~~~~~~~~~~~~~~~i~~~g~~~s~r-----G~~~~~ii~DE~~~~~~~~~s~~~~~~~~~~~~~~~~~~  536 (881)
                         .......   ..+..|...+...-..     +.+++++|+||++......            +...+..+
T Consensus         195  ~~~~~~~---~~~~~~i~v~t~~~l~~~~~~~~~~~~~vivDEah~~~~~~~~~~~~~~~~~~~~~l~~~  249 (282)
T d1rifa_           195  ASKDDKY---KNDAPVVVGTWQTVVKQPKEWFSQFGMMMNDECHLATGKS------------ISSIISGL  249 (282)
T ss_dssp                CSSTTCC---CTTCSEEEECHHHHTTSCGGGGGGEEEEEEETGGGCCHHH------------HHHHTTTC
```

```
T ss_pred                  CCccccc---cCCCCEEEEcHHHHHhChHHHHHcCCEEEEeChhhcCccc------------HHHHHHHh

Q ss_pred                  cCCCCeEEEEccccCcccHHHHHH
Q Q_7621124_2       537    KAPTYREVLVMTRWHQDDLAGRLL  560 (881)
Q Consensus         537    ~~~~~~~i~i~T~~~~~d~~~~l~  560 (881)
                           .....++++.+||.....-+..++
T Consensus         250    ~~~~~~i~ltaTp~~~~~~~~~~  273 (282)
T d1rifa_           250    NNCMFKFGLSGSLRDGKANIMQYV  273 (282)
T ss_dssp                  TTCCEEEEECSSCCTTSTTHHHHH
T ss_pred                  ccCcEEEEEEeeCCchHHHHHHHh
```

Template alignment | Template 3D structure | PDBe

97. **1OA8_D ATAXIN-1; RNA BINDING, HIGH MOBILITY GROUP; 1.7A {HOMO SAPIENS} SCOP: b.145.1.1; Related PDB entries: 1OA8_C 1OA8_B 1OA8_A 4J2J_A 4J2J_B 4J2J_C 4J2L_B 4J2L_A 4AQP_D 4AQP_C 4AQP_B 4AQP_A 2M41_B 4APT_D 4APT_C 4APT_B 4APT_A**

Probability: 89.85 E-value: 4.2 Score: 38.45 Aligned Cols: 74 Identities: 15% Similarity: 0.147

```
Q ss_pred                  eCCCCCccccCCCcEECCCc-cEEHHHcCCCCEEECCCCCE------EEEEEEecCC-CCeEEEEeCCCC
Q Q_7621124_2       83     TPSQVGKLVAHDTPVPTPTG-WTTHGELRPGDEVYHPSGKV------VTVRAISADA-HASIRVSTSDGG  144 (881)
Q Consensus         83     g~~g~gkC~~~dt~Vlt~~G-~~~i~~i~~gd~v~~~~g~~-------~~v~~~~~~-~~~~~i~t~~G~  144 (881)
                           .......|+..++.+.+..| ..+|+++..|+.+....+..      ..+..... ...+.+.+..+.
T Consensus         6      ~~~~~~~~~~g~~~~~~g~~~~i~~~~~g~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~  75 (133)
T 10A8_D            6      APPTLPPYFMKGSIIQLANGELKKVEDLKTEDFIQSAEISNDLKIDSSTVERIEDSHSPGVAVIQFAVGE  75 (133)
T ss_dssp                  STTTSCCGGGTTCEEECTTSCEEEGGGCCHHHHHHHHHHCSSEEEEEEEEEEEEEECSSTTEEEEEEEETT
T ss_pred                  CCCCCCCcccCCCCEEEcCCCCEEEHHHCCcccEEEecccCCCCceeeeEEEEEEcCCCCCeEEEEEEeCC

Q ss_pred                  -----eEEECCCCeEEE
Q Q_7621124_2       145    -----SIVVHPRHEWTV  156 (881)
Q Consensus         145    ------~i~~T~~H~~~~  156 (881)
                                .+.+|++|++++
T Consensus         76     ~~~~~~~~~~~~~~~~  92 (133)
T 10A8_D            76     HRAQVSVEVLVEYPFFV  92 (133)
T ss_dssp                  TTEEEEEEEETTCCEEE
T ss_pred                  CcceeEEEEcccccEEE
```

Template alignment | Template 3D structure | PDB | NCBI

98. **d1dq3a3 d.95.2.2 (A:129-226) PI-Pfui intein {Pyrococcus furiosus [TaxId: 2261]}**

Probability: 89.82 E-value: 2.0 Score: 38.23 Aligned Cols: 71 Identities: 14% Similarity: 0.142

```
Q ss_pred                  HHHHHHHHHHHHHcCCeeCCCC-----------eEEEEeCCHHHHHHHHHHHHHCCCcEEEEecCCCCCC
Q Q_7621124_2       280    ESSRRALLAGLIDSDGTIAKSG-----------QVSFINTNRRLYDGVVELIRTLGYRATIHAPLQPSTS  338 (881)
Q Consensus         280    ~~~~~~fL~Gl~dgDG~~~~~~~~~~~~~~~~~i~~~t~s~~l~~~l~~Ll~~lGi~~~i~~~~~~~~~  338 (881)
                           .....++|-||+.||||.....           +++++...++++..|+.+|.+++.......+
T Consensus         7      ~~~fL~WlIGf~eGDGsf~~~~~~~~~~~~~~~rf~I~~~d~~vL~kIr~~Lg~~FG~v~~~~~------  70 (98)
T d1dq3a3           7      KFIFDYWLAGFIAGDGCFDKYHSHVKGHEYIYDRLRIYDYRIETFEIINDYLEKTFGRKYSIQK------  70 (98)
T ss_dssp                  CCCHHHHHHHHHHHHEEEEEEEECCBTTBCCEEEEEEEEESCHHHHHHHHHHHHHHSCCCCCEE------
T ss_pred                  chhHHHHHHHHHcccceeeeeccccCCCCcceeEEEEEEcCCHHHHHHHHHHHHHhhCeEEEEec------

Q ss_pred                  CCCccCeeeEEEEEEecCCCCCCc
Q Q_7621124_2       339    SSGVAGTRVLYRVSFTPHDGIPPA  362 (881)
Q Consensus         339    ~~~~~~~~~~y~~~i~~~~~~~~f  362 (881)
                                 ....|++.+.....+..|
T Consensus         71     ------~~~~~~~~~v~~r~~v~~l  88 (98)
T d1dq3a3           71     ------DRNIYYIDIKARNITSHY  88 (98)
T ss_dssp                  ------SSSCEEEEECCHHHHHHH
T ss_pred                  ------CCCeEEEEEecchHHHHH
```

Template alignment | Template 3D structure | PDBe

99. **5K08_A RecA mini intein; cisplatin, Zeise's salt, inhibitor, intein; HET: TCE; 1.401A {Mycobacterium tuberculosis}; Related PDB entries: 5I0A_A 3IFJ_A 2IN8_A 2IN0_A 2IN9_A 3IGD_A 2L8L_A 3IFJ_B**

Probability: 89.8 E-value: 2.5 Score: 39.73 Aligned Cols: 66 Identities: 20% Similarity: 0.238

```
Q ss_pred                  cccCCCCcEECC-Ccc-EEHHHcCCCCE---EECCCCC-----EEEEEEEecCC-CCeEEEEeCCCCeEEE
Q Q_7621124_2       90     LVAHDTPVPTP-TGW-TTHGELRPGDE---VYHPSGK-----VVTVRAISADA-HASIRVSTSDGGSIVV  148 (881)
Q Consensus         90     C~~~dt~Vlt~-~G~-~~i~~i~~gd~---v~~~~g~-------~~~v~~~~~~-~~~~~i~t~~G~~i~~  148 (881)
                           |+..++.+.+. +|. ..++++..|+.   ++..+ .     ...+..+.... ..++.+.+..|..+.+
T Consensus         1      ~~~~~~~~~~~~g~~~~i~~~~~~~~~~~~~~~~-~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~~~  69 (142)
T 5K08_A            1      CLAEGTRIFDPVTGTTHRIEDVVDGRKPIHVVAAA-KDGTLHARPVVSWFDQGTRDVIGLRIAGGAILWA  69 (142)
T ss_dssp                  CEETTCEEECTTTCCEEEHHHHHHHTTCCCEEEEEC-TTSCEEEEEEEEEEEEEEEEEEEEETTSCEEEE
T ss_pred                  CCCCCCEEEcCCCCcEEEHHHhccCCCCeEEEEEC-CCCCEEEEeceEEEeCCCCcEEEEEECCCCEEEE

Q ss_pred                  CCCCeEEE
```

```
Q Q_7621124_2       149    HPRHEWTV  156 (881)
Q Consensus         149    T~~H~~~~  156 (881)
                           |++|++++
T Consensus         70     t~~~~~~~  77 (142)
T 5K08_A            70     TPDHKVLT  77 (142)
T ss_dssp                  CTTCEEEE
T ss_pred                  CCCCeeec
```

Template alignment | CDD

100. **PF02075.17 ; RuvC ; Crossover junction endodeoxyribonuclease RuvC**

Probability: 89.8 E-value: 8.6 Score: 37.41 Aligned Cols: 133 Identities: 12% Similarity: 0.055

```
Q ss_pred                  EEEEeCCCCCCCcCCcEEEEEEEECCCCcEEEEecccccCcch-------HHHHHHHHHHHhCCCEEEE
Q Q_7621124_2       678    VVGVDPSGGEGARHDTAGISAVGLDEHQHAWFLEDRTAVLTPLE-------WPRAVCLLAYERDASMIVY  740 (881)
Q Consensus         678    ~~~iD~a~~~~~~~D~tai~v~~~~~~g~~~v~~~~~~~~~~~~~-------~~~~i~~~~~~~~~~~i~i  740 (881)
                           ++|||||..      .++++++... .+.+.+++...-..+...       +.+.+.+++++|+++.|++
T Consensus         1      ilgiD~g~~-------~~G~av~~~~-~~~~~~~~~~~~~~~~~~~~~r~~~~~~~l~~~i~~~~~~~ivi  63 (148)
T PF02075.17        1      ILGIDPGSR------KCGYAIISHA-SNKLSLITAGFINITTTRLQEQILDLIEALDCLLDRYEVNEVAI  63 (148)
T ss_pred                  CeEEccCCC------ceEEEEEEec-CCeeEEEEEeEEecCCCCHHHHHHHHHHHHHHHHHHcCCCEEEE

Q ss_pred                  EcccCchHH------HHHHHHHHHHhccCCCCCCccccCcccCCCCceeeccCCCCHHHHhHHHHHHHH
Q Q_7621124_2       741    EKNYGGGMA------SALITQAWAALQNEPINADTDETMIPKSANCPYVKGVSAKISKVLRAEPIAQAVK  804 (881)
Q Consensus         741    E~~~~g~~~-------~~~l~~~~~~~~~~~~~~~~~~~~~~~~~i~~~~~~~~K~~ri~~l~~~~~  804 (881)
                           |....+...      ..+...+...+...               +++ +..+....-|....
T Consensus         64     E~~~~~~~~~~~~~~~~~g~i~~~~~~~----------~~~-v~~v~~~~~k~~~~~~~~~~  109 (148)
T PF02075.17        64     EDIFFGYNPKSVIKLAQFRGALSLKILER---------------IGN-FSEYTPLQVKKALT--------  109 (148)
T ss_pred                  ecccCCCCHHHHHHHHHHHHHHHHHHHh---------------CCc-eEEeCHHHHHHHh--------

Q ss_pred                  cCCeEEcccCccHHHHHHHhccCCCCC--CCCcHHHHHHHHHH
Q Q_7621124_2       805    TGRAKFAQLGNLGSLTNEFTLWQPGST--WSPGALDAAVYGATE  846 (881)
Q Consensus         805    ~g~i~~~~~~~~~~l~~el~~~~~~~~-~~~dD~~Dal~~~~~~  846 (881)
                            |.-.-..    ..+.+.+..+.....  ..+|.+||++.++..
T Consensus         110    -~~~~~~K----~~~~~~~~~~~~~~~~~~~~d~aDA~~i~~~~  148 (148)
T PF02075.17        110    -GNGKAAK----EQVAFMVKRLLNITSEIKPLDISDAIAVAITH  148 (148)
T ss_pred                  -CCCCCCH----HHHHHHHHHHhCCCCCCCCChHHHHHhhHhcC
```

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