



(/#!/)

## HHpred ?

Created: Jul 20, 2017 3:36 PM

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

InputParametersResults (/api/job/result/1419573/hhpred/Results)



Raw Output (HHR) (/api/job/result/1419573/hhpred/Raw Output (HHR))



Number of hits: **250**



Probability Plot (/api/job/result/1419573/hhpred/Probability Plot)



Query Template MSA (/api/job/result/1419573/hhpred/Query Template MSA)



## Visualization

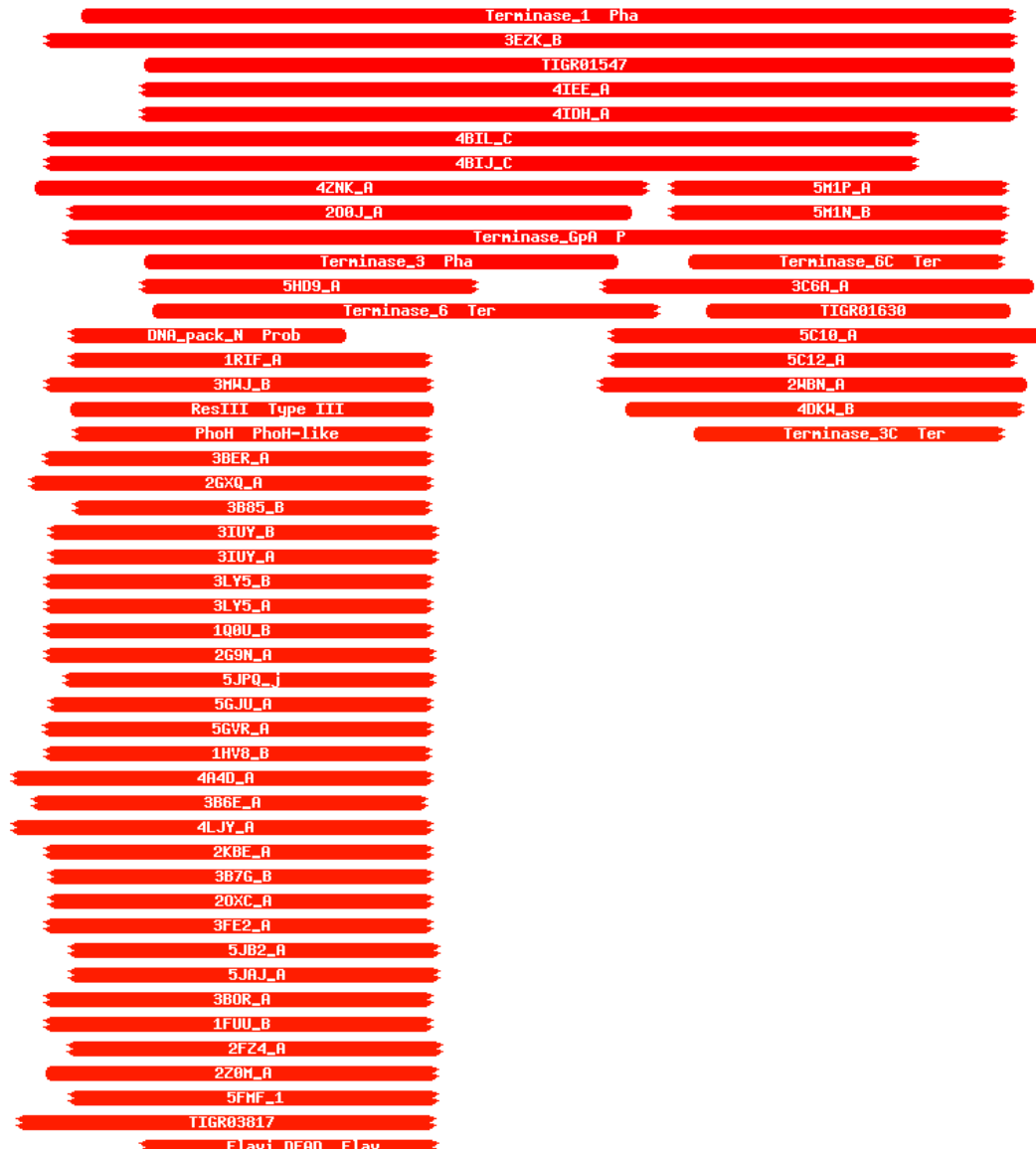
Query MSA (/api/job/result/1419573/hhpred/Query MSA)

[Resubmit section](#)



35

480



[Vis](#)[Hits](#)[Aln](#)[Select all](#)[Forward](#)[Forward Query MSA](#)[Color Seqs](#)[Unwrap Seqs](#)

	2J0U_A
	1UJ_A
	5SUP_B
	1M36_D
	TIGR04895
	3DKP_A
	2PL3_A
	1VEC_B
	5IVL_B
	3PEY_A
	5LD2_D
	4A4Z_A
	30IY_B
	3FHT_B
	1Z63_B
	5SUQ_C
	4CT4_B
	TIGR00643
	1Z6A_A
	3TBK_A
	2DB3_A
	5JC3_B
	3LLM_A
	5JC3_A
	4M7S_B
	4M7S_A
	3P4X_B
	4XGT_A
	5DZR_A
	4D26_A
	4D25_A
	TIGR00580
	2EYQ_A
	5AGA_A
	1S2H_A
	4C9B_A
	2ZJ8_A
	3G0H_A
	2P6R_A
	2FMR_A
	TIGR00603
	1GM5_A
	2XGJ_A
	2I4I_A
	TIGR04121
	3FH0_B
	4A36_B
	1MF9_A
	1MP9_E
	4U4C_A
	TIGR00348
	1T6N_A
	5DTU_A
	3SQM_A
	5XDR_A
	4QQH_A
	4QQH_G
	4TYN_A
	5FFJ_A
	5FFJ_B
	3DHQ_A
	TIGR02621
	3H1T_A
	2VA8_B
	Helicase_RecD_H
	3I5X_A
	DEAD_DEAD/DEAH
	2Z83_A
	4NHQ_A
	TIGR01447
	5LJ5_Q
	5MSG_e
	5GM6_Y
	5LQM_O
	1Z3I_X
	TIGR01448
	5HQF_q
	4CBH_B
	2JLU_B
	4DDV_B
	4DDU_A
	5AOR_A

[Vis](#)[Hits](#)[Aln](#)[Select all](#)[Forward](#)[Forward Query MSA](#)[Color Seqs](#)[Unwrap Seqs](#)

4F91_B
3E1S_A
3GP8_A
5H2R_A
4XJX_A
4Q2D_A
4Q2C_A
2M74_B
4F91_B
5DCA_A
4XQK_A
4Q47_A
4Q48_B
1OYM_A
5JMH_A
5DCA_A
5M59_E
5M59_G
TIGR00614
3MHY_M
1MRB_A
5M59_E
5M59_G
5JXR_A
TIGR03714
TIGR04397
AAA_19 AAA domai
4CBL_A
TIGR01389
5EAN_A
TIGR04221
1GL9_B
308B_B
2ZPA_B
AAA_34 P-loop co
TIGR01054
TIGR01587
TIGR00963
1GKU_B
TIGR02562
1YKS_A
3UPU_A
AAA_11 AAA domai
5B7I_A
3JB9_X
2FSF_B
UTP25 Utp25, U3
5X0X_0
4PJ3_A
TIGR01967
4NL4_H
2VDA_A
3KGN_A
1M74_A
3JUX_A
4UHQ_A
4YS0_A
TIGR01970
2XZL_A
SecA_DEAD SecA
2IPC_A
2IPC_D
2MHX_A
2VBC_A
3BXZ_B
5LTJ_A
5D0U_A
TIGR02768
3VKW_A
2XZ0_A
2XZP_A
TIGR00376
UvrD-helicase U
1TF5_A
AAA_30 AAA domai
4N0N_A
5M2N_A
3RC0_A
3RC3_A
4B3F_X
SNF2_N SNF2 fan
1NKT_A
4NL2_A

Align

Select all

Forward

Forward Query MSA

Color Seqs

Unwrap Seqs

2MY\_A

2P3C\_A

4ZCF\_C

TIGR02760

Podovirus\_Gp16

TIGR02760

TIGR00631

5FTB\_A

403H\_A

3U4Q\_A

4CEJ\_A

5FMF\_Y

2VL7\_A

TIGR01073

Herpes\_ori\_bp 0

1UAA\_B

1UAA\_A

5MQ0\_V

5FTF\_A

1D2H\_A

1C40\_A

TIGR01075

5IY9\_H

5IVW\_H

4C2U\_D

TIGR02785

TIGR01074

5LB3\_B

Hitlist

Show 25 entries

Nr	Hit	Name	Probability
<input type="checkbox"/>	1	PF03354.14 ( <a href="http://pfam.xfam.org/family/PF03354.14#tabview=tab0">http://pfam.xfam.org/family/PF03354.14#tabview=tab0</a> )	; Terminase_1 ; Phage Terminase  100
<input type="checkbox"/>	2	3EZK B ( <a href="http://pdb.rcsb.org/pdb/explore.do?structureId=3EZK">http://pdb.rcsb.org/pdb/explore.do?structureId=3EZK</a> )	DNA packaging protein Gp17; pentameric motor, DNA packaging, Alternative; 34.0A {Bacteriophage T4}  99.95
<input type="checkbox"/>	3	TIGR01547 ( <a href="http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR01547">http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR01547</a> )	phage_term_2; phage terminase, large subunit, PBSX family. This model detects members of a highly divergent family of the large subunit of phage terminase.  99.95
<input type="checkbox"/>	4	4IEE A ( <a href="http://pdb.rcsb.org/pdb/explore.do?structureId=4IEE">http://pdb.rcsb.org/pdb/explore.do?structureId=4IEE</a> )	Gene 2 protein; DNA packaging, terminase, ATPase, nuclease; HET: AGS; 1.89A {Shigella phage Sf6}  99.94

[Vis](#)[Hits](#)[Align](#)[Help](#)[Select all](#)[Forward](#)[Forward Query MSA](#)[Color Scales](#)[Unwrap Sequences](#)[Probability](#)

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[4IDH A \(http://pdb.rcsb.org/pdb/explore.do?structureId=4IDH\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4IDH)

Gene 2 protein;  
DNA packaging,  
terminase,  
ATPase, nuclease;  
1.69Å {Shigella  
phage Sf6}

99.94



6

[4BIL C \(http://pdb.rcsb.org/pdb/explore.do?structureId=4BIL\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4BIL)

DNA MATURASE B;  
HYDROLASE,  
PACKAGING  
MOTOR,  
CONNECTOR,  
DNA; 29.0Å  
{ENTEROBACTERIA  
PHAGE T7}

99.91



7

[4BIJ C \(http://pdb.rcsb.org/pdb/explore.do?structureId=4BIJ\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4BIJ)

DNA MATURASE B;  
HYDROLASE,  
ATPASE, DNA  
TRANSLOCATION,  
SINGLE-PARTICLE;  
16.0Å  
{ENTEROBACTERIA  
PHAGE T7}

99.91



8

[4ZNK A \(http://pdb.rcsb.org/pdb/explore.do?structureId=4ZNK\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4ZNK)

Phage terminase  
large subunit;  
DNA  
Translocation,  
VIRAL PROTEIN;  
HET: SO4; 1.931Å  
{Thermus phage  
P7426}

99.66



9

[2O0I A \(http://pdb.rcsb.org/pdb/explore.do?structureId=2O0I\)](http://pdb.rcsb.org/pdb/explore.do?structureId=2O0I)

DNA packaging  
protein Gp17;  
nucleotide-  
binding fold,  
HYDROLASE; HET:  
ADP; 1.8Å  
{Enterobacteria  
phage T4}

99.65



10

[PF05876.11  
\(http://pfam.xfam.org/family/PF05876.11#tabview=tab0\)](http://pfam.xfam.org/family/PF05876.11#tabview=tab0)

; Terminase\_GpA ;  
Phage terminase  
large subunit  
(GpA)

99.58



11

[PF04466.12  
\(http://pfam.xfam.org/family/PF04466.12#tabview=tab0\)](http://pfam.xfam.org/family/PF04466.12#tabview=tab0)

; Terminase\_3 ;  
Phage terminase  
large subunit

99.5



12

[3C6A A \(http://pdb.rcsb.org/pdb/explore.do?structureId=3C6A\)](http://pdb.rcsb.org/pdb/explore.do?structureId=3C6A)

Terminase large  
subunit;  
terminase  
nuclease, VIRAL  
PROTEIN; 1.16Å  
{Enterobacteria  
phage RB49}

99.21

Align	Hits	Select all	Forward	Forward Query MSA	Color Segs	Unwrap Spans	Probability
<input type="checkbox"/>	13	<a href="http://pdb.rcsb.org/pdb/explore.do?structureId=5M1P">5M1P A (http://pdb.rcsb.org/pdb/explore.do?structureId=5M1P)</a>				Terminase large subunit; large terminase, nuclease domain, Hydrolase; 1.1A {Thermus phage G20c}	99.13
<input type="checkbox"/>	14	<a href="http://pdb.rcsb.org/pdb/explore.do?structureId=5M1N">5M1N B (http://pdb.rcsb.org/pdb/explore.do?structureId=5M1N)</a>				Large terminase protein; large terminase, nuclease domain, viral; HET: SO4, BTB; 1.2A {Thermus phage G20c}	99.13
<input type="checkbox"/>	15	<a href="http://pfam.xfam.org/family/PF03237.14#tabview=tab0">PF03237.14 (http://pfam.xfam.org/family/PF03237.14#tabview=tab0)</a>				; Terminase_6 ; Terminase-like family	98.89
<input type="checkbox"/>	16	<a href="http://pdb.rcsb.org/pdb/explore.do?structureId=5HD9">5HD9 A (http://pdb.rcsb.org/pdb/explore.do?structureId=5HD9)</a>				Encapsidation protein; ASCE fold, VIRAL PROTEIN; HET: MSE; 1.941A {Bacillus phage phi29}	98.86
<input type="checkbox"/>	17	<a href="http://pdb.rcsb.org/pdb/explore.do?structureId=5C10">5C10 A (http://pdb.rcsb.org/pdb/explore.do?structureId=5C10)</a>				Gene 2 protein; nuclease domain, metal binding site; 1.55A {Enterobacteria phage Sf6}	98.84
<input type="checkbox"/>	18	<a href="http://pdb.rcsb.org/pdb/explore.do?structureId=5C12">5C12 A (http://pdb.rcsb.org/pdb/explore.do?structureId=5C12)</a>				Gene 2 protein; nuclease domain, metal binding site; 1.517A {Enterobacteria phage Sf6}	98.81
<input type="checkbox"/>	19	<a href="http://pdb.rcsb.org/pdb/explore.do?structureId=2WBN">2WBN A (http://pdb.rcsb.org/pdb/explore.do?structureId=2WBN)</a>				TERMINASE LARGE SUBUNIT; LARGE TERMINASE, NUCLEASE, VIRAL PROTEIN; 1.9A {BACILLUS PHAGE SPP1}	98.68
<input type="checkbox"/>	20	<a href="http://pfam.xfam.org/family/PF02500.14#tabview=tab0">PF02500.14 (http://pfam.xfam.org/family/PF02500.14#tabview=tab0)</a>				; DNA_pack_N ; Probable DNA packing protein, N-terminus	98.53
<input type="checkbox"/>	21	<a href="http://pfam.xfam.org/family/PF17289.1#tabview=tab0">PF17289.1 (http://pfam.xfam.org/family/PF17289.1#tabview=tab0)</a>				; Terminase_6C ; Terminase RNaseH-like domain	98.4

Align	Hit	Select all	Forward	Forward Query MSA	Color Segs	Unwrap Segs	Probability
<input type="checkbox"/>	22	<a href="http://pdb.rcsb.org/pdb/explore.do?structureId=1RIF">1RIF A (http://pdb.rcsb.org/pdb/explore.do?structureId=1RIF)</a>				DNA helicase uvsW; Bacteriophage, T4, Helicase, UvsW, RecG; 2.0A {Enterobacteria phage T4} SCOP: c.37.1.23	98.33
<input type="checkbox"/>	23	<a href="http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR01630">TIGR01630 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR01630)</a>				psiM2_ORF9; phage uncharacterized protein (putative large terminase), C-terminal domain. This model represents the C-terminal region of a set of phage proteins typically about 400-500 amino acids in length, although some members are considerably shorter.	98.33
<input type="checkbox"/>	24	<a href="http://pdb.rcsb.org/pdb/explore.do?structureId=3MWJ">3MWJ B (http://pdb.rcsb.org/pdb/explore.do?structureId=3MWJ)</a>				Heat resistant RNA dependent ATPase; RNA HELICASE, RIBOSOME BIOGENESIS, THERMOPHILIC; HET: SO4; 1.4A {Thermus thermophilus}	98
<input type="checkbox"/>	25	<a href="http://pfam.xfam.org/family/PF04851.14#tabview=tab0">PF04851.14 (http://pfam.xfam.org/family/PF04851.14#tabview=tab0)</a>				; ResIII ; Type III restriction enzyme, res subunit	97.98

Showing 1 to 25 of 250 entries

Previous 1 2 3 4 5 ... 10  
Next

Alignments

☐ 1. [Template alignment | CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam03354\)](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam03354)  
[PF03354.14 \(http://pfam.xfam.org/family/PF03354.14#tabview=tab0\)](http://pfam.xfam.org/family/PF03354.14#tabview=tab0) ; Terminase\_1 ; Phage Terminase

Probability: 100.0    E-value: 1.1E-32    Score: 281.43    Aligned Cols: 411    Identities: 15%    Similar

Q ss\_pred

Q Klein\_Draft

Q Consensus

35

35

HHHHHHHHHHccChhHhhccCCcchh---hhheeEeeEecCCCCHHHHHHHHHHHHH  
PWQELCLHEALKESDELVLQLESGAWVK---KWAASSFGLVVSQRQNGKGSILEALELAGL  
~~Q~~~~~g~~~~~rg~GKT~~~~~

[illegible]





Q ss_pred		eeEeeEEecCCCCHHHHHHHHHHHHHHHcCeeEEEEcCHHHH-HHHHHHHHHHHHcc
Q Klein_Draft	65	ASSFGLVSRQNGKGSILEALELAGLILFGERLIIHSAHEFKTA-VNGMERLESLIAKSG
Q Consensus	65	~~~~~rg~GKT~~~~~i~~~~t~~~a-~~~~~ +++++.+   +    +....+++.+.+.+.+.+.+.+.+.+.+
T Consensus	1	~~~~~rg~GKT~~~~~
T TIGR01547	1	HEEIIAKGGRGSGKTFAIALKLVEKAARNKPQNILCARKVQNSIRDSVFKDIEDLLSIEG
T ss_pred		CceEEEEeCCCCCHHHHHHHHHHHHHHCCcCeEEEEECCHHHHHHHHHHHHHhhCc
Q ss_pred		CceEEEeCCCC-CcEEEEEC--CCCCccccce-eEEEEcHHhcCHHHHHHHhhhcC
Q Klein_Draft	134	AESIEILDGNPNP-GARVIFQTR--TDRSLGLTA-DRVIFDEAMTITPGSKALAPTSS
Q Consensus	134	~~~~i~~~~~g~~~~i~~~~~G~~~~v~~~~iDE~~~~~l~~~~~ ...+.+. +  +. .+.+. +.++++ .+. +++++ +.++.+.+.+.++++.
T Consensus	71	~~~~i~~~~~g~~~~i~~~~~G~~~~~i~~~~DE~~~~~l~~~~~
T TIGR01547	71	SMEIKIL---NTGKKFIKGLNDKPNKLKSGAGIAIWFEEASQLTKEDIKELIPRLRE
T ss_pred		cceEEEE---CCCCEEEEEcCCCCccccCCcCeEEEEechhhCCHHHHHHHHHhhCc
Q ss_pred		ecCCCCCCCchhchHHHHHHHHHHhCc--CCCCEEEEeCCCCCCCCcCHHHHHH
Q Klein_Draft	199	GTAADQRTQPYCHTFGGVRYRALEQLRTG--ERKRCLFLWSAPDDLPEEKFGDPQYWM
Q Consensus	199	stp~~~~~ +  +.+. + ++ +.+. . .+++..+.+. .
T Consensus	137	~tp~~~~~
T TIGR01547	137	SNPESPLH--W---VY---KRFIE--NMEDEFRICIIHSTY-----R
T ss_pred		eCCCCCc--H---HH---HHHH--ccccccCEEEEEEc-----c
Q ss_pred		HHHHHHHHHHHhChhhhHHhCCCCCCC-CCCCCCCCHHHHHhCCCCcccCCcEE
Q Klein_Draft	267	EKILDEYEEMWANLRDFGVDRLGIDWPQF-GAGISEIPLDKWRRLDNPEPDLAGARAL
Q Consensus	267	~el~~~~~f~~~~e~~~~g~~~~~f~~~~~p~~~~~ .++++++.+.+.+. .++ +.  ... + +.+ +.+.+.+.+.+.+.+.+
T Consensus	175	~~~~~f~~~~~
T TIGR01547	175	EVTIQEI EELKRRDPALYRRIWLGE--WVSALG--GILYKKLDVKAAAYIK-ESPNHPIDF
T ss_pred		HHHHHHHHHHhCCHHHHHHHhCcC--cchhc--cceechHHhhhhccC-CCCCCEE
Q ss_pred		EEEEEEEEeCCCC-EEEEeccCCC-----CHHHHHHHHHHHHHHCCCEEEEcCccHH
Q Klein_Draft	336	WAIVGSQRCTDGR-IHVEVGAGMD-----PVDRVVDKFIQAITAWGP EEILVRGGAA
Q Consensus	336	tai~~~~~g~~~~v~~~~~i~~~~~i~~~~d~~~~ng +++++.+.+. ++++.+.+. .+.+.+.+.+.+.+.+.+.+.+
T Consensus	240	~a~~~~~v~~~~~i~~~~~i~~~~~

Q ss_pred		HHHHHHHHHhCCHHHhHHHHCCCCCCCCCCCCCHHHHHhcCCC---CCcCCCE
Q Klein_Draft	269	KILDEYEEWMANLRDFGVRLGIGDWPQFGAGISEIPLDKWRRLDNP---EPDLAGARA
Q Consensus	269	~l~~~~~f~~e~~ng~~~~~f~~~~~-----p~~~~~ +++++.+...++.. .+++ .  ...+ ++.+ +.+++..t... .t.....++
T Consensus	204	~~~~~f~~e~~ng--~~~~~f~~~~i~~~~~
T 4IEE A	204	LRLEEMEECKRRNPTLYRHIWLGE--PVSAS-DMAIKREWLEAATDAHKKLGWKAKGAVV

Q ss_pred		CCcEE-EecCCCCcEEEEEECC--CCCCccc-eeEEEEcHHhcCHHHHHHHHHhhc
Q Klein_Draft	133	GAESIE-ILDGPNPGARVIFQTRT--DRSGLGLT-ADRVIFDEAMTITPGSLKALLPTVS
Q Consensus	133	~~~~i~~~~~~g~i~~~~~--~~~~G~--~v~iDE~~~~~ +...+. +. ++. .+.+. +.+++ . + +++++   +.+.++++ .+.+.+





6.

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/4bil\)](#)[4BIL\\_C \(http://pdb.rcsb.org/pdb/explore.do?structureId=4BIL\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4BIL) DNA MATURASE B; HYDROLASE, PACKAG  
DNA; 29.0A {ENTEROBACTERIA PHAGE T7}

Probability: 99.91 E-value: 1.5E-24 Score: 222.39 Aligned Cols: 359 Identities: 12% Similar

```
Q ss_pred          HHHHHHHH-HHcC---CCCCHHHHHHHHHHccChHHhccCCcchhhheeEeeEEe
Q Klein_Draft    18 AGQEAIIDLA-AACG---LILDPWQELCLHEALKESDELVLQLESGAWVKWAASSFGLVV
Q Consensus      18 ~~~~~~1~~~~~Q~~~~~g~~~~~
      +...+.|+ ..++   +.+.|+.+++++. . . . .      .+...+.
T Consensus      15 ~~~d~~~f~~~~~Q~~~~~
T 4BIL_C         15 LKGDFAFLFVLWKALNLPVPTKCQIDMAKVLANGD-----NKKFILQA
T ss_dssp        HHHHHTCCCCBTTTBSCCCCCHHHHHHHSSSS-----CSEEEEC
T ss_pred        HHcHHHHHHHHHcCCCCCHHHHHHHHcC-----CCeEEEC
```

```
Q ss_pred          HHHHHHHHHhCCeEEECCHHHHHHHHHHHHHccchhhceec--cCCeEEEC
Q Klein_Draft    83 EALELAGLILFGERLIIHSAHEFKTAVNGMERLESIAKSLKYAKQA--HGAESIEIL
Q Consensus      83 ~~~~~~i~~~~~t~~~~~a~~~~~1~~~~~
      +...+.+.|+.+++++.+++++.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.
T Consensus      69 ~~~~~~p~~~~~i~~~~~s~~~~~t~~~~~a~~~~~i~~~~~
T 4BIL_C         69 CAFVWVSLWRDPQLKILIVSASKERADANSIFIKNIIDLLPFLSELKPRPGQRDSVISFD
T ss_dssp        HHHHHHHHTSSSCEEEEECSTHHHHHHHHHHHTTSCTTTCCCSBTTSCSCBS
T ss_pred        HHHHHHHHHhCCCCEEEEECCHHHHHHHHHHHHHcCHHHHHCCCCCCCCCeeEee
```

```
Q ss_pred          --CcEEEEECccccccceEEECcHHhC-----HHHHHHHh--hCcccc
Q Klein_Draft    146 --GARVIFQTRDRSGLGLTADRIVFDEAMTIT-----PGSLKALLP--TVSSRPN
Q Consensus      146 --g~~~~i~~~~~G~~~~~V~iDE~~~~~1~~~~~
      |+.|.+.+.+. +++|.+++++|.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.
T Consensus      135 ~~~g~~~~i~~~~~G~~~~~V~iDE~~~~~
T 4BIL_C         135 DHSPSVKSVGITG-QLTGSRADIIADDVEIPNSATMGAREKLWTLVQEFAALLKPLPS
T ss_dssp        EEEECTTTTHH-HHHCSEEEEEETTTCTTHHHHHHHHHSSHHHHHTTCCC
T ss_pred        CCCCcEEEEECcC-ccccCCcEEEEECcCCcCCcCHHHHHHHHHHHHHHCCCC
```

```
Q ss_pred          CCCCcchhchHHHHHHHHHHcCCCCEEEEECcC-----
Q Klein_Draft    203 DQRTQPYCHTFGGVRYALEQLRTGERKRLCFLEWSAPD-----
Q Consensus      203 ~~~~~~
      +.++ + ++ ++... +. |...+++.
T Consensus      204 ~~~~~~
T 4BIL_C         204 TEMT--L---YK---ELEDN-----RGYTTIWPALYPRTREENLYYSQRLAPMLRAE
T ss_dssp        TTSH--H---HH---HHHH-----HTTCCCCCSTTSGGGBCCTSCBCTTHHHH
T ss_pred        CcCC--H---HH---HHHhC-----CCceEEecCCcchhchhccccchHHHHH
```

```
Q ss_pred          ccccCHHHHHHHcCCCCcCHHHHHHHHHHHcHHhhHHHHCCCCCCCCCCCCC
Q Klein_Draft    245 EEKFGDPQYWAMANPGLGYRQTEEKILDEYEMWANLRDFGVDRLGIGDWPQFGAGISEI
Q Consensus      245 ~~~~~~nP~~~~~e~1~~~~~f~~~~~g~~~~~f~~~~~
      ..+|.+.+.+.+++++.++ ++.|.++|. |...+ +.+.
T Consensus      257 -----~~~~~~e~1~~~~~f~~~~~ey~~~~~f~~~~~
T 4BIL_C         257 -----AGTPTDPVFRDRLRERELEY--GKAGFTLQFMLN--PNLSD--AEKY
T ss_dssp        -----THHHHTTCCCTTSCSBSSCHH--HHTTCCCCC-----CSSSE--EESS
T ss_pred        -----CCCCCcCCHHHHHHHHH--cHHHHHHhC--CCCc--cccc
```

```
Q ss_pred          -----HHHHhCcc-----CCcCCcEEEEECcCC
Q Klein_Draft    306 -----LDKWRLDNP-----EPDLAGARALILYRTPEG
Q Consensus      306 -----~~~~~~g~D~a~
      +.+. . . . .      .+.+.+.++|. |.+.
T Consensus      310 ~~~~~~g~D~a~
T 4BIL_C         310 ALDLEKAPMHYQWLPNRQNIIEDLPNVGLKGDDLHTYHDCSNNSGQYQKILVIDPSGRG
T ss_dssp        EEBCCSSTTSCEEEEECSSSEEEEEECSSSSHHHHHHHHHTTSCEEEE
```

```

Q ss_pred          eCCCCEEEEcccC-CCCHHHHHHHHHHHHHCCCEEEeCcCHH-HHHHHHHH-----
Q Klein_Draft      344 CTDGRIHVEVGYAG-MDPVDRVVDKFIQAITAWGPEEILVGRGGAA-EVIPQIEA-----
Q Consensus        344 ~~~g~~~V~~~~~i~~~~~i~iD~~~g~~~l~~~~~
      .+.+.+.+.+. .+.+.+.+.|.+.+.|.+.+.|.+.+.|.+.+.|.+.+.|.+.
T Consensus        380 ~~~~~V~~~~~i~~~~~i~iE~~~g~~~l~~~~~
T 4BIL_C           380 TLNGYIYLMAGGFRDGYSDKTLLELLAKKAKQWGVQTVVYESNFGDGMFGKVFSPILLKH
T ss_dssp          HTSSSSSSCCSCEECSSSSCSSEECSTHHHHHHHHHHHHHTTSECCCSHHHHHHHTT
T ss_pred          EcCEEEEEeCcCCCCcHHHHHHHHHHHHhCCCEEEeccccchHHHHHHHHHHh

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Q ss_pred          HHHHHHHhHHHH-HhhcCCCCcceeCCc
Q Klein_Draft      407 SEEAQACGGFLN-DALVDPENPLLSHGNQ 434 (510)
Q Consensus        407 ~~~~~~l~~~~~g~~~~~ 434 (510)
      +..+|.. ++. .|...+++|++..+.
T Consensus        449 ~~~K~~-ri~~~l~~~~~g~~~~~ 475 (476)
T 4BIL_C           449 ARGMKEM--RICDTLEPVMQTHRLVIRDE 475 (476)
T ss_dssp          ECTTCCC--HHHHHHHHHHHHHSGGGTT
T ss_pred          cCCcHHH--HHHHchHHHHhCcEEEEcC

```

☐ 7.

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

**4BIJ\_C (<http://pdb.rcsb.org/pdb/explore.do?structureId=4BIJ>) DNA MATURASE B; HYDROLASE, ATPASE, PARTICLE; 16.0A {ENTEROBACTERIA PHAGE T7}**

Probability: 99.91 E-value: 1.5E-24 Score: 222.39 Aligned Cols: 359 Identities: 12% Similar

```

Q ss_pred          hHHHHHHHH-HHcC---CCCCHHHHHHHHHHhccChhHhhccCCcchhhheeEeeEEe
Q Klein_Draft      18 AGQEAIOLA-AACG---LILDPWQELCLHEALKESDELVLQLESAGWVKWAASSFGLV
Q Consensus        18 ~~~~~~l~~~~~Q~~~~~g~~~~~
      +...+.|+ ..++ +.+.|+.+++++.+. .+.+.+.
T Consensus        15 ~~~d~~~~f~~~~~Q~~~~~
T 4BIJ_C           15 LKGDFVAFLFVLWKALNLPVPTKCQIDMAKVLANGD-----NKKFILQA
T ss_dssp          HHHHHTCCCCBTTTBSCCCCCHHHHHHHHHSSSS-----CSEEEEEc
T ss_pred          HHhCHHHHHHHHHhCCCCCHHHHHHHHHHhCC-----CcEEEEe

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```

Q ss_pred          HHHHHHHHHhCCeEEEEeCCHHHHHHHHHHHHHhccchhhceec--cCCeEEEE
Q Klein_Draft      83 EALELAGLILFGERLIIHSAHEFKTAVNGMERLESIAKSLKYAKQA--HGAESIEIL
Q Consensus        83 ~~~~~i~~~~~t~~~~~a~~~~~l~~~~~i~~~~~
      +.++++.+.|+.+++++.+++++.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.
T Consensus        69 ~~~~~p~~~~~i~~~~~s~~~~~t~~~~~a~~~~~i~~~~~
T 4BIJ_C           69 CAFVWVSLWRDPQLKILIVSASKERADANSIFIKNIIDLLPFLSELKPRPGQRDSVISFD
T ss_dssp          HHHHHHHHTSSSCCEEEECSTHHHHHHHHHHHTTSTTTCCCSBTTSCSCBS
T ss_pred          HHHHHHHHHhCCCCEEEEeCCHHHHHHHHHHHHHhCHHHHHHCCCCCCCCcEeEe

```

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```

Q ss_pred          --CcEEEEEECCCCCCCCcEEEEEcHHhC-----HHHHHHHHh--hCcccc
Q Klein_Draft      146 --GARVIFQTRTDRSGLGLTADRVIDEAMTIT-----PGSLKALLP---TVSSRPN
Q Consensus        146 --g~i~~~~~G~~~~~V~iDE~~~~~l~~~~~
      |+.|.+.+.+. +++|.+++++|.+.+. .+.+.+.+.+.+.+.
T Consensus        135 ~~~g~i~~~~~G~~~~~V~DE~~~~~
T 4BIJ_C           135 DHSPSVKSVGITG-QLTGSRADIIADDVEIPSNSATMGAREKLWTLVQEFAALLKPLPS
T ss_dssp          EEEEECTTTTHH-HHHCSEEEEEETTTCTTHHHHHHHHHSSHHHHHTTCCC
T ss_pred          CCCCCEEEEcCC-ccccCCCEEEcCCCCcCCCHHHHHHHHHHHHHHHCCCCC

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```

Q ss_pred          CCCCCcchhchHHHHHHHHHHhCCCCCEEEEEeCCC-----
Q Klein_Draft      203 DQRTQPYCHTFGGVRYRALEQLRTGERKRLCFLEWSAPD-----
Q Consensus        203 ~~~~~
      +.++ + ++ ++... +.|...+++..
T Consensus        204 ~~~~

```

<a href="#">T 4BIJ_C</a>	204	TEMT--L---YK-----ELEDN-----RGYTIIWPALYPRTREENLYSQR LAPMLRAE
Select all	Forward	T TSH--H---HH---HHHH-----HTTCCCCCCSTTSGGGGBCTTSCBCC-CHHHH
T ss_dssp		Color Segs Unwrap Segs
T ss_pred		CcCC--H--HH---HHHhc-----CCceEEEcCcCChhhchhccccchHHHHHH
Q ss_pred		ccccCCHHHHHHHHCcccccccCHHHHHHHHHHHHhCHhhhHHHhCCCCCCCCCCCCCCC
Q Klein_Draft	245	E EKFGDPQYWAMANPGLGYRQTEEKILDEYEEMWANLRDfGVDRlGIGDWpQGAGISEI
Q Consensus	245	~~~~~n P~~~~~e~l~~~~~f~~~g~~~~~ ..+ .+.+.+.+++++.++ ++.  .++ +.  ...+ +.+
T Consensus	257	-----~e~l~~~~~f~~~ey~~~-----f
T 4BIJ_C	257	-----AGTPDTPVFRDDLREREL EY--GKAGfTLQFMlN--PNLSd--AEKY
T ss_dssp		-----THHHHTTTCCCTTSCSBSSCHH--HHTTCCCCCCCC--CSSSE--EESS
T ss_pred		-----CCCCCccCCHHHHHHHHHHH--cHHHHHHHHhC- -CCcC- -ccc
Q ss_pred		-----HHHHHhC CCC-----CCcCCCEEEEEEC CCC
Q Klein_Draft	306	-----LDKWRR LDNP-----EPDLA GARALILY RTPEG
Q Consensus	306	-----~p~~~~~g~D~a~~~ +.+. . . . . .+.+. . .+++ + +.++
T Consensus	310	~~~~~g~D~a~~~
T 4BIJ_C	310	ALDLEKAPMHYQWLPNRQNIEDLPNVGLKGDDLHTYHD CSNNSGQYQQKILVIDPSGRG
T ss_dssp		EEBCCCC-CCEEEEEEECSSSSEEEEEEEESC C SSSSHHHHHHHHHHTTSC EEEE
T ss_pred		cCCcccCCcEEcCCcchhhcCCCCCCCCCcccccccCcCccCceeEEEECCCCC
Q ss_pred		eCCCCEEEEeccC-CCCHHHHHHHHHHHHHHCCEEEEEcC c HH-HHHHHHHH----
Q Klein_Draft	344	CTDGRIHVEVG YAG-MDPVD R VVKF IQAITAWGP EE ILVGRGGA A-EVIPQIEA----
Q Consensus	344	~~~g~~~V~~~~~i~~~~~i~D~~~g~-~~~~~l~~~~~ ..++.+.+.+. . .+++++.  .++++.  +..+++ .++.  .+.+. ++
T Consensus	380	~~~~~V~~~~~i~~~~~i~E~~~g~-~~~~~l~~~~~
T 4BIJ_C	380	TLNGYIYLMEAGGFRDYGSDKTLELLAKKAKQWGVQT VVYESNF GDGMFGKV FSPILLKH
T ss_dssp		HTSSSSSSCSCEECSSSSCSSECCSTHHHHHHHHHHHHHTTSEECCSCHHHHHHTS
T ss_pred		EeCEEEEEEEcC cCCCCCHHHHHHHHHHHHHCCCEEEEEec c c chHHHHHHHHHHh
Q ss_pred		HHHHHHhhHHH-HhhcCCCCceeeCCc
Q Klein_Draft	407	SEEAQACGGFLN-DALVPENPLL SHGNQ 434 (510)
Q Consensus	407	~~~~~l~~~~~g~i~~~~~ 434 (510) +.+ . . ++.  . . .+++ ++.+.
T Consensus	449	~~~K~~-ri~~~l~~~~~g~i~~~~~ 475 (476)
T 4BIJ_C	449	ARGMKEM--RICDTLEPVMQTHR LVIRDE 475 (476)
T ss_dssp		ECTTCCC--HHHHHHHHHHHHHS GGGTT
T ss_pred		cCCcHHH--HHHHchHHHHhCCEEEecC

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

8. [4ZNK A \(http://pdb.rcsb.org/pdb/explore.do?structureId=4ZNK\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4ZNK) Phage terminase large subunit; DNA  
HET: SO4; 1.931A {Thermus phage P7426}

Probability: 99.66    E-value: 4.0E-17    Score: 154.88    Aligned Cols: 232    Identities: 14%    Similar

Q ss_pred		CCCCchHH-HHHHHH-HHcCCCCCHHHHHHHHHHhccChhHhhccCCcchhhheeEeeE
Q Klein_Draft	13	EA NSSAGQ- EAIDL A-AACGLILDPWQELCLHEALKESEDELVLQLESGAWVKWAASSFGL
Q Consensus	13	~~~~~1~~~Q~~~~~g~~~~~ .+.+. . . ++.  + . .+++ . ++ . +++..+ .+.+++
T Consensus	1	~~~~~Q~~~~~
T 4ZNK_A	1	GPGGSMKRLRP SDKFFEL LGYKPHHVQLAIHRST-----AKRRVA
T ss_dssp		-----CCCCCHHHHHHTTCCCHHHHHHHHCC-----CSEEEE
T ss_pred		CCCCccccCchHHHHhhCCCCCHHHHHHHhCC-----CcEEEEE
Q ss_pred		HHHHHHHHHHHHCCeeEEEEcCCHHHHHHHHHHHHHHhcc- cchhhceeccCCceEEE
Q Klein_Draft	81	ILEALELAGLILFGERLIISAHAEFKTAVNGMERLESIAKS-GLKYKAKQAHGAESIEI
Q Consensus	81	~~~~~i~~~~t~~~~a~~~~~1~~~~~i~~~~~



Q ss_pred		CCCCCHHHHHHHHHhhccChhHhhccCCcchhhhhheeEeeEeccccCCCCHHHHHHHHHH
Q Klein_Draft	29	CGLILDPWQELCLHEALKESDELVLQLESGAWVKWAASSFGLVVSQRQNGKGSILEALELA
Q Consensus	29	~~~~l~~~Q~~~~~g~~~~~rg~GKT~~~~~ .++. .++ .+++..+..+.+++++  +  ++++.+++
T Consensus	160	~~~~l~p~Q~eil~l~l~-----~r~i~i~ngRq~GKTt~a~a~l~
T 200J_A	160	IKVQLRDYQRDLKIMSS-----KRMTVCNLSRQLGKTTVVAIFLAH
T ss_dssp		EECCCCHHHHHHHHHHHH-----SSEEEEECSSCHHHHHHHHHHH
T ss_pred		eccCCCCHHHHHHHHHHcc-----CCeEEEEcCCCCChHHHHHHHHHH
Q ss_pred		EEEcCCHHHHHHHHHHHHHHHcccc-hhhceeccCCceEEeEcCCCCcEEEEEECCCC
Q Klein_Draft	99	IHSAHEFKTAVNGMERLESIAKSL-KYKAKQAHGAESIEILDGPNPGARVIFQTRTDR
Q Consensus	99	~i~nt~t~a~a~a~a~a~a~a~a~l~-----i~n~n~g~i~n~n~n~ +++++.++++.++..+.+++..+. . . . .+. . .+. . .+ +. .+.+.+
T Consensus	212	liia~t~n~qa~l~l~i~i~l~l~p~l~l~-----nGs~I~n~s~n~n~
T 200J_A	212	GILAHKGMSAEVLDRTKQAIELLPDFLQPGIVEWNKGSIELD---NGSSIGAYASSPD
T ss_dssp		EEEESSHHHHHHHHHHHHHHHHHSCTTTSCEEEECSSEEEET----TSCEEEEEECSSH
T ss_pred		EEeEcChHHHHHHHHHHHHHHHHCHHHhcCCeeecCCCEEEeC----CCCEEEEEcCCCC
Q ss_pred		EEeChHhChH- -HHHHHHHHhhcCCCCCEEEEEcCCCCCcchhchHHHHHHHHHHHH



			~W~~~~p~~~~i~~~~1~~~~p~~~~a~~~~a~~~~f~n~L	
Select all	Forward	Forward Query MSA	Color Segs	Unwrap Segs
T Consensus	265	RGFVVTINLDAGRRRRRTTSADGLLCFRSGWRLEAKQWREAGTLEWETLQSEA		GLVGFFENGKA
T PF05876.11	265			
T ss_pred		CceeeccccCCCCceEEEEEEeeccCCHHHHHHHHHHHHHHHHHHCCHH-HhhheeeCcc		
Q ss_pred		CCC--CCCHHHHHhcc-----CCcCCcCeEEEEEEcCCCCeEEEEEEEEcCCCCEE		
Q Klein_Draft	300	GIS--EIPLDKWRRLDN-----PEPDLAGARALILYRTPEGGPWAIVGSQRCTDGRIVH		
Q Consensus	300	~~~--~f~~~~~-----~p~~~~~g~D~a~~~~d~t~a~i~~~~~g~~~~v		
		... .++.+.+.+.+. . . .... .++ + +. . . .++.+.+.+.+. .++		
T Consensus	331	~~~~~n~~~~~i~~~~~p~~~~~GvD~q~~~~~V~~~~~		
T PF05876.11	331	LSGEPPIEIKTLAARRRKGWKLGTPVAGVKVIVITVDVQAN--RFECAAVGYGDGLECWV		
T ss_pred		CCCCCCCCHHHHHHHHHCcCCcCCCCCceEEEEEEecCC--EEEEEEEEcCCcEEE		
Q ss_pred		-----CCHHHHHHHHHHHHHH-----HCCCEEEEcC-cHH-HHHHHHHHC		
Q Klein_Draft	359	-----DPVDRVVDKFIQAITA-----WGPEEILVGRG-GAA-EVIPQIEAA		
Q Consensus	359	-----~i~~~~~-----~i~~~~~iD~g~g~~~~~l~~~~~		
		....+.+.+. .++++. .+++.++  . .+. .+.+.+.+. .+		
T Consensus	399	~g~~~~~l~~~~~g~~~~~i~~~~~iD~g~~~~t~~~~v~~~~~		
T PF05876.11	399	DGLTSVQPLRYREHWAALLPLFSRDWPLADGSGQAQALTVADARGGESDLVTGFWHLC		
T ss_pred		CCCCCcCcccccHHHHHHHHHHHCccccCCCCCceEEEEEEECccccHHHHHHHHhh		
Q ss_pred		-----CCeEcCCHHHHHHHhhHHHHHHhC-Cc		
Q Klein_Draft	398	-----GFTVYSPNQSEEAQACGGFLNDALVD-PE		
Q Consensus	398	-----g~~~~~l~~~~~		
		+.+.+.+. .+ . .+.+.+. .+		
T Consensus	469	~~~~g~~~~~V~~~~~kd~-----l~~~~~		
T PF05876.11	469	TLLQGGNNPRAELISRARRSDEKAGGGVKRNSPAKWTVN-VHALKNI--LDARLRREKPG		
T ss_pred		EEEcCCCCCceeeccccccccCCCCccCCEEEeC-hHHHHHH--HHHHhCCCCC		
Q ss_pred		cHHHHHHHHhcEEEECCCCceeeCccCHHHHHHHHHHHH		
Q Klein_Draft	434	QHSLNAAISRRAKRDLPSSGGFVWDCIEQSTYAQLMGVTLGRWA	476 (510)	
Q Consensus	434	~~~l~~~l~~~~~D~~~dA~~~a~~~	476 (510)	
		...+.+  +.+.+. .+. .+.+. .+ .+.+.+. .+		
T Consensus	536	~~~~~qltae~~~~~g~--W~~~~~nh~~~d~~~ya~~~a	572 (578)	
T PF05876.11	536	RELHFDeltaEEKQD---GK--WKKIR-PRNETLDMVMSYAA	572 (578)	
T ss_pred		CHHHHHHheeeEeeC---Cc---eeeCC-CCHHHHHHHHHHHH		

Template alignment | CDD (<http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam04466>)

11. [PF04466.12 \(http://pfam.xfam.org/family/PF04466.12#tabview=tab0\)](http://pfam.xfam.org/family/PF04466.12#tabview=tab0) ; Terminase 3 ; Phage terminase I

Probability: 99.5	E-value: 1.4E-15	Score: 136.98	Aligned Cols: 194	Identities: 12%	Similarity: 12%
-------------------	------------------	---------------	-------------------	-----------------	-----------------

Q ss_pred		eeEeeEEecCCCCHHHHHHHHHHHHHHHh--CCeeEEEEcCCHHHHh-HHHHHHHHHHh
Q Klein_Draft	65	ASSFGLVVSQRQNGKGSILEALELAGLILF--GERLIHSAHEFKTAV-NGMERLESLIA
Q Consensus	65	~~~~~rg~GKT~~~~~--~~~~~i~~~~~t~~~~a~~~~~ .+.+++..+++ +   ++++..+++..+...+. .++++ +..++++.+.+.+.+.+
T Consensus	1	~~~~~rg~GKT~~~~~--~~~~~
T PF04466.12	1	HLTEVWYGGASSGKSHGVVQKVVLKSLQHWNVPR-KVLWLRLKVDRTVKNSIFTDVTCLSL
T ss_pred		CcEEEEECcCCCChHHHHHHHHHHHHHhCcccc-eEEEEEcchHHhhHHHHHHHHHHh
Q ss_pred		ccCCceEEEEcCCCCcEEEEEECC-CCCCccc-ceeEEEEcHHhcCHHHHHHHHHhhc
Q Klein_Draft	131	AHGAESIEILDGPNPGARVIFQTRT-DRSGLGL-TADRVIFDEAMTITPGSLKALLPTVS
Q Consensus	131	~~~~~i~~~~~rg~~~~~i~~~~~--~~~~~G~~~~~v~~~~~i~~~~~DE~~~~~l~~~~~ .....+.+. .+ .+.+.+. .+++ . .+++++  ++..+.+.+.+.+.+
T Consensus	70	~~~~~-----g~~~~~i~~~~~--~~~~~g~~~~~i~~~~~DE~~~~~l~~~~~
T PF04466.12	70	NRSDKTIVLP---NGAIFLFQGMDDPEKIKSIKGLSDVVMEEASEFNHNDYTQLTLRLR
T ss_pred		eCccEEEECC---CCEEEEEEcCCHHHhccccCcceEEEEccccCCHHHHHHHHHHHh
Q ss_pred		EEeCCCCCCCCchhchHHHHHHHHHHHhCCCCCEEEEEEEcCCCCCCCCcCCHHHHHHh





Q ss_pred		heeEeeEeeCCCCHHHHHHHHHHHHHHHHhCCeeEEEEcCCHHHHHHHHHHHHHHHhccc
Q Klein_Draft	64	AASSFGLVVSQRNGKGSILEALELAGLILFGERLIHSAHEFKTAVNGMERLESIAKSG
Q Consensus	64	~~~~~rg~GKT~~~~~i~i~nt~a~~~~~ ..+.+++. +   ..+++..+..+.+.+++++.++++.+.+.+.+
T Consensus	13	~~~~~ggrgsGKT~~~~~l~~~~~i~p~t~~~~~l~~~~~l~~~~~
T 5HD9_A	13	DRILNFVIGARGIGKSYAMKVYPINRFIKY-GEQFIYVRRYKPELAKV-SNYFNDVAQEF
T ss_dssp		CCSEEEECSCSSHHHHHHHHHHHHHHHHH-CCEEEEESSGGGGTTG-GGGGGTGGGC
T ss_pred		CCEEEEEEcCCCCChhhhhHHHHHHHHHHh-CCEEEEEcCHHHHHH-HHHHHHHhhc

Q ss_pred		CceEEEEcCCCCCEEEEEECC-CCCccccc--e-eEEEEcHHhc----	H---H---	HHH
Select all		Forward	Color Segs	UniqSegs
Q Kiehn_Draft	134	AESLEEDGPIPGARVLTFRDRLSGGLTAA	DRVFIDAMITLTPP	GSL
Q Consensus	134	~~~~~i~~~~~g~~~n~~~~~r~~~~~v~~~~ide~~~~~		
T Consensus	79	...+.+. + +. .++.+ ..+++ .+	.++++   ++.	+.
T SHD9_A	79	~~~~i~~~~----~g~~~~If~~~~~lR~~~~~in~~~~deA~~~~~		
T ss_dssp		GRRFYID----	GKLAGWAIPLSVVQSEKSNAYPNVSTIVFDEFIREKDNSNYIPNEVSAL	
T ss_pred		TTEEEET-----TEEeeeeEGGGHHHTSCSSS	EEEEEEETCSCSSCCCTTHHHHH	
T ss_pred		CcEEEEEC----	CeEEEEEEcCCChHHccccCCcccEEEEecceccccCCCChhHHHHH	

Q ss_pred		CCCCEEE-----EecCCCCCCCchhchHHHHHHHHHH	
Q Klein_Draft	190	RPNPQIVY-----TGTAADQRTQPYCHTFGGVRYRALEQ	223 (510)
Q Consensus	190	~~~~~i~-----~stp~~~~~	223 (510)
		.+..++++ ++  .+...   ++ +.+.	
T Consensus	145	~~~~~i~~~~g~~~~~NP~~~~~	175 (194)
T 5HD9_A	145	RERVRCICLSNAVSVVNPYFLFF--N---LV---PDVNK	175 (194)
T ss_dssp		STTCEEEEECCSCCSSHSHHHHH--T---CC---CCTTC	
T ss_pred		CCCceEEecCCcccCchHHhh--c---cc---cchhh	

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/5c10\)](http://www.ebi.ac.uk/pdbe/entry/pdb/5c10)

17. [5C10 A \(http://pdbr.rcsb.org/pdb/explore.do?structureId=5C10\)](http://pdbr.rcsb.org/pdb/explore.do?structureId=5C10) Gene 2 protein; nuclease domain, metz  
{Enterobacteria phage Sf6}

Probability: 98.84    E-value: 4.7E-10    Score: 105.44    Aligned Cols: 197    Identities: 11%    Similar

Q ss_pred		HhCCCCCCCCCCCCCHHHHHhCcc---CCcCCcEFFFFFFCccCcEEEEEE
Q Klein_Draft	288	RLGIGDWPQFGAGISEIPLDKWRRLDNP---EPDLAGARALILYRTPEGGPWAIVGSQR
Q Consensus	288	~g~f~p~g~D~a~n~d~t~a~i~n~  .+.  ... +. +.+++. ... .+.+.+.++ + +.++++.++++.~
T Consensus	12	~~~~~f~~~~i~a~~~~~GvDvA~G~D~svi~v~
T 5C10_A	12	SGLV--PRGSH--MAIIKREWLEAATDAHKKLGWKAKGAVVSAHDPSDTGPDAKGYASRH
T ss_dssp		-----CBSSCHHHHHHHBTHHHHTCCCCSCEEEEEECSSSSCEEEEEEE
T ss_pred		CCcC--CCCC--cceeHHHHHHHHHHhhhhcccCCCEEEEEeccCCCCCEEEEEEE

Q ss_pred		cccCCCCHHHHHHHHHHHHHHHHCCCEEEeCcCHH-HHHHHHHHC---CCeEcCCHHH
Q Klein_Draft	354	GYAGMDPVDRVVDKFIQAITAWGP EEILVGRGGAA-EVIPQIEAA---GFTVYSNPQSE
Q Consensus	354	~~~~~i~~~~~i~iD~~g~g~~~~~l~~~~~g~~~~~ .+. .+.+.+.+.+.+.+. +.+.+. .+. . .+. .+. .+.+.+.+.+
T Consensus	76	~~~~~a~~~~~l~~~~~i~iD~~GvGvgv~d~l~~~~~
T 5C10_A	76	EGL-LMDINEGADWATSLAIEDGADHYLWDGDGVGAGLRRQTTEAFSGKKITATMFKGSE
T ss_dssp		EEC-SCCHHHHHHHHHHHHHHTTSCSEEEECSSGGGGCHHHHHHHHTTTSCSEEEECTTS
T ss_pred		Eec-CCCHHHHHHHHHHHHHhCCCEEEECCECCChHHHHHHHHHCCECCeEEEEeCCC

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Q ss_pred          -----HHHHHHHHHHhhcCCCC-----Cce-----
Q Klein_Draft     409 -----EAQACGGFLNDALVDPEN-----PLL-----
Q Consensus       409 -----~::~~1~::~~-----g~i-----
                   .+. .  ++.+.+.+.+++      +.+
T Consensus       145 ~::~~f~n~Rae-----~1~1~::~~p~::~~
T 5C10_A          145 AGAWADEVVQGDNVRTIGDVFNRKRAQ--FYALADRLYLTYRAVVHGEYADPDDMLSFD
T ss_dssp         C-----CCBHHHHBSSHHHH--HHHHHHHHHHHHHHHHCCCCGGGCCCEEC
T ss_pred         cCccccccccCccccchhhHHHHHH--HHHHHHHHHHHHccceecCCCCchhccccC

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Q ss_pred		HHHHHHHccEEEECCCCceeeecC-----CCcHHHHHHHHHHHHHHHHccccCC-CC
Q Klein_Draft	436	SLNAAISRAVKRDLPSGGFVWDCI-----EQSTYAQLMGVTLGRAWLLKHAINAA-PT
Q Consensus	436	~l~~~l~~~~~D~~dA~~~a~~~~~  .  .  . +. ++. ++++++. + . +.  + .+ + ++ ++.....+.... --
T Consensus	213	~l~~eL~~~~~Gk~~i~~K~~ik~~g~~spD~~adAl~~la~~~~~
T 5C10_A	213	KLFAELTQIQRFNNNGKLELMTKVEMKQKLGI PSNLADALMCMCHCPALVREETEIVY
T ss_dssp		HHHHHHHTTCBBCCTTSCBCBCHHHHHHHHHCCCCCHHHHHHHHTTCCCC-----
T ss_pred		HHHHHHHhcCeEEeCCCCCEEEeHHHHHHHHCCCCCHHHHHHHHHhcCccccCccccccC





Q ss_pred	EEEEcccC-CCCHHHHHHHHHHHHHCCCEEEEcCcHHHHHHHHHH-CCCe-EeCCCH
Q Klein_Draft	350 HVEVGATG-MDPVDRVDRKT-IOAITANGPEELLVGRGGAELVLPQTEA-AGFT-VYSPNQ
Q Consensus	350 ~V~~~~~i~iD~g~g~l~g~ ++...+. .+.+++++. .++. ++...++ +++ .+.+.+ . .+. +....
T Consensus	79 ~~~~e~~~~~i~~~~~D~~~~~l~~~~g~~~~~
T 2WBN_A	79 YAIDELVDHKVSLKRTADFVRKNK--YESARIADSSEP-RSIDALKLEHGINRIEGAKK
T ss_dssp	EEEEEESSCCHHHHHHHHHHTT--CTTSCEEECTTCH-HHHHCCCCCTCCTTEEECCS
T ss_pred	EEEEecccCCCCHHHHHHHHHhCC--CccCEEEcCCH-HHHHHHHHHhCcccccccCC
Q ss_pred	HHHhCCCCCceecC-CcHHHHHHHhCCCEEECCCCceecCCCCcHHHHHHHHHHH
Q Klein_Draft	417 LNDALVDPENPLL SHG-NQHS LNAAISR AVKRDLP SGGFVWDIEQSTYAQLMGVTLGRW
Q Consensus	417 ~~~l~~~~~g~i~~~~~l~~~~~D~~dA~~a~~ ++.+. . . . .+++ + +.++++ .+++++.+.+. .+.+.+++ .+. +.+++.
T Consensus	144 i~~~~~l~~~~~i~~~~~c~~~~~e~~~~y~~~~~p~~~~dH~~Da~rY~~~
T 2WBN_A	144 ERWLDE--LDAIVIDPLRTPNIAREFENIDYQTDKNGDP-IPRLEDKNHTIDATRYAFE
T ss_dssp	HHHHHT--SSEEEECTTTCHHHHHHHHHCCEEECTTCE-EEEESSSCHHHHHHHHTG
T ss_pred	HHHHHh--CCeEECCCCCHHHHHHHHhcccCccccC-CCCCCCCCCHHHHHHHHHH
Q ss_pred	CC
Q Klein_Draft	486 PT 487 (510)
Q Consensus	486 ~~ 487 (510) ++
T Consensus	211 ~~ 212 (212)
T 2WBN_A	211 WG 212 (212)
T ss_dssp	--
T ss_pred	CC

☐ 20. [Template alignment | CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam02500\)](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam02500)  
[PF02500.14 \(http://pfam.xfam.org/family/PF02500.14#tabview=tab0\)](http://pfam.xfam.org/family/PF02500.14#tabview=tab0) ; DNA\_pack\_N ; Probable DNA pac  
 Probability: 98.53 E-value: 1.5E-8 Score: 94.3 Aligned Cols: 116 Identities: 16% Similarity:

Q ss_pred	CCCCCHHHHHHHHHhccChhHhccCCc----ch-----
Q Klein_Draft	30 GLILD PWQELCLHEALKESDELVLQLESGA----WV-----
Q Consensus	30 ~~~l~~~~Q~~~~~g~----- ++. .   .++.++ +  +
T Consensus	122 ~~~LepfQk~i~l~~~~~f~~~~~f~~~~~
T PF02500.14	122 VHWLEPFQQQLVMHTF-----FFLVSIKAPQKTHQLFGLFKQYFGLFETPNSV
T ss_pred	CccCCHHHHHHHHHH-----HHHhccCchhhHHHHHHHHhCCCCCccc
Q ss_pred	EEecCCCCCHHHHHHHHHHHHHCCeeEEEEcCCHHHHHHHHHHHHHhccchh--h
Q Klein_Draft	70 LVVSRQNGKGSILEALELAGLILFGERLIIHSAHEFKTAVNGMERLESIAKSGLKY--K
Q Consensus	70 ~~~~rg~GKT~~~~~i~~~~t~~~~a~~~~~l~-- +. .   .++++.+++..+.+.+++++.++ .+++..+.++++. .
T Consensus	180 i~v~RqnGKT~l~aai~l~l~~~~g~i~v~A~t~Q~A~v~f~i~i~p~~~~
T PF02500.14	180 FLIPRRHGKTIWVVAIISMLLASVENINIGYVAHQHVANSVFAEIIKTLCRWFPPKNLN
T ss_pred	EEeCCCCCHHHHHHHHHHHHHhCCceEEEEcCCHHHHHHHHHHHHHHhCCCCcc
Q ss_pred	EEeCCCCC--cEEEEEECC-CCCCcc
Q Klein_Draft	138 EILDGPNPG--ARVIFQTRT-DRSGLG 161 (510)
Q Consensus	138 ~~~~g~--~i~~~~~G 161 (510) ++.    +. .+++ +.+++
T Consensus	250 ~f~---nG~~S~I~~~Sa~n~~siRG 272 (272)
T PF02500.14	250 TRP----GGRSSSLMCATCFNKNSIRG 272 (272)
T ss_pred	EeC---CCCeEEEEEECCCCCcCc



Q ss_pred		ECC-----CCCCccceeeEEEEcHHhcCH---HHHHHHHHhhcCCCCEEEEEcC
Q Klein_Draft	153	TRT-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRNPQIVYTGTA
Q Consensus	153	~~~~~-----~~~~~G~~~~~v~iDE~~~~~-----~~~~~~~~~~l~~~~~i~~~~~stp

Q ss_pred	EEEEecHHhcCHHHHHHHhhhcCCCCEEEEecC
Q Klein_Draft	166 RVIFDEAMTITPGSLKALLPTVSSRPNPQIVYTGT 201 (510)

<u>Q Consensus</u>	166	v~v~iDE~~~~~l~~~~~i~~~~stp	201 (510)
<u>Select all</u>	<u>Forward</u>	<u>Forward Query MSA</u>	<u>Color Segs</u>
T Consensus	122	~lliDEa~~~~~ll~~~~~--~~~~ii~gd~	155 (205)
T PF02562.15	122	FIIIDEAQNNTAEQMKMFLTRIGF--GSKAVITGDI	155 (205)
T ss_pred		EEEEECCHhhCCHHHHHHHHHHhccC--CcEEEEECCH	

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

27. [3BER A \(http://pdb.rcsb.org/pdb/explore.do?structureId=3BER\)](http://pdb.rcsb.org/pdb/explore.do?structureId=3BER) Probable ATP-dependent RNA helicase  
AMP, Structural; HET: PGE, AMP; 1.4A {Homo sapiens}

Probability: 97.89    E-value: 3.2E-6    Score: 79.36    Aligned Cols: 164    Identities: 13%    Similarity

Q ss_pred		cHHHHHHHHHHHCC-CCCHHHHHHHHHhcChhHhhccCCcchhhhheeEeeEEecCC
Q Klein_Draft	17	SAGQEAIIDLAAACGL-ILDPWQELCLHEALKESDELVLQLESgAWVKKWAASSFGLVVSRL
Q Consensus	17	~~~~~1~~~Q~~~~~g~~~~~rg .+. .+.+.+.+.+.  +++ . +++.+.+. .+. +++.+
T Consensus	49	~1~~~~~1~~~~~Q~~~~~i~~~~~-----~~~~~i~~~~~tG
T 3BER_A	49	GVTDLVCEACDQLGWTKPTKIQIEAIPALQ-----GRDIIGLAETG
T ss_dssp		TCCHHHHHHHHTTCCSCCHHHHHHHHHHT-----TCCEEEECCTT
T ss_pred		CCCCHHHHHHHHCCCCCCHHHHHHHHHHC-----CCcEEEEcCCC

Q ss_pred		HHHHHHHhC-CeeEEEEcCCHHHHHHHHHHHHHHHhhcc--chhhceeccCCeEEEcC-
Q Klein_Draft	86	ELAGLILFG-ERLIISHAHEFKTAVNGMERLESIAKS--GLKYKAKQAHAESIEILDG
Q Consensus	86	~~~~~i~~~~t~~~a~~~~~ ++..+...+ ..++++ +.+.+.+.+.+.+. . . . +. . . . .
T Consensus	101	~~~~~livP~~~l~~q~~~~~
T 3BER_A	101	ILNALLETQRLFALVLTPTRELAFAQISEQFEALGSSIGVQSASIVGGIDSMQSLAL--
T ss_dssp		HHHHHHHSCSSCEEEECSSHHHHHHHHHHHHHHHGGGTCEEECTTCHHHHHHHH--
T ss_pred		HHHHHhCCCCCeEEEEcCCHHHHHHHHHHHHHHHhhcCCCEEEECCHHHHHHH--

Q ss_pred		ECC-----CCCCcccccEEEEEcHHhCH---HHHHHHHHhhcCCCCEEEEEEc
Q Klein_Draft	153	TRT-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRPNPQIVYTG
Q Consensus	153	~~~~~-----~~~~~G~~~~~V~iDE~~~~~-----~~~~~l~~~~~i~~~~~st +..                   .....+++++  +.+.           ..+.+.+.+.   ...+++.+
T Consensus	168	t~~~l~~~~~liiDEa~~~l~~~~~i~~~~~i~~~~~i~~SAT
T 3BER_A	168	TPGRLIDHLENTKGFNLRALKYLVMEADRILNMDFETEVDKILKVIPRD-RKTLFSAT
T ss_dssp		CHHHHHHHHHHSTTCCTTCCEEEECSHHHHHHTTCHHHHHHHHSSCSS-SEEEEEESS
T ss_pred		chHHHHHHHHHCCCCHhhCCEEEEcCHHHHcCCCHHHHHHHHcCCCC-CEEEEEEC

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

28. [2GXQ A \(http://pdb.rcsb.org/pdb/explore.do?structureId=2GXQ\)](http://pdb.rcsb.org/pdb/explore.do?structureId=2GXQ) heat resistant RNA dependent ATPase resolution, AMP; HET: AMP; 1.2A {*Thermus thermophilus* HB27}

Probability: 97.88    E-value: 1.9E-6    Score: 77.56    Aligned Cols: 170    Identities: 14%    Similarity

Q ss_pred		CCCCCchHHHHHHHHHHHCCCCCHHHHHHHHHHhccChhHhhccCCcchhhheeEeeE
Q Klein_Draft	11	SPEANSSAQGEAIDLAACGLILDWPQELCLHEALKESDELVQLESGAWVKKWAASSFGL
Q Consensus	11	~~~~~1~~~~~Q~~~~~g~~~~~ ..+. . . . . + - . . . . . + + + +   . + . + . + . . . . . + . + + +
T Consensus	2	~~~~~1~~~~~Q~~~~~-----~~~~~i
T 2GXQ_A	2	EFKDFPLKPEILEALHGRGLTTPTIQAAALPLALE-----GKDLIG
T ss_dssp		CGGGSCCCHHHHHHHHHTTCCSCCHHHHHHHHHHT-----TCCEEE
T ss_pred		ChhhCCCCCHHHHHHHHCCCCCCHHHHHHHHHHC-----CCCEEE

Q ss_pred		HHHHHHHHHHH---CCeEEEECCHHHHHHHHHHHHHccchhhceecCCE
Q Klein_Draft	81	ILEALELAGLILF---GERLIISHAHEFKTAVNGMERLESIAKSGLYKAKQAHAES
Q Consensus	81	~~~~~i~~~~t~~~a~~~~~l~~~~~ ++...+...+... +...++++ +...+...+...+.....
T Consensus	54	~~~~~linp~~~~~

T 2GXQ_A	54	AFALPIAERLAPSQERGRKPRALVLTPTRELALQVASELTAVAPHLKVVAVYGGTGYGKQ
Select all	Forward	Forward Query MSA
T ss_dssp		Color Segs Unwrap Segs
T ss_pred		HHHHHHHHCCCCCFCCEEEECSSHHHHHHHHHHHCTFCEEEECSSSCSHHH
		HHHHHHHHHhcchhhcCCCCEEEEechHHHHHHHHHHHHHCCCeEEEECCCCHHHH
Q ss_pred		cEEEEEECC-----CCCcccccEEEEEcHHhcCH---HHHHHHHhhcCCCCCEE
Q Klein_Draft	147	ARVIFQTRT-----DRSLGLTADRVIFDEAMTITP----GSLKALLPTVSSRPNPQI
Q Consensus	147	~i~~~~~-----~~~G~~~~~ViDE~~~~~-----~~~~~l~~~~~i ..+.+.+.. ..+.++++ +++.+.. ..+.+.+.+... ..+
T Consensus	121	~i~i~t~~~i
T 2GXQ_A	121	ADAVVATPGRALDYLQGVLDSLREVAVLDEADEMLSMGFEEVEEALLSATPPS-RQTL
T ss_dssp		CSEEEECHHHHHHHHHHTSSCCTTCSEEEESHHHHHHTTCHHHHHHHHTSCTT-SEEE
T ss_pred		CCEEEEcHHHHHHHHHCCHCCCHhccEEEEcCHHHhhhCCCHHHHHHHHCCHCC-CEEE

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/3b85\)](http://www.ebi.ac.uk/pdbe/entry/pdb/3b85)  
**29. [3B85 B \(http://pdb.rcsb.org/pdb/explore.do?structureId=3B85\)](http://pdb.rcsb.org/pdb/explore.do?structureId=3B85) Phosphate starvation-inducible protein glutamicum, PhoH2, ATPase, PFAM::; HET: SO4; 2.35A {Corynebacterium glutamicum ATCC 13032}**  
 Probability: 97.82    E-value: 9.4E-7    Score: 79.43    Aligned Cols: 147    Identities: 19%    Similarity

Q ss_pred		CCCHHHHHHHHHHhccChhHhhccCCcchhhhheeEeeEEecCCCCHHHHHHHHHHHHHHH
Q Klein_Draft	32	ILDpWQELCLHEALKESDELVLQLESGAWVKKWAASSFGLVSRQNGKGSILEALELAGLI
Q Consensus	32	~l~m~Q~g~r~g~GKT~ . +++ .+++...+... ...+++. ++ +  +++...+...+
T Consensus	7	~l~m~q~i~g~G~GKT~
T 3B85_B	7	PKTLGQKHYVDAIDT-----NTIVFGLGPAGSGKTYLAMAKAVQALQ
T ss_dssp		CCSHHHHHHHHHHHH-----CSEEEEEECCTTSSTTHHHHHHHHHHHHHH
T ss_pred		CCCHHHHHHHHHHHhC-----CcEEEEECCECCCCHHHHHHHHHHHHHHH

Q ss_pred		cCCHHHHHHHHHHHHHHcc----cchhhceecCCceEEEcCCCCCEEEEECCC
Q Klein_Draft	102	AHEFKTAVNGMERLESIAKS----GLKYKAKQAHAESIEILDGPNPGARVIFQTRTD
Q Consensus	102	~t~~~a~~~~~-----~l~~~~~i~~~~~g~~~i~~~~~ + +.+
T Consensus	59	~~~~~-----
T 3885_B	59	RPAVEAGEKLGLPGLTNEKIDPYLRPLHDALRDMVEPEVIPKL--MEAGIVEVAPLAY
T ss_dssp		ECSCCTTCCCSGCC-----CTTHHHHHHTTTSTCTTHHHH---HHHTSEEEEEGGG
T ss_pred		eCCcHHHHhhcccCCChHhhhHHHHHHHHHHHHhhcChhhhHHH---HHCCCEEEcChHH

Q ss_pred		EEEcHHhcCHHHHHHHHhhcCCCCEEEEEC	
Q Klein_Draft	167	VIFDEAMTITPGSLKALLPTVSSRPNPQIVYTGTA	201 (510)
Q Consensus	167	v~iDe~~~~~l~~~~~i~~~stp +++   +..+...+..+...+. . .++++  +	201 (510)
T Consensus	126	i iide~~~~~--~~~~i~lg~	158 (208)
T 3B85_B	126	VILDEAQNTTPAQMKMFLTRLGF--GSKMVTGDI	158 (208)
T ss_dssp		EEECGGGCCHHHHHHHHTBCS--SCEEEEEC-	
T ss_pred		EEeEChhhCCHHHHHHHHhccC--CcEEEEEC	

30. [Template alignment](http://www.ebi.ac.uk/pdbe/entry/pdb/3iuy) | [Template 3D structure](http://www.ebi.ac.uk/pdbe/entry/pdb/3iuy) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/3iuy\)](http://www.ebi.ac.uk/pdbe/entry/pdb/3iuy)  
[3IUY B \(http://pdbs.rcsb.org/pdb/explore.do?structureId=3IUY\)](http://pdbs.rcsb.org/pdb/explore.do?structureId=3IUY) Probable ATP-dependent RNA helicase  
**Structural Genomics, Structural; HET: AMP; 2.4A {Homo sapiens}**  
 Probability: 97.8    E-value: 5.7E-6    Score: 76.17    Aligned Cols: 162    Identities: 15%    Similarity:

Q ss_pred		HHHHHHHHHCC-CCCHHHHHHHHHhccChhhhhccCCcchhhheeEeeEEecCCCCH
Q Klein_Draft	20	QEAIIDLAACGL-ILDWPQELCLHEALKESDELVLQLESGAWVKKWAASSFGLVSRQNGK
Q Consensus	20	~~~~~l~Q~~~~~g~~~~~rg~GK ...+-.++ .+++ .+++..+.. .+.+++ +
T Consensus	29	~~~~~Q~~~~~-----~~~~~li~~~~~g~GK
T 3IUY_B	29	PDLLKSIIRVGILKPTPIQSQAWPIILQ-----GIDLIVVAQTGTGK
T ss_dssp		HHHHHHHHHHTCCSCCHHHHHHHHHHT-----TCCEEEECCTTSCH

<u>T ss_pred</u>		HHHHHHHHHCCCCCHHHHHHHHHHHHHHC-----CCCEEECCCCCH
<u>Select all</u>	<u>Forward</u>	<u>Forward Query MSA</u> <u>Color Seqs</u> <u>Unwrap Seqs</u>
Q ss_pred		HHHHHc-----CeeEEEECCCHHHHHHHHHHHHHHHhhcc-cchhhceeccCCeEEEe
Q Klein_Draft	89	GLILFG-----ERLIHSAHEFKTAVNGMERLESLAKS-GLKYKAKQAHAESIEIL
Q Consensus	89	~~~~~ ~~~~~ +.++. .+.....   +.+.+.+.+.+. .+.....
T Consensus	81	~~~~~lii~p~~~~~
T 3IUY_B	81	HLDSQPISREQRNGPGMLVLTPTRELALHVEAECSKYSYKGLKSICITYGGRNRNQIEDI
T ss_dssp		HHTC-----CCCSEEEECSSHHHHHHHHHHHHHCCTTCCEEEEC-----
T ss_pred		HHhcCCcchhcCCCeEEEEcCHHHHHHHHHHHhhcccCCeEEEEcCCChHHHHHH
Q ss_pred		EEEC-----CCCCccccceEEEEcHHhcCH---HHHHHHhhhcccCCCEEEEEe
Q Klein_Draft	151	FQTRT-----DRSGLGLTADRVFIDEAMTITP---GSLKALLPTVSSRPNPQIVYTG
Q Consensus	151	~~~~~G~~~~~v~ID~~~~~ ~~~~~ +.+. .+.....   +.+. .+.. .+.. .+....
T Consensus	148	v~t~~~~~iiide~~~~~i~~~~~--~~~~~i~s
T 3IUY_B	148	IATPGRNLNDQMNSVNLRISITYLVIDEADKMLMEFEPQIRKILLDVRP--DRQTVMTS
T ss_dssp		EECHHHHHHHHTTSCCTTCCEEEECCHHHHHHTTCHHHHHHHHHHSCS--SCEEEEE
T ss_pred		EECHHHHHHHhhCCCcccccccEEEEcCHHHhhcccCHHHHHHHHHhCCc--cCeEEEE

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

31. [3IUY A \(http://pdbe.rcsb.org/pdb/explore.do?structureId=3IUY\)](http://pdbe.rcsb.org/pdb/explore.do?structureId=3IUY) Probable ATP-dependent RNA helicase  
Structural Genomics, Structural; HET: AMP; 2.4A {Homo sapiens}

Probability: 97.8    E-value: 5.7E-6    Score: 76.17    Aligned Cols: 162    Identities: 15%    Similarity:

Q ss_pred		HHHHHHHHHCC-CCCHHHHHHHHHhccChhHhhccCCcchhhheeEeeEEecCCCCH
Q Klein_Draft	20	QEAI DLAAACGL-ILD PQWELCLHEALKEDELVQLESGAWVKKWAASSFGLVVS RQNGK
Q Consensus	20	~~~~~1~~~~~Q~~~~~g~~~~~r~GK ...+-.+...++ .+++ .+++...+... . . .+++ .+++ +
T Consensus	29	~~~~~Q~~~~~-----~~~~~li~~~~~g~GK
T 3IUY_A	29	PDLLKSIIRVGILKPTPIQSQAWPIILQ-----GIDLIVVAQTGTGK
T ss_dssp		HHHHHHHHHTCCSCCHHHHHHHHHHT-----TCEEEEECCTTSCH
T ss_pred		HHHHHHHHHCCCCCHHHHHhHHHHhHC-----CCCEEECCCCCH

Q ss_pred		HHHHC-----CeeEEEEcCCHHHHHHHHHHHHHHHcc-cchhhceeccCCeEEE
Q Klein_Draft	89	GLILFG-----ERLIHSAHEFKTAVNGMERLESLIAKS-GLKYKAKQAHAESIEIL
Q Consensus	89	~~~~~-----~ini~~ntt~~a~~~~~l~~~~~in~~ +.+++           ...+++++ +...+.++...+.         .....
T Consensus	81	~~~~~liip~~~~~
T 3IUY_A	81	HLDSQPISREQRNGPGLVLTPTRELALHVEAECSKYSYKLGKSICITYGGRNRNQIEDI
T ss_dssp		HHC-----CCCSEEEECSSHHHHHHHHHHHHHCCTTCCEEEEC-----CHHHH
T ss_pred		HHhcCCcchhcCCCCEEEEcCCHHHHHHHHHHHhccCCCCEEEECChHHHHHH

Q ss_pred		EEEEC-----CCCCccceEEEEcHHhcCH---HHHHHHHHhhcCCCCEEEEEE
Q Klein_Draft	151	FQTRT-----DRSGLGLTADRVFDEAMTITP---GSLKALLPTVSSRPNPQIVYTG
Q Consensus	151	~~~~~-----~~~~~G~~~~~V~IDE~~~~~-----~~~~~l~~~~~i~~~~~ +.+. . . . .+.+++++  +.+. . .+.+. . .+. . .+++++
T Consensus	148	v~t~~~~~i~IDE~~~~~i~~~~~-----i~~~~~
T 3IUY_A	148	IATPGRNLNDQMNSVNLRSITYLVIDEADKMLDMEFEPQIRKILLDVRP--DRQVTMTS
T ss_dssp		EECHHHHHHHHHTTCCCTTTCCEEEECCHHHHHHTTCHHHHHHHHHHSCS--SCEEEEE
T ss_pred		EECHHHHHHHHhCCCCccccccEEEEEcHHHHHccccHHHHHHHHhCCc--cCeEEEE

Template alignment | Template 3D structure | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/3ly5>)

32. [3LY5 B \(http://pdbe.rcsb.org/pdb/explore.do?structureId=3LY5\)](http://pdbe.rcsb.org/pdb/explore.do?structureId=3LY5) ATP-dependent RNA helicase DDX18 (E. Structural Genomics, Structural Genomics; 2.8Å {Homo sapiens})

Probability: 97.79	E-value: 7.3E-6	Score: 77.48	Aligned Cols: 163	Identities: 12%	Similarity
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Vis	Hits	Aln	Select all	Forward	Forward Query MSA	Color Segs	Unwrap Segs
			Q ss_pred		HHHHHHHHHHCC-CCCHHHHHHHHHHHCCCHHHhccCCCHHHhheEeeEEecCCC		
			Q Klein_Draft	18	AGQEAI DLAAACGL-ILDPWQELCLHEALKESDELVLQLESGAWVKKWAASSFGLVVSQRN		
			Q Consensus	18	~~~~~1~~~Q~~~~~g~~~~~rg~		
					+...+.+.+++ . +++ .+.+.+. . . . .+++ +		
			T Consensus	61	~~~~~1~~~~~Q~~~~~1~~~~~Gs		
			T 3LY5_B	61	VNENTLKAIKEMGFTNMTEIQHKSIRPLLE-----GRDLLAAAKTGS		
			T ss_dssp		CCHHHHHHHHTTCCBCCHHHHHHHHHHH-----TCCCEECCTTS		
			T ss_pred		cCHHHHHHHHCCCCCHHHHHHHHHHC-----CCeEEEECCCC		
			Q ss_pred		HHHHH----hCCeeEEEEcCHHHHHHHHHHHHHHcc--cchhhceeccCCeEEE		
			Q Klein_Draft	87	LAGLIL----FGERLIHSAHEFKTAVNGMERLESIAKS--GLKYKAKQAHAESIEI		
			Q Consensus	87	~~~~~i~~~~~t~~~~~a~~~~~1~~~~~i~~		
					...+. . .+.++++ +.+.+.+.+. . . . .		
			T Consensus	113	~~~~~li~p~~~1~~~~~		
			T 3LY5_B	113	VELIVKLRFMPRNGTGVILSPTRELAMQTFGVLELMTHHVHTYGLIMGGSNRSAEAQK		
			T ss_dssp		HHHHHTTCCCTTCCCEEEECSSHHHHHHHHHHHHHTTCCCEEEECSSSCHHHHHHH		
			T ss_pred		HHHHHHhccccccceEEEEcCHHHHHHHHHHHHHhccCCCeEEEEcCCCHHHHHHH		
			Q ss_pred		EEEECC-----CCCCcccccEEEEEcHHhCH---HHHHHHhhhhCCCCCEEE		
			Q Klein_Draft	150	IFQTRT-----DRSGLGLTADRVI FDEAMTITP----GSLKALLPTVSSRPNPQIVY		
			Q Consensus	150	~~~~~G~~~~~V~iDE~~~~~1~~~~~i~~		
					+.+. . . . .+++ + +++. . .+.+.+. . . .+++		
			T Consensus	180	iv~t~~~~~1~~~~~V~iDE~h~~~~~i~~~~~v~1		
			T 3LY5_B	180	IVATPGRLLDHMQNTPGFMYNLQCLVIDEADRI LDVGFEELKQIKLLPTR-RQTM LF		
			T ss_dssp		EECHHHHHHHHHCTTCCCTTCCCEEECSHHHHHTTCHHHHHHHHHHSCSS-SEEEEE		
			T ss_pred		EEEcHHHHHHHHhCCCCcChhccEEEEcHHHHhCCHHHHHHHHHCCCC-CEEEEE		

33. [Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/3ly5\)](#)  
[3LY5 A \(http://pdb.rcsb.org/pdb/explore.do?structureId=3LY5\)](#) ATP-dependent RNA helicase DDX18 (E. Structural Genomics, Structural Genomics; 2.8A {Homo sapiens})

Probability: 97.75 E-value: 8.7E-6 Score: 76.95 Aligned Cols: 163 Identities: 12% Similarity

Q ss_pred		HHHHHHHHHHCC-CCCHHHHHHHHHHccChhHhccCCcchhhheeEeeEEecCCC
Q Klein_Draft	18	AGQEAI DLAAACGL-ILDPWQELCLHEALKESDELVLQLESGAWVKKWAASSFGLVVSQRN
Q Consensus	18	~~~~~1~~~Q~~~~~g~~~~~rg~
		+...+.+.+++ . +++ .+.+.+. . . . .+++ +
T Consensus	61	~~~~~1~~~~~1~~~Q~~~~~1~~~~~G~
T 3LY5_A	61	VNENTLKAIKEMGFTNMTEIQHKSIRPLLE-----GRDLLAAAKTGS
T ss_dssp		CCHHHHHHHHTTCCBCCHHHHHHHHHHH-----TCCCEECCTTS
T ss_pred		cCHHHHHHHHCCCCCHHHHHHHHHHC-----CCeEEEECCCC
Q ss_pred		HHHHH----hCCeeEEEEcCHHHHHHHHHHHHHHcc--cchhhceeccCCeEEE
Q Klein_Draft	87	LAGLIL----FGERLIHSAHEFKTAVNGMERLESIAKS--GLKYKAKQAHAESIEI
Q Consensus	87	~~~~~i~~~~~t~~~~~a~~~~~1~~~~~i~~
		...+. . .+.++++ +.+.+.+.+. . . . .
T Consensus	113	~~~~~vli~p~~~1~~~~~
T 3LY5_A	113	VELIVKLRFMPRNGTGVILSPTRELAMQTFGVLELMTHHVHTYGLIMGGSNRSAEAQK
T ss_dssp		HHHHHTTCCGGGCCCEEEECSSHHHHHHHHHHHHHTTCCSCEEECSSSCHHHHHHH
T ss_pred		HHHHHHhccccccceEEEEcCHHHHHHHHHHHHHhccCCCeEEEEcCCCHHHHHHH
Q ss_pred		EEEECC-----CCCCcccccEEEEEcHHhCH---HHHHHHhhhhCCCCCEEE
Q Klein_Draft	150	IFQTRT-----DRSGLGLTADRVI FDEAMTITP----GSLKALLPTVSSRPNPQIVY
Q Consensus	150	~~~~~G~~~~~V~iDE~~~~~1~~~~~i~~
		+.+. . . . .+++ + +++. . .+.+.+. . . .+++
T Consensus	180	iv~t~~~~~1~~~~~V~iDE~h~~~~~i~~~~~i~1
T 3LY5_A	180	IVATPGRLLDHMQNTPGFMYNLQCLVIDEADRI LDVGFEELKQIKLLPTR-RQTM LF
T ss_dssp		EECHHHHHHHHHCTTCCCTTCCCEEECSHHHHHTTCHHHHHHHHHHSCSS-SEEEEE



- ☐ 34. [Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/1q0u\)](#)  
[1Q0U\\_B \(http://pdb.rcsb.org/pdb/explore.do?structureId=1Q0U\)](#) BstDEAD; DEAD PROTEIN, RNA BINDING  
stearothermophilus} SCOP: c.37.1.19

Probability: 97.74 E-value: 7.3E-6 Score: 74.41 Aligned Cols: 163 Identities: 13% Similarity

```
Q ss_pred      hHHHHHHHHHCC-CCCHHHHHHHHhccChhHhccCCcchhhheeEeeEEecCCC
Q Klein_Draft  18 AGQEAI DLAAACGL-ILD PWQELCLHEALKESDELVLQLESGAWVKWAASSFGLVVSQRN
Q Consensus    18 ~~~~~~1~~~Q~~~~~g~~~~~rg~
      +.....+.+.+.+. +++++|.+.+.+.+. . . . . +. +. +. +. +
T Consensus    11 ~~~~~~Q~~~~~-----~i~~~~~G~
T 1Q0U_B       11 FQPFIEAIKTLRFYKPTETIERIPGALR-----GESMVGQSQTGT
T ss_dssp      CCHHHHHHHHTTCCSCCHHHHHHHHHHT-----TCCEEEECCTTS
T ss_pred      CCHHHHHHHHCCCCCCHHHHHHHHHHc-----CcEEEECCCCC

Q ss_pred      HHHHHHhC-CeeEEEEcCHHHHHHHHHHHHHHc-----ccchhhceeccCCeEEEE
Q Klein_Draft  87 LAGLILFG-ERLIHSAHEFKTAVNGMERLESIAK-----SGLKYKAKQAHAESIEI
Q Consensus    87 ~~~~~~i~~~~~t~~~a~~~~~1~~~~~i~~~~~
      .+.+.+. . . . +++++|.+.+.+.+. . . . . +. +. +. +. +
T Consensus    63 ~~~~~~lv~~p~~~~~
T 1Q0U_B       63 MEKIKPERAEVQAVITAPTRELATQIYHETLKITKFCPKDRMIVARCLIGGTDKQKALEK
T ss_dssp      HHCCTTSCSCCEEEECSSHHHHHHHHHHHHHTTSCGGGCCCEEEECSSHHHHHHCC
T ss_pred      HHHHhccCcCEEEEcCHHHHHHHHHHHHhccCCcCeEEEEEEcCCCHHHHHH

Q ss_pred      EEEEC-----CCCCccceEEEEcHHhCH---HHHHHHhCCHCCCEEEEE
Q Klein_Draft  150 IFQTRT-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRPNQIVYT
Q Consensus    150 ~~~~~~G~~~~~V~iDE~~~~~1~~~~~i~~~~~
      .+.+. . . . . +++++|.+.+.+. . . . +. +. +. +. +
T Consensus    130 ~v~t~~~~~i~iDE~~~~~i~~~~~s
T 1Q0U_B       130 VIGTPGRINDFIREQALDVHTAHILVVDEADLMDMGFITDQVIAARMPKD-LQMLVFS
T ss_dssp      EEECHHHHHHHHTTSCCTTCCEEECSHHHHHHHTTCHHHHHHHHTSCTT-CEEEEE
T ss_pred      EEECHHHHHHHHCCCCChcCEEEEcCHHHHccCCHHHHHHHHCCCC-cEEEEE
```

- ☐ 35. [Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/2g9n\)](#)  
[2G9N\\_A \(http://pdb.rcsb.org/pdb/explore.do?structureId=2G9N\)](#) Eukaryotic initiation factor 4A-I (E.C.3  
DDX2A, RNA, Structural; 2.25A {Homo sapiens} SCOP: c.37.1.19

Probability: 97.72 E-value: 1.1E-5 Score: 73.83 Aligned Cols: 166 Identities: 14% Similarity

```
Q ss_pred      hHHHHHHHHHCCCC-CCCHHHHHHHHhccChhHhccCCcchhhheeEeeEEecCCC
Q Klein_Draft  18 AGQEAI DLAAACGLI-LDPWQELCLHEALKESDELVLQLESGAWVKWAASSFGLVVSQRN
Q Consensus    18 ~~~~~~1~~~Q~~~~~g~~~~~rg~
      +.....+.+.+.+. +++++|.+.+.+.+. . . . . +. +. +. +. +
T Consensus    22 ~~~~~~Q~~~~~i~~~~~-----~G~
T 2G9N_A       22 LSESLLRGIYAYGEKPSAIQQRAILPCIK-----GYDVIAQAQSGT
T ss_dssp      CCHHHHHHHHTTCCSCCHHHHHHHHHH-----TCCEEEECCTTS
T ss_pred      CCHHHHHHHHCCCCCCHHHHHHHHHHc-----CCEEEECCCCC

Q ss_pred      HHHHHHhC-CeeEEEEcCHHHHHHHHHHHHHHhccchhhceeccCCeEEECCTTS
Q Klein_Draft  87 LAGLILFG-ERLIHSAHEFKTAVNGMERLESIAKSGSKYKAKQAHAESIEILDGPNP
Q Consensus    87 ~~~~~~i~~~~~t~~~a~~~~~1~~~~~i~~~~~
      .+.+. . . . +++++|.+.+.+.+. . . . . +. +. +. +. +
T Consensus    74 ~~~~~~li~~p~~~~~
T 2G9N_A       74 LQQIELDLKATQALVLAPTRELAAQQIQKVMALGDYMGASCHACIGGTNVRAEVQKLQME
T ss_dssp      HHHCCTTCCSCCEEEECSSHHHHHHHHHHHHHTTTTCCEEEECCTTS
T ss_pred      HHHHHHhccCCCCEEEEcCHHHHHHHHHHHHHhCCEEEEcCCCHHHHHHHHHH
```



T Consensus	62	~~~~~1~~~~~p~~~~~
Select all	Forward	Forward Query MSA
T 5GJU_A	62	NLDPELRAPQLVLEAPFRELAQVAEAMTDFSKHMRGVNVVAETGGGRTDVQLRAL---R
T ss_dssp		TSCTTCCSCCEEEECSSHHHHHHHHHHHHHTTTSTTCCEEEEC-----CHHHHH---H
T ss_pred		HhchhhCCCEEEEEcCHHHHHHHHHHHHHHccCCCCEEEEEECCcCHHHHHHHH---h
Q ss_pred		C-----CCCCccceEEEEcCHhCH---HHHHHHHhChCCCCCEEEEEcCC
Q Klein_Draft	155	T-----DRSGLGLTADRVIIDEAMTITP----GSLKALLPTVSSRPNPQIVYGTAA
Q Consensus	155	~~~~~G~~~~~V~iD~~~~~1~~~~~i~~~~~stp~
		. . . . . ++++++    + + . + . . . + . + . . + . . . . + + + +   + .
T Consensus	129	~1~~~~~liiD~~~~~i~~~~~sat~
T 5GJU_A	129	GRLLDHLKRGTLDSLKSLGLVLDEADEMLRMGFIEDVETIMAQIPEG-HQTALFSATMP
T ss_dssp		HHHHHHHHHTSSCCTTCCEEEESHHHHHHTTCHHHHHHHHTSCSS-CEEEECSSCC
T ss_pred		HHHHHHHHhCCCCHHhcCEEEEcCHHHHHhcCCHHHHHHHhCCCC-CEEEEEcCCC

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/5qvr\)](http://www.ebi.ac.uk/pdbe/entry/pdb/5qvr)

38. [5GVR A \(http://pdb.rcsb.org/pdb/explore.do?structureId=5GVR\)](http://pdb.rcsb.org/pdb/explore.do?structureId=5GVR) Probable ATP-dependent RNA helicase protein, HYDROLASE; 1.5A {Homo sapiens}

Probability: 97.62    E-value: 2.2E-5    Score: 72.39    Aligned Cols: 164    Identities: 11%    Similarity

Q ss_pred		chHHHHHHHHHCC-CCCCHHHHHHHhhcChhhhccCCcchhhheeEeeEEecCC
Q Klein_Draft	17	SAGQEADLAAACGL-ILDPWQLCLHEALKESDELVLQLESGAWVKKWAASSFGLVVSRL
Q Consensus	17	~~~~~l~~~~~q~~~~~g~~~~~rg +. . . . +. . . . +. + + +   . +. +. +. +. . . . + + +. + + +
T Consensus	19	~~~~~l~~~~~q~~~~~-----~~~~~li~~~~~g
T 5GVR_A	19	KFPAAILRGLKKGIHHPPTPIQIQIPTILS-----GRDMIGIAFTG
T ss_dssp		TCCHHHHHHHHTTCCSCCHHHHHHHHHHT-----TCCEEEECCTT
T ss_pred		CCCHHHHHHHHCCCCCCcHHHHhHHHHHHhc-----CCcEEEEcCCC

```
Q ss_pred          HHHHHHHhh-----CCeeEEEEcCCHHHHHHHHHHHHHHHHhc-----ccchhhc
Q Klein_Draft      86 ELAGLILF-----GERLIHSAHFETAVNGMERLESIAK-----SGLKYKA
Q Consensus        86 ~~~~~~-----~i~n~t~a~~~~~-----~l~n~
                   ++.+...    ....++++|+...+.++...+.....    .....
T Consensus        71 ~~~~~~~~~~~li~~p~~~~~
T 5GVR_A           71 VIMFCLEQEKRLPFSKREGPYGLIICPSRELARQTGHILEYCRLLQEDSSPLRLCALCI
T ss_dssp          HHHHHHHHHHSCCTTCCCSEEEECSCHHHHHHHHHHHHHHHHTTSCCCCEEEEC
T ss_pred          HHHHHHHHHhhCCCCCCCCeEEEecChHHHHHHHHHHHHHHHC CCCCceEEEEe
```

Q ss_pred		EeCCCCCCEEEEEEC-----CCCCccceEEEEEcHHhcH---HHHHHHhhhh
Q Klein_Draft	139	ILDGPNPGARVIFQTRT-----DRSGLGLTADRVIIDEAMTITP---GSLKALLPTV
Q Consensus	139	~~~~~g~~~i~~~~~-----~~~~~G~~~~~v~iDE~~~~~-----~~~~~l .. ..+.+ .+.+. . . . . .+++++  ++.+. . .+.+.+.+
T Consensus	141	~-::~~~~~~i~v~t~~~~~l~~~~~vviiDE~~~~~::~~~~~~i~~~~~
T 5GVR_A	141	TI---RHGVHMVATPGRLDLLQKKMVSLDICRYLALDEADRMIDMGFECDRTIFSYP
T ss_dssp		HH---HTCCSEEEEECHHHHHHHHHTSSCTTCCEEEEEESHHHHHHTTCHHHHHHHHTTC
T ss_pred		HH---hcCCCCEEEECHHHHHHHHhCCCChhhccEEEEecHHHHhhCcCHHHHHHHhhc

Q ss_pred		EecCC	
Q Klein_Draft	198	TGTAA	202 (510)
Q Consensus	198	~stp~	202 (510)
		++ +.	
T Consensus	207	sat~~	211 (234)
T 5GVR_A	207	SATMP	211 (234)
T ss_dssp		ESCCC	
T ss_pred		EccCC	

**1HV8 B** (<http://pdb.rcsb.org/pdb/explore.do?structureId=1HV8>) DEAD BOX HELICASE; Helicase, RNA-binding protein  
Select all | Forward | Forward Query MSA | Color Segs | Unwrap Segs  
[PDB Entry 1HV8 B](#) | [Metamaps](#) | [DocGen](#) | [Annotations](#) | [SeqOP](#): c.37.1-19

Probability: 97.59    E-value: 1.5E-5    Score: 78.78    Aligned Cols: 162    Identities: 12%    Similarity

Q ss_pred		hhhhhhhhhHHcCC-CCCHHHHHHHHHHhcChhHhhccCCCchhhhhheeEeeEEecCCC
Q Klein_Draft	18	AGQEAIIDLAACGL-ILDPWQELCLHEALKESDELVLQLESGAWVKKWAASSFGLVVSQRN
Q Consensus	18	~~~~~1~~~Q~~~~~g~~~~~rg~ +.....++..+ . +++ .+.+.+. . . . .+++ .+++ +
T Consensus	13	~~~~~1~~~~~Q~~~~~-----1~~~~G~
T 1HV8_B	13	LSDNILNAIRNKGFKEPTDIQMVIPLFLN-----DEYNIVAQARTGS
T ss_dssp		CCHHHHHHHHHHTCCSCCHHHHHHHHHHH-----TCSEEEEECCSSS
T ss_pred		CCHHHHHHHHHCCCCCChHHHHhhHHHhc-----CCCEEEEeCCCC

```

Q ss_pred          HHHHHHHhCCeeEEEEcCCHHHHHHHHHHHHHHHHHHhcc--cchhhceecCCCeEEEEcCCC
Q Klein_Draft      87  LAGLILFGERLIHSAHEFKTAVNGMERLESIAKS--GLKYKAKQAHGAESIEILDGPN
Q Consensus        87  ~~~~~~i~i~nt~a~~~~~--l~~~~~i~~~~~
                    ...+...+...++++|+...+...+.....+.~.....
T Consensus        66  ~~~~~~liv~p~~~l~~~~~-----
T 1Hv8_B           66  IELVNENNGIEAII LPTRELAIQVADEIESLKGKNLKIAYIGGKA IYPQIKAL----
T ss_dssp          HHHSCSSSSCCEEEECSCHHHHHHHHHHHHHHSCSCCEEEECTTSCHHHHHHHH----
T ss_pred          HHHHHhCCcCEEEECCHHHHHHHHHHHHHhCCCCcEEEEECcCCcHHHHHHHH----

```

Q ss_pred		C-----CCCCccceEEEEEcHHhcCH---HHHHHHHHhhcCCCCEEEEEEcC
Q Klein_Draft	155	T-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRPNPQIVYTGTA
Q Consensus	155	~-----~G~~~~~V~iDE~~~~~-----~l~~~~~i~~~~~stp
		.        .....++++++  ++....    .+.+.+.+.+.+.+.+++++
T Consensus	132	~l~~~~~v~iDE~h~~~~~-----~i~~~~~sat~
T 1Hv8_B	132	GRILDHINRGTLNLKNVKYFILDEADEMLNMGFIKDVEKILNACNKD-KRILLFSATM
T ss_dssp		HHHHHHHHHTTSSCGGGCCEEEEETHHHHHHTTTTHHHHHHHHHTSCSS-CEEEEEESSC
T ss_pred		HHHHHHHHcCCCChhcccEEEEEEcHHHHhccchHHHHHHHHhhCCCC-cEEEEEEcCC

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/4a4d\)](http://www.ebi.ac.uk/pdbe/entry/pdb/4a4d)

40. [4A4D A \(http://pdb.rcsb.org/pdb/explore.do?structureId=4A4D\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4A4D) PROBABLE ATP-DEPENDENT RNA HELICASE, RNA-BINDING; 2.7A {HOMO SAPIENS}

Probability: 97.58    E-value: 2.7E-5    Score: 72.9    Aligned Cols: 179    Identities: 12%    Similarity:

Q ss_pred		CCCCCCEeCCCCCchHHHHHHHHHhCCCCCHHHHHHHHHhccChhHhccCCcchh
Q Klein_Draft	2	GVQEPRIWLSPEANSSAQGEAIDLAAACGLILDPWQELCLHEALKESDELVLQLESgAWVK
Q Consensus	2	~~~~~1~~~Q~~~~~g~~~~~ +.+. .....+.....+.++++ .+++.+..
T Consensus	35	~~~~~1~~~~~Q~~~~~-----
T 4A4D_A	35	GHNCPKPVLFNFYEANFPANVMDVIARQNFTEPTAIQAGWPVALS-----
T ss_dssp		SSSSCCCCSSGGGSCCCHHHHHHHHHHCCSCCHHHHHHHHHHT-----
T ss_pred		CCCCCCCCcchHCCCCCHHHHHHHHHCCCCCCHHHHHHHHHHhC-----

Q ss_pred		ecCCCCHHHHHHHHHHHHHHHhC-----CeeEEEEcCCHHHHHHHHHHHHHHhc--c-
Q Klein_Draft	72	VSRQNGKGSILEALELAGLILFG-----ERLIISHAHEFKTAVNGMERLESIAKS--G
Q Consensus	72	~r~g~GKT~::~::~::~::~::~::~::~::~::~::~::~i~n~t~t~a~::~::~::~::~::~::~
		+++ +   .++...++..+...+. . .+++++ +...+..+...+..... .
T Consensus	87	~r~g~GKT~::~::~::~::~::~::~::~::~::~::~::l~i~p~::~::~::~::~::~::~
T 4A4D_A	87	AQTGSGKTL SYLLPAIVHINHQPFL ERGDGPICLV LAPTRELAQQVQQA EYCRACRLK
T ss_dssp		CCTTSSCHHHHHHHHHHHHHSSCCCTTCCCSEEECSHHHHHHHHHHHHHTTTTC
T ss_pred		cCCCCHHHHhhHHHHHHHHhCc ccccccCceEEEEcChHHHHHHHHHHHHHHhCCCe

Q ss_pred		CceEEEeCCCCcEEEEEECC-----CCCcccccEEEEEcHHHcCH---HHHHH
Q Klein_Draft	134	AESIEILDGPNPGARVIFQTRT-----DRSGLGLTADRVIFDEAMTITP---GSLKA
Q Consensus	134	~~~~~i~~~~~g~~~~~i~~~~~-----~~~~~G~~~~~v~ID~~~~~-----~~~~~ .....+.++.. .+.+..+.++++ . +.+.+.+.+



Q ss_pred		CCCCCcEeCCCCCchHHHHHHHHHhCC-CCCHHHHHHHHHhccChhHhhccCCch
Q Klein_Draft	2	GVQEPRIWLSPEANSSAQGEAIDLAAACGL-ILDPWQELCLHEALKESDELVLQLESGAWV
Q Consensus	2	~~~~~ +... .....+. .+++ . +++ .+++..+..
T Consensus	42	~~~~~f~~~~~l~~~~~l~~~~~Q~~~~i~~~~i~~~~-----
T 4LJY_A	42	GTGCPKPVTKWSQLGLSTDMVLITEKLHFGSLTPIQSQALPAIMS-----
T ss_dssp		SSCCCCCCCCGGGSCCHHHHHCCCCSCCCSCCHHHHHHHHHHT-----
T ss_pred		cCCCCCCCCcHHhCCCCHHHHHHHHHhCCCCCHHHHHHHHHHC-----

Q ss_pred		EecCCCCCHHHHHHHHHHHHHHHHhC-----CeeEEEEcCCHHHHHHHHHHHHHHHHhcc-
Q Klein_Draft	71	VVSRQNGKGSILEALELAGLILFG-----ERLIHSAHEFKTAVNGMERLESIAKS-
Q Consensus	71	~~~rg~GKT~~~~~-----~~~i~i~ntt~~a~~~~~ .+++ +   .++...++..+...+ .+++ ++ +...+.++...+.+...+
T Consensus	94	~~~tGsGKT~~~~~lil~P~~~l~~q~~~~~
T 4LJY_A	94	ISKTGSGKTI SYLLPLLRQVKAQRPLSKHETGPMGLIAPTRELALQIHEEVTKFTEADT
T ss_dssp		ECCTTSCHHHHHHHHHHHHHHTSCCCCTTCCCCSEEEECSSHHHHHHHHHHHHHTTCT
T ss_pred		EcCCCCcHHHHhhHHHHHHHHHhCccCccCCCCcEEEECCcHHHHHHHHHHHHHhCccc

```
Q ss_pred          ccCCcEeEEEcCCCCCEEEEEEC-----CCCcccccEeEEEcHHhc---C
Q Klein_Draft      131 AHGAESIEILDGPNPGARVIFQTRT-----DRSGLGLTADRIVFDEAMTI---T
Q Consensus        131 ~~~~~i~~~~~g~~~i~~~~~-----~~~~~G~~~~~v~iDe~~~~~
                    .....   .+.|.+.+.+           .....++++|+|+++.   .
T Consensus        164 ~~~~~-~~~~~iiiT~~~~l~~~~~-----iViDeah~~~~~
T 4LJY_A           164 SEMKKQITDL--KRGTEIIVATPGRFIDILTLNDGKLSTKRITFVVMDEADRLFDLG
T ss_dssp           SCTHHHHHHH--TTCCSEEECHHHHHHTTHHHHTSSCSTTCCEEETTHHHHHHTTC
T ss_pred          ccHHHHHHHH--HhCCCEEECHHHHHHHHHCCCCeCCceEEEcCHHHhhCc
```

Q ss_pred		hCCCCCEEEEEeCC	
Q Klein_Draft	187	VSSRPNPQIVYGTAA	202 (510)
Q Consensus	187	l~~~~~i~~~~stp	202 (510)
		+... ..+ttt+ +.	
T Consensus	231	~~~~~i~~SaT~	245 (493)
T 4LJY_A	231	VRPD-KQCVLFSATFP	245 (493)
T ss_dssp		SCTT-CEEEEEESCCC	
T ss_pred		CCCC-CEEEEECCCC	

Q ss_pred		hhhhhhhhhhhhcCC-CCCHHHHHHHHHHhccChhHhhccCCcchhhhe--eEeEEeEc
Q Klein_Draft	18	AGQEAIIDLAAACGL-ILDPWQELCLHEALKESDELVLQESGAWVKKWA--SSFGLVVS
Q Consensus	18	~~~~~1~~~Q~~~~~g~~~~~ +...+.+...++ .+++ .+.+.+. . .+++.
T Consensus	29	~~~~~Q~~~~~-----i~~~
T 2KBE_A	29	LAPELLKGIYAMKFQPSKIQRALPLLLH-----NPPRNMIAQSQS
T ss_dssp		SCHHHHHHHHHSSSSCCSCHHHHHHHHSSC-----CSSCCEEEESST
T ss_pred		CCHHHHHHHHHCCCCCCHHHHHHHHHhC-----CCCCCEEEeCC

```

Q ss_pred          HHHHHHHHhC-CeeEEEEcCCHHHHHHHHHHHHHHHHHccccchhceecCCceEEEcCC
Q Klein_Draft      85  LELAGLILFG-ERLIISAHFEKTVANGMERLESIAKSGLYKAKQAHGAESIEILDGP
Q Consensus         85  ~~~~~~i~~~~t~~~~a~~~~~l~~~~~i~~~~~
                      .+. . . . .+. . . . .+++++|+. . .+. . . .+. . . . .

```

Q ss_pred		HHHHHHHHHCC-CCCHHHHHHHHHhccChhHhhccCCcchhhheeEeeEEecCCCCH
Q Klein_Draft	20	QEAIIDLAAACGL-ILDPWQELCLHEALKESDELVLQLESGAWVKKWAASSFGLVSRQNGK
Q Consensus	20	~~~~~1~~~~~g~~~~~rg~GK ...+-.+.+++ .+.++ .+.+.+.+. .+.+++. +
T Consensus	33	~~~~~1~~~~~Q~~~~~-----~~~~~i~~~~~g~GK
T 20XC A	33	RPVLEGLRAAGFERPSPVLKAIPLGRC-----GLDLIVQAKSGTGK

Vis

Hits

Aln

T ss\_dssp

Select all

Forward

HHHHHHHHHTTCCSCCHHHHHHHHHHT

Forward Query MSA

Color Segs

Unwrap Segs

HHHHHHHHHTTCCSCCHHHHHHHHHHTTCCSEEEECCTTSSH

Q ss\_pred

Q Klein\_Draft

89

Q Consensus

89

T Consensus

85

T 20XC\_A

85

T ss\_dssp

T ss\_pred

Q ss\_pred

Q Klein\_Draft

155

Q Consensus

155

T Consensus

151

T 20XC\_A

151

T ss\_dssp

T ss\_pred

Q ss\_pred

Q Klein\_Draft

18

Q Consensus

18

T Consensus

36

T 3FE2\_A

36

T ss\_dssp

T ss\_pred

Q ss\_pred

Q Klein\_Draft

87

Q Consensus

87

T Consensus

88

T 3FE2\_A

88

T ss\_dssp

T ss\_pred

Q ss\_pred

Q Klein\_Draft

149

Q Consensus

149

T Consensus

155

T 3FE2\_A

155

T ss\_dssp

T ss\_pred



46.

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/3fe2\)](http://www.ebi.ac.uk/pdbe/entry/pdb/3fe2)[3FE2 A \(http://pdb.rcsb.org/pdb/explore.do?structureId=3FE2\)](http://pdb.rcsb.org/pdb/explore.do?structureId=3FE2) Probable ATP-dependent RNA helicase  
ADP, ATP-binding; HET: ADP, SO4; 2.6A {Homo sapiens}

Probability: 97.55 E-value: 3.0E-5 Score: 72.08 Aligned Cols: 163 Identities: 12% Similarity



47.

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/5jb2\)](http://www.ebi.ac.uk/pdbe/entry/pdb/5jb2)[5JB2 A \(http://pdb.rcsb.org/pdb/explore.do?structureId=5JB2\)](http://pdb.rcsb.org/pdb/explore.do?structureId=5JB2) LGP2/RNA Complex; Innate immune pa  
HET: ADP, GTP; 2.2A {Gallus gallus}





Q ss_pred		HHHHHHHC-CeeEEEEcCCHHHHHHHHHHHHHHHHcc--cchhceecCCceEEEcCC
Q Klein_Draft	87	LAGLILFG-ERLIHSAAHEFKTAVNGMERLESIAKS--GLKYAKAQAHGAESIEILDGP
Q Consensus	87	~~~~~i~nt~~a~~~~~l~~~~~i~~~~~ +..+... ..++++ +..+.++..+..... ..
T Consensus	80	~~~~~lvvp~~~l~~~~~---
T 1FUU_B	80	LQRIDTSVKAPQALMLAPTRELALQIQKVMALAFHMDIKVHACIGGTSFVEDAEGL---
T ss_dssp		HHHCCTTCCSCCEEEECSSHHHHHHHHHHHHHTTSCCCEEEECSSCHHHHHHHH---
T ss_pred		HHHHhccCCCCeEEEEcCCHHHHHHHHHHHHHhCCCCEEEEECcCCChhchHHh---



Probability: 97.49	E-value: 2.5E-5	Score: 86.17	Aligned Cols: 178	Identities: 13%	Similarity
--------------------	-----------------	--------------	-------------------	-----------------	------------

Vis

### Hits

Aln[illegible]

[Template alignment | CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam07652\)](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam07652)

55. [PF07652.13 \(http://pfam.xfam.org/family/PF07652.13#tabview=tab0\)](http://pfam.xfam.org/family/PF07652.13#tabview=tab0) ; Flavi\_DEAD ; Flavivirus DEAD domain  
Probability: 97.48 E-value: 2.0E-5 Score: 66.28 Aligned Cols: 134 Identities: 16% Similarity

Q ss_pred		heeEeeEecCCCCCHHHHHHHHHHHHCCeeEEEEcCCHHHHHHHHHHHHHccccc
Q Klein_Draft	64	AASSFGLVVSQRNGKGSILEALELAGLILFGERLIHSAHEFKTAVNGMERLESIAKSG
Q Consensus	64	~~~~~rG~GKT~~~~~i~i~~t~~~a~~~~~ ..+.+++. ++ +   +++...++..+. ++..+++++ +...+...+.....
T Consensus	3	~~~~~G~GKT~~~~~
T PF07652.13	3	KKQLIVLDPHPGAGKTRKVLPEFIHQAVE--RLWTLALAPTRVVAAEMAELNGLPVRYL
T ss_pred		CCcEEEEECCCCCHHHHHHHHHHHHHhh-CCcEEEEEchHHHHHHHHHHhcCCCcccc
Q ss_pred		CceEEEEcCCCCcEEEEEECCCCCcccccEEEEEchHhcCHHHHH--HHHhhhccc
Q Klein_Draft	134	AESIEILDGPNGPARVIFQTRTDRLSGLGLTADRVIFDEAMTITPGSLK--ALLPTVSSRP
Q Consensus	134	~~~~i~~~~~g~i~~~~~G~~~~v~iDE~~~~~l~~~~~ ..... +...+..... ..+.+++++  +++.+.+. .+.+.+.+
T Consensus	72	~~~~~---~~~~~iiDE~~~~~
T PF07652.13	72	KEIVDLM---CHATFTMRLLS--GGRVPNYNMFIMDEAHFTDPSSIAARGYSTKVDMG
T ss_pred		CceEEEE---EechHHHHhhc--CCcCCcCEEEEcHhCcChhhhhHHHHheecC
Q ss_pred		CCCC
Q Klein_Draft	201	AADQ    204 (510)
Q Consensus	201	p~~~    204 (510)  ...
T Consensus	136	~~~~~ 139 (148)





[illegible]

### Template alignment

**60.**

**TIGR04095** (<http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR04095>) dnd\_restrict\_1; DN restriction enzyme. The DNA phosphorothioate modification system dnd (DNA instability during electri shown to provide a modification essential to a restriction system.

Probability: 97.44    E-value: 2.2E-5    Score: 80.17    Aligned Cols: 148    Identities: 14%    Similarity

Q ss_pred		CCCCCHHHHHHHHHHccChhHhhccCCcchhhhhheeEeeEEecCCCCCHHHHHHHHHHH	
Q Klein_Draft	30	GLILDPWQELCLHEALKESDELVLQLESGAWVKKWAASSFGLVVSQRNGKGSILEALELAG	
Q Consensus	30	~~~l~~~Q~~~~~g~~~~~rg~GKT~~~~~ .+. +++ .+++..+. . . . . ++.+++ +  +.++..+...	
T Consensus	6	~~~l~~~Q~~~~~li~~~tG~GKT~~~~~	
T TIGR04095	6	TFELRDYQKEAIRAWFK-----NNGRGILKMATGTGKTLTALAAASKL	
T ss_pred		CCCCCHHHHHHHHHHHh-----hCCCEEEecCCCCCHHHHHHHHHHH	
Q ss_pred		EEcCCHHHHHHHHHHHHH-----HHccccchhceeccCCceEEEcCCC	
Q Klein_Draft	100	HSAEHFKTAVNGMERLESL-----IAKSGLKYKAKQAHGAESIEILDGPN	
Q Consensus	100	i~~~t~~~a~~~~~l~~~~~i~~~~~  ++ +...+.+...+.+ -...+.+.	
T Consensus	59	vi~P~~~l~~~q~~~~~i~~~	
T TIGR04095	59	VVCPYQHLVDQWAREAEKFGLNPILCYESVSNWQSELSTGLYNLNSGNQKFLAIIT---	
T ss_pred		EEechHHHHHHHHHHHHhCCCCEEecCCCCcchHhHhHhHhccCCCCceEEEE---	
Q ss_pred		CCCCCccceEEEEecHHhcCHHHHHHHHhhcCCCCCEEEEcC	
Q Klein_Draft	155	TDRSGLGLTADRVIIDEAMTITPGSLKALLPTVSSRNPQIVYTGTA	201 (510)
Q Consensus	155	~~~~~G~~~~~v~iDE~~~~~l~~~~~i~~~~~stp	201 (510)
		...-...+.++ + +++.+...+... ..+.+++	
T Consensus	125	~~~~~iViDE~h~~~~~l~saTp	168 (451)
T TIGR04095	125	QSQLRRFPGKTLTIGDEAHNLGAPRIRESLPDNI---GFRLGLSATP	168 (451)
T ss_pred		HHHHhhCCCCcEEEEecHHHcCchHHHHhCCcC---ceEEEEecCC	



Q ss_pred		hHHHHHHHHHHhCC-CCCHHHHHHHHHhCcChhHhhccCCcchhhhhheeEeeEEecCCC
Q Klein_Draft	18	AGQEAIIDLAACGL-ILDPWQELCLHEALKESDELVLQLESGAWVKKWAASSFGLVVSQRN
Q Consensus	18	~~~~~1~~~Q~~~~~g~~~~~rg~ +...+~+...++ .++++ .+.+.+. . .+.+.+.+.+ +
T Consensus	36	1~~~~~Q~~~~~-----i~~~~G~
T 3DKP_A	36	INSRLQNIIDAGFMPTPIQMQAIPVMLH-----GRELLASAPTGS
T ss_dssp		CCHHHHHHHHHTTCCSCCHHHHHHHHHHT-----TCCEEEECCTTS
T ss_pred		CCHHHHHHHHCCCCCcHHHHHHHHHhC-----CCcEEEECCCC

Q ss_pred		HHHHHH--hcCeeEEEEcCHHHHHHHHHHHHHHccchhhceecCCCeEEEcCCC
Q Klein_Draft	87	LAGLIL--FGERLIHSAHEFKTAVNGMERLESLIAKSGLYKAKQAHAESIEILDGPN
Q Consensus	87	~~~~~i~i~~t~~a~~~~~l~~~~~i~~~~~ +..+. . . . +++++ +..+. +...+. +...+. +.....+
T Consensus	88	~~~~~lv~~p~~~~~
T 3DKP_A	88	LMQLKQPANKGFRALIISPTRELASQIHRELIKISEGTGFRIHMIHKAAVAANKFGPKSS
T ss_dssp		HHHHCSCSSSCCEEEECSSHNNNNNNNNNNNHTTSTCCCECCCHNNNNHTTTSTTSC
T ss_pred		HHHHCchhcCCcCEEEcCHHHHHHHHHHHHHHCCCEEEEcchHHHHHChhhh

Q ss_pred		C-----CCCCccceeEEEEcHHhcCH-----HHHHHHhhHhCccccEEEEE
Q Klein_Draft	155	T-----DRSGLGLTADRVIFDEAMTITP-----GSLKALLPTVSSRPNPQIVYT
Q Consensus	155	~-----~~~~G~~~~v~IDe~~~~~-----~~~~~l~~~~~i~~~ .....+++++  +++.       +.+.+.+.+.+.+++++
T Consensus	158	~l~~~~~lviDe~~~~~l~~~~~i~~~S
T 3DKP_A	158	NRLIYLLKQPPGIDLASVEWLVDSDKLFDGKTGRDQLASIFLACTSHKVRRAMFS
T ss_dssp		HHHHHHHHSSSCSCCTTCCEEESSHNNHHHC--CHNNHHHHHHHCCCTTCCEEEEE
T ss_pred		HHHHHHhhCCCCChhCCEEEEECHHHHhccccchHHHHHHhhCcccCcEEEEE

Q ss_pred		CCCHHHHHHHHHHccChhHhhccCCcchhhhheeEeeEEecCCCCHHHHHHHHHHHHHH
Q Klein_Draft	32	I LDPWQELCLHEALKESDELVLQLESGAWVKKWAASSFGLVVSQRNGKGSGILEALELAGLI
Q Consensus	32	~l~~~Q~~~~~g~~~~~rgGKT~~~~~ .++++ .+
T Consensus	47	~~~~~Q~~~l~~~~~-----~~~~~ll~~~~~G~GKT~~~~~
T 2PL3_A	47	LVTETIQQTIGLALQ-----GKDVLGAAKTGSGLTLAFLVPVLEALY
T ss_dssp		BCCHHHHHHHHHHT-----TCCEEEEECTTSCHHHHHHHHHHHHH
T ss_pred		CCcHHHHHHHHHHHC-----CCCEEEEECCCCCHHHHHHHHHHHHH

Q ss_pred		eEEEEcCCHHHHHHHHHHHHHHhc--cchhhceeccCCeEEEcCCCCcEEEEEC
Q Klein_Draft	97	LIIHSAHEFKTAVNGMERLESIAKS--GLKYAKAQHAESIEILDGPNPGARVIFQTR
Q Consensus	97	~i~i~~t~n~~a~~~~~-----l~~~~~i~~~~g~i~~~~ +.++++ +...+.++...+.+.... .. ... . .... +.+.
T Consensus	99	~lliip~~~~~-----~~~~i~v~t~
T 2PL3_A	99	GVLIIISPTRLAYQTFEVLRKVGKNHDFSAGLIIGGDKLKHEAERI----NNINILVCTP
T ss_dssp		CEEEECSSHHHHHHHHHHHHHTTTSSCCEEEECCC--CHHHHHH---TTCSEEEECH
T ss_pred		cEEEEeCCHHHHHHHHHHHHHhcCCCEEEEECCCCHHHHHHH---cccCEEECh

Q ss_pred		CCCCccceEEEEEcHHhc----	HHHHHHHHhhC	CCCCCEEEEcCC	
Q Klein_Draft	157	RSGLGLTADRIVFDEAMTIT----	PGSLKALLPTVSSRPNPQIVYGTAA		202 (510)
Q Consensus	157	~~~~G~~~~~V~IDE~~~~~----	~~~~~l~~~~~i~~~~stpn		202 (510)
		.....+++++  +++. .	.+.+.+.+.+. .	.....+++++  .	



[Vis](#)[Hits](#)[Aln](#)

T ss\_dssp

Select all

[Forward](#)

HHHCCTTCCSCCEEEECSSHHHHHHHHHHHHHTTTTTCCEEEECTTSCHHHHHHHG--

HHHCCTTCCSCCEEEECSSHHHHHHHHHHHHHTTTTTCCEEEECTTSCHHHHHHHG--

[Color Segs](#)[Unwrap Segs](#)

Q ss\_pred

CC-----CCCCcccccEEEEEcHHhcCH---HHHHHHhhcCCCCEEEEEEcCC

Q Klein\_Draft

154

RT-----DRSGLGLTADRVI FDEAMTITP----GSLKALLPTVSSRPNPQIVYTGTAA

Q Consensus

154

~-----G~V~iDE~-----1~-----i~st~

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

T Consensus

128

~~1~-----V~iDE~h~-----i~sat~

T 5IVL\_B

128

PGRIIDHINRGTLRL EHVHTVVLDEADEMLNMGFI EDIEAILSHVPAE-RQTLLFSATMP

T ss\_dssp

HHHHHHHHHTCSCCTTCCEEEEESHHHHHHTTCHHHHHHHHSCSS-CEEEEEESCCC

T ss\_pred

HHHHHHHHhCCCCCHhCCEEEECCHHHHHhccCHHHHHHHHCCCHH-ceEEEEEECCC



65.

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/3pey\)](#)[3PEY A \(http://pdb.rcsb.org/pdb/explore.do?structureId=3PEY\)](#) ATP-dependent RNA helicase DBP5 (E.CATPase, Helicase, mRNA-export; HET: NO3, ADP; 1.401A {*Saccharomyces cerevisiae*}

Probability: 97.42

E-value: 5.3E-5

Score: 75.93

Aligned Cols: 161

Identities: 14%

Similarity

Q ss\_pred

HHHHHHHHHhCC-CCCHHHHHHHHHhccChhHhccCCcchhhhe--eEeeEEecC

Q Klein\_Draft

18

AGQEAI DLAAACGL-ILDPWQELCLHEALKEDELVQLESGAWVKKAA--SSFGLVVS

Q Consensus

18

~-----1~Q~-----g~-----r

+.....+.+++ .|+++|.+++..+. .+.+++.

T Consensus

12

1~-----Q~-----1~-----

T 3PEY\_A

12

LAPELLKGIYAMKFQKPSKIQERALPLLLH-----NPPRNMIAQSQS

T ss\_dssp

CCHHHHHHHHTTCCSCCHHHHHHHHHHC-----SSCCEEEEECT

T ss\_pred

CCHHHHHHHHCCCCCCHHHHHHHHHhC-----CCCCeEEecCC

Q ss\_pred

HHHHHHHHhC-CeeEEEEcCHHHHHHHHHHHHHHhccchhhceecCCceEEecCC

Q Klein\_Draft

85

LELAGLILFG-ERLIHSAHEFKTAVNGMERLESIAKSGLK YAKAQHGAESIEILDGP

Q Consensus

85

~-----~i~t~a~-----1~-----i~-----

.++.+.+.+. .++++|+.+.+.+.+. .++++.

T Consensus

64

~-----vli~p~1~-----

T 3PEY\_A

64

TMLTRVNPEDASPQAICLAPSRELARQTLEVQEMGFKITSQLIVPDSFEKNKQ----

T ss\_dssp

HHHHHCCTTCCSCCEEEECSSHHHHHHHHHHHHHTTSCCEEEESTTSSCTTSC----

T ss\_pred

HHHHHhCccccCEEEECCHHHHHHHHHHHHHhCCEEEECcCHHHHHh----

Q ss\_pred

CC-----CCCCcccccEEEEEcHHhc-----CHHHHHHHhhcCCCCEEEEEEcC

Q Klein\_Draft

154

RT-----DRSGLGLTADRVI FDEAMTI----TPGSLKALLPTVSSRPNPQIVYTGT

Q Consensus

154

~-----G~V~iDE~-----1~-----i~st~

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

T Consensus

129

~~1~-----i~iDE~h~-----i~sat~

T 3PEY\_A

129

PGTVLDLMRRKLMQLQKIKIFVLDEADNMLDQQLGQDCIRVKRFLPKD-TQLVLFSA

T ss\_dssp

HHHHHHHHHTTBCCTTCCEEEEETHHHHHHSTTHHHHHHHHTSCTT-CEEEEEESCC

T ss\_pred

HHHHHHHHhCCCCCHhCCEEEECCHHHHhccCCHHHHHHHCCCC-eEEEEEECCC



66.

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/5ld2\)](#)[5LD2 D \(http://pdb.rcsb.org/pdb/explore.do?structureId=5LD2\)](#) RecBCD enzyme subunit RecB, RecBCDHomologous Recombination; HET: ANP; 3.83A {*Escherichia coli* (strain K12)}

Probability: 97.41

E-value: 7.3E-5

Score: 80.4

Aligned Cols: 133

Identities: 20%

Similarity

Q ss\_pred

CCCHHHHHHHHHhccChhHhccCCcchhhheEeeEEecCCCHHHHHHHHHHH

Q Klein\_Draft

32

ILDPWQELCLHEALKEDELVQLESGAWVKKWAASSFGLVVSQRNGKGSILEALELAGLI

Q Consensus

32

~1~Q~-----g~-----r~GKT~-----

.+.++|+.+++.+. .+.++|.++|+|+++.+.+. .

T Consensus

150

~Q~a~-----i~G~t~GKT~1~1~

T 5LD2\_D

150

DEINWQKVAAAVALT-----RRISVISGGPGTGKTTTAKLLAALI

T ss\_dssp

SSCCHHHHHHHHH-----BSEEEEEECTTSSHHHHHHHHHHHH

T ss\_pred

CCCHHHHHHHHHh-----CCEEEEECCCCCHHHHHHHHHHH

Probability: 97.38	E-value: 4.9E-5	Score: 77.42	Aligned Cols: 162	Identities: 14%	Similarity
--------------------	-----------------	--------------	-------------------	-----------------	------------



[Vis](#)[Hits](#)[Aln](#)[Select all](#)[Forward](#)[Forward Query MSA](#)[Color Segs](#)[Unwrap Segs](#)

```
Q ss_pred          CC-----CCCCcccccEEEEcHHhcCH-----HHHHHHHHhhcCCCCEEEEEEc
Q Klein_Draft      154 RT-----DRSGLGLTADRVIFDEAMTITP-----GSLKALLPTVSSRPNQIVYGT
Q Consensus        154 ~~~~~G~~~~V~iDE~~~~~l~~~~~i~~~~~st
                      ..      ....-...+++|+|+++.~      .....+...+... ..+++++|
T Consensus        151 ~~~l~~~~~iIiDE~h~~~~~i~~~~~Sat
T 3FHT_B           151 PGTVLDWCSKLKFDPKKIKVFLDEADVMIAITQGHQDQSIRIQRMLPRN-CQMLLF SAT
T ss_dssp          HHHHHHHHTTSCSCGGGCCEEEEETHHHHHSTTTTHHHHHHHHTTSCTT-CEEEEEESC
T ss_pred          HHHHHHHHHCCCCCHhCCEEEEcHHHHHHhCCCHHHHHHHHHCCCC-CEEEEEEC
```



70.

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/1z63\)](#)[1Z63 B \(http://pdb.rcsb.org/pdb/explore.do?structureId=1Z63\)](http://pdb.rcsb.org/pdb/explore.do?structureId=1Z63) Helicase of the snf2/rad54 family/DNA; HYDROLASE-DNA complex COMPLEX; 3.0A {Sulfolobus solfataricus} SCOP: c.37.1.19

Probability: 97.37 E-value: 5.4E-5 Score: 79.09 Aligned Cols: 154 Identities: 16% Similarity

```
Q ss_pred          cCCCCCHHHHHHHHHhccChhHhhccCCcchhhheeEeeEEcCCCCHHHHHHHHHH
Q Klein_Draft      29 CGLILDPWQELCLHEALKESDELVLQLESGAWVKKWAASSFGLVSRQNGKGSILEALELA
Q Consensus        29 ~~~~l~~~Q~~~~~g~~~~~rg~GKT~~~~~
                      ...|+++|.+.+.+.~      .+.+++.|+|+.+.+.~
T Consensus        34 ~~~~l~~~Q~~~~~tG~GKT~~~~~
T 1Z63_B           34 IKANLRPYQIKGFSWMRFMKNL-----GFGICLADDMGLGKTLQTIQVFS
T ss_dssp          CSSCCHHHHHHHHHHHHT-----TCCEEECCCTTSCHHHHHHHHHH
T ss_pred          ccccChHHHHHHHHHHHH-----CCCEEEcCCCCCHHHHHHHHH

Q ss_pred          EEEcCHHHHHHHHHHHHHccchhhceccCCcEEEEcCCCCcEEEEEECC--
Q Klein_Draft      99 ILSAHEFKTAVNGMERLESLIAKSGLYKAKQAHAESIEILDGPNPGARVIFQTRT--
Q Consensus        99 ~i~~~t~~~a~~~~~l~~~~~i~~~~~g~~~i~~~~~
                      ++++| ....+.+.+.+.~      ...+.~      .+.|.+.+.~
T Consensus        90 lvv~p~~~~l~q~~~~~i~~~~~v~t~~~l~
T 1Z63_B           90 LVICP-LSVLKNWEEELSKFAPHLRFA---VFHEDRSKIKL---EDYDIILTYAVLL
T ss_dssp          EEEEC-STTHHHHHHHHHHCTTSCEE---ECSSSTTSCCG---GGSSEEEEEHHHT
T ss_pred          EEEEE-HHHHHHHHHHHHCCcCEEE---EECCccccch---hhCCEEEcHHHHH

Q ss_pred          eEEEEcHHhcCHHHHHHHhhcCCCCEEEEEEcCCCC
Q Klein_Draft      165 DRVIFDEAMTITPGSLKALLPTVSSRPNQIVYTGTAADQR 205 (510)
Q Consensus        165 ~~V~iDE~~~~~l~~~~~i~~~~~stp~~~~ 205 (510)
                      ++|+|+++.~      .....+++++|+|....
T Consensus        151 ~~vIvDE~H~~~~~l~lTaTp~~~~ 191 (500)
T 1Z63_B           151 KYIVIDEAQNIKNPQTKIFKAVKELKSKYRIALTGTPIENK 191 (500)
T ss_dssp          EEEEEETGGGSCCTTSHHHHHHTSCEEEEEECCSSCTTC
T ss_pred          cEEEEcHHHccChHHHHHHHHcCCCcEEEEcCCCCC
```



71.

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/5suq\)](#)[5SUQ C \(http://pdb.rcsb.org/pdb/explore.do?structureId=5SUQ\)](http://pdb.rcsb.org/pdb/explore.do?structureId=5SUQ) ATP-dependent RNA helicase SUB2 (E. HYDROLASE; HET: KEG; 6.0A {Saccharomyces cerevisiae (strain ATCC 204508 / S288c)}

Probability: 97.36 E-value: 6.5E-5 Score: 77.14 Aligned Cols: 163 Identities: 10% Similarity

```
Q ss_pred          hHHHHHHHHHCC-CCCHHHHHHHHHhccChhHhhccCCcchhhheeEeeEEcCCC
Q Klein_Draft      18 AGQEAIDLAAACGL-ILDPWQELCLHEALKESDELVLQLESGAWVKKWAASSFGLVSRQN
Q Consensus        18 ~~~~~~l~~~Q~~~~~g~~~~~rg~
                      +....+.+.+++|.+++|.+.+.~      .+.+++.|+
T Consensus        69 l~~l~~~l~~~~~Q~~~i~~~~~i~~~~~tGs
T 5SUQ_C           69 LKPELSRAIIDCGFHPSEVQQHTIPQSIH-----GTDVLCQAKSGL
T ss_dssp          CCHHHHHHHHTTCCSCCHHHHHHHHTT-----TCCEEEECCTTS
T ss_pred          CCHHHHHHHHCCCCCCHHHHHHHHHc-----CCcEEEECCCC
```

Q ss_pred		HHHHHHHc-CeeEEEEcCCHHHHHHHHHHHHHHHHHcc-----chhhceeccCCceeEE
Select all	Forward	LAGEFLFG-LRELLTHSAHLKLTAVNGMKRLLSLAKSG-----LKTRAKQAHGAEISIEI
Q Kiein_Draft	87	~~~~~i~~nt~~a~~~~~l~~~~~i~~
Q Consensus	87	+..+..+ ..++ ++ +...+.++...+.+...+ +.....
T Consensus	121	~~~~~lii~P~~~l~~q~~~~~
T 5SUQ_C	121	LQQLDPVPGEVAVVVICNARELAYQIRNEYLRFSKYMPDVKTAVFYGGTPISKDAELLKN
T ss_dssp		HHHCCCCCTCCCEEEECSSHHHHHHHHHHHHHTTTCTTCCEEECTTSCHHHHHHHHHHC
T ss_pred		HHHHCCCCCcEeEEEEcCcHHHHHHHHHHHHHHhhCCCceEEEeCCCCchHHHHHHhc

Q	ss_pred		EEEECC-----CCCCcccceEEEEcHHhcCH----HHHHHHHHhhcCCCCEEEE
Q	Klein_Draft	150	IFQTRT-----DRSGLGLTADRVIFDEAMTITP----GSLKALLPTVSSRPNPQIVY
Q	Consensus	150	~~~~~-----~~~~~G~~~~~v~iDe~~~~~-----~~~~~l~~~~~i~ .+.+. . . . .-..+++   +++.+. . .+.+.+.+. . .+++
T	Consensus	188	~i~T~~~~~l~~~~~v~iDeEah~~~~~-----~~~~~i~
T	5SUQ_C	188	VVATPGRLKALVREKYIDLSHVKNFVIDECDKVL EELDMRRDVQEIFRATPRD-KQVM MF
T	ss_dssp		EEECHHHHHHHHTTTSSCCTTCEEEEEETHHHHHHSHHHHHHHHHHTTSCSS-SEEEEE
T	ss_pred		EEECHHHHHHHHHhCCCCHHhCEEEEEcHHHHHHhCChHHHHHHHHhCCCC-CEEEEE

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/4ct4\)](http://www.ebi.ac.uk/pdbe/entry/pdb/4ct4)

72. [4CT4 B \(http://pdb.rcsb.org/pdb/explore.do?structureId=4CT4\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4CT4) CCR4-NOT TRANSCRIPTION COMPLEX S PROTEIN, DEADENYLATION, TRANSCRIPTION; 2.3A {HOMO SAPIENS}

Probability: 97.36    E-value: 7.5E-5    Score: 74.28    Aligned Cols: 165    Identities: 13%    Similarity

Q ss_pred		chHHHHHHHHHHcCC-CCCHHHHHHHHHhccChhHhhccCCcchhhhhheeEeeEEecCC
Q Klein_Draft	17	SAGQEaIDLAACGL-ILDPWQELCLHEALKESDELVLQLESGAWVKWAASSFGLVVSrq
Q Consensus	17	~~~~~l~~~Q~~~~~g~~~~~rg .+. . . . .+. .+++ . +++ .+++ .+. . . . .+. .+++ .+++
T Consensus	11	~l~~~l~~~~~Q~~~~~i~-----~~~~~l~~~~~g
T 4CT4_B	11	CLKRELLMGIFEMGWKPSPIQEESIPIALS-----GRDILARAKNG
T ss_dssp		CCCHHHHHHHHTTCCSCCHHHHHHHHHHT-----TCCEEEECCSS
T ss_pred		CCCHHHHHHHHHcCCCCCHHHHHHHHHhcc-----CCcEEEECCcC

Q ss_pred		HHHHHHHhC-CeeEEEEcCHHHHHHHHHHHHHHHhhcc--cchhhceeccCCceEEEc
Q Klein_Draft	86	ELAGLILFG-ERLIHSAHEFKTAVNGMERLESIAKS--GLKYKAKQAHAESIEILD
Q Consensus	86	~~~~~i~n~t~a~~~~~l~~~~~i~n~ +++.+.+.+...++++ +.+.+.+.+.+.+.+.+.+.+.+.+.+.+
T Consensus	63	~~~~~li~p~~~l~~~~~
T 4CT4_B	63	LLERLDLKDN IQAMVIVPTRELALQVSQICIQVSKHMGGAKVMATTGGTNLRDDIMRL-
T ss_dssp		HHHHHCCTTCSCCEEEECSSHHHHHHHHHHHHHTTTSSSCCEEEECTSCHHHHHHT-
T ss_pred		HHHHhccccCCCCeEEEEcCHHHHHHHHHHHHHhhcCCCEEEECcCHHHHHhc-

Q ss_pred		EECC-----CCCCcccccEEEEEcHHhcCHHHHHHHHHhhcC---CCCCEEEEEcC
Q Klein_Draft	152	QTRT-----DRSGLGLTADRVIIDEAMTITPGSLKALLPTVSS---RPNQIVYTGTA
Q Consensus	152	~~~~~-----~~~~~G~~~~~v~iDE~~~~~l~~~~~i~~~~~stp .+. . . . .- .+++++  +.+. . . .+. . . . .+ . . . .+++++ +
T Consensus	130	~t~~~~~iiIDE~h~~~~~i~~~~~sat~
T 4CT4_B	130	ATPGRILDLIKGVAKVDHVQMIVLDEADKLLSQDFVQIMEDIILTPKNRQILLYSATF
T ss_dssp		ECHHHHHHHHHTTSSCCTTCCEEEESHHTSTTTTHHHHHHHHTTSCCTTCCEEEESC
T ss_pred		ECHHHHHHHHC CCCccccccEEEEEcHHHhcChhHHHHHHHHHHCCCCCEEEEECC

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

73. [4DKW B \(http://pdb.rcsb.org/pdb/explore.do?structureId=4DKW\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4DKW) Large terminase protein; DNA-packaging terminase; HET: SO4; 2.02Å {Enterobacteria phage P22}

Probability: 97.36      E-value: 4.0E-4      Score: 63.61      Aligned Cols: 174      Identities: 8%      Similarity:

Q ss_pred	CCCCCCCCCHHHHHhCCCCCc-CCcEEEEEEcCCCCcEEEEEEEEcC-CCEEE
Q Klein Draft 295	PQFGAGISEIPLDKWRRLDNPEPDL-AGARALILYRTPEGGPWAIVGSQRCTD-GRIHVE

<u>Q Consensus</u>	<u>Select all</u>	<u>Forward</u>	<u>Query MSA</u>	<u>Color Segs</u>	<u>Unwrap Segs</u>
T Consensus	1	~~~~-G~vy~~f~~~~~p~~~g~D~a~~d~t~ai~~~~~g~~v~			
T 4DKW_B	1	TMGS--GRIFQIPEETIKCQPFECPDHFYVIDAQDFGW-NHPQAHIQLWWDKDAADVFLA			
T ss_dssp		CCBT--EESCCSCHHHHEEECCCCCTTSEEEEEEECCSS-SCEEEEEEEEETTTEEEEE			
T ss_pred		CCCC--ccccCCcchcccCCCCCCCeCeEEEEecCCC-CeEEEEEEeCCCCEEEE			
Q ss_pred		H H H H H H H H H H H H C C E E E E e C c c - - - - - H H - H H H H H H H C C C e E e C - - - - - C C H H H			
Q Klein_Draft	362	DRVVDKFIQAITAWGP EE ILVGRGG - - - - - AA-EVIPQIEAA GFTVYS - - - - - P N Q S E			
Q Consensus	362	~~~~~i~~~~~n~~~~~i~d~n~g~- - - - ~g~-~~~~l~~~~g~~~~~ - - - - ~~~~~ +.++++.+... ..++ +. + . + . + .   ++ .   + . + . ....			
T Consensus	68	~~~~~i~~~~~ - - - - - D~~~~~l~~~~G~~~~~			
T 4DKW_B	68	VQAWGA VKSWA --NKIPVA WPHDG HQ HEKG GG EQ L K T Q Y A D A G F S M L P D H A T F P D G G N S			
T ss_dssp		H H H H H H H H H H H --TTCEE EEC C S S C S S S S C H H H H H H H H H H T C E E C S S C C C C T T S C C C			
T ss_pred		H H H H H H H H H H C --C C C C e e c c C C c c c c C C C h H H H H H H H C C C c c c c c c c C C C C C C			
Q ss_pred		HhhCCCCCeeeeeCCcH H H H H H H H H H c E E E E C C C C e e e e c C C C c c H H H H H H H H H H H H H H H			
Q Klein_Draft	419	DALVDPENPLL SHGNQHSLNAAISR AVKRDLPSGGF VWD C IEQSTY AQLMGVTL GR WALL			
Q Consensus	419	~l~~~~~g~i~~~~~l~~~~l~~~~~ - - - - - D~ndA~~~~a~~~~~ . + . . . . +++ .   + . +++   . ++ . + . + . . + . . . . +   +   + . + . + . . . .			
T Consensus	135	~l~---~m~l~v~~~~~i~el~y~~~~~ - - - - - p~~~~~dH~~Da~rY~~~~~			
T 4DKW_B	135	LML ---EGRFKVNTCEPFEEFRLYHRDENG-----KIVKTND DVLDATRYGYMMRR			
T ss_dssp		HHH ---TTCEE EETTC H H H H H H H H H H C E E C T T S -----CBCCSCCH H H H H H H H H H H TGG			
T ss_pred		HHh ---cCEEE EeCCCH H H H H H H H H H H C eeCCCC-----CCCCCcH H H H H H H H H H H H hh			

## Template alignment

74. [TIGR00643 \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR00643\)](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR00643) recG; ATP-dependent metabolism, DNA replication, recombination, and repair].

Probability: 97.35    E-value: 1.2E-4    Score: 79.25    Aligned Cols: 157    Identities: 16%    Similarity

Q ss_pred		HHHHHHHhCCCCCHHHHHHHHHhhcChhHhhccCCcchhhh-----eeEeeEEecC	
Q Klein_Draft	21	EAlDLAAACGLILDpWQELCLHEALKESDELVLQLESGAWVKKWA-----ASSFGLVVSr	
Q Consensus	21	~~~~~l~~~Q~~~~~g~~~~~ ...+..+++. ++ .+++..+. . . . . ++.+++	
T Consensus	224	~~~~~l~~~Q~~~i~~i~-----~~~~~li~~~t	
T TIGR00643	224	LlTKFLASLPFKLTRAQKRvvKEIL-----QDLKSDVPmNRLlQGdV	
T ss_pred		HHHHHHHhCCCCCHHHHHHHHHH-----HHccCCCCcEEEEeCC	
Q ss_pred		HHHHHHHHHCceEEEEcCHHHHHHHHHHHHHHccccchhceeccCCceEEE----	
Q Klein_Draft	85	LELAGLIlfGERLIIHSAHEfKTAVNGMERLESIAKSLKYKAQAHAESIEI----	
Q Consensus	85	~~~~~i~~~t~~~a~~~~~l~~~~~i~~~ .+.+. . . +.++++ +.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+	
T Consensus	276	~~~~~--~~~~liiP~~~l~~q~~~~~v~~~~~	
T TIGR00643	276	AMLAaIEA- GyQVALMAPEITLaEQHYNSLRnLLAPLGIEVALLTGSLKGRRkELLEt	
T ss_pred		HHHHHHHC-CCeEEEEcCHHHHHHHHHHHHHhhhhCCeEEEEcCCCHHHHHHHHH	
Q ss_pred		EEEEEECC-CCCCcccccEEEEEchHhCCHHHHHHHHHhhcCC-CCCEEEEcC	
Q Klein_Draft	148	RVIHQTRT-DRSGLGTADRVIFDEAMITPGSLKAllPTVSSR-PNPQIVYTGTa	2
Q Consensus	148	~i~~~~~G~~~~v~iDE~~~~~l~~~~~i~~~~~stP . .+..+. . . . . +++++ + ++.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+	2
T Consensus	340	~iii~T~~~l~~~~~viDeah~~~~~i~LSaTp	3
T TIGR00643	340	HLVGTHALIqEKVEfKRAlViIDEQHrfGVeqRKklREKGQGGFTPHVLvMSATP	3
T ss_pred		cEEEEechhhhhhcccccEEEEccccccCHHHHHHHHHhCCCCCcEEEEECcC	





T 5JC3 B 57 GKVIVLVNKKVPLVEOHLRKEFNPELKHWHYOVIGLSGDSSELKISFPEV---VKRYDVIICT

Q ss_pred		C-----CCccccceEEEEcHHhcCHHHH-HHHHHhhcC-----CCCCC
Q Klein_Draft	157	R-----SGLGLTADRVIFDEAMTITPGSL-KALLPTVSS-----RPNPQ
Q Consensus	157	~-----~~~G~~~~~v~iDe~~~~~l~~~~~
		. . . . . + + + +   +   + + + . . . . . . + + . . . . .
T Consensus	124	~~~~~l~i~D~E~H~~~~~i~~~~~l~~~~~i
T 5JC3_B	124	ATEEDESVRLSDFSLLIIDQCHHTQKEGVYNNIMRRYLKEKIKNRKQAKENKPLIPQPQI
T ss_dssp		SCCC--CCCGGGCSEEEETGGGSCSTTCHHHHHHHHHHHHHHHHHHHHC--CCCCCEE
T ss_pred		CCCCCCCcHhhceEEEEcHHHccccHhHHHHHHHHHHHHhhchhhhcCCCCCCCeE

Q ss_pred		C	
Q Klein_Draft	205	R	205 (510)
Q Consensus	205	~	205 (510)
		.	
T Consensus	194	~	194 (701)
T 5JC3_B	194	G	194 (701)
T ss_dssp		T	
T ss_pred		C	

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

79. [3LLM A \(http://pdb.rcsb.org/pdb/explore.do?structureId=3LLM\)](http://pdb.rcsb.org/pdb/explore.do?structureId=3LLM) ATP-dependent RNA helicase A (E.C.3. Structural Genomics, Structural Genomics; HET: ADP; 2.8A {Homo sapiens})

Probability: 97.32    E-value: 1.3E-4    Score: 67.4    Aligned Cols: 160    Identities: 15%    Similarity:

Q ss_pred		hhHHHHHHHHCcC-CCCHHHHHHHHHhcChhHhhccCCchhhhheeEeeEEecCCC
Q Klein_Draft	18	AGQEAIIDLAAACGL-I LDPWQELCLHEALKESDELVLQLESGAWVKKWAASSFGLVVSQRQN
Q Consensus	18	~~~~~l~~~Q~~~~~g~~~~~rg~ +. . . +. . . ++ . +++  . +++ . +. . ~~~~~+
T Consensus	46	~~~~~Q~~~~~-----gs
T 3LLM_A	46	QDHDQLQAILQERELLPVKKFESEILEAISQ-----NSVVIIRGATGC
T ss_dssp		HCHHHHHHHHTSGGGGGHHHHHHHH-----CSEEEEEECTTS
T ss_pred		cCHHHHHHHhhcCCHHHHHHHHHhh-----CCEEEEECCCC

Q ss_pred		HHHHHH--hCCeeEEEEcCCHHHHHHHHHHHHHHHHccccchhceecCCceEEEcCC
Q Klein_Draft	87	LAGLIL--FGERLIIHSAHEFKTAVNGMERLESIAKSGLYKAKQAHGAESIEILDGP
Q Consensus	87	~~~~~--~~~~~i~i~t~a~~~~~l~~~~~i~~~~~ ...+..+...++++ +...+...+.....
T Consensus	98	~~~~~vlii~p~~~~~
T 3LLM_A	98	LDDFIQNDRAAECNIVVTQPRRISAVSVAERVAFERGEEPGKSGYSYRFESILPR----
T ss_dssp		HHHHHHTTCGGGCEEEEEESSHHHHHHHHHHHHHTTCTTSSEEEEETTEEECCC----
T ss_pred		HHHHHHcCCCCCEEEEEcCCHHHHHHHHHHHHHHCCCCccccceehccCCC----

Q ss_pred		CCCCCCC---ccceeEEEEeCHHhCHHH-----HHHHHHhhcCCCCCEEEEEeCC
Q Klein_Draft	154	RTDRSGL---GLTADRVIFDEAMITPGS-----LKALLPTVSSRPNPQIVYTGTA
Q Consensus	154	~~~~~---G~~~~v~iDE~~~~~-----~~~~~l~~~~~i~~~~stp~
		...-... ..+.++++ ++...+. ..+.+. .... ..++++ +.
T Consensus	163	~~~l~~~~~i~iDE~h~~~~~-----~~~i~~sat~~
T 3LLM_A	163	VGVLRLKLEAGIRGISHVIVDEIHERDINTDFLLVLRDVQYAYE--VRIVLMSATID
T ss_dssp		HHHHHHHHHCTTCCEEEECCTTSCCHHHHHHHHHHHHHHCTT--SEEEEEECSSC
T ss_pred		HHHHHHHHHhccCCCCEEEEcCCcccChHHHHHHHHHHHHHCCC--CEEEEECCCC

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/5jc3\)](http://www.ebi.ac.uk/pdbe/entry/pdb/5jc3)

80. [5JC3 A \(http://pdbe.rcsb.org/pdb/explore.do?structureId=5JC3\)](http://pdbe.rcsb.org/pdb/explore.do?structureId=5JC3) LGP2/RNA Complex; Innate immune pat  
HET: ADP: 2.6A {Gallus gallus}



Q ss_pred		c cchhhceeccCCcEEFecCCCCcEEEEEECC-----CCCcccccEeEFecHHH
Q Klein_Draft	122	SGLKYKAKQAHAESIEILDGPNPGARVIFQTRT-----DRSGLGLTADRVIFDEAMT
Q Consensus	122	~l~~~~~i~~~~g~~i~~~~~-----~~~~G~~~~v~iDE~~~ .....+.+++++ .++.. ..+...+    ++.
T Consensus	164	~~~~~iv~T~~~~l~~~~~IViDeah~
T 4W7S_B	164	CKVISIVGGHSLEEISFSL---SEGCDILVATPGRLLDSLENHLLVMKQVETLVLEADK
T ss_dssp		CCEEEECTTSCHHHHHHHHG---GGCCSEEEECHHHHHHHHTTCCCTTCCEEEECSHHH
T ss_pred		cEEEEeCCCCHHHHHHHH--hcCCCSEEEECHHHHHHHHCccccCCEEEeCHHH
Q ss_pred		HhhhCC-----CCEEEEEEc
Q Klein_Draft	184	LPTVSSR-----PNPQIVYTGT     200 (510)
Q Consensus	184	~~~l~-~-~i~~st     200 (510) ...+...     ...++++.+.
T Consensus	231	~~~~~i~~sa     254 (463)
T 4W7S_B	231	TNILT KVDINADSAVN RQTLMFTA     254 (463)
T ss_dssp		HHHHHHHHHSC T TCCEEEEEES
T ss_pred		HHHHHhCCcCCCCcCCEEEEEEC

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/4w7s\)](http://www.ebi.ac.uk/pdbe/entry/pdb/4w7s)

82. [4W7S A \(http://pdb.rcsb.org/pdb/explore.do?structureId=4W7S\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4W7S) S.cerevisiae Prp28 (127-588 aa); splicir ATPase; HET: P6G, MSE, ANP; 2.542A {Saccharomyces cerevisiae}

Probability: 97.31    E-value: 5.6E-5    Score: 77.93    Aligned Cols: 181    Identities: 11%    Similarity

Q ss_pred		CCCCCCEeCCCCCchHHHHHHHH-HHcCC-CCCHHHHHHHHHhccChhHhhccCCc
Q Klein_Draft	2	GVQEPRIWLSPEANSSAQGEAIDLA-AACGL-ILDPWQELCLHEALKESDELVQLESGAW
Q Consensus	2	~~~~~1~~~Q~~~~~g~ +...+.+...+.+...+.+...+.+...+.+...+.+...+.+...+.+...+.+...+
T Consensus	39	~~~~~Q~~~~~i~~~~~-----
T 4W7S_A	39	GGTVENPLRNWEELNIIPDLLRVIIQELRFPSPPTPIQRITIPNVCNMKQ-----
T ss_dssp		SSSSSSSSSSSTTCCSCHHHHHCCCCCTCCSSCHHHHHHHHHHSCCTTC-----
T ss_pred		CCCCCCCCCHHhCCCCHHHHHHHHHHcCCCCCHHHHHHHHHHhccc-----

Q ss_pred		EEeCCCCCHHHHHHHHHHHHHHhC-----CeeEEEEcCCHHHHHHHHHHHHHHH
Q Klein_Draft	70	LVVSRQNGKGSILEALELAGLILFG-----ERLIISAHFKTAVNGMERLES LI
Q Consensus	70	~~~~rg~GKT~~~~~ +.+++ +  ..+...++..+...+.....+++++ +.+.+.+.+.+.++
T Consensus	94	i~~tGsGKT~~~~~liiP~~l~q~~~~~
T 4W7S_A	94	GVASTGSGKTLAFVIPILIKMSRSPRPPLSLKIIDGPKALILAPTRELVQQIQKETQKV T
T ss_dssp		EECCTTSSHHHHHHHHHHHHHTSCCCCHHHHHHHHCCSEEEECSSHHHHHHHHHHHHHH
T ss_pred		EEcCCCCCHHHHHHHHHHHHHhC CCCCCCcCCCCCcEEEEcCCHHHHHHHHHHHHHHH

Q ss_pred		ccchhhceeccCCcEEEcCCCCcEEEEEC-----CCCccccceEEFcHHH
Q Klein_Draft	122	SGLKYKAKQAHAESIEILDGPNPGARVIFQTRT-----DRSGLGLTADRVIFDEAMT
Q Consensus	122	~l~~~~~i~~~~~g~~i~~~~~-----~~~~~G~~~~~v~iDe~~~ .....+.+++++.. .+.+. . . . .-..++++ +  ++.
T Consensus	164	~~~~~-----~~~~~ivi~T~~~l~~~~~~~~~~lViDeah~
T 4W7S_A	164	CKVISIVGGHSLEESISL---SEGCDILVATPGRGLDSLENHLLVMKQVETLVLDADK
T ss_dssp		CCEEEECTTCCHHHHHHHH---TTCCSEEEECHHHHHHHHTTCCC-CCCCEEEETTTHH
T ss_pred		cEEEEeCCCCHHHHHHHH---hcCCCEEEECHHHHHHHHCcCcccCCEEEeCHHH

Q ss_pred		HhhhcCC-----CCCEEEEEec	
Q Klein_Draft	184	LPTVSSR-----PNPQIVYGT	200 (510)
Q Consensus	184	~..1~..-----~..i~..st	200 (510)
		...t... ..+...t.	

[Vis](#)[Hits](#)[Aln](#)

T Consensus 231 ~~~~~i~sa 254 (463)  
Select all Forward Forward Query MSA Color Segs Unwrap Segs  
T ss\_dssp HHHHHHHHHHCCTTCCCEEEEEES  
T ss\_pred HHHHHHCCCCCCCCCEEEEEEC

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/3p4x\)](http://www.ebi.ac.uk/pdbe/entry/pdb/3p4x)

☐ 83. [3P4X\\_B \(http://pdb.rcsb.org/pdb/explore.do?structureId=3P4X\)](http://pdb.rcsb.org/pdb/explore.do?structureId=3P4X) reverse gyrase helicase-like domain; T SUPERCOILING, ARCHAEA, HELICASE; HET: ADP; 2.41A {thermotoga maritima}

Probability: 97.31 E-value: 6.6E-5 Score: 76.48 Aligned Cols: 162 Identities: 14% Similarity

```
Q ss_pred          HHHHHHH-HHcCCCCCHHHHHHHHHHhccChhHhhccCCcchhhheeEeeEEecCCCCH
Q Klein_Draft      20 QEAILDLA-AACGLILDPWQELCLHEALKESDELVLQESGAWKKWAASSFGLVVSQRNGK
Q Consensus        20 ~~~~~-~~~~~l~~~~Q~~~~~g~~~~~rg~GK
                   ..+.+. .+.+.|+++|.+.+.+. .+.+.+.+.|+|
T Consensus        7  ~~~~~l~~~~Q~~~~~-----l~~~~tG~GK
T 3P4X_B           7  EDFRSFFKKKFGKDLTGYQRLWAKRIVQ-----GKSFTMVAPTGVGK
T ss_dssp          HHHHHHHHHHSSCCCHHHHHHHHHHT-----TCCECCSCCTTH
T ss_pred          HHHHHHHHHHCCCCCHHHHHHHHHHc-----CCCEEEcCCCCCH

Q ss_pred          HHHHhCCeeEEEEcCHHHHHHHHHHHHHHhcc-cchhhceecCCceEEE----ecC
Q Klein_Draft      89 GLILFGERLIIHSAHEFKTAVNGMERLESIAKS-GLKYKAKQAHGAESIEI----LDG
Q Consensus        89 ~~~~~i~i~t~a~~~~~l~~~~~i~-----~
                   ... .+.+++++|+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.
T Consensus        59 ~~-~~~~lii~P~~~~l~q~~~~~-----
T 3P4X_B           59 LAR--KGKKSALVFPTVTLVKQTLERLQKLADEKVKIFGFYSSMKKEEKEKFEKSFE--
T ss_dssp          HHT--TTCEEEEESSHHHHHHHHHHHSCCTTSCEEEECTTSCHHHHHHHHHHH--
T ss_pred          HHH--cCCcEEEEcCHHHHHHHHHHHHhccCCcEEEEccCCHHHHHHHHHhh--

Q ss_pred          ECC-----CCCCccceEEEEcHHhCH-----HHHHHHhhhc---
Q Klein_Draft      153 TRT-----DRSGLGLTADRIVFDEAMTITP-----GSLKALLPTVS---
Q Consensus        153 ~~------G~~~~~V~iDE~~~~~-----l~---
                   +.. .+.+.+.+++++|++.+. .+.+.+.+.+.
T Consensus        123 t~~~l~~~~~V~iDE~h~~~~~l~~~~~
T 3P4X_B           123 STQFVSKNREKLSQKRFDFVDDVDVAVLKASRNIDTLMMVGIFEIIRKAFSTIKQGK
T ss_dssp          EHHHHHHHHHTTCCCEEEESCCHHHSHHHHHHHHHHTTCCHHHHHHHHHHHTTCC
T ss_pred          cHHHHHhCHHHHhccCCCEEEcCHHHHHhhcCHHHHHHcCCCHHHHHHHHHhCCc

Q ss_pred          CCEEEEEcCCCC
Q Klein_Draft      192 NPQIVYTGTAAQQR 205 (510)
Q Consensus        192 ~~~i~~~stp~~~~ 205 (510)
                   ...+++++|....
T Consensus        193 ~~~~~sat~~~~~ 206 (413)
T 3P4X_B           193 GILVSSATAKPRG 206 (413)
T ss_dssp          CEEEECCSSCCCT
T ss_pred          cEEEEEcCCCCc
```

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

☐ 84. [4XGT\\_A \(http://pdb.rcsb.org/pdb/explore.do?structureId=4XGT\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4XGT) FRQ-interacting RNA helicase; ATPase 3.09A {Neurospora crassa}

Probability: 97.29 E-value: 1.2E-4 Score: 83.71 Aligned Cols: 142 Identities: 16% Similarity

```
Q ss_pred          cCCCCCHHHHHHHHHHhccChhHhhccCCcchhhheeEeeEEcCCCCHHHHHHHHHH
Q Klein_Draft      29 CGLILDPWQELCLHEALKESDELVLQESGAWKKWAASSFGLVVSQRNGKGSILEALELA
Q Consensus        29 ~~~l~~~~Q~~~~~g~~~~~rg~GKT~~~~~
                   +.+.|+++|.+.+.+. .+.+.+.+.|+|+.+.+.
T Consensus        64 ~~~l~~~~Q~~i~~~~~-----v~l~a~TGSgKTl~~~~i~
T 4XGT_A           64 YSFKLDPFQALSVASIER-----EESVLVSAHTSAGKTVVAEYIAIQ
```

Q ss_pred		EEECCHHHHHHHHHHHHHHHHccccchhhceccCCeEEEcCCCCCEEEEECC---
Q Klein_Draft	99	IHSAEHFKTAVNGMERLESLIAKSGLKAKQAHAESIEILDGPNPGARVIFQTRT---
Q Consensus	99	~i~~t~a~~~~~l~~~~~i~~~~~g~i~~~~~ ++++ +. .+. +. .+. .+. .+. . . . . . . . . . .+. +. +. +. +.
T Consensus	114	l~vP~aL~q~~~~~v~i-----tgd~~~~~-----~iI~T~e~L~
T 4XGT_A	114	IYTSPIKALSNQKYRDFQAEFGDVGLM-----TGDTVIN---PTASCLVMTEILR
T ss_dssp		EEEESchHHHHHHHHHHHHHSCEEEE-----CSSCEEC---TTCSEEEEEHHHHH
T ss_pred		EEECcCHHHHHHHHHHHHHHcccccee-----eccccCC---CCCCEEEEeHHHHH

Q ss_pred		cceeEEEEcHhHcCH---HHHHHHHHhhcCCCCEEEEecCCC	
Q Klein_Draft	162	LTADRVI FDEAMTITP---GSLKALLPTVSSRPNPQIVYGTAA	203 (510)
Q Consensus	162	~~~~~v~IDe~~~~~---~~~~~l~~~~~i~~~~~stp~~	203 (510)
		.++++ + + +.+.+ .++.+.+.+.+.+.+.+.+.+.+.+	
T Consensus	172	~~~~~VI~DEaH~i~~~~r~~~~e~~~~i~~~~l~~~~~v~lSAT~n	216 (993)
T 4XGT_A	172	REVAWVVFDEIHYMRDKIRGVVWEETIILLPKD-VRYVFLSATIPN	216 (993)
T ss_dssp		HHEEEEEESC GGGGGCTTTHHHHHHHHHTSCTT-SEEEEEESCCTT	
T ss_pred		HheeEEEEechHhccccccHHHHHHHHHCCCC-CEEEEEeCCCCC	

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/5dzt\)](http://www.ebi.ac.uk/pdbe/entry/pdb/5dzt)

85. [5DZR A \(http://pdb.rcsb.org/pdb/explore.do?structureId=5DZR\)](http://pdb.rcsb.org/pdb/explore.do?structureId=5DZR) FRQ-interacting RNA helicase; helicase BINDING; 3.161A {*Neurospora crassa*}

Probability: 97.29    E-value: 1.2E-4    Score: 83.71    Aligned Cols: 142    Identities: 16%    Similarity

Q ss_pred		cCCCCCHHHHHHHHHHccChhhHhhcCCcchhhhheeEeeEEecCCCCCHHHHHHHHHH
Q Klein_Draft	29	CGLILDpqwELCLHEALKESDELVLQLSGAWVKWAASSFGLVVSrqNGKGSILEALELA
Q Consensus	29	~~~~~l~~~Q~~~~~g~~~~~rg~GKT~~~~~ +.+. +++ .+.+..+.+.+++.+++   .++.+.. 
T Consensus	64	~~~~~l~~~Q~~~~i~~~~-----vvlv~a~TgsGkTl~~~~~i~~
T 5DZR_A	64	YSFKLDPFqALSVASIER-----EESVLvSAHTSAGktVVAEYAIaq
T ss_dssp		TTCCCCHHHHHHHHHHNT-----TCCEEEEECGGGCTHHHHHHHHH
T ss_pred		CCCCCCHHHHHHHHHHhc-----CCEEEEeccccCHHHHHHHHHH

Q ss_pred		EEEcCCHHHHHHHHHHHHHHccchhhceecCCcEEEcCCCCCEEEEEEC---
Q Klein_Draft	99	IHSAEHFKTAVNGMERLESLIAKSGLYKAKQAHAESIEILDGPNPGARVIFQTRT---
Q Consensus	99	~i~~~t~~~~a~~~~~l~~~~~i~~~~~g~i~~~~~ ++++ +. .+. +. .+. .+. .+. .+. .+. .+. .+. .+. .+. .+. .+
T Consensus	114	l~vP~naL~nq~~~~~v~i-----tgdn~~~~~-----~iIl~Tv~eL~
T 5DZR_A	114	IYTSPIKALSNQKYRDFQAEFGDVGLM-----TGDTVIN----PTASCLVMTEILR
T ss_dssp		EEEESSHHHHHHHHHHHHHTSCEEEE-----CSSCBCC---TTSSEEEEEHHHHH
T ss_pred		EEEcCcHHHHHHHHHHHHHHcccccee-----ecccccCC---CCCCEEEeHHHHH

Q ss_pred		cceeEEEEcHHhcCH---- <td></td>	
Q Klein_Draft	162	LTADRVI FDEAMTITP----GSLKALLPTVSSRPNPQIVYTGTAAD	203 (510)
Q Consensus	162	~~~~~v~iDE~~~~~----~~~~~l~~~~~i~~~~~stp~~	203 (510)
		.++++ + + +.+.+ .++.+.+.+.+.+.+.+.+.+.+	
T Consensus	172	~~~~~VI~DEAh~i~~~~~r~~~~~e~~~~~i~~~~~l~~~~~v~i~lSAT~~n	216 (993)
T 5DZR_A	172	REVAWVVFDEIHYMRDKIRGVVWEETIILLPDK-VRYVFLSATIPN	216 (993)
T ss_dssp		GSEEEEEEEESGGGGGCTTTHHHHHHHHHHSCCTT-CEEEEEECCTT	
T ss_pred		HheeEEEEechHhcccccccHHHHHHHHHCCCC-CEEEEEeCCCCC	

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/4d26\)](http://www.ebi.ac.uk/pdbe/entry/pdb/4d26)

86. [4D26 A \(http://pdb.rcsb.org/pdb/explore.do?structureId=4D26\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4D26) BMVLG PROTEIN; HYDROLASE, PIRNA, TRANSPOSON; HET: ADP; 2.1A {BOMBYX MORI}

[Select all](#)[Forward](#)[Forward Query MSA](#)[Color Seqs](#)[Unwrap Seqs](#)

Q ss_pred		hHHHHHHHHHCC-CCCHHHHHHHHhccChhHhccCCcchhhheeEeeEEecCCC
Q Klein_Draft	18	AGQEAI DLAAACGL-ILDPWQELCLHEALKESDELVLQESGAWVKKWAASSFGLVVSQRN
Q Consensus	18	~~~~~1~~~Q~~~~~g~~~~~rg~ +.....-+...++ . +++ .+++..+.. .+.+++. + T Consensus 57 1~~~1~~~1~~~~~Q~~~~~i~~~~~li~~~tGs
T 4D26_A	57	LRKYVLDNVLKAGYRKPTPIQKNAIPIIMS-----GRDLMGCAQTGS
T ss_dssp		CCHHHHHHHHTTCCSCCHHHHHHHHHHT-----TCCEEEECCTTS
T ss_pred		CCHHHHHHHHCCCCCCHHHHHHHHHHC-----CCeEEEECCCC
Q ss_pred		HHHHHHhC-----CeeEEEEcCHHHHHHHHHHHHhcc--cchhhceeccCC
Q Klein_Draft	87	LAGLILFG-----ERLIHSAHEFKTAVNGMERLESIAKS--GLKYKAKQAHGA
Q Consensus	87	~~~~~i~~~~t~~~a~~~~~1~~~~~ +..+...+ ...++ ++ +...+...+...+...+...+...+ T Consensus 109 ~~~~~livp~~~l~~q~~~~~
T 4D26_A	109	INMLLQDPKDLISENGCAQPQVIVSPTRELTQIFNEARKFSYGSVLKVAVAYGGTAVR
T ss_dssp		HHHHHHSCCCCEETTECCSEEEECSSHHHHHHHHHHHTTTSSCCEEEECTTSCHH
T ss_pred		HHHHhCChHHcCCCCCCCCeEEECCHHHHHHHHHHHhCCCCeEEEECCCCCHH
Q ss_pred		CCeEEEEEECC-----CCCCccceEEECCHHHhCHHHH-HHHHhC-----C
Q Klein_Draft	145	PGARVIFQTRT-----DRSGLGLTADRVIFDEAMTITPGSL-KALLPTVSS-----R
Q Consensus	145	~g~~i~~~~~G~~~~~V~iDE~~~~~1~~~~~ +.. .+.+.+ .....-..+++++  ++..+...+ ..+...+ T Consensus 176 ~~~i~v~t~~~1~~~~~liiDE~h~~~~~
T 4D26_A	176	RGCHILVATPGRLHDFVERNRFVFGSVRFVLDQADCLDMGFMPSEIKMMLHPTMVETT
T ss_dssp		TCCSEEECHHHHHHHHTTBCCTTCCEEEETHHHHTSTTTTHHHHHHTTCTTSCCGG
T ss_pred		hCCCEEECHHHHHHHhCCcCccCEEEECCHHHHhCCHHHHHHHhCCcCCCC
Q ss_pred		CC
Q Klein_Draft	201	AA 202 (510)
Q Consensus	201	p~ 202 (510) +. T Consensus 246 ~~ 247 (434)
T 4D26_A	246	FP 247 (434)
T ss_dssp		CC
T ss_pred		CC

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/4d25\)](#)

87.

[4D25 A \(http://pdb.rcsb.org/pdb/explore.do?structureId=4D25\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4D25) BMVLG PROTEIN; HYDROLASE, PIRNA, TRANSPOSON; HET: ANP; 1.9A {BOMBYX MORI}

Q ss_pred		hHHHHHHHHHCC-CCCHHHHHHHHhccChhHhccCCcchhhheeEeeEEecCCC
Q Klein_Draft	18	AGQEAI DLAAACGL-ILDPWQELCLHEALKESDELVLQESGAWVKKWAASSFGLVVSQRN
Q Consensus	18	~~~~~1~~~Q~~~~~g~~~~~rg~ +.....-+...++ . +++ .+++..+.. .+.+++. + T Consensus 57 1~~~1~~~1~~~~~Q~~~~~i~~~~~li~~~tGs
T 4D25_A	57	LRKYVLDNVLKAGYRKPTPIQKNAIPIIMS-----GRDLMGCAQTGS
T ss_dssp		CCHHHHHHHHTTCCSCCHHHHHHHHHHT-----TCCEEEECCTTS
T ss_pred		CCHHHHHHHHCCCCCCHHHHHHHHHHC-----CCeEEEECCCC
Q ss_pred		HHHHHHhC-----CeeEEEEcCHHHHHHHHHHHHhcc--cchhhceeccCC
Q Klein_Draft	87	LAGLILFG-----ERLIHSAHEFKTAVNGMERLESIAKS--GLKYKAKQAHGA
Q Consensus	87	~~~~~i~~~~t~~~a~~~~~1~~~~~ +..+...+ ...++ ++ +...+...+...+...+...+...+ T Consensus 109 ~~~~~livp~~~l~~q~~~~~
T 4D25_A	109	INMLLQDPKDLISENGCAQPQVIVSPTRELTQIFNEARKFSYGSVLKVAVAYGGTAVR



Probability: 97.27    E-value: 1.2E-4    Score: 84.55    Aligned Cols: 157    Identities: 9%    Similarity:

Vis

### Hits

Aln

<u>Select all</u>	<u>Forward</u>	<u>Forward Query MSA</u>	<u>Color Segs</u>	<u>Unwrap Segs</u>
Q ss_pred		HHHHHHHHHhCCCCCHHHHHHHHHhhcCChHhccCCcchhhh-----eeEeeEEe		
Q Klein_Draft	19	GQEATDLAAACGLIEDPWOELCLHEALKESDLVLVQLSGAWYKKWA-----ASSFGLVV		
Q Consensus	19	~~~~~l~~~Q~~~~~g~~~~~ .....+...+++. +++ .+.+.+. . ....++++		
T Consensus	590	~~~~~l~~~Q~~~ai~~~i~~~~~ll~~~		
T 2EQ_A	590	REYQLFCDSFPFETTPDQAQAINAVL-----SDMCQPLAMDRLVCG		
T ss_dssp		HHHHHHHHHTTCCSCCHHHHHHHHHHH-----HHHHSSSCCEEEEEEC		
T ss_pred		HHHHHHHHHhCCCCCHHHHHHHHHHH-----HHccccCCCCCEEEec		
Q ss_pred		HHHHHHHHHHhCcEEEEEcCCHHHHHHHHHHHHHhhcccchhceeccCcEEEEE---		
Q Klein_Draft	83	EALELAGLILFGERLIISHAHEFKTAVNGMERLESIAKSLGKYKAKQAHGAESIEI---		
Q Consensus	83	~~~~~i~~~t~~~a~~~~~l~~~~~i~~~-- ...++. . . +.+++++ +.+.+.+.+.+.+.+.+. . . . .		
T Consensus	642	l~~~~~v~lilvPt~La~Q~~~~~i~v~~~~~		
T 2EQ_A	642	MRAAF LAVDN--HKQ VAVLVPTTL LAQQHYDNFRDRFANWPVRIEMISRF RSAKEQTQIL		
T ss_dssp		HHHHHHHHHTT--TCEEEECSSHHHHHHHHHHHHHSTTTTCCEEEESTTSCHHHHHHHHH		
T ss_pred		HHHHHHHHhC--CCeEEEEechHHHHHHHHHHHHhCCCCeEEEEecCCCCHHHHHHHH		
Q ss_pred		CcEEEEEECC--CCCCccceEEEEEcHHhcCHHHHHHHhhcCCCCCEEEEcC		
Q Klein_Draft	146	GARVIFQTRT--DRSGLGLTADRIVFDEAMTITPGSLKALLPTVSSRPNQIVYTGT A		
Q Consensus	146	g~i~~~~~G~~~~~V~IDe~~~~~l~~~~~i~~~~~st p ... .+.+. . . .-.+++++ + +.+. . . .+. . . . .+.+.+++		
T Consensus	706	~~~IvI~T~~~L~~~~~l~lvIDE~H~~~~~l~~~~~--~~~l~lSATP		
T 2EQ_A	706	KIDILIGTHKLQSDVKFKDLGLLVIDEEHRFGVRHKERIKAMRAN--VDILT LTATP		
T ss_dssp		CCSEEEECTHHHSCCCCSSEEEEEESGGSCHHHHHHHHHHTT--SEEEEEESSC		
T ss_pred		CcEEEEechHHhccCCCCccCEEeechhcChhHHHHHHhccC--CCEEEEECC		

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/5aga\)](http://www.ebi.ac.uk/pdbe/entry/pdb/5aga)

**90.**

**5AGA A** (<http://pdb.rcsb.org/pdb/explore.do?structureId=5AGA>) DNA POLYMERASE THETA (E.C.2.7.7.7); REPAIR; HET: FLC, ANP; 2.9A {HOMO SAPIENS}

Probability: 97.27    E-value: 1.1E-4    Score: 82.42    Aligned Cols: 162    Identities: 17%    Similarity

Q ss_pred		HHHHHHHHHcCC-CCCHHHHHH--HHHccChhhCcCchhhhheeEeeEEecC
Q Klein_Draft	18	AGQEAI DLAAACGL -ILD PWQELCL --HEALKESDEL VQL ES GA WVKKWAASSF GLVVS R
Q Consensus	18	~~~~~l~~~Q~~~~-~~~~g~~~~ +...+. +... + .  + + .+++ ..+.. .+.+++.+ +
T Consensus	12	l~~~~gi~~l~~~Q~~~l~~~~-----ii~~pt
T 5AGA_A	12	L PKAVLEKYHSFG VKKMFEWQA ECL L LGQV LE -----GKNLVYSAPT
T ss_dssp		CCHHHHHHHHTSSCCB CCHHHHHHHSHSSTTT-----TCCEEEEECT
T ss_pred		CCHHHHHHHHhCCccc CHHHHHHHhc ccc cC-----CCeEEEECC
Q ss_pred		HHHHHHHHHcCCeEEEEcCCHHHHHHHHHHHHHHhcccc hhceecc CCceEEEecCCC
Q Klein_Draft	85	L ELA G L I L FGERLI HSA HEFKT AVNGMERLES LI AKSG L KYAKAQ HA GES IE IL DGP N
Q Consensus	85	~~~~~i~i~~~t~~~a~~~~~l~~~~~i~~~~~ .++.+. +.+. +++++ +. +. +. +. +. +. +. -. +. +. +. +.
T Consensus	64	~il~~~~~-v liv ~P~~~~l~~~~~l~~~~~V~~~~~g~~~~~----
T 5AGA_A	64	L I L KRVLEM RK - KALFILPFVSVAKEKKYYL QSL FQEVGIKV DG YMG STSPSRHF ----
T ss_dssp		H H H H H H H T TC - E E E E S S H H H H H H H H H H H G G G T C C E E E E C T T C C S S C G ----
T ss_pred		H H H H H H h h c C - c E E E E C C H H H H H H H H H H H H H C C E E E E e c C C C c c c h ----
Q ss_pred		CC-----CCCCccceeEEEEcHHhCCH---HHHHHHHhhc-----
Q Klein_Draft	155	TD-----RSGLGL TAD RVIFDEAMTITP ---GS L KALLPTVS-----
Q Consensus	155	~~~~~G~~~~~v~iD~~~~~l~~~~~ .. ....-. ++++  +    ++.+. + ..+.+. +. +.
T Consensus	128	e~l~~ll~~~~~l~~~~VVVD E~H~l~~~~r~~~~e~ll~~l~~~~~
T 5AGA_A	128	E RANGLINRLIEENKMDLLGMVVDELHMLGD SHRGYLL ELLLTKICYITRKSASCQADL
T ss_dssp		H H H H H H H H H HT CGGGEEEEESC GG G GS CS STTHHHHHHHHHHHHHHTGGGCC-
T ss_pred		H H H H H H H H H H h c c h h c C E E E E C H h c C C C c h H H H H H H H H h c c h h c h h h

[Vis](#)[Hits](#)[Aln](#)[Select all](#)  
Q ss\_pred[Forward](#)[Forward Query MSA](#)[Color Seqs](#)[Unwrap Seqs](#)

EEEEeCCCC

Q Klein\_Draft 195 IVYTGTAAD 203 (510)

Q Consensus 195 i~~~stp~~ 203 (510)

+.+++|+..

T Consensus 198 I~lSATl~~ 206 (830)

T 5AGA\_A 198 VGMSATLPN 206 (830)

T ss\_dssp EEEESCCTT

T ss\_pred EEEeCCCC

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/1s2m\)](#)☐ 91. [1S2M A \(http://pdb.rcsb.org/pdb/explore.do?structureId=1S2M\)](http://pdb.rcsb.org/pdb/explore.do?structureId=1S2M) Putative ATP-dependent RNA helicase binding, Helicase, RNA BINDING; 2.1A {Saccharomyces cerevisiae} SCOP: c.37.1.19

Probability: 97.26 E-value: 1.6E-4 Score: 72.82 Aligned Cols: 162 Identities: 12% Similarity

Q ss\_pred hHHHHHHHHHhCCC-CCCHHHHHHHHHhccChhHhccCCcchhhheeEeeEEeCCCC

Q Klein\_Draft 18 AGQEAIIDLAAACGL-ILDPWQELCLHEALKESDELVLQESGAWVKKWAASSFGLVVSQRN

Q Consensus 18 ~~~~~~1~~~Q~~~~~g~~~~~rg~

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

T Consensus 28 l~~~l~~~l~~~~~Q~~~~~-----~l~~~~Gs

T 1S2M\_A 28 LKRELLMGIFEAGFEKPSPIQEEAIPVAIT-----GRDILARAKNGT

T ss\_dssp CCHHHHHHHHTTCCSCCHHHHHHHHHH-----TCCEEEECCTTS

T ss\_pred CCHHHHHHHHhCCCCCHHHHHHHHHhC-----CCeEEEECCCC

Q ss\_pred HHHHHHh-CCeeEEEEcCHHHHHHHHHHHHHHHhccccchhcecccCCe---EEeEcC

Q Klein\_Draft 87 LAGLILF-GERLIIHSAHEFKTAVNGMERLESIAKSGLKAKQAHAES---IEILDG

Q Consensus 87 ~~~~~~i~~~~t~~~~a~~~~~l~~~~~i~~~~~

+.+. .+.++++|+.+.+.+.+.+.+.+.+.+. . . . .

T Consensus 80 ~~~~~~li~p~~~l~~~~~-----~

T 1S2M\_A 80 LEKVKPKLNKIQALIMVPTRELALQTSQVVRTLGKHCGISCMVTTGGTNLRDDILRLN--

T ss\_dssp HHHCCTTSCSCSEEEECSSHHHHHHHHHHHHHTTTTTCCEEEECSSSCHHHHHHTT--

T ss\_pred HHHHchhhcCceEEEEcCHHHHHHHHHHHHHhCCeEEEEcCCCCHHHHHHHh--

Q ss\_pred ECC-----CCCCccceeeEEEEcHHhCCH---HHHHHHhHhCCCCCEEEEcC

Q Klein\_Draft 153 TRT-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRPNPQIVYTGTA

Q Consensus 153 ~~~~~~G~~~~v~iDE~~~~~l~~~~~i~~~~~stp

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

T Consensus 146 t~~~l~~~~~v~iDE~h~~~~~i~~sat~

T 1S2M\_A 146 TPGRVLDLASRKVADLSDCLFIMDEADKMLSRDFKTIIEQILSFLPPT-HQSLFLSATF

T ss\_dssp CCHHHHHHHHTTCCSCCTTCEEEESHHSCHHHHHHHHTTSCSS-CEEEEEESC

T ss\_pred cHHHHHHHHhCCCCChhCCEEEEcCHHHHhccchHHHHHHhCCCC-CEEEEEccC

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/4c9b\)](#)☐ 92. [4C9B A \(http://pdb.rcsb.org/pdb/explore.do?structureId=4C9B\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4C9B) EUKARYOTIC INITIATION FACTOR 4A-II DEAD-BOX HELICASE, NMD, MRNP; HET: GOL; 2.0A {HOMO SAPIENS}

Probability: 97.25 E-value: 8.7E-5 Score: 75.06 Aligned Cols: 163 Identities: 16% Similarity

Q ss\_pred hHHHHHHHHHhCCC-CCCHHHHHHHHHhccChhHhccCCcchhhheeEeeEEeCCCC

Q Klein\_Draft 18 AGQEAIIDLAAACGL-ILDPWQELCLHEALKESDELVLQESGAWVKKWAASSFGLVVSQRN

Q Consensus 18 ~~~~~~1~~~Q~~~~~g~~~~~rg~

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

T Consensus 45 l~~~~~Q~~~~~-----~l~~~~tGs

T 4C9B\_A 45 LREDLLRGIYAYGFKPSAIQQRAIKQIIK-----GRDVIAQSQSGT

T ss\_dssp CCHHHHHHHHTTCCSCCTTHHHHHHHHT-----TCCEEEECSTTS

T ss\_pred CCHHHHHHHHhCCCCCHHHHHHHHHHhC-----CCCEEECCCCC

Q ss_pred		hHHHHHHHHHHcCC-CCCHHHHHHHHHhccChhHhhccCCcchhhhe--eEeeEEecC
Q Klein Draft	18	AGQEAIDLAAACGL-ILDPWQELCLHEALKESDELVLQESGAWVKKAA--SSFGLVVS

Q Consensus	18	~~~~~1~~~Q~~~~~g~~~~~
Select all	Forward	Forward Query MSA
T Consensus	48	1~~~~~1~~~~~Q~~~~~-----11~~~t
T 3G0H_A	48	LKPQLLGQVYAMGFNRPSKIQENALPLMLA-----EPPQNLIQSQS
T ss_dssp		CCHHHHHHHHTTCCSCCHHHHHHHHHHHS-----SSCCEEEECCT
T ss_pred		CCHHHHHHHHCCCCCCHHHHHHHHHHhc-----CCCceEEEECC
Q ss_pred		HHHHHHHHhC-CeeEEEEcCCHHHHHHHHHHHHHHccchhhceeccCCceEEEEcCC
Q Klein_Draft	85	LELAGLILFG-ERLIHSAHEFKTAVNGMERLESLIAKSGLYKAKQAHAESIEILDGP
Q Consensus	85	~~~~~i~i~~~t~~~a~~~~~1~~~~~i~~~~~
		.++.+. . . . .++++ +.+.+.+.+.+. . . . .
T Consensus	100	~~~~~lii~p~~~l~~~q~~~~~-----
T 3G0H_A	100	AMLSQVEPANKYPQCLCLSPTYELALQTGKVI EQMGKFYPELKLAYAVRGNKLERGQ---
T ss_dssp		HHHTTCCTTSCSCCEEEECSSHHHHHHHHHHHHHSTTSTTCCCEEEESTTCCCCTTC---
T ss_pred		HHHHhccccCCCCeEEEEeCchHHHHHHHHHHHHhhcCCcEEEEeCcchhccc---
Q ss_pred		CC-----CCCCccceeeEEEEchHhCCH-----HHHHHHHHhhcCCCCEEEEEEc
Q Klein_Draft	154	RT-----DRSGLGLTADRVIFDEAMTITP-----GSLKALLPTVSSRPNPQIVYTGT
Q Consensus	154	~~~~~G~~~~~v~iDE~~~~~-----1~~~~~i~~~~~
		. . . . .++++ + +.+. . . .+.+.+.+. . . . .++++
T Consensus	167	~~~1~~~~~vIvDe~h~~~~~-----i~~~SaT
T 3G0H_A	167	PGTVLDWCSKLKFDIPKKIKVFVLDEADVMIAQTGQHQQSIRIQRMLPRN-CQMLLFSAT
T ss_dssp		HHHHHHHTTTTCCSCGGGCSEEEEEETHHHHSTTTTHHHHHHHHHTSCSS-CEEEEEESC
T ss_pred		HHHHHHHHhCccccHhCCEEEEEeCHHHHHhCCHHHHHHHHHHCCCC-CEEEEEEC

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/2p6r\)](http://www.ebi.ac.uk/pdbe/entry/pdb/2p6r)

95. [2P6R A \(http://pdbs.rcsb.org/pdb/explore.do?structureId=2P6R\)](http://pdbs.rcsb.org/pdb/explore.do?structureId=2P6R) afUHEL308 HELICASE/DNA Complex; Pf HELICASE, ARCHAEL; 3.0A {Archaeoglobus fulgidus} SCOP: a.4.5.43, a.289.1.2, c.37.1.19

Probability: 97.25    E-value: 1.9E-4    Score: 78.73    Aligned Cols: 161    Identities: 16%    Similarity

Q ss_pred		chHHHHHHHHHCC-CCCHHHHHHHHHhcChHHhhccCCCchhhhheeEeeEEecCC
Q Klein_Draft	17	SAGQEAIIDLAACGL-ILDPWQELCLHEALKESDELVLQLESAGAWVKWAASSFGLVVSQR
Q Consensus	17	~~~~~l~~~Q~~~~~g~~~~~rg .+. . . . . +.+   + .  +++ . . +++ . +. . . . . +.+   +
T Consensus	9	~l~~~~~l~~~~g~~~~l~~~~Q~~~~~-----~lv~apTG
T 2P6R_A	9	SISSYAVGILKEEGIEELFPQPQAEAVEKVFS-----GKNLLLAMPTA
T ss_dssp		HNNNNNNNNHHCC---CCCCCHNNNNNNHTT-----CSCEEEECSSH
T ss_pred		hcCHHHHHHHHHCCcCCCHHHHHHHHHhhc-----CCeEEEECCC
Q ss_pred		HHHHHHHhCcEeeEEEEcCCHHHHHHHHHHHHHHHhcccchhhceeccCcCeEEEecCCCC
Q Klein_Draft	86	ELAGLILFGERLIISAHFKTAVNGMERLESLIAKSGLKAKQAHAESI EILDGNPNP
Q Consensus	86	~~~~~i~i~ntt~~~a~~~~~l~~~~~i~~~~~ +++.+. . +.+++++ +.+.+.+.+.+. . +.-. . . . . . . . . . .
T Consensus	61	i l ~~~~~-~~~~~l v ~ P ~~~~ L ~~~~ q ~~~~~~v ~~~~ g ~~~~~~-----~
T 2P6R_A	61	MVREAIK--GGKSlyVVPLRALAGEKYESFKKWEK-IGLRIGISTGDYESRDEHL----G
T ss_dssp		HHNNNHT--TCCEEEEESSHNNNNNNNNNNHTTTT-TTCCEEEECSSCBCSSCS---T
T ss_pred		HHNNNNH--cCeEEEEcChHHHHHHHHHHhHHh-cCCeEEEEecCCcchhhh---c
Q ss_pred		-----CCCCccccceeEEEEecHHhcCH-----HHHHHHHHhhcCCCCEEEEEEecC
Q Klein_Draft	156	-----DRSGLGLTADRVIDEAMTITP-----GSLKALLPTVSSRPNPQIVYTGT A
Q Consensus	156	-----~~~~~G~~~~~v~IDE~~~~~-----~~~~~l~~~~~i~~~~~stp . . . . . +++++ +   ++.+. . +.-. . . . . . . +.+++ +
T Consensus	124	~l~~~~~liIvDe~Hi~~~~r~~~~e~~~~~l~~~~~-~ii~lSAT~
T 2P6R_A	124	KADSLIRNRASVIKAVSCLVDIEIHL DSEKR GATLEILVTKMRRMNKA-LRVIGLSATA
T ss_dssp		HHNNNNHTTCSGGGGCCEEEET TGGGGGCTTHHHHHHHHHHHHHHCTT-CEEEEEECCC
T ss_pred		HHNNNNHCCHHHHHhhcCEEEEcHhHCcCCcccCHHHHHHHHHHHhCcCc-cceEEEEeCCC

**96.**

Probability: 97.24    E-value: 1.1E-4    Score: 76.2    Aligned Cols: 137    Identities: 17%    Similarity:

Q ss_pred		EEEEecHHhcCHHHHHHHhhcCCCCEEEEECcccc	
Q Klein_Draft	166	RVIFDEAMTITPGSLKALLPTVSSRNPQIVYTGAADQ	204 (510)
Q Consensus	166	~v~IDe~~~~~l~~~~~i~~~stp~~~ ++ +  +++. . . +. . . +. . . . . ++.+++  . . .	204 (510)
T Consensus	195	~iViDe~h~~~~~-----~i~lSaTp~~~	231 (472)
T 2FWR_A	195	LLIFDEVHHLPAESYVQIAQMSIA--PFRGLGTATFERE	231 (472)
T ss_dssp		EEEEETGGGTTSTTTTHHHHTCCC--SEEEEEESCccCT	
T ss_pred		EEEEEChhhCCchHHHHHHhhccC--CEEEeeceeeecC	

**97.**

Probability: 97.24      E-value: 6.3E-5      Score: 82.59      Aligned Cols: 149      Identities: 12%      Similarity

Q ss_pred		-CCCCccceeEEEEcHHhCCHHHHHHHhhcCCCCEEEEcCCCCC	
Q Klein_Draft	156	-DRSGLGLTADRVI FDEAMTITPGSLKALLPTVSSRNPQIVYTGTAADQRT	206 (5
Q Consensus	156	-~~~~~G~~~~~v~iDE~~~~~l~~~~~i~~~~~stp~~~~~	206 (5

Q ss_pred		HCCCEeEeCCHHHHHHHhhHHHHHhcCCCCceeeCCcHHHHHHHhcCEEEECCECe
Q Klein_Draft	396	AAGFTVYSPNQSEEAQACGGFLNDALVDPENPLLSHGNQHSLNAAISRVRKRDLPSSGGFV
Q Consensus	396	~g~~~~~l~~~~~gi~~~~~l~~~l~~~~~ +. +..+. .+.+.+. .++++. +.... .+++.+.+.+
T Consensus	68	~G~~~~~--gi~~~~~--i~~~~c~~~~iel~y~~~~~
T PF17288.1	68	QHGFNMVGARKYQGSRLQ--YTKIKRFRK--IICSDRCNTIELKPLAYATDKLGNII
T ss_pred		HcCCcceeccccCCHHH--HHHHHhHCe--EEeCCCCHHHHHHHhhcccccCCCCCc





[Vis](#)

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Hildebrand A, Renner M, Egert A, Söding J. *Proteins* 2009; 71:Suppl 9:128-32  
(<http://onlinelibrary.wiley.com/doi/10.1002/prot.22499/abstract;jsessionid=6FF63B8F61E35391B79F4681BB12DB2C.f02t>)

Automatic Prediction of Protein 3D Structures by Probabilistic Multi-template Homology Modeling.  
Meier A, Söding J. *PLoS Comput Biol*. 2015 Oct 23;11(10):e1004343  
(<http://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004343>).

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