



(/#/)

HHpred ?

Created: Jul 20, 2017 3:25 PM

ID	Date	Tool
8036569		HHPR
2963036		HHPR
6553686		HHPR
5422889		HHPR

Input Parameters Results (/api/job/result/2963036/hhpred/Results)



Raw Output (HHR) (/api/job/result/2963036/hhpred/Raw Output (HHR))



Number of hits: **250**



Probability Plot (/api/job/result/2963036/hhpred/Probability Plot)



Query Template MSA (/api/job/result/2963036/hhpred/Query Template MSA)

Visualization

Query MSA (/api/job/result/2963036/hhpred/Query MSA)

[Resubmit section](#)



1

225

	42NK_A
	200J_A
	4BIL_C
	4BIJ_C
	3EZK_B
	TIGR01547
	Terminase_3 Pha
	Terminase_1 Pha
	4IEE_A
	4IDH_A
	Terminase_GpA P
	1RIF_A
	5FMF_1
	3BER_A
	2FZ4_A
	PhoH PhoH-like
	ResIII Type III
	220M_A
	3H4J_B
	TIGR00603
	5J82_A
	5J8J_A
	2FWR_A
	5H09_A
	4BUJ_A
	3LY5_B
	3LY5_A
	1F0U_B
	5DZR_A
	4XGT_A
	4A4Z_A
	1Q0U_B
	2GXQ_A
	2XGJ_A
	3IUY_B
	3IUY_A
	2J8U_A
	Terminase_6 Ter
	5SUP_B
	20XC_A
	3B7G_B
	5GJU_A
	5JC3_B
	5JC3_A
	1VEC_B
	4U4C_A
	3B6F_A

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

4LJY_A
35HT_B
1S2M_A
3B85_B
4CT4_B
3G6H_A
TIGR04095
3FE2_A
1M36_D
5SUQ_C
4A4D_A
3B0R_A
5IVL_B
5GVR_A
3LLH_A
2P6R_A
3PEY_A
2G9N_A
2PL3_A
2KBE_A
1HV8_B
3DKP_A
4C9B_A
5LD2_D
TIGR00643
3FH0_B
1MP9_A
3TBK_A
3DMQ_A
TIGR00580
5XDR_A
1MP9_E
3OIY_B
5MOF_q
2EYQ_A
2ZJ8_A
5JFQ_j
4A36_B
3SQW_A
3P4X_B
AAA_11 AAA domai
2I4I_A
TIGR00614
20B3_A
4CBH_B
10YM_A
1GM5_A
5AGA_A
4Q48_B
4Q47_A
3H1T_A
1T6N_A
3I5X_A
4D26_A
4D25_A
5FFJ_B
5FFJ_A
TIGR00348
4TYN_A
1Z63_B
5LQW_D
5GM6_Y
5DCA_A
2Z83_A
4M7S_B
4M7S_A
308B_B
1Z6A_A
DNA_pack_N Prob
TIGR01389
TIGR03817
TIGR04121
4XQK_A
2XZL_A
5A0R_A
5LJ5_Q
5MSG_e
5DTU_A
DEAD DEAD/DEAD
2JLU_B
2V1X_B
2HWY_A

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

3GP8_A
3P1S_A
4F91_B
TIGR01447
4NH0_A
5DCA_A
1Z3I_X
2VA8_B
4XJX_A
4QQW_A
4QQW_G
3KQN_A
TIGR01448
4CBL_A
2XZP_A
2XZ0_A
5JHH_A
Flavi_DEAD Flav
5M59_E
5M59_G
4DDV_B
4DDU_A
2M74_B
4F91_B
403M_A
TIGR01967
5HZR_A
AAA_19 AAA domai
1MRB_A
5EAN_A
TIGR01970
5MZN_A
TIGR03714
AAA_34 P-loop co
3UPU_A
4B3F_X
5LBS_B
TIGR02621
1GKU_B
2ZFA_B
TIGR02768
Helicase_RecD H
1GL9_B
5M59_G
5M59_E
5JXR_A
5FHH_A
5FHH_B
4Q2D_A
4Q2C_A
TIGR00963
UTP25 Utp25, U3
4NL4_H
3HWY_W
TIGR04397
5X0X_0
TIGR04221
TIGR02562
TIGR01054
3VKW_A
4N0N_A
TIGR01587
1YKS_A
5B7I_A
5D8U_A
5LTJ_A
3BXZ_B
5FTB_A
2MHX_A
4UAD_A
2VBC_A
2FSF_B
TIGR02760
3RC8_A
3RC3_A
2VDA_A
SecA_DEAD SecA
5FTF_A
SNF2_N SNF2 fan
TIGR02760
TIGR03158
1M74_A
RT54 RT54-His

Align

Select all

Forward

Forward Query MSA

Color Seqs

Unwrap Seqs

TIGR01407

AAA_2

TIGR00631

1TF5_A

3JUX_A

Herpes_orf_0

1NL3_A

1NKT_A

4YS0_A

3JB9_X

2IPC_D

2IPC_A

4PJ3_A

TIGR00376

102H_A

5MQ0_V

1C40_A

4ZCF_C

TIGR00595

TIGR03117

UvrD-helicase_U

2VL7_A

DUF2075_Uncharac

3E2I_A

3CRV_A

TIGR01650

TIGR02640

TIGR01073

4CEJ_A

3U40_A

1UAA_B

1UAA_A

TIGR01075

5FMF_Y

2J87_D

2J87_B

DUF3638_Protein

TIGR01074

Hitlist

Show 25 entries

Nr	Hit	Name	Probability
<input type="checkbox"/> 1	4ZNK A (http://pdb.rcsb.org/pdb/explore.do?structureId=4ZNK)	Phage terminase large subunit; DNA Translocation, VIRAL PROTEIN; HET: SO4; 1.931A {Thermus phage P7426}	99.76
<input type="checkbox"/> 2	2O0I A (http://pdb.rcsb.org/pdb/explore.do?structureId=2O0I)	DNA packaging protein Gp17; nucleotide-binding fold, HYDROLASE; HET: ADP; 1.8A {Enterobacteria phage T4}	99.73

Vis

Hits

Align	Hit	Select all	Forward	Forward Query MSA	Color Seps	Unwrap Seps	Probability
<input type="checkbox"/>	3	4BIL_C (http://pdb.rcsb.org/pdb/explore.do?structureId=4BIL)				DNA MATURASE B; HYDROLASE, PACKAGING MOTOR, CONNECTOR, DNA; 29.0A {ENTEROBACTERIA PHAGE T7}	99.67
<input type="checkbox"/>	4	4BIJ_C (http://pdb.rcsb.org/pdb/explore.do?structureId=4BIJ)				DNA MATURASE B; HYDROLASE, ATPASE, DNA TRANSLOCATION, SINGLE-PARTICLE; 16.0A {ENTEROBACTERIA PHAGE T7}	99.67
<input type="checkbox"/>	5	3EZK_B (http://pdb.rcsb.org/pdb/explore.do?structureId=3EZK)				DNA packaging protein Gp17; pentameric motor, DNA packaging, Alternative; 34.0A {Bacteriophage T4}	99.64
<input type="checkbox"/>	6	TIGR01547 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR01547)				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.	99.61
<input type="checkbox"/>	7	PF04466.12 (http://pfam.xfam.org/family/PF04466.12#tabview=tab0)				; Terminase_3 ; Phage terminase large subunit	99.56
<input type="checkbox"/>	8	PF03354.14 (http://pfam.xfam.org/family/PF03354.14#tabview=tab0)				; Terminase_1 ; Phage Terminase	99.54
<input type="checkbox"/>	9	4IEE_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4IEE)				Gene 2 protein; DNA packaging, terminase, ATPase, nuclease; HET: AGS; 1.89A {Shigella phage Sf6}	99.39
<input type="checkbox"/>	10	4IDH_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4IDH)				Gene 2 protein; DNA packaging, terminase, ATPase, nuclease; 1.69A {Shigella phage Sf6}	99.39

Align	Hit	Select all	Forward	Forward Query MSA	Color Scales	Unwrap Sequences	Probability
<input type="checkbox"/>	11	PF05876.11 (http://pfam.xfam.org/family/PF05876.11#tabview=tab0)					; Terminase_GpA ; Phage terminase large subunit (GpA) 99.11
<input type="checkbox"/>	12	1RIF A (http://pdb.rcsb.org/pdb/explore.do? structureId=1RIF)					DNA helicase uvsW; Bacteriophage, T4, Helicase, UvsW, RecG; 2.0A {Enterobacteria phage T4} SCOP: c.37.1.23 99.09
<input type="checkbox"/>	13	5FMF 1 (http://pdb.rcsb.org/pdb/explore.do? structureId=5FMF)					DNA REPAIR HELICASE RAD25, SSL2; TRANSCRIPTION, PRE-INITIATION COMPLEX, RNA POLYMERASE; 6.0A {SACCHAROMYCES CEREVISIAE} 98.81
<input type="checkbox"/>	14	3BER A (http://pdb.rcsb.org/pdb/explore.do? structureId=3BER)					Probable ATP- dependent RNA helicase DDX47; RNA HELICASE, DEAD, AMP, Structural; HET: PGE, AMP; 1.4A {Homo sapiens} 98.8
<input type="checkbox"/>	15	2FZ4 A (http://pdb.rcsb.org/pdb/explore.do? structureId=2FZ4)					DNA repair protein RAD25; RecA-like domain, DNA damage recognition; 2.4A {Archaeoglobus fulgidus} SCOP: c.37.1.19 98.79
<input type="checkbox"/>	16	PF02562.15 (http://pfam.xfam.org/family/PF02562.15#tabview=tab0)					; PhoH ; PhoH-like protein 98.73
<input type="checkbox"/>	17	PF04851.14 (http://pfam.xfam.org/family/PF04851.14#tabview=tab0)					; ResIII ; Type III restriction enzyme, res subunit 98.72
<input type="checkbox"/>	18	2Z0M A (http://pdb.rcsb.org/pdb/explore.do? structureId=2Z0M)					337aa long hypothetical ATP- dependent RNA; helicase, ATP- binding, Hydrolase, Nucleotide- binding, RNA; 1.9A {Sulfolobus tokodaii} 98.72

Align	Hits	Select all	Forward	Forward Query MSA	Color Scales	Unwrap Sequences	Probability
<input type="checkbox"/>	19	3MWJ B (http://pdb.rcsb.org/pdb/explore.do?structureId=3MWJ)				Heat resistant RNA dependent ATPase; RNA HELICASE, RIBOSOME BIOGENESIS, THERMOPHILIC; HET: SO4; 1.4A {Thermus thermophilus}	98.72
<input type="checkbox"/>	20	TIGR00603 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR00603)				rad25; DNA repair helicase rad25. All proteins in this family for which functions are known are DNA-DNA helicases used for the initiation of nucleotide excision repair and transacription as part of the TFIIH complex.	98.71
<input type="checkbox"/>	21	5JB2 A (http://pdb.rcsb.org/pdb/explore.do?structureId=5JB2)				LGP2/RNA Complex; Innate immune pattern recognition receptor; HET: ADP, GTP; 2.2A {Gallus gallus}	98.71
<input type="checkbox"/>	22	5JAI A (http://pdb.rcsb.org/pdb/explore.do?structureId=5JAI)				LGP2/RNA Complex; Innate immune pattern recognition receptor; HET: ADP, EDO; 1.5A {Gallus gallus}	98.71
<input type="checkbox"/>	23	2FWR A (http://pdb.rcsb.org/pdb/explore.do?structureId=2FWR)				DNA repair protein RAD25; DNA Unwinding, DNA Repair, XPB; HET: IPA, PO4; 2.6A {Archaeoglobus fulgidus} SCOP: c.37.1.19	98.71
<input type="checkbox"/>	24	5HD9 A (http://pdb.rcsb.org/pdb/explore.do?structureId=5HD9)				Encapsidation protein; ASCE fold, VIRAL PROTEIN; HET: MSE; 1.941A {Bacillus phage phi29}	98.7

<u>Vis</u>	<u>Hits</u>	<u>Aln</u>	<u>Select all</u>	<u>Forward</u>	<u>Forward Query MSA</u>	<u>Color Segs</u>	<u>Unwrap Segs</u>
			Q ss_pred		HHHHCcCchccCEEEecCCEEEEEEecCCC-----CcEEEEeCCCCCccceecEE		
			Q Klein_Draft	64	KMGDRGPGTWSVIQSSKTNGRLSVSTSLCGA-----FGQVDFLPYGRGSARGLIADLV		
			Q Consensus	64	~~~~~ ..+...+.+...+.... ..+...+.+ .+ +...+.+.+.+.+. .+++++		
			T Consensus	103	~~~~~g~~i~~~~~G~~~~~V		
			T 4BIL_C	103	NIIDLPLFSELKPRPG-QRDSVISF---DVGPNPDHPSPVKSVGITG-QLTGSRADII		
			T ss_dssp		HHHTTSCTTTCCSCCB-STTSCSCB---SCSSSSCEEECTTTTTTHH-HHHCSEEEEE		
			T ss_pred		HHHHcCHHHHHHCCCC-CCCeeEe---ecCCCCCCCCcEEEecCC-ccccCCcEE		
			Q ss_pred		-----HHHHHHhhh---hhcc-cCCeEEEEeccch-HHHHHHHHCCCCCeEEEecCC		
			Q Klein_Draft	126	-----PEVLGDIYP---TVLT-TGGKIAAFGLLHK-QGLLAHVAGVADGRRVWGGPC		
			Q Consensus	126	-----~l~-----~i~t~p~----- ...+++.+. ++. .+++++++ .+. +++.+.+. . . .		
			T Consensus	168	-----Tp-----		
			T 4BIL_C	168	SATMGAREKLWTLVQEFAALLKPLPSSRVLYLGTPQTEMTLYKELEDNRGYTTIIPALY		
			T ss_dssp		HHHHHHHHHHSSSHHHHHHTTCCCCCEEEECCTTSHHHHHHHHHHTTCCCCCCCST		
			T ss_pred		CCCHHHHHHHHHHHHHHHHCCCCCeEEEECCCCcCHHHHHHhcCCceEEEcCC		
			Q ss_pred		-----HHHCccccCCHHHHHHHhhCCHHHHHHHhCCCCChhhc		
			Q Klein_Draft	182	-----AEANPALGHFLTREQVGRELKILPREVFARDRLGITPPKVEF		
			Q Consensus	182	-----~p~----- ...+ .+.+.+.+.+++++.++++. .++ + .+.+.+		
			T Consensus	238	-----e~l~-----f~ey-----		
			T 4BIL_C	238	SQRLAPMLRAEYDENPEALAGTPTDPVRFRDDLRERELEYKGAGFTLQFMLNPNLSDAE		
			T ss_dssp		SCBC TTHHHHHHHHTSCTTHHHHTTTCCTTSCSBSSCHHHHTTCCCCCCCCSSSEEE		
			T ss_pred		ccccHHHHHHHhcChhHhCCCCCcccCHHHHHHHHHHhCHHHHHHHhCCCCccc		

Aln[illegible]

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

7. [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: 99.56 E-value: 9.2E-16 Score: 107.63 Aligned Cols: 181 Identities: 10% Similar

Q ss_pred		CCeEEEEcCCCCcHHHHHHHHHHhC-----CCeEEEEcCCHHHHh-HHHHHHHHHHhC
Q Klein_Draft	17	SSVSFAAPRQNGKTYAAVNVALRY-----PGRVLVYFSGRFREAR-CAFDLAVKMGDR
Q Consensus	17	~~~~~i~~~~g~GKT~~~~~ .+.+++. + .++...+...+.++++ +.+++ .++..+...+..
T Consensus	1	~~~~~g~GKT~~~~~
T PF04466.12	1	HLTEVWYGGASSGKSHGVVQKVVLKSLQHWNVPRKVLWLRKVDRTVKNSIFTDVTCLSG
T ss_pred		CcEEEEEcCCCCcHHHHHHHHHHHHhC-----CcEEEEEcchHHHHhHHHHHHHHhC

Q ss_pred		eecCEEEEEEEcCCCCEEEEECcccc-CCccc-eecEEEEcCHHHcCHHHHHHHhhhhh
Q Klein_Draft	79	SKTNGRLSVSTSLCGAFGQVDFLPYGRG-SARGL-IADLVILDDADEVEPEVLGDIIPTV
Q Consensus	79	~~~~~iiiiiiiii~De~~~~~l~~~+..+.+++..+...+...+ ++..+..+..+..+
T Consensus	70	~~~~~g~iiiiiiiii~De~~~~~l~~~
T PF04466.12	70	NRSDKTIVLP----NGAIFLFQGMDPEKIKSIKGLSDVVMEAESEFNHNDYTQLTLRL
T ss_pred		eCccceEEEC-----CCCEEEEeCCCHHHhcCCCcCeEEEcCCCCCHHHHHHHHHHHH

Q ss_pred		EEEeccch-HHHHHHhCCC----
Q Klein_Draft	144	AAFGLLHK-QGLLAHVAGVA----DGRRVWVGPGPCESWDQATIAEANPALGHLFTREQV
Q Consensus	144	~~~~tp~-----p~~~~~ ++++ .. .++++....+.+.+.+.+.+.+.+ .+ +.+++
T Consensus	135	~~~~tP~-----dnP~-----
T PF04466.12	135	FCMFNPVSKLNWTYQTWFDPADYSRVSRAIHQSTY-----KDNRFLL--DEDNI
T ss_pred		EEEECCCCCcCceeeeeeeCCCCCCCCCeEEEEccc-----ccccCC---CHHHH

Q ss_pred		CCeEEEEeCCCCCHHHHHHHHHHc----	CCeEEEEeCCHHHH-HHHHHHHHHHHHcCc
Q Klein_Draft	17	SSVSFAAAPRQNGKTYAAVNYALRY----	PGRVLYFSRGFREA-RCAFDLAVKMGDRGPG
Q Consensus	17	~~~~i~~~~g~GKT~~~~~	~~~~~
T Consensus	35	.+.+++.+ +++..+..	.+++++.+++ +.+++..+..+. +.
T 4IEE_A	35	r~~~~~rg~GKT~~~~~	p~i~a~t~a~~~~~i~i~
T ss_dssp		HRYKVAKGGRGSGKSWAIARLLVEAARRQPV	RILCARELQNSISDSVIRLLEDTIER-EG
		CSEEEEEECTSSHHHHHHHHHHHHTTSC	EEEEEESSCGGGSTHHHHHHHHHH-HT

<u>T ss_pred</u>		<u>CCEEEEECCCCCHHHHHHHHHHCCceEEEEEcCCHHHHHHHHHHHHHHH--cc</u>
Select all	Forward	Forward Query MSA Color Seqs Unwrap Seqs
Q ss_pred		CCEEEEEEcCCCCcEEEEeCC-CC-CCccc-eEIEEEcHHHCCHHHHHHHhhhhhcc
Q Klein_Draft	82	NGRLSVSTSLCGAFGQVDFLPYG-RG-SARGLI-ADLVILDDADEVEPEVLGDIIPTVLT
Q Consensus	82	~~~~~i~~~~~g~~~iiDE~~~~~l~~~~~ ...+.... ++++.++++ .. .+ . +++++ +++.++++.++.+.+++..
T Consensus	102	~~~i~~~~---ngs~i~~~~G~~g~~~iiDE~~~~~i~~~~l~~
T 4IEE_A	102	RSMIRHLG----TNAEFMFYGIKNPNTIKISLEGIDICWVEEAETKESWDILIPTIRK
T ss_dssp		TTEEEETT----TCCEEEEEETTTCHHHHHHCCCCCEEECSSGGGCCHHHHHHHGGGCCS
T ss_pred		cceEEEcC----CCCEEEEEecCChhhccccCCCCEEEechhhCCHHHHHHHHHHhc
Q ss_pred		cch-HHHHHH-CCCCCCCeEEEcCCCcCCHHHHHHhccccCCHHHHHHHhh--hc
Q Klein_Draft	149	LHK-QGLLAHV-AGVADGRRVWGGPCSEWDQATIAEANPALGHFLTREQVGRELK--IL
Q Consensus	149	p~-::~:-:::p~-:::-::: .. .++++.+.+. .+ . + .++++.+. + ..
T Consensus	168	P~~~~~np~~~~~
T 4IEE_A	168	PKNILDDTYQRFFVNPPDDICLLTVNY-----TDNPHF----PEVLRLEMEECKRR
T ss_dssp		CCBTTSHHHCCCCSCCSSEEEEEEG-----GGCTTC----CHHHHHHHHHHHHH
T ss_pred		CCCCCCHHHHeeeCCCCCeEEEEec-----ccCCCC---CHHHHHHHHHHHhh
Q ss_pred		CCCCChhh-ccc
Q Klein_Draft	215	GITPPKVE-FKR 225 (229)
Q Consensus	215	~~~~~ 225 (229) +. +.
T Consensus	225	g~~~~~f 236 (490)
T 4IEE_A	225	GEPVSASDMAII 236 (490)
T ss_dssp		CCCBCCCTTBSS
T ss_pred		CckcccCccee

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

10. [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, termi {Shiella phage Sf6}

Probability: 99.39 E-value: 7.0E-13 Score: 105.81 Aligned Cols: 189 Identities: 12% Similar

Q ss_pred		CCeEEEEeCCCCCHHHHHHHHHHC---CCeEEEEeCCHHHH-HHHHHHHHHHHHCcCc
Q Klein_Draft	17	SSVSFAAAPRQNGKTYAAVNVALRY---PGRVLYFSRGFREA-RCAFDLAVKMGRGPG
Q Consensus	17	~~~~~i~~~~g~GKT~~~~~-----~~~~~ .+.+++..+++ + +++...+.. ..++++++..+++ +.++..+...+.+. +.
T Consensus	35	~r~~~~~rg~GKT~~~~~p~i~~~~a~t~~~~a~~~~~i~~~~i~--
T 4IDH_A	35	HRYKVAKGGRGSGKSWAIARLLVEAARRQPVRI LCARELQNSISDSVIRLLED TIER-EG
T ss_dssp		CSEEEEECTTCCHHHHHHHHHHHHTTSCSEEEEEESCSSGGGSHHHHHHHHHH-HT
T ss_pred		CCEEEEeCCCCCHHHHHHHHHHHHHHCcCeEEEEECcHHHHHHHHHHHHHHH-cC
Q ss_pred		CCEEEEEEcCCCCcEEEEeCC-CC-CCcCe-ecEEEEcCHHHcCHHHHHHHhhhhcc
Q Klein_Draft	82	NGRLSVSTSLCGAFGQVDFLPYG-RG-SARGLI-ADLVILDDADEVEPEVLGDIYPTVLT
Q Consensus	82	~~~~~i~~~~~--~ng~n~--~ii~DE~~~~~l~~~~~ ...+.... ++++.+.+.+. . .+ . + ++++++ +++.++++.+.+.+.+. .
T Consensus	102	~~~i~~~~~---ngs~i~~~~~G~ng~ii~DE~~~~~i~~~~l~
T 4IDH_A	102	RSMIRHLG---TNAEFMFYGIKNPTIKISLEGIDICWVEEA EAVTKESWDILIPTIRK
T ss_dssp		TTEEEETT---TCSEEEEEETTCCHHHHHHCCCCCEEEESC GGGCCHHHHHHGGGCCS
T ss_pred		cceEEEC---CCSEEEEEECcChhhcccCCCCEEEEechhhcCHHHHHHHHHHhcC
Q ss_pred		cch-HHHHHH-cCCCCcEEEEcCCCcCCHHHHHHHCccccCCHHHHHHHHh--hc
Q Klein_Draft	149	LHK-QGLLAHV-AGVADGRRVWGGPCESWDQATIAEANPALGHLFTREQVGRELK--IL
Q Consensus	149	p~--~~~~~-----~~~~~p~~~~~ .. .++++.+.+.+. . .+ . + .++++.+.+. .
T Consensus	168	P~~~~~-----~~~~~p~--~~~~~

T 4IDH_A	168	PKNILDDTYQRFVVNPPDDICLLTVNY-----TDNPHF----	PEVLRLEMEECKRR
<u>Select all</u>	<u>Forward</u>	<u>Forward Query MSA</u>	<u>Color Segs</u>
T ss_dssp		CCBTFSHHHCCCCCSCCSSEEEECG-----GGCTTC-----	CHHHHHHHHHHHHHH
T ss_pred		CCCCCChHHHeeeCCCCCeEEEEec-----ccCCCC----	CHHHHHHHHHHHHHH
Q ss_pred		CCCCChhh-ccc	
Q Klein_Draft	215	GITPPKVE-FKR	225 (229)
Q Consensus	215	~~~~~	225 (229)
	++ .+	
T Consensus	225	g~~~~~f	236 (490)
T 4IDH_A	225	GEPVSASDMAII	236 (490)
T ss_dssp		CCCBCCCTTBSS	
T ss_pred		CccccCCccee	

Probability: 99.11 E-value: 4.2E-11 Score: 97.61 Aligned Cols: 167 Identities: 11% Similarity: 11%

Q ss_pred		CCcHHHHHHHHhh--cCCeEEEEeCCCCcHHHHHHHHHhC----CceEEEEeCCHHH	
Q Klein_Draft	1	MELLAHQKLIHETID--NSSVSFAAAPRQNGKTYAAVNYALRY---PGRVLVFSRGFRE	
Q Consensus	1	~1~Q~-----~i~g~GKT~-----	
		+.+.++ .+++++. .+.+++..++++ +++.+++. ..++++ +.++	
T Consensus	22	~~~~p~Q~i~-----v~v~r~q~GKT~-----p~i~vapt~q	
T PF05876.11	22	PETLPWQMEIMDALGDPEVAEVGLMGPAGAKGSEIGLAWLGSIEHDPAGFMICQPSKVL	
T ss_pred		cccCHHHHHHHHHCCCCCEEEEEcCCCCCHHHHHHHHHHHHCCCCCEEEeCCHHH	
Q ss_pred		HHHHcCcchccEEE-eecCEEEEEEEcCCCCeEEEEeCCCC-CCccccecEEEEcCH	
Q Klein_Draft	64	KMGDRPGTWSVIQS-SKTNGRLSVSTSLCGAFGQVDFLPYGRG-SARGLIADLVILDDA	
Q Consensus	64	~~~~~i~-----g~-----ii~DE~	
		..+++..+.+.+.+. .+.+.+.+.+. .+.+.+.+.+. .+.+.+.+.+. +.+	
T Consensus	92	~i~-----l~-----i~-----g~-----a~-----l~G~-----vi~DE~	
T PF05876.11	92	PMIKSTSALRGQLLSEVGADNMFLKQF---R-AMLLTSIWPTAENFRARPVPRGWVDDY	
T ss_pred		HHHHcCHHHHhccccCCCCeEEEEe---c-ceEEEEecCCHHHhccCccCEEEEcCH	
Q ss_pred		--HHHHhhhhcc--cCCeEEEEecchH--HHHHHhCCCCCceEEEcC	
Q Klein_Draft	128	--VLGDYIPTVL--TGGKIAAFGLLHKQ--GLLAHVAGVADGRVWGGP	172 (22
Q Consensus	128	--~~~~l~-----~i~-----tp~-----	172 (22
		..+.+.+.+. .+.++++ .. .+.+.+.+.+.+.+.+.+.+	
T Consensus	157	~~~~~r~-----i~STP~~~~~i~-----q~-----Cp	207 (57
T PF05876.11	157	GSAVSLMDDRAATFEGRDTKFISSPADEKGGKIEAFVKGGTHERLMPPCP	207 (57
T ss_pred		CCHHHHHHHhhhhccccCEEEEEeCCCCcCCCCcHHHhCCCCCEEEeCC	

Probability: 99.09	E-value: 8.5E-12	Score: 92.63	Aligned Cols: 143	Identities: 12%	Similarity: 12%
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Q ss_pred		CCcchHHHHHHHHhhcCCeEEEEcCCCCcHHHHHHHHHHCC--C-eEEEEcCCHHHH
Q Klein_Draft	1	MELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNVALRYP--G-RVLVYFSRGFREAR
Q Consensus	1	~1~~Q~~~i~~~g~GKT~ .. +++ .+++..+...+.+++.+ .++..+...+ +++++ +...+.
T Consensus	112	~1~~Q~~av~~~i~~~GsGKT~ ~1~~Q~~av~~~i~~~GsGKT~
T 1RIF_A	112	IEPHWYQKDAVFEGLVNRRIILNLPTSAGRSLIQALLARYLYENYEGKILIIVPTTALT
T ss_dssp		CCCCHHHHHHHHHHHHHSEEECCCTTSCHHHHHHHHHHHHHCSSEEEECSSHHHHH
T ss_pred		CCCCHHHHHHHHHHHHhCCcEEEEcCCCCcHHHHHHHHHHHhCCcEEEEcCCHHHH
Q ss_pred		HcCcchhccEEEEecCEEEEEecCCCCcEEEEecCC--CC-CCccecEEEEcCHH

[illegible]

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

13. [5FMF 1 \(http://pdb.rcsb.org/pdb/explore.do?structureId=5FMF\)](http://pdb.rcsb.org/pdb/explore.do?structureId=5FMF) DNA REPAIR HELICASE RAD25, SSL2; TF INITIATION COMPLEX, RNA POLYMERASE; 6.0A {SACCHAROMYCES CEREVISIAE}

Probability: 98.81 E-value: 7.9E-10 Score: 88.58 Aligned Cols: 140 Identities: 13% Similarity: 13%

Q ss_pred		CCcHHHHHHHHHhhC---CeEEEEeCCCCCHHHHHHHHHhCCCeEEEEeCCHHHHHH
Q Klein_Draft	1	MELLAHQKLIHETIDNS---SVSAFAAPRQNGKTYAAVNVALRYPGRVLYFSRGFREARC
Q Consensus	1	~l~~~Q~~~~~-----~i~~~g~GKT~~~~~ .. +++ .+++..+...+.++.++ + .++..+.....++++ +...+
T Consensus	67	~l~~~Q~~~~i~~~~~ll~~~TGSgKT~~~~~liv~p~~~l~~~q
T 5FMF_1	67	TQIRPYQEKSLSKMFGNGRARSGIIVLPCGAGKTLVGITAACITIKSKSIVILCTSSVSVMQ
T ss_dssp		CCCCHHHHHHHHHTTSSSSSEEEECGGGCHHHHHHHHHHCSCEEEEESSHHHHHH
T ss_pred		CCCCHHHHHHHHHhcCCCCCEEEEeCCCCCHHHHHHHHHhCCEEEEEecChhHHHH
Q ss_pred		cCcchhcceEEeeCCEEEEEEcCCCCeEEEEeCCCCCcc-----ce
Q Klein_Draft	68	RPGTWSVIQSSKTNGLRSVSTSLCGAFGVDFLPYGRGSARG-----LI
Q Consensus	68	~~~~~i~~~~~g----- ..+.....+.....+.++.+++.+-....
T Consensus	137	~~~~~i~i~t~~~l~~~~~
T 5FMF_1	137	LQPENCAVFTSDNKEMFQ-----TESGLVSTYSVMANTRNRSHDSQKVMDFLTGRE
T ss_dssp		SSSTTCCEBSSSCBCCC-----TTTSEEESCSSSSSSCHHHHTTSCSSSSSSS
T ss_pred		CChhhEEEEecCCcchhc-----ccCeEEecHHHHHhCccccChHHHHHHHhCcc

Q ss_pred		HcCHHHHHHHhhhhccCCeEEEEecc	
Q Klein_Draft	123	EVEPEVLGDIYPTVLTGGKIAAFGLL	149 (229)
Q Consensus	123	~~~~~l~~~~~i~~~~tp	149 (229)
		+.+.+.+.+.+.+.+.+++++	
T Consensus	199	~~~~~l~lSaT~	224 (492)
T 5FMF_1	199	VVPAAMFRRVSTIAA-HAKLGLTATL	224 (492)
T ss_dssp		GTTSTTTTHHHHTCCC-CEEEEEESCC	
T ss_pred		cCCcHHHHHHHHhhhh-cCEEEeCCC	

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

14. [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: 98.8 E-value: 5.3E-10 Score: 81.56 Aligned Cols: 147 Identities: 13% Similarity

```

Q ss_pred          CchHHHHHHHHHHhCCeEEEEeCCCCchHHHHHHHHHhC-----CC-eEEEEeCCHHHH
Q Klein_Draft      2  ELLAHQKLIHETIDNSSVSFAAPRQNGKYAAVNVALRY----PG-RVLYFSRGFREA
Q Consensus        2  ~1~~~~Q~~~~~i~~~~gGKT~~~~~

```


Q ss_pred		HHcCcchhccEEEEecCEEEEEEEecCCCCEEEEEECCCC-----CCccee
Q Klein_Draft	66	GDRPGTWSVIQSSKTNGRLSVSTSLCGAFGQVDFLPYGRG-----SARGLIAD
Q Consensus	66	~~~~~i~~~~~ +.+.+.+.+.+.+.+.+
T Consensus	77	~~~~~v~~~~g~~~~~i~~~~~ivI~T~~~~l~~~~l~~~~~
T 5JB2_A	77	LRDAFKVTAVSGDSSHCKFFGQLA----KGSDVVICTAQILQNALLSGEEEARVELTDFS
T ss_dssp		GGGTSCCCCBCTTTGGGSGCHHHHH----HTCCC-CEHHHHHHHHHCCSTTTCGGGGCS

<u>T ss_pred</u>	<u>hccCceEEEEeCCccccchHHH- ---hcCEEEECHHHHHHHhhcCcCCCCcccce</u>			
<u>Select all</u>	<u>Forward</u>	<u>Forward Query MSA</u>	<u>Color Seqs</u>	<u>Unwrap Seqs</u>
Q ss_pred		CH-----HHHHHHhhhcccccCeEEEEecc		
Q Klein_Draft	125	EP-----EVLGDIYPTVLTGGKIAAFGLLH	150	(229)
Q Consensus	125	~-----l~~~~~i~~~~tp~	150	(229)
		.. .+.+.+.+.+.+.+.+.+		
T Consensus	143	~~~~~ii~LTaTp~	177	(680)
T 5JB2_A	143	QEAVYNKIMLSYLQKKLSGQRDLQPQLGLTASPG	177	(680)
T ss_dssp		STSHHHHHHHHHHHHTTCCCCCEEEESCCE		
T ss_pred		cCCHHHHHHHHHHHhhcCCCCCcEEEEcCCC		

22. [5JAJ A \(http://pdbe.rcsb.org/pdb/explore.do?structureId=5JAJ\)](http://pdbe.rcsb.org/pdb/explore.do?structureId=5JAJ) LGP2/RNA Complex; Innate immune pat ADP, EDO; 1.5Å {Gallus gallus}

Probability: 98.71 E-value: 1.1E-9 Score: 91.18 Aligned Cols: 146 Identities: 15% Similarity

Q ss_pred		CCchHHHHHHHHhhcCCEEEEEeCCCCCHHHHHHHHHhc----	CC-eEEEEeCCHHHH
Q Klein_Draft	1	MELLAHQKLIHETIDNSSVSFAAPRQNGKYAAVNYALRY---	PG-RVLYFSRGFREA
Q Consensus	1	~l~~~Q~~~~~i~~~~g~GKT~~~~~-----~	~ .. .++ .+++...+.+.+.+.+ .+.+.+.+.+. +. ++++++ +.+.+
T Consensus	8	~lr~Q~~~~~g~~~~i~~~~tGsGKT~a~~~~~vllilP~~~l~	
T 5JAJ_A	8	SELHGyQL EAVAPALGRNSIVWLP TGAGKTRA AVHVCRRHLEGRGRGVAVLVNKVHLV	
T ss_dssp		-CCCHHHHHHHHHHTTCCEEEECCTTSCHHHHHHHHHHHHTSSSCCEEEEEESSHHHH	
T ss_pred		CCchHHHHHHHHHHCCCCEEEEeCCCCCHHHHHHHHHHHHC	CCCCEEEEeCcCHHHH

Q ss_pred		HHCcCchhcceEEeeCCCEEEEEECccccEeCCCC-----Ccceeec
Q Klein_Draft	66	GDRPGTWSVIQSSTNGRLSVSTSLCGAFGQVDFLPYGRG-----SARGLIAD
Q Consensus	66	~~~~~iiiiiii~ +.....+.++++-++
T Consensus	78	~~~~~VV~~g~~~~~----~~~~IvIt~~l~~l~~~~~
T 5JAJ_A	78	LKDAFKVTAVSGDSSHCKFFGQLA---KGSDVICTAQILQNALLSGEEEARVELTDFS
T ss_dssp		GGGTSCREEECTTTTSSCHHHH--HTCSEEEEEHHHHHHHHCCCSTTTCCCGGGCS
T ss_pred		hccCEEEEEECcccChhhH---hCCCEEECHHHHHHHhCcccccChhhce

Q ss_pred		CHH-----HHHHhhhhhcc---CCeEEEEecc	
Q Klein_Draft	125	EPE-----VLGDIYPTVLT---GGKIAAFLGLH	150 (229)
Q Consensus	125	~~~~~l~~~~~i~~~~tp~ ...+...+. . .+.+++ .	150 (229)
T Consensus	144	~~~~~ii~LTaTp~	178 (681)
T 5JAJ_A	144	QEAVYNKIMLSYLQKKLSGQRDLPIQLGLTASPG	178 (681)
T ss_dssp		STSHHHHHHHHHHHHTTCCCCCEEEEEEESCCC	
T ss_pred		CCCcHHHHHHHHHHHHhcCCCCCcEEEEECccc	

23. [2FWR A \(http://pdbe.rcsb.org/pdb/explore.do?structureId=2FWR\)](http://pdbe.rcsb.org/pdb/explore.do?structureId=2FWR) DNA repair protein RAD25; DNA Unwinding factor A. PO4: 2.6Å {Archaeoglobus fulgidus} SCOP: c.37.1.19

Probability: 98.71 E-value: 2.5E-9 Score: 85.25 Aligned Cols: 133 Identities: 15% Similarity

Q ss_pred		CCcHHHHHHHHHhhCCEEEEECCCCCHHHHHHHHHhCCCCEEEEECCHHHHHHHHH
Q Klein_Draft	1	MELLAHQKLIHETIDNSSVSFAAPRQNGKYAAVNYALRPGRVLYFSRGFREARCAFD
Q Consensus	1	~l~~~Q~~~~~i~~~g~GKT~~~~~ +. .++ .+++..+..+..+..+ + .++.+.+.+.+++++ +...+.+..
T Consensus	92	~l~~~Q~~~~~i~~~tGsGKT~~~~~lil~P~~~l~~q~~
T 2FWR_A	92	ISLRDYEQKALERWLVDKRGCIVLPTGSGKTHVAMAAINELSTPTLIVVPTLALAEQWKE
T ss_dssp		CCBCHHHHHHHHHHTTTTEEEECCTTSCHHHHHHHHHHHCSEEEEESHHHHHHHHH
T ss_pred		CCCCHHHHHHHHHHhCCEEEEECCCCCHHHHHHHHHhCCCCEEEECCHHHHHHHHH

[illegible]

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/3ly5\)](http://www.ebi.ac.uk/pdbe/entry/pdb/3ly5)

26. [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: 98.69 E-value: 2.5E-9 Score: 78.45 Aligned Cols: 154 Identities: 18% Similarity

Q ss_pred		CchHHHHHHHHhhcCCeEEEEeCCCCCHHHHHHHHHh-----CCC-eEEEEeCC
Q Klein_Draft	2	ELLAHQKLIHETIDNSSVSFAAPRQNGKYAAVNYALR-----YPG-RVLVFSRG
Q Consensus	2	~l~~~Q~~~~~i~~~~g~GKT~~~~~ .++++ .+++..+...+.+++. + .++..+.. T Consensus 76 ~~~~~Q~~~~~l~~~~GsGKT~~~~~liv~p~
T 3LY5_B	76	NMTEIQHKSI RPLLEGRDLLAAAKTGSGKTLAFLIPAVELIVKLRFMPRN GTGLVLSPT
T ss_dssp		BCCHHHHHHHHHTCCCEECCTTSSHHHHHHHHHHHTTCCTTTCCCEEEECSS
T ss_pred		CCCHHHHHHHHHCCCCeEEEEeCCCCCHHHHHHHHHHHhccccCCCCceEEEEeCC
Q ss_pred		HHHHHHcCcchhcEEEEecCEEEEEEcCCCCeEEEEeCCCC-C-----Ccccee
Q Klein_Draft	62	AVKMGRGP GTSVIQSSTNGRLSVSTSLCGAFGQVDLPYGRG-S-----ARGLIA
Q Consensus	62	~~~~~i~~~~~g~~~ +..... ..+.+.+.+-+
T Consensus	146	~~~~~iivt~l~~~~~
T 3LY5_B	146	LKELMTHHVHTYGLIMGGSNRSAEQKL--GNGINIVATPGRLLDHMQNTPGFMYKNL
T ss_dssp		HHHHHTTCCCEEEECSSSCHHHHHHH--HTCCSEEEECHHHHHHHHCTTCCTTC
T ss_pred		HHHHhcCCCeEEEEeCCCHHHHHHH--cCCCeEEEEcHHHHHHHHhCCCCcHhc
Q ss_pred		cCH---HHHHHhhhcccCEEEEEeccch--HHHHHHH
Q Klein_Draft	124	VEP---EVLGD IYPTVLTGGKIAAGLLHK--QG LLAHV 158 (229)
Q Consensus	124	~~~l~~~~~tp~~~~~ 158 (229) +.+ ..+.+.+.+.++++ +. .++.+
T Consensus	213	~~~~~i~~~~~v~lsat~~~~~ 253 (262)
T 3LY5_B	213	ILDVGFEELKQIKLLPTRRQTMLFSATQRKVEDLARIS 253 (262)
T ss_dssp		HHHTTCHHHHHHHHSCSSSEEEECSSCHHHHHHHHH
T ss_pred		HhHCCHHHHHHHHHCCCCCEEEECCHHHHHHHHH

```
Q ss pred      ---HHHHHhhhhhcccCCeEEEEeccch
```


0 Consensus 68 ~~~~~i~~~~~-----~~~~~g~~~~~ii~DE

Q ss_pred		CCcchHHHHHHHHhhcCCeEEEEcCCCCHHHHHHHHHhC-----CC-eEEEEcCHHH
Q Klein_Draft	1	MELLAHQKLIHETIDNSSVSAFAAPRQNGKTYAAVNYALRY-----PG-RVLYFSRGFRE
Q Consensus	1	~1~~~~~Q~~~~~i~~~~g~GKT~~~~~-----~ ..++++ .++++.+...+.+++..++++ + .++...+... .. ++++++ +...
T Consensus	25	~~~~~Q~~~~~i~~~~G~GKT~~~~~l~v~p~~~~~

T 1Q0U_B	25	YKPTIEIQRIRIPGALRGESVMGQSQTGTGKTHAYLLPIMEIKIKPERAEVQAIVTAPREL
Select all	Forward	Forward Query MSA
T ss_dssp		Color Segs Unwrap Segs
T ss_pred		CSCCHHHHHHHHHHHCCEEEECSSHHHHHHHHHHHCCCTTSCSCEEEECSHHH
		CCCCHHHHhhHHHHHhCCceEEEEcCCCCCHHHHHHHHHHHHHhhccCccEEEEeCcHHH
Q ss_pred		HHHcCc---chhcceEEecCEEEEEEcCCCCeEEEEeCC-----CCCcccee
Q Klein_Draft	65	MGDRGP---GTWSVIQSSKTNGRLSVSTSLCGAFGQVDFLPYG-----RGSARGLIA
Q Consensus	65	~~~~~--~-~~~~~i~~~~~g~~~+.+.+.+.+.....
T Consensus	95	~~~~~i~v~t~~~~~
T 1Q0U_B	95	ITKFCPKDRMIVARCLIGGTDKQKALEKL--NVQPHVIGTGPRINDFIREQALDVHTA
T ss_dssp		HHTTSCGGGCCCEEEECSSHHHHHHHCCC--SSCCSEEEECHHHHHHHHHTTSCCCTTC
T ss_pred		HhccCCCcceEEEEEEecCCcHHHHHHHh--cCCCCEEECHHHHHHHHHhCCCChhcC
Q ss_pred		cCH---HHHHHHhhhcccCeEEEEeccch--HHHHHHcCCCCCeeEEec
Q Klein_Draft	124	VEP---EVLGDYIPTVLTTGGKIAAFGLLHK--QGGLAHVAGVADGRRVWWGG 171
Q Consensus	124	~~~--~-~~~~l~~~~~i~~~~tp~~-~~~~~ 171 +.. .+.+.+.+.+.+.++++ +. .+.+.+.+.+.+.+
T Consensus	162	~~~~~i~sat~~~~~p~~~~~ 215
T 1Q0U_B	162	MLDMGFITDVDQIAARMKDLQMLVFSATIKEKLPFLKKYMNPTFVHVLEHH 215
T ss_dssp		HHHTTCHHHHHHHHHTSCTTCEEEEEESCCGGGHHHHHHHhCSSCEEEEC---
T ss_pred		HcccCcHHHHHHHHHhCCCCceEEEEEcCCHHHHHHHHHHhccCCchhhcccc

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

33. [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; 1.2Å {*Thermus thermophilus* HB27}

Probability: 98.62 E-value: 1.2E-9 Score: 76.73 Aligned Cols: 152 Identities: 13% Similarity

Q	ss_pred		CchHHHHHHHHhhcCCeEEEEeCCCCCHHHHHHHHHhc-----CC-eEEEEeCCH
Q	Klein_Draft	2	ELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNYALRY-----PG-RVLYFSRGF
Q	Consensus	2	~l~~~Q~~~~~i~~~~gGKT~~~~~ .+++ .+++++.+++.+++ + .++.+...+. .++++ +
T	Consensus	23	~~~~Q~~~~~i~~~~gGkt~~~~~li~p~
T	2GXQ_A	23	TPTIQAAAALPLALEGKDILIGQARTGTGKTLAFALPIAERLAPSQERGRKPRLVLTPTR
T	ss_dssp		SCCHHHHHHHHHHTTCEEEECCTTSCHHHHHHHHHHHCCCCCTTCCSSEEEECSSH
T	ss_pred		CCCHHHHHHHHHHCCCCEEECCCCCCHHHHHHHHHHhchhcCCCCEEEEechH

Q ss_pred		HHHHHCcCchhcEEeEcCEEEEEECcCCcCEEEEeCCCC-----CcceecE
Q Klein_Draft	63	VKMGRPGTWSVIQSSKTNGRLSVSTSLCGAFGQVDFLPYGRGS-----ARGLIADL
Q Consensus	63	~~~~~i~~~~~ ...+
T Consensus	93	~~~~~i~t~~~~~
T 2GXQ_A	93	TAVAPHLKVVAVYGTTYGKGKEALL----RGADAVVATPGRALDYLRQGVLDSLRIEV
T ss_dssp		HHHCTTSCEEEESCSSHNNNNNNNNN----HCCSEEEECHNNNNNNNNHTSSCCTTCSE
T ss_pred		HHhCCCeEEEEECCHNNNNNNNNN----cCCEEEcHHNNNNNNNNcCCChhhccE

Q ss_pred		H---HHHHHhhhhhccCCEEEeccch--HHHHHHH	
Q Klein_Draft	126	P---EVLGDIYPTVLTGGKIAAFGLLHK--QGLLAHV	158 (229)
Q Consensus	126	~-----l~~~~~i~~~~tp~-~~~~~ . .+.+.+.+.+.++++ +. .++.+	158 (229)
T Consensus	158	~~~~~i~~sat~~~~~	196 (207)
T 2GXQ_A	158	SMGFEEEVEALLSATPPSRQTLLFSATLPWAKRLAERY	196 (207)
T ss_dssp		HTTCHHHHHHHHSTCTTSEEEEECSCHHHHHHHHHH	
T ss_pred		hCCCHHHHHHHHcCCCCEEEEECCHHHHHHHHHH	

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

Q ss_pred		--HHHHHHhhhhccCCEEEEEccch	
Q Klein_Draft	127	--EVLGDIYPTVLTGGKIAAFGLLHK	151 (229)
Q Consensus	127	--~~~~~l~~~~~i~~~~tp~~	151 (229)
		..+..+.....+ttt+ ..	
T Consensus	160	~~~~~i~~~~sat~~~	186 (374)
T 2J0U_A	160	FKEQIYDVYRYLPATQVVLISATLPH	186 (374)
T ss_dssp		CHHHHHHHHTSCTTCEEEEEESCCCH	
T ss_pred		hHHHHHHHHHCcCccEEEEeCCCCH	

[Template alignment | CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam03237\)](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=pfam03237)

38. [PF03237.14 \(http://pfam.xfam.org/family/PF03237.14#tabview=tab0\)](http://pfam.xfam.org/family/PF03237.14#tabview=tab0) ; Terminase_6 ; Terminase-like far

Probability: 98.6 E-value: 5.9E-11 Score: 85.36 Aligned Cols: 188 Identities: 15% Similarity

Q ss_pred		EEEECCCCCHHHHHHHHHHhC---CC-eEEEEeCCHHHHHH-HHH--HHHHHHHhCcC
Q Klein_Draft	21	AFAAPRQNGKTYAAVNALRY---PG-RVLYFSRGFREARC-AFD--LAVKMGDRGPG
Q Consensus	21	~i~n~g~GKT~~~~~ +++.+++ + +++.+++.+.+.+++++.++++.++.++.+.+.+.+.+
T Consensus	1	~~~~~r~GKT~~~~~
T PF03237.14	1	IIIEIPPQHGKSTVITETFPAYYLMRHPDSLVMVVSYSKELFQKFGKRNREKFRFLFSD-QL
T ss_pred		CcccCCCCCHHHHHHHHHHHHHhCcccEEEEeCCHHHHHHhHHHHHHHHHHhC-HH

Q ss_pred		CCCEEEEEeCCCCe-EEEECCC---CCCccceeeEEEEcCHHHcCHHHHHHHhhhh
Q Klein_Draft	82	NGRLSVSTSLCGAFGQ-VDFLPYGR---GSARGLIADLVILDDADEVEPEVLGDIYPTV
Q Consensus	82	~~~~~i~~~~~g~~~~ii~DE~~~~~l~~~~+++ .+.+.+. .+. .+++++ +.+.+.+.+.+
T Consensus	66	~~~~~g~~~~i~~~~~G~~~~i~~~~DE~~~~~
T PF03237.14	66	SETSSVS-----EWGVEGHLGSLYSTSILGGATGRGARLLIIDDPKRNRAEAEKTI RDK
T ss_pred		Ccccccc-----ccccccccceEEEEcCCCCcCCCCEEEEcCCCCCHHHhcCHHHHHH

Q ss_pred		eccccHHHHHHHcCCCC-----CeEEEcCCCCcCHHHHHHcccccCC
Q Klein_Draft	147	GLLHKQGLLAHVAGVADG-----RRVWGGGPCESWDQATIAEANPALGHLFT
Q Consensus	147	~tp~~~~~p~~~~~ + ...+++++.+. ++.++
T Consensus	131	stp~~~~~-----
T PF03237.14	131	SRLTADASVIVIMTRWHEDDLA GRLLKEQTL PWEEIKIPAI-----AEDDDLGRKPG
T ss_pred		cCCCCCcEEEEeccccCcCHHHHccccCCCCcEEEEccee-----ccCccccCCCC

Q ss_pred		CCHHHHHHHhC	CCCCC-----	hhhccc	
Q Klein_Draft	204	LPREVFARDRLGITPP-----	KVEFKR	225 (229)	
Q Consensus	204	~~~~~	~~~~~	225 (229)	
		+++.. +++++++.		
T Consensus	194	~~~~~g~~~~~g~	f	225 (232)	
T PF03237.14	194	EEWAAKTAVTGSRGWAALYQQRPT	PAGGNIF	225 (232)	
T ss_pred		HHHHHHHHHHhChHHHHHHHH	CCCCCCCCCc		

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

39. [5SUP B \(http://pdb.rcsb.org/pdb/explore.do?structureId=5SUP\)](http://pdb.rcsb.org/pdb/explore.do?structureId=5SUP) ATP-dependent RNA helicase SUB2, YR HYDROLASE-RNA complex; HET: BEF, ADP: 2.6Å {*Saccharomyces cerevisiae*}

Probability: 98.59	E-value: 2.0E-8	Score: 77.59	Aligned Cols: 145	Identities: 12%	Similarity
--------------------	-----------------	--------------	-------------------	-----------------	------------

Q ss_pred		CchHHHHHHHHHHhCCeEEEEeCCCCchHHHHHHHHHhC-----CC-eEEEEeCCHHHH
Q Klein_Draft	2	ELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNYALRY-----PG-RVLYFSRGFREA
Q Consensus	2	~1~~~~~Q~~~~~i~~~~~gGKT~~~~~-----~-----

Q ss_pred		CCcchHHHHHHHHhhccCCEEEEEeCCCCCHHHHHHHHHhc-----CC-eEEEEeCCHHH	
Q Klein_Draft	1	MELLAHQKLIHETIDNSSVSFAAPRQNGKYAAVNYALRY-----PG-RVLYFSRGFRE	
Q Consensus	1	~l~~~Q~~~~~i~~~~g~GKT~~~~~-----~::~~ ..+++ .+++..+...+.+++.+++ + .++...+...+. .++++ +...	
T Consensus	45	~~~~~Q~~~~~i~~~~g~Gkt~~~~~l~~~~p~~~~	
T 20XC_A	45	ERPSPVQLKAIPLGRGLDLIVQAASGTGKTCVFSTIALDSLVLLENLSTQILILAPTREI	
T ss_dssp		CSCCHHHHHHHHHHTTCCEEEECTTS SHHHHHHHHHHHHCCTTSCSCCEEEECSSHHH	
T ss_pred		CCCCHHHhhHHHHhCCCCeEEEEcCCCCCHHHHHHHHHHHhccccCeEEEEcCCHHH	
Q ss_pred		HHHcCcchhccEeeeecCEEEEEEcCCCCeEEEEeCC-----CCCCceeecccEE	
Q Klein_Draft	65	MGDRGPWTWSVIQSSKTNGRLSVSTSLCGAFGQVDFLPYG-----RGSARGLIADLVI	
Q Consensus	65	~~~~~i~~~~~-----~::g~~~~ii+.+.+. +++++	
T Consensus	115	~~~~~--~~~~i~int~~~l~~~~~ii	
T 20XC_A	115	IGIKMEGLECHVFVGITPLSQDKTR--LKKCHIAVSGSPRIKQLIELDYLNPGSIRLFI	
T ss_dssp		HTTTSTTCCEEEECTTSCHHHHHH--T TSCSEEEECHHHHHHHHTTSSCGGGCCEEE	
T ss_pred		HhhcccCeEEEECCCCChHHHH--HcCCCEEEECCHHHHHHHCCcCccCCEEE	
Q ss_pred		-CHHHHHHHhhhcccccCeEEEEeccch	
Q Klein_Draft	125	--EPEVLGDIIPTVLTGGKIAAFLHLK	151 (229)
Q Consensus	125	--~~~~~l~~~~~i~~~~tp~~	151 (229)
	 +. +. +. +. +. +. +. +. +. +. +.	
T Consensus	182	~~~~~l~~~~~i~~~~sat~~	210 (230)
T 20XC_A	182	GsfQEINWIYSSLPA SKQMLAVSATYPE	210 (230)
T ss_dssp		TSSH HH HH HH HHH SCSSCEEEEEESCCH	
T ss_pred		CCHHHHHHHHHhCCCCeEEEEEcCCH	

T 5JC3_A	76	EFNPF LKH WYQVIGLSGDS ELKIS FP EV ---VKRYDVI ICTAQ IL ENSL LNATEE DSVR
Select all	Forward	Forward Query MSA
T ss_dssp		Color Segs
T ss_pred		Unwran Segs
T ss_dssp		CCHHHHTT TT SEEEEL CCSS SCCHHH---HHK SEEELHHHHHHHH CSCC--CCC
T ss_pred		HhHHHh cC eEEEE eC Ccc CC ChHH---Hh hC EEEE ch HHHHHHHh cC CCCC cC c
Q ss_pred		CHHH cC H-HHHHHhhhh hC -----cc C eEEEE eC cc
Q Klein_Draft	120	DADEV EP -EVLGDI YPT VL-----TTGGKIA AF GLLH 150 (229)
Q Consensus	120	E~~~~~ ~~~~~ l~~~~~ ~~~~~ -----~~~~~ ~~~~~ i~~~~~ ~~~~~ tp~ 150 (229)
		+ +... ..+.+.+.+++ .
T Consensus	143	E~H~~~~~ ~~~~~ i~~~~~ ~~~~~ l~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~ ~~~~~ il~LTATp~ 191 (701)
T 5JC3_A	143	QCHHTQKEGVNNIMRRYLKEIKNRKQAKENKPLIPQPQILGLTASPG 191 (701)
T ss_dssp		TGGG CST TCHHHHHHHHHHHHHHHHHHHHHHC---CCCC CEEEEE ESCCC
T ss_pred		cHHHh ccc ChHHHHHHHHHHHHHh ch hhhh cC CCCC CC eEEEE eC CCC

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/1vec\)](http://www.ebi.ac.uk/pdbe/entry/pdb/1vec)

45. [1VEC B \(http://pdb.rcsb.org/pdb/explore.do?structureId=1VEC\)](http://pdb.rcsb.org/pdb/explore.do?structureId=1VEC) ATP-dependent RNA helicase p54; RNA PROTEIN, RNA; HET: TLA; 2.01Å {Homo sapiens} SCOP: c.37.1.19

Probability: 98.57 E-value: 1.3E-8 Score: 72.05 Aligned Cols: 148 Identities: 13% Similarity

Q ss_pred		CCcchHHHHHHHHHHhCCEeEEEEeCCCCCHHHHHHHHHHhC-----CC-eEEEEeCCHHH
Q Klein_Draft	1	MELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNVALRY-----PG-RVLYFSRGFRE
Q Consensus	1	~1~~~Q~~~~~i~~~~g~GKT~~~~~-----~::~~ ..+++. .+++.+.+.+.+++.+++ + .+.+.+.+.+.+.+.+.+.+.+.+.+++++ +...
T Consensus	24	~~~~~Q~~~~~i~~~~G~GKT~~~~~li~p~~~~
T 1VEC_B	24	EKPSPIQEESIPIALSGRDILARAKNGTGKSGAYLIPLLERLDLKKDNIQAMVIVPTREL
T ss_dssp		CSCCHHHHTTHHHHHHTCCEEEECSSSTTHHHHHHHHHHCCCTTSCSCCEEEECSSHHH
T ss_pred		CCCCHHHHHHHHHHHCCCCEEECCECCCCCHHHHHHHHHHHhCccCCCCeEEEEeCCHHH

Q ss_pred		HHHhCcchhc-cEEEEcCCEEEEEEcCCCCcEEEEcC-----CCCCccceecEE
Q Klein_Draft	65	MGDRGPGTWS-VIQSSKTNGRLSVSTSLCGAFGQVDFLPYG-----RGSARGLIADLV
Q Consensus	65	~~~~~i~~~~~++..+..+..+.....++++
T Consensus	94	~~~~~i~v~t~l~~~~~l
T 1VEC_B	94	VSKHMGGAkVMATTGGTNLRDDIMRL---DDTVHVVIATPGRILDLIKKGVAkVDHVQMI
T ss_dssp		HTGGGSCCCEEEECTTSCHHHHHHHH---TSCCCEEECHHHHHHHHHTTSSCCTTCCEE
T ss_pred		HHhhcCCcEEEEEEcCCcHHHHHHhhc---cCCCEEECHHHHHHHHhCCcChhcceEE

Q ss_pred		----	HHHHHHhhhhcccccCEEEEEccch	
Q Klein_Draft	127	----	EVLGDIYPTVLTGKIAAFGLLHK	151 (229)
Q Consensus	127	-----	~~~~~l~~~~~i~~~~tp~~	151 (229)
			..+..+.....++++ +..	
T Consensus	161	~~~~~	~~~~~l~lsat~~	189 (206)
T 1VEC_B	161		QDFVQIMEDIILTLPKNRQILLYSATFPL	189 (206)
T ss_dssp			TTTHHHHHHHHTSCTTCEEEEEESCCCH	
T ss_pred			CCHHHHHHHHHcCCCCcEEEEEECCCH	

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/4u4c\)](http://www.ebi.ac.uk/pdbe/entry/pdb/4u4c)

46. [4U4C A \(http://pdbe.rcsb.org/pdb/explore.do?structureId=4U4C\)](http://pdbe.rcsb.org/pdb/explore.do?structureId=4U4C) Mtr4, Dob1 (E.C.3.6.4.13), Air2-Trf4 Fusi poly(A)polymerase, RNA degradation; HET: SO4, PG4; 2.4Å {*Saccharomyces cerevisiae*}

Probability: 98.57 E-value: 1.3E-8 Score: 88.59 Aligned Cols: 144 Identities: 15% Similarity

Q ss_pred		CCcHHHHHHHHHhhCCEEEEECCCCCHHHHHHHHHhC--CC-eEEEEeCCHHHHH
Q Klein_Draft	1	MELLAHQKLIHETIDNSSVSFAAPRQNGKYAAVNVALRY--PG-RVLYFSRGFREARC
Q Consensus	1	~L~~~Q~~~~~i~~~~g~GKT~~~~~--~-~~~~~ ++ +++ .+++..+.++.+...+ .+.+.+.+. .+ +++++++.+
T Consensus	73	~L~~~Q~~ai~l~~~~vll~antGsGKTl~~~~i~~~l~~~~~lv~P~~aL~~q
T 4U4C_A	73	FTLDPFQDTAISCIDRGESVLVSAHTSAGKTVVAEYAIQAQLKNKRVIYTSPIKALSNQ
T ss_dssp		SCCCHHHHHHHHHHTTCEEEECGGGCHHHHHHHHHHHHTTCEEEEEESSHHHHH

T ss_pred		CCCCHHHHHHHHHCCeEEEEcCCCCHHHHHHHHHHHCCEEEEEEcCchHHHHH		
Select all	Forward	Forward Query MSA	Color Seqs	Unwrap Seqs
Q ss_pred		cCcchccEEEEecCEEEEEEEcCCCCeEEEEEC-----CCCccceecEEEEcC		
Q Klein_Draft	68	RPGTWSVIQSSKTNGRLSVSTSLCGAGFQVDFLPYG-----RGSARGLIADLVILDD		
Q Consensus	68	~~~~~i~~~~~g~~~~~ii~DE ...+.+..+.+.+. .++++ +		
T Consensus	143	~v~~~g~~~~~-----~~~~~ilI~T~e~l~~~l~~~~~vI~DE		
T 4U4C_A	143	DVGLMTGDITIN-----PDAGCLVMTEILRSMLYRGSEVMREVAWVIFDE		
T ss_dssp		CEEEECSSCEE-----TTCEEEEEHHHHHHHHHTCTHHHHEEEEEETT		
T ss_pred		CeEEEcCCCC-----CCCCEEehHHHHHHhcCCHHHHhcEEEEcC		
Q ss_pred		HHHHhhhhhccccCeEEEEeccchHHHHHHH		
Q Klein_Draft	127	EVLGDIYPTVLTGGKIAAFGLLHKQGLLAHV	158 (229)	
Q Consensus	127	~~~~~l~~~~~i~~~~tp~~~~~ ..+++. ...+.....++++ +. +. +. +.	158 (229)	
T Consensus	199	~~~e~~i~~~l~~~~~i~LSATI~n~~e~~~	230 (998)	
T 4U4C_A	199	VVWEETIIILLPDKVRVVFLSATIPNAMEFAEW	230 (998)	
T ss_dssp		HHHHHHHHHSCTTCEEEEEECCTTHHHHHHH		
T ss_pred		hhHHHHHHhCCCCCEEEEEcCCCCHHHHHHH		

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/3b6e\)](http://www.ebi.ac.uk/pdbe/entry/pdb/3b6e)

47. [3B6E A \(http://pdb.rcsb.org/pdb/explore.do?structureId=3B6E\)](http://pdb.rcsb.org/pdb/explore.do?structureId=3B6E) Interferon-induced helicase C domain-DExD/H RNA-binding helicase, innate; 1.6A {Homo sapiens}

Probability: 98.56 E-value: 1.0E-8 Score: 72.62 Aligned Cols: 145 Identities: 13% Similarity

Q ss_pred		CCcHHHHHHHHHhhccCeEEEEeCCCCCHHHHHHHHHhc-----CC-eEEEEecC	
Q Klein_Draft	1	MELLAHQKLIHETIDNSSVSFAAPRQNGKYAAVNYALRY-----PG-RVLYFSRG	
Q Consensus	1	~l~~~Q~~~~~i~~~g~GKT~~~~~+ . +++++ . +++++ . +...+.+++.+++ + .++.+...+..+.	
T Consensus	32	~l~~~Q~~~~~G~Gkt~~~~~ili~~p	
T 3B6E_A	32	LQLRPYQMEVAQPALLEGKNIIICLPTGS GKTR VAVYIAKDHLDKKKKASEPGKVIVLVNK	
T ss_dssp		CCCCHHHHHHHHHTTCEEEECSCHHHHHHHHHHHHHHHHHTTCCCCCEEES	
T ss_pred		CCCCHHHHHHHHHHCCEEEEeCCCCCHHHHHHHHHHHhccccCCCceEEEEch	
Q ss_pred		HHHHHHCcChhcccEEEEecCEEEEEEcCCCCeEEEEeCCCC-----C	
Q Klein_Draft	62	AVKMGRGPWTWSVIQSSTNGRLSVSTSLCGAFGQVDLPYGRGS-----A	
Q Consensus	62	~~~~~i~~~~~+.+.+.+.+-.	
T Consensus	102	~~~~~i~v~t~~~~~	
T 3B6E_A	102	EFPFLKKWYRVIGLSGDTQLKISFPEV--VKSCDIIISTAQILENSLLNLENGEDAGV	
T ss_dssp		CCHHHHTTTSCHEEECC---CCCCHHH--HHHCSEEEEEHHHHHHHHHC-----CC	
T ss_pred		HhHhhhCcCeEEEEcCCceeeccc hH--h c C E E E e c H H H H H H h c c c C C c c c c	
Q ss_pred		cCHHHcCHH-HHHHHhhhhccc-----CCeEEEEec	
Q Klein_Draft	119	DDADEVEPE-VLGDIYP TVLT-----GGKIAAFGL	148 (229)
Q Consensus	119	DE~~~~~l~~~~~i~~~~t +.+.+.+.+.+.+.+.+.+.+	148 (229)
T Consensus	169	DE~h~~~~~sa	215 (216)
T 3B6E_A	169	DECHHTNKEAVNNIMRHYLMQKLKNNRLKENKPVIPLPQILGLTA	215 (216)
T ss_dssp		TTC-----CHHHHHHHHHHHHHHHHTTCCCCCCCCCCEEEEEC	
T ss_pred		ECHhccChhHHHHHHHHHHHHhhchccccCCCCCCCCceeeeec	

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

48. [4LJY A \(http://pdb.rcsb.org/pdb/explore.do?structureId=4LJY\)](http://pdb.rcsb.org/pdb/explore.do?structureId=4LJY) Pre-mRNA-processing ATP-dependent R box, RNA splicing; HET: MRD, ADP; 1.95Å {*Saccharomyces cerevisiae*}

Probability: 98.56	E-value: 3.9E-9	Score: 84.45	Aligned Cols: 148	Identities: 15%	Similarity
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Vis	Hits	Aln	Select all	Forward	Forward Query MSA	Color Segs	Unwrap Segs
			Q ss_pred		CchHHHHHHHHHHCCCEEEECCECCCHHHHHHHHHHC		-----CCeEEEEe
			Q Klein_Draft	2	ELLAHQKLIHETIDNSSVSAFAAPRQNGKTYAAVNYALRY		-----PGRVLYFS
			Q Consensus	2	~l~~~Q~~~~~i~~~g~GKT~~~~~		-----
					. +++ .++..+.+++..+++ + .++..+..		...+++++
			T Consensus	73	~l~~~Q~~~~i~~i~~~~~l~~~~tGsGKT~~~~~		~~~~~lil~
			T 4LJY_A	73	SLTPIQSQALPAIMSGRDVIGISKTGSGKTISYLLPLLRQVKAQRPLSKHETGPMGLILA		
			T ss_dssp		SCCHHHHHHHHHHTTCCEEEECCTTSCHHHHHHHHHHHTSCCCCTTCCCCSEEEEC		
			T ss_pred		CCCHHHHHHHHHHCCEEEECCECCCHHHHHHHHHHHHC		CCcCCCCCEEEEC
			Q ss_pred		HHHHHHHHCcchhccEEEEecCEEEEEECCECCCEEEECCECC		-----CCc
			Q Klein_Draft	60	DLAVKMGDRGPGTWSVIQSSKTNGRLSVSTSLCGAFGQVDFLPYGRG		-----SAR
			Q Consensus	60	~~~~~i~~~~~		-----
					..+.....+.....		..+..+..+..+..- ...
			T Consensus	143	~~~~~ii~T~~~~l~~~~~		~~~~~
			T 4LJY_A	143	EEVTKFTEADTSIRSVCTGSGEMKKQITDL--KRGTEIVVATPGRFIDILTNDGKLLS		
			T ss_dssp		HHHHHHHTTCTTCEEEESSCCTHHHHHHH--TTCSEEECHHHHHHHHTTHHHHTSSC		
			T ss_pred		HHHHHHHCCECCCEEEECcCHHHHHHHH--HhCCCEEECHHHHHHHHHCCCCeEC		
			Q ss_pred		CHHHcCH---HHHHHhhhhcccCCeEEEEecch		
			Q Klein_Draft	120	DADEVEP---EVLGDIYPTVLTGGKIAAFGLLHK	151 (229)	
			Q Consensus	120	E~~~~~l~~~~~i~~~~tp~~	151 (229)	
					+ .+.+ ..+.+.+.+.+.+.+.+.+.+.+.+		
			T Consensus	211	Eah~~~~~i~~SaT~~~	246 (493)	
			T 4LJY_A	211	EADRLFDLGFEPQITQIMKTVRPDKQCVLFSATFPN	246 (493)	
			T ss_dssp		THHHHHHTTCHHHHHHHHHHSCCTTCEEEEEESCCCH		
			T ss_pred		CHHHHhCcCHHHHHHHHHCCCCCEEEEEECCH		

49.	Template alignment Template 3D structure PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3fht) 3FHT B (http://pdb.rcsb.org/pdb/explore.do?structureId=3FHT) ATP-dependent RNA helicase DDX19B (box helicase, RNA dependent; HET: ANP, GOL; 2.2A (Homo sapiens)						
	Probability: 98.56	E-value: 2.3E-8	Score: 78.05	Aligned Cols: 145	Identities: 14%	Similarity	
			Q ss_pred		CchHHHHHHHHHhC--CeEEEECCCCCHHHHHHHHHHC		-----CC-eEEEEeCCHH
			Q Klein_Draft	2	ELLAHQKLIHETIDNS--SVSAFAAPRQNGKTYAAVNYALRY		-----PG-RVLYFSRGFR
			Q Consensus	2	~l~~~Q~~~~~i~~~g~GKT~~~~~		-----
					.++++ .+++..+.+. +.+++..+++ + .++..+..		+ .++++ +. .
			T Consensus	47	~~~~~Q~~~~~i~~~~tGsGKT~~~~~		~~~~~liip~~~
			T 3FHT_B	47	RPSKIQENALPLMLAEPQNLIAQSQSGTGKTAAFVLAMLSQVEPANKYPQCLCLSPTYE		
			T ss_dssp		SCCHHHHHHHHHHTSSSCCEEEECCTTSSHHHHHHHHHHHCCTTSCSCCEEEECSSH		
			T ss_pred		CCCHHHHHHHHHHCCECCeEEEECCCCCHHHHHHHHHHhcccCCCCeEEEEcCHH		
			Q ss_pred		HHHHcCchhccEEEEecCEEEEEECCECCCEEEECCECC		-----CCcceeEC
			Q Klein_Draft	64	KMGDRGPGTWSVIQSSKTNGRLSVSTSLCGAFGQVDFLPYGRG		-----SARGLIADL
			Q Consensus	64	~~~~~i~~~~~g~~~~~		-----
				+..+..+..-++
			T Consensus	117	~~~~~iiv~t~~~~l~~~~~		~~~~~
			T 3FHT_B	117	QMGKFYPELKLAYAVRGNKLERGQK----ISEQIVIGTPGTVDWCSKLKFDPKKIKV		
			T ss_dssp		HHTTTCTTCEEEECTTCC-----CCCSEEECHHHHHHHHTTSCSCGGGCCCE		
			T ss_pred		HHHhCcCeEEEEeCCChhcccc-----cCCCEEECHHHHHHHHHCCCCChhCCCE		
			Q ss_pred		H----HHHHHhhhhcccCCeEEEEecch		
			Q Klein_Draft	126	P----EVLGDIYPTVLTGGKIAAFGLLHK	151 (229)	
			Q Consensus	126	~~~~~l~~~~~i~~~~tp~~	151 (229)	
				+.+.+.+.+.+.+.+.+.+.+.+		
			T Consensus	182	~~~~~i~~SaT~~~	212 (412)	
			T 3FHT_B	182	ATQGHQDQSIRIQRMLPRNCQMLLFSAFED	212 (412)	
			T ss_dssp		STTTTHHHHHHTTSCCTTCEEEEEESCCCH		

Vis

Hits

Aln

Select read

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Local Query MSA

Color Segs

Unwrap Seqs

Q_Klein_Draft	132	IYPTVLTITGGKIAAFGLLHK	151 (229)
Q_Consensus	132	1~~~~~i~~~~tp~~ +...+.. ..++++ + .+	151 (229)
T_Consensus	142	~~~~~i~lg~~~~q	160 (208)
T_3885_B	142	FLTRLGF-GSKMVTGDITQ	160 (208)
T_ss_dssp		HHTTBCS-SCEEEEEEC---	
T_ss_pred		HHHhccC-CcEEEEECcHHH	

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

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

Probability: 98.53 E-value: 2.2E-8 Score: 77.0 Aligned Cols: 148 Identities: 15% Similarity:

Q ss_pred		CchHHHHHHHHHHhCCeEEEECCCCChHHHHHHHHHhC----	CC-eEEEEeCCHHHH
Q Klein_Draft	2	ELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNALRY----	PG-RVLYFSRGFREA
Q Consensus	2	~l~~~Q~~~~~i~~~~g~GKT~~~~~	~~~~~
T Consensus	27	~~~~Q~~~~i~~~~~l~~~~g~GKT~~~~~	~~~~~li~~p~~~l~
T 4CT4_B	27	KPSPIQEESIPIALSGRDILARAKNGTGKSGAYLIPLLERDLK	KDNIQAMVIVPTRELA
T ss_dssp		SCCHHHHHHHHHHTTCCEEEECCSSGGGHHHHHHHHHHHCC	CTTCCSCCEEEEECCSHHHH
T ss_pred		CCCHHHHHHHHHHhCCcEEEECCCCCHHHHHHHHHHHHh	ccCCCCcEEEEcCCHHHH

Q ss_pred		HHCcCchhcEEEEEeCCCCCEEEEEECCECCCEEEEEEC-----CCCCccceEEEEE
Q Klein_Draft	66	GDRPGTWSVIQSSKTNGRLSVSTSLCGAFGQVDFLPYG-----RGSARGLIADLVIL
Q Consensus	66	~~~~~iiiiiiiii~+
T Consensus	97	~~~~~iiiiit~~~~~iiii
T 4CT4_B	97	SKHMGGAkvMATTGGTNLRDDIMRL--DDTVHVVIATPGRILDLIKGVAKVDHVQMIVL
T ss_dssp		TTTSSSCCEEEECTTSCHHHHHHTT--TSCSEEEECHHHHHHHHTTSSCCTTCCEEEE
T ss_pred		HhhCCCCCEEEEEECcCHHHHHhcc--ccCCCCCEEECHHHHHHHHcCCCCccccEEEEE

Q ss_pred		--HHHHHHhhhhcccccEEEEEeccch	
Q Klein_Draft	127	--EVLGDIYPTVLTGGKIAAFGLLHK	151 (229)
Q Consensus	127	--~~~~~l~~~~~i~~~~tp~~	151 (229)
		..+..+..+..+..+..+..+..+..+..	
T Consensus	165	~~~~~i~~~~sat~~	191 (378)
T 4CT4_B	165	FVQIMEDIILTLPKNRQILLYSATFPL	191 (378)
T ss_dssp		THHHHHHHHTTCTTCEEEEEESCCCH	
T ss_pred		HHHHHHHHHHCCCCCEEEEEECCH	

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/3g0h\)](http://www.ebi.ac.uk/pdbe/entry/pdb/3g0h)

3G0H A (<http://pdb.rcsb.org/pdb/explore.do?structureId=3G0H>) ATP-dependent RNA helicase DDX19B RNA COMPLEX, DBP5, Structural Genomics; HET: ANP; 2.7Å {Homo sapiens}

Probability: 98.52 E-value: 3.5E-8 Score: 77.39 Aligned Cols: 145 Identities: 14% Similarity

Q ss_pred		CchHHHHHHHHHhC-.-CeEEEECCCCCHHHHHHHHHHC-----CC-eEEEEcCHH
Q Klein_Draft	2	ELLAHQKLIHETIDNS--SVSAFAAPRQNGKYAAVNYALRY----PG-RVLVYFSRGFR
Q Consensus	2	~l~~~Q~~~~~-----~in~~g~GKT~~~~~-----~ .++++ .+++..+...+.+++. + .+.....+... .. .++++ +..
T Consensus	63	~~~~~Q~~~~~ll~~tGsGKT~~~~~liip~~
T 3G0H_A	63	RPSKIQENALPLMLAEPQNLIAQSQSGTGKTAAFVLAMLSQVEPANKYPQCCLCSPTYE
T ss_dssp		SCCHHHHHHHHHSSSCCEEEECCTTSCHHHHHHHHHTTCCTTSCSCEECEECSSH
T ss_pred		CCCHHHHHHHHHhCcccCeEEEECCCCcHHHHHHHHHHhhcccccCeEEEEcChH

Q ss pred HHHHcCcchccEEEecCEEEEEEEcCCCCeEEEEeCCCC-----CCcccceecE

T 3FE2_A	51	EPTAIIQAQGWPVALSLDMVGVAQTGSGKTLSYLLPAIVHINHQPFLERGDGPICLVLPAP
Select all	Forward	Forward Query MSA
T ss_dssp		Color Segs Unwrap Segs
T ss_pred		CCcHHHHhhHHHHhCCCCCEEEECccccCHHHHHHHHHHHHHhccccccCCCCCeEEEEeC
Q ss_pred		HHHHHHhcCcchcccEEEecCEECEEEEcCCCCcEEEEeCC-----CCCcccee
Q Klein_Draft	61	LAVKMGRDGPGTWSVIQSSTNGRLSVSTSLCGAFGQVDFLPYG-----RGSARGLIA
Q Consensus	61	~~~~~i~~~~~g~~ +. +. +
T Consensus	121	~~~~~i~v~t~n~l~~~~~
T 3FE2_A	121	VAAEYCRACRLKSTCIYGGAPKGPQIRDL--ERGVEICIATPGRILDFLECGKTNLRT
T ss_dssp		HHHHHHHHHTTCEEEECTTSCHHHHHHHH--HHCCSEEEECHHHHHHHHHHTSCCTTC
T ss_pred		HHHHHHhhcCCeEEEEECcChHHHHHH--hhCCCEEEeCHHHHHHHHHhCCCChhhC
Q ss_pred		cCH---HHHHHhhhhcccCCeEEEEeccch
Q Klein_Draft	124	VEP---EVLDGIYPTVLTTGGKIAAFGLLHK 151 (229)
Q Consensus	124	~~~~~l~~~~~tp~~ 151 (229) +.. +++++ +.
T Consensus	188	~~~~~i~nsat~~ 219 (242)
T 3FE2_A	188	MLDMGFEPQIRKIVDQIRPDQRTLMSATWPK 219 (242)
T ss_dssp		HHHTTCHHHHHHHHTTSCSSCEEEEEESCCCH
T ss_pred		HhhcCCHHHHHHHHHhCcCEEEEEECcCh

Template alignment | Template 3D structure | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/1w36>)

56. [1W36 D \(http://pdb.rcsb.org/pdb/explore.do?structureId=1W36\)](http://pdb.rcsb.org/pdb/explore.do?structureId=1W36) EXODEOXYRIBONUCLEASE V BETA CH/ RECOMBINATION, HELICASE, NUCLEASE, HYDROLASE, DNA; 3.1A {ESCHERICHIA COLI} SCOP: c.37.1.19

Probability: 98.51 E-value: 1.0E-8 Score: 84.49 Aligned Cols: 145 Identities: 12% Similarity

Q ss_pred		CchHHHHHHHHHHhCCeEEEEeCCCCCHHHHHHHHHhC-----CC-eEEEEeCCHHH
Q Klein_Draft	2	ELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNYALRY-----PG-RVLYFSRGFRE
Q Consensus	2	~l~~~Q~~~~~i~~~~gGKT~~~~~ .+.++ +.++..+...+.++. ++ + +++..++..+.+++++ +...
T Consensus	149	~~~~~Q~~~a~~~~~iG~~GTGKTt~i~l~~~l~~~~~i~~~apT~~a
T 1W36_D	149	DEINWQKVAALTRRISVISGGPGTGKTTTAKLLAALIQMADGERCRIRLAAPTGKA
T ss_pred		CCCHHHHHHHHHHHhCCeEEEEeCCCCCHHHHHHHHHHHhCCeEEEEeCCHHH

Q ss_pred		HHHCcchhccEEEEecCEEEEEEEcCCCCcEEEEeCCCCCccceecEEEEcHHHC
Q Klein_Draft	65	MGDRGPGTWSVIQSSKTNGRLSVSTSLCGAFGQVDFLPYGRGSARGLIADLVILDDADEV
Q Consensus	65	~~~~~i~~~~~g~~~~~iiDE~~~~~+ -+.....++ ++.
T Consensus	219	~~~~~Ti~~~~~l~~~~~d~iIIDEasmv
T 1W36_D	219	ALRQLPLTDEQKKRIPEDASTLHRL---LGAQPGSQRLRHAGNPLHLDLVLVDEASMI
T ss_pred		HHHCcCCCHHHHhcCCcccchHHH---hcCCCCccccccCCCCCCCCEEEEcCCCC

Q ss_pred		hhcccCceEEEEeccch	
Q Klein_Draft	135	TVLTGTGGKIAAFGLLHK	151 (229)
Q Consensus	135	~~~~~i~~~~tp~~	151 (229)
		.+. .+.++++ ++.+	
T Consensus	285	~l~--~rIlvGD~Q	300 (608)
T 1W36_D	285	ALPD-HARVIFLGDRDQ	300 (608)
T ss_pred		hCCC-CcEEEEEEChhh	

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

57. [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; 6.0Å [*Saccharomyces cerevisiae* (strain ATCC 204508 / S288c)])

Probability: 98.51	E-value: 4.4E-8	Score: 77.46	Aligned Cols: 134	Identities: 13%	Similarity
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Vis

Hits

Aln

Q ss_pred		CchHHHHHHHHhhcCCeEEEECCCCCHHHHHHHHhC-----CC-eEEEEcCHHHH
Select all		Forward Query MSA Color Segs Unwrap Segs
Q Klein_Draft	2	ELLANQLIETIDNSSVSAPAAPRONGKTYAAYNYALRY----PG-RVLYFSRGFREA
Q Consensus	2	~l~~~Q~~~~~i~~~~gGKT~~~~~+..++++ +...+
T Consensus	84	~~~~Q~~~i~~~~~il~~~tGsGKT~~~~~lii~P~~~l~
T SSUQ_C	84	HPSEVQQHTIPQSIHGTDVLCQAkSGLGKTAVFVLSTLQQLDPVPGEVAVVVICNARELA
T ss_dssp		SCCHHHHHHHHHHTTTCCEEEECCTTSSSHHHHHHHHHHCCCCCTTCCCEEEECSSHHHH
T ss_pred		CCCHHHHHHHHHhCCCcEEEEcCCCCCHHHHHHHHHHCCCCCcEeEEEEcChHHH
Q ss_pred		HHCcChhcceEEeeCCEEEEecCCCCCe-----EeeeeCC----
Q Klein_Draft	66	GDRGPGTWSVIQSSTNGRLSVSTSLCGAFGQ-----VDFLPYG----
Q Consensus	66	~~~~~i~~~~~+.....+.+. .+.++.
T Consensus	154	~~~~~I~i~T~~~l~
T SSUQ_C	154	SKYMPDVKTAVF-----YGTPISKDAELLKNKDTAPHIVVATPGR LKA
T ss_dssp		TTTCTTCEEEEE-----CTTschHHHHHHHCTTTCCSEEEECHHHHHH
T ss_pred		HhhCCCceEEEE-----eCCCCchHHHHHHhCCCCCEEEECHHHHHH
Q ss_pred		eecEEEEcCHHHcCH-----HHHHHhhhcccccCEEEEEeccch
Q Klein_Draft	112	IADLVILDDADEVEP-----EVLGDIYPTVLTGGKIAAFGLLHK 151 (229)
Q Consensus	112	~~~~ii~DE~~~~~l~~~~~i~~~~tp~~ 151 (229) .++++ + +.+. .+.+.+.+.+.+.++++ +..
T Consensus	208	~~~~vIiDeah~~~~~i~~sat~~ 252 (446)
T SSUQ_C	208	HVKNFVIDECDKVLEELDMRRDQVEIFRATPRDKQVMMSATLSQ 252 (446)
T ss_dssp		TCEEEETTHHHHHSHHHHHHHHHHTTSCSSSEEEESCCT
T ss_pred		hCEEEEcCHHHHHHChHHHHHHHHhCCCCCEEEECCH

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

58. [4A4D A \(http://pdbe.rcsb.org/pdb/explore.do?structureId=4A4D\)](http://pdbe.rcsb.org/pdb/explore.do?structureId=4A4D) PROBABLE ATP-DEPENDENT RNA HELICASE, RNA-BINDING; 2.7A {HOMO SAPIENS}

Probability: 98.5 E-value: 1.8E-8 Score: 73.29 Aligned Cols: 147 Identities: 14% Similarity:

Q ss_pred		CchHHHHHHHHHHhCCeEEEEcCCCCHHHHHHHHHHhC-----CcEEEEeC
Q Klein_Draft	2	ELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNYALRY-----PGRVLYFSR
Q Consensus	2	~l~m~Q~i~m~g~GKT~ .+++ .+++..+..+++.+++ + ..+...+... ..++++
T Consensus	65	~~~~~Q~~~~~i~~~~~g~GKT~~~~~lii~p
T 4A4D_A	65	EPTAIQAQGWPVALSGLDMVGVAQTGSGKTLSYLLPAIVHINHQPFLERGDGPICLVLP
T ss_dssp		SCCHHHHHHHHHHHTTCEEEEECTTSSCHHHHHHHHHHHSSCCCTTCCCSEEEECs
T ss_pred		CCcHHHHhHHHHHHhCCCEEEEEcCCCCHHHHHHHHHHhCccccCCCCceEEEEcC

[illegible]

Q ss_pred		cCH---HHHHHHhhhhccCCeEEEEeccch	
Q Klein_Draft	124	VEP---EVLGDIIPTVLTGKGIAAFGLLHK	151 (229)
Q Consensus	124	~~~~~l~~~~~i~~~~tp~~ +.. ..+.+.+.+.+.++++ +..	151 (229)
T Consensus	202	~~~~~i~~~~st~~~~	233 (253)
T 4A4D_A	202	MLDMGFEPQIRKIVDQIRPDRQLTLMWSATWPK	233 (253)
T ss_dssp		HHHTTCNNNNNNHHTTSCTTSEEEEEESCCH	
T ss_pred		HHhcCCHNNNNNNHHhcCcCCEEEEEECCH	

Vis

Hits

Aln

Q Consensus	63	~~~~~i~~~~~i~			
Select all	Forward	Forward Query MSA	Color Segs	Unwrap Segs	...+++ +
T Consensus	130	~~~~~i~v~t~l~~~~~iii			
T 3LLM_A	130	AFERGEPEGKSCGYSVRFESILP-----RPHASIMFCTVGVLRLKLEAGIRGISHVIV			
T ss_dssp		HHTTTCCTTSSEEEEEETTEECC-----CSSSEEEEEHHHHHHHHHCCCTTCEEEEE			
T ss_pred		HHHhCCCCCccccccehhccCC-----CCCCeEEEEeHHHHHHHHHhccCCCeEEE			
Q ss_pred		-----HHHhhhhhcccccEEEEEeccchHHHHHHH			
Q Klein_Draft	129	-----LGDYPTVLTGGKIAAFGLLHKQGLLAHV	158 (229)		
Q Consensus	129	-----~l~~~~~i~~~~~tp~~~~~	158 (229)		
		+..+..... ..+++++ +...+...+			
T Consensus	193	~~~~~i~sat~~~~~	227 (235)		
T 3LLM_A	193	DFLLVLRDVQAYPE-VRIVLMSATIDTSMFCEYF	227 (235)		
T ss_dssp		HHHHHHHHHHHHHCTT-SEEEEEECSSCCHHHHHHT			
T ss_pred		HHHHHHHHHHHHHCCC-CEEEEEeCCCCHHHHHHHh			

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

63. [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: 98.48 E-value: 4.3E-8 Score: 82.29 Aligned Cols: 150 Identities: 15% Similarity

Q ss_pred		CchHHHHHHHHHHhCCeEEEEeCCCCchHHHHHHHHHhC--CC-eEEEEeCCHHHHHHH
Q Klein_Draft	2	ELLAHQKL I HETIDNSSVSFAAPRQNGKTYAAVNALRY--PG-RVLYFSRGFR EARCA
Q Consensus	2	~l~~~Q~~~~~i~~~~gGKT~~~~~ .+.++ .++++.+.++.+++.+ + + .++...+... .. ++++++ ...+.+
T Consensus	25	~l~~~Q~~~~~lv~apTgSGKT~a~~~il~~~~~lv~pP~~~L~~q~
T 2P6R_A	25	ELFPQAEAEVKVFSGKNLLAMPTAAGKTLAEMAMVREAIKGGKSLYVVPRLALAGEK
T ss_dssp		CCCCCHHHHHHHHTTCSCEEEECSSHHHHHHHHHHHHHHHHHTTCEEEEEESSHHHHHHH
T ss_pred		CCCHHHHHHHHHHHhCCeEEEEeCCCCchHHHHHHHHHHHHhCceEEEEeCchHHHHHHH

Q ss_pred		CcchhccEEEecCCEEEEEEecCCCCEEEEeCC-----CCCCccceecEEEEcCH
Q Klein_Draft	69	GPGTWSVIQSSKTNGRLSVSTSLCGAFGQVDFLPYG-----RGSARGLIADLVILDDA
Q Consensus	69	~~~~~i~~~~~g~~~~~ii~DE~+.+.++.+ + +
T Consensus	94	~~~~V~~~~g~~~~~Iiv~T~e~l~~~~~liivDE~
T 2P6R_A	94	-IGLRIGISTGDYESRDEHL-----GDCDIIVTTSEKADSLIRNRASWIKAVSCLVVDIEI
T ss_dssp		-TTCCEEEECSSCBCSSCS-----TTCSEEEEEHHHHHHHHHTTCSGGGGCCEEEETTGT
T ss_pred		-cCCeEEEecCCcchhhh-----cCCCEEEeCHHHHHHHHCHHHhhccEEEEecH

Q ss_pred		HHHHHHhhhhccccc---CCeEEEEecccHHHHHHHH	
Q Klein_Draft	128	VLGDYPTVLTT---GGKIAAFLGKQGLLAHV	158 (229)
Q Consensus	128	~~~~l~~~~~---~i~~~~tp~~~~~ .++.+.+.+.+.+.+.+.+.+.+.+.+.+.+	158 (229)
T Consensus	158	~~e~~~~~l~~~~~ii~lSAT~~~~~l~~~	191 (702)
T 2P6R_A	158	TLEILVTKMRRMNKALRVIGLSATAPNVTEIAEW	191 (702)
T ss_dssp		HHHHHHHHHHHHCTTCEEEEEECCTTHHHHHHH	
T ss_pred		HHHHHHHHHHHhCccccEEEEECCHHHHHHH	

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

64. [3PEY A \(http://pdbs.rcsb.org/pdb/explore.do?structureId=3PEY\)](http://pdbs.rcsb.org/pdb/explore.do?structureId=3PEY) ATP-dependent RNA helicase DBP5 (E.C. ATPase, Helicase, mRNA-export; HET: NO3, ADP: 1.401A {*Saccharomyces cerevisiae*})

Probability: 98.48 E-value: 2.4E-8 Score: 77.3 Aligned Cols: 143 Identities: 13% Similarity:

Q ss_pred		CchHHHHHHHHhhcC-CeEEEECCCCChHHHHHHHHHhC-----CcEEEEcCHH
Q Klein_Draft	2	ELLAHQKLIHETIDNS--SVSAFAAPRQGKTYAAVNVALRY-----PGRVLVYFSRGFR
Q Consensus	2	~l~~~Q~~~~~i~~~~gGKT~~~~~ .++++ .+++..+...+.++++.++ .++...++...+..++++ +..

T Consensus		27	~~~~~Q~~~~~1~~~~~G~GKT~~~~~vli~p~~~	
Select all	Forward	27	Forward Query MSA	Color Segs Unwrap Segs
T 3PEY_A		27	PKPSIQERALPELLHMPFRNIQAQSQSGTGKTAATSLTMTLRVNPEDASPOAICLAPSRE	
T ss_dssp			SCCHHHHHHHHHHHHSCSCCEEEECCTTSCHHHHHHHHHHHHCCTTCCSCCEEEECSSH	
T ss_pred			CCCHHHHHHHHHHHHCCCCeEEEEcCCCcHHHHHHHHHHHHHcCcccCCCeEEEEcChHH	
Q ss_pred			HHHHcCcchhccEEEEecCEEEEEEEecCCCCeEEEEeCCCC-----CCccceecEE	
Q Klein_Draft	64		KMGDRGPGTWSVIQSSKTNGRSLVSTSLCGAFGQVDFLPYGRG-----SARGLIADLV	
Q Consensus	64		~~~~~i~~~~~g~~~~~i+.+.++..-.....++++	
T Consensus	97		~~~~~i~v~t~~~1~~~~~i	
T 3PEY_A	97		EMGKFTKITSQLIVPDSFEKNK-----QINAQVIVGTPGTVDLDMRRKLMQLQKIKIF	
T ss_dssp			HHTTSCCCEEEESTSSCTTS-----CBCCSEEECHHHHHHHHTTCBCCTTCCEE	
T ss_pred			HHHhhcCcEEEEECcChHHHHh-----hcCCCEEECHHHHHHHHhCCHChhCCEE	
Q ss_pred			----H~~~~~h~~~~~c~~~~~c~~~~~e~~~~~e~~~~~c~~~~~h	
Q Klein_Draft	127		----EVLGDIYPTVLTGTGGKIAAFGLLHK 151 (229)	
Q Consensus	127		----~~~~~l~~~~~i~~~~~t~~~~~p~~~~~ 151 (229) ..+.+.+.+.+.+.++++ +..	
T Consensus	160		~~~~~i~~~~~s~~~~~a~~~~~t~~~~~ 189 (395)	
T 3PEY_A	160		QQGLGDQCIRVKRFLPKDTQLVLFSATFAD 189 (395)	
T ss_dssp			STHHHHHHHHHHTSCTTCEEEEEESCCH	
T ss_pred			ccCchHHHHHHHHHCCCCeEEEEEECCCH	

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/2g9n\)](http://www.ebi.ac.uk/pdbe/entry/pdb/2g9n)

65. [2G9N A \(http://pdb.rcsb.org/pdb/explore.do?structureId=2G9N\)](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: 98.47 E-value: 7.4E-9 Score: 73.77 Aligned Cols: 148 Identities: 14% Similarity

[illegible]

Template alignment | Template 3D structure | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/2pl3>)

Q ss_pred		CcchHHHHHHHHHhCCeEEEECCCCCHHHHHHHHHhh-----CCC-eEEEECC
Q Klein_Draft	2	E LLAHQKLIHETIDNSSVSFAAPRQNGKYAAVNYALR-----YPG-RVLVFSRG
Q Consensus	2	~l~~~Q~~~~~i~~~~g~GKT~~~~~ .++++ .+++..+..+.+++.+++ + .++...+. .+. .++++ +
T Consensus	47	~~~~~Q~~~~~l~~~~~ll~~~~~G~GKT~~~~~lii~p~
T 2PL3_A	47	LVTIEIQQTIGLALQGKDVLGAAKTSGSKTLAFLVPVLEALYRLQWSTDGLGVLIISPT
T ss_dssp		BCCHHHHHHHHHHTTCCEEEECCTTSCHHHHHHHHHHHHTTCCGGGCCCEEEECSS
T ss_pred		CCcHHHHHHHHHHHCCCEEEEECCCCCHHHHHHHHHHHhhccCCCCCCEEEEeCc

Q ss_pred		HHHHHHcCccchccEEEEecCEEEEEEEcCCCCEEEEEEcCCC-C-----Ccccee
Q Klein_Draft	62	AVKMGDRPGTWSVIQSSKNTGRSLVSTSLCAGAGQVDFLPYGRG-S-----ARGLIA
Q Consensus	62	~~~~~i~~~~~ +.....+.+.+.+.~.....
T Consensus	117	~~~~~i~v~t~l~~~~~
T 2PL3_A	117	LRKVGKNHDFSAGLIIGGKDLKHEAERI---NNINILVCTPGRLLQHMDETVSFHTDL
T ss_dssp		HHHHHTTSSCCEEEEECC--CHHHHHHH---TTCSEEECHHHHHHHHHHCSSCCCTTC
T ss_pred		HHHHhhcCCCCCCCCCHHHHHHH---cCCCCEEChHHHHHHHHhccCcCHHH

Q ss_pred		CC---HHHHHHHHhhcccCeEEEEeccch	
Q Klein_Draft	124	VE---PEVLGDIYPTVLTTGGKIAAFGLLHK	151 (229)
Q Consensus	124	~-----l~i~t~p~	151 (229)
		+ . . . + . . + + + + + + . .	
T Consensus	183	~i~l~s~a~t~	214 (236)
T 2PL3_A	183	ILDMGFADTMNAVIENLPKKRQTLFSAQTQK	214 (236)
T ss_dssp		HHHTTTTHHHHHHHHTSCTTSEEEEEESSCCH	
T ss_pred		HcccCcHHHHHHHHHhCCCEEEEEECcCCCH	

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

67. [2KBE A \(http://pdbs.rcsb.org/pdb/explore.do?structureId=2KBE\)](http://pdbs.rcsb.org/pdb/explore.do?structureId=2KBE) ATP-dependent RNA helicase DBP5 (E. coli) Helicase, Hydrolase, Membrane; NMR {*Saccharomyces cerevisiae*}

Probability: 98.46 E-value: 6.3E-8 Score: 69.12 Aligned Cols: 144 Identities: 13% Similarity

Q ss_pred		CCchHHHHHHHHHHhC--CeEEEECCCCCHHHHHHHHHHhC----CC-eEEEEeCCH
Q Klein_Draft	1	MELLAHQKLIHETIDNS--SVSAFAAPRQNGKTYAAVNVALRY----PG-RVLYFSRGF
Q Consensus	1	~~l~~~~Q~~~~~i~~~~g~GKT~~~~~ ..++++ .+++.+...+.+++. + .++...+... .. .++++ +.
T Consensus	43	~~~~~Q~~~~~i~~~~G~GkT~~~~~lii~p~
T 2KBE_A	43	QKPSKIQERALPLLLHNPPRNMAIQSQSGTGKTAAFSLTMLTRVNPEDASPAICLAPSR
T ss_dssp		SCCCHHHHHHHHSSCCSCCEEEESTTCHHHHHHHHHHHCCCTTCCCCEEEECSH
T ss_pred		CCCCHHHHHHHHHhCCCCeEEEEcCCCCCHHHHHHHHHHhCCcCCCCeEEEEcCH

Q ss_pred		HHHHHcCcchccEEeEcCEEEEEECcCCcCEEEEcCCCC-----CCcccceE
Q Klein_Draft	63	VKMGRGPGTWSVIQSSTNGRLSVSTSLCGAFGVDFLPYGRG-----SARGLIADL
Q Consensus	63	~~~~~i~~~~~g~~~~~+.+.+.-.....++
T Consensus	113	~~~~~i~v~t~l~~~~~
T 2KBE_A	113	QEMGFKTKI---TSQLIVPDSFEKNKQ---INAQVIGTPGTVLDMRRKLMLQKIKI
T ss_dssp		HHHSTTCSC---CCEEESTTSCCSSC---CCCSEEECTTTHHHHHHTTSCCTTSCCE
T ss_pred		HHhcccCcc---EEEEecCCchhhhhh---hCCcEEEECHHHHHHHHCcCCccccce

	Q ss_pred		HH-----H HHHhhhhhccccCeEEEEeccch	
	Q Klein_Draft	126	PE-----VLGDIYPTVLTGTGGKIAAFGLLHK	151 (229)
	Q Consensus	126	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ i ~ ~ ~ t p ~ ~	151 (229)
			. . + . + . + + + + + + .	

Q ss_pred		chHHHHHHHHhhcCCeEEEEeCCCCChHHHHHHHHhC-----CC-eEEEEeCCHHHH
Q Klein_Draft	3	LLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNALRY-----PG-RVLYFSRGFREA
Q Consensus	3	l~~~Q~~~~~i~~~~~g~GKT~~~~~ +.++ +.++..+..+.++. ++ + +++..++..+. ++++++ +..+
T Consensus	151	~~~~Q~~~a~~~~~ii~G~~GtGKT~~~~l~~~l~~~~~i~l~apt~~aa
T 5LD2_D	151	EINWQKVAAAVALTRRISVISGPGTGKTTTVAKLAAALIQMADGERCRIRLAAPTGKAA
T ss_dssp		SCCHHHHHHHHHHHBSEEEEEECTTSSHHHHHHHHHHHHHCSSSCCEEEEEESHHHH
T ss_pred		CCHHHHHHHHHHHhhcCEEEEEeCCCCCHHHHHHHHHHHhhcCCcCeEEEEeCCHHHH

Q ss_pred		HHHHCcCchhcEEeEcCEEEEEecCCCCeEEEEcCC-----CCCCccceeeEEE
Q Klein_Draft	64	KMGDRPGTWSVIQSSTNGRLSVSTSLCGAFGQVDFLPYG-----RGSARGLIADLVI
Q Consensus	64	~~~~~i~~~~~g~~~~ii ..+.+++++.....+
T Consensus	102	~~~~~V~~~~~Iv~T~~l~~l~~~l~~~l~~~~V
T 5XDR A	102	DEM DVM LG QEV GYSIR F EDCSS-----AK I LK YMTDGM LLRE AMNDP LLERYGV II



86.

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/3sqw\)](http://www.ebi.ac.uk/pdbe/entry/pdb/3sqw)[3SQW_A \(http://pdb.rcsb.org/pdb/explore.do?structureId=3SQW\)](http://pdb.rcsb.org/pdb/explore.do?structureId=3SQW) ATP-dependent RNA helicase MSS11c
RNA dependent ATPase; HET: ANP; 1.909A {*Saccharomyces cerevisiae* S288c}

Probability: 98.36 E-value: 1.2E-7 Score: 77.92 Aligned Cols: 146 Identities: 16% Similarity

```
Q ss_pred          CchHHHHHHHHhhc--CCeEEEECCCCCHHHHHHHHHhC-----CC-eEEEEe
Q Klein_Draft      2  ELLAHQKLIHETIDN--SSVSFAAPRQNGKTYAAVNYALRY-----PG-RVLYFS
Q Consensus        2  ~l~Q~i~g~GKT~
      .+++|.+++..+.+.+++|+||.++..++..      ..+++++
T Consensus        43  ~lt~Q~i~il~l~v~a~TGsGKTla~l~i~li~
T 3SQW_A           43  GLTPVQQTIKPILSSEDHDIARAKTGTGKTF AFLIPFQHLINTKFSQYMKAVIVA
T ss_dssp          SCCHHHHHHHHHHHCSSEEEEEECCTTSCHHHHHHHHHHHHTTSTTSCCEEEEC
T ss_pred          CCHHHHHHHHHhhcCCCCCEEECCCCCHHHHHHHHHHHhhcCCCCcCeeEEEEe
```

```
Q ss_pred          HHHHHHHHCcchhccEEeECCE-----EEeECCECCcEEEEeEC-----C
Q Klein_Draft      60  DLAVKMGDRGPGTWSVIQSSKTNGRL-----SVSTSLCGAFGQVDFLPYG-----R
Q Consensus        60  ~~~~~i~
      ..+.....+.....      ....      ....|.+.+++      .
T Consensus        113 ~~~~~IiV~Tp~l~l~
T 3SQW_A           113 AEVKKIHD MN YGLKKYACVSLVGGTDFRAAMNKMNK----LRPNIV IATPGR LIDVLEKY
T ss_dssp          HHHHHHHHCGGGTTSCEEEECTTSCHHHHHHHHH----HCCSEEECHHHHHHHHH
T ss_pred          HHHHHHHhccccceEEeECCHHHHHHHH----cCCEEECHHHHHHHH
```

```
Q ss_pred          EEEcCHHHcCH---HHHHhhhhcc-----cCCEEEEcch
Q Klein_Draft      116 VILDDADEVEP---EVLGDIYPTVLT-----TGGKIAAFLHLHK 151 (229)
Q Consensus        116 ii~DE~l~i~tp~
      +|+|+|.+.+      ..+.+.+.+.      ....++++|+.
T Consensus        179 lViDEah~l~l~l~l~l~l~l~l~l~SATl~ 225 (579)
T 3SQW_A           179 KVLDEADRLLEIGFRDLETISGILNEKNSKADNIKTLLFSATLDD 225 (579)
T ss_dssp          EEEETHHHTSTTTTHHHHHHHHHHHHHCSSCTTCCEEEESSCTT
T ss_pred          EEEcCHHHhhcCCHHHHHHHHHhchcCCCCCceEEEEcCCCH
```



87.

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/3p4x\)](http://www.ebi.ac.uk/pdbe/entry/pdb/3p4x)[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: 98.36 E-value: 8.5E-8 Score: 75.35 Aligned Cols: 137 Identities: 19% Similarity

```
Q ss_pred          CCchHHHHHHHHhhcCCeEEEECCCCCHHHHHHHHHhC--CC-eEEEEeCCHHHHH
Q Klein_Draft      1  MELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNYALRY--PG-RVLYFSRGFREARC
Q Consensus        1  ~l~Q~i~g~GKT~
      .|+++|...+.+.+.+.+++|+||.++..+...      .+ .++++|+.+.+.+
T Consensus        19  ~l~Q~l~t~G~GKT~l~i~P~l~q
T 3P4X_B           19  KDLTG YQRLWAKRIVQGKSFTMVAPTVGKTTFGMMTALWLARKGKKSALVFPTVTLVKQ
T ss_dssp          SCCCHHHHHHHHHHTTCEEECCSCCTTHHHHHHHHHHHHTTTCCEEEESSHHHHH
T ss_pred          CCCCCHHHHHHHHHHCCCEEEECCECCCCCHHHHHHHHHHHhhcCCeEEEEeCCHHHHH
```

```
Q ss_pred          cCchhccEEeECCEEEEEecCC-----CCeEEEEeCCCC-----Ccc
Q Klein_Draft      68  RGP GTWSVIQSSKTNGRLSVSTSLCG-----AFGQVDFLPYGRGS-----ARG
Q Consensus        68  ~~~~~i~
      ....+.....      .      ....+.+.+.+.      ...
T Consensus        89  ~~~~~iV~t~l~
T 3P4X_B           89  EKVKIFGFYSSMK-----KEEKEKFEKSFEEDDYHILVFSTQFVSKNREKLSQ
T ss_dssp          TTSEEEECTTSC-----HHHHHHHHHHHHTTCCSEEEEHHHHHHHHHHTT
T ss_pred          CCCEEEecCC-----HHHHHHHHHHhhCCeEEEEeCHHHHHhCHHHHH
```


Similarity

Q ss_pred		CCcHHHHHHHHHHhCCEEEEECCCCCHHHHHHHHHHC-----CCeEEEE
Q Klein_Draft	1	MELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNALRY-----PGRVLYFS
Q Consensus	1	~1~Q~i~g~GKT~-----~
T Consensus	77	~Q~li~
T 2DB3_A	77	KIPTPIQKCSIPVISSGRDLMACAQTGSGKTA AFLLPILSKLLED PHELELGRPQVIVIS
T ss_dssp		CSCCHHHHHHHHTTCCEEEECCTTSCCHHHHHHHHHHHHSCCCCBTTBCSEEEEC
T ss_pred		CCCCHHHHHHHHCCCCeEEECCECCCHHHHHHHHHHHHCcchhCCEEEEEE
Q ss_pred		HHHHHHHHCcchhccEEEEecCEEEEEECCEEEECCEEEECCEEEECCEEEEC-----CCccee
Q Klein_Draft	60	DLAVKMGDRGPGTWSVIQSSKTNGRLSVSTSLCGAFGQVDFLPYGRG-----SARGLI
Q Consensus	60	~i~g~
T Consensus	147	~i~V~T~L~
T 2DB3_A	147	NEARKFAFESYLKIGIVYGGTSFRHQNECI---TRGCHVVIATPGRLLDFVDRTFITFED
T ss_dssp		HHHHHHTTSSCCEEEECSSSCHHHHHHHH---HTCCSEEEECHHHHHHHHHTSSCCTT
T ss_pred		HHHHHHhCCEEEEEECCCHHHHHHHH---HcCCEEEECcHHHHHHHhCCcChh
Q ss_pred		HcCH---HHHHHhHHhccc-CCeEEEEec
Q Klein_Draft	123	EVEP----EVLGDIYPTVLTT-GGKIAAFGL 148 (229)
Q Consensus	123	~i~t 148 (229)
T Consensus	214	~i~sa 244 (434)
T 2DB3_A	214	RMLDMGFSEDMRRIMTHVTMRPEHQTLMFSA 244 (434)
T ss_dssp		HHTSHHHHHHHHTCTTSCSSCEEEEEE
T ss_pred		HHHhCCHHHHHHHhCCCCCCEEEEEec

92.

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/4cbh\)](#)
4CBH_B (http://pdb.rcsb.org/pdb/explore.do?structureId=4CBH) SERINE PROTEASE NS3 (E.C.3.4.21.113, HELICASES, FLAVIVIRIDAE NS3; 2.51A {CLASSICAL SWINE FEVER VIRUS})

Probability: 98.33 E-value: 9.9E-8 Score: 77.24 Aligned Cols: 138 Identities: 12% Similarity

Q ss_pred		CCcHHHHHHHHHHhCCEEEEECCCCCHHHHHHHHHHC--CC-eEEEEcCHHHHHH
Q Klein_Draft	1	MELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNALRY--PG-RVLYFSRGFREARC
Q Consensus	1	~1~Q~i~g~GKT~-----~
T Consensus	28	~q~li~tGsgKT~i~vli~P~l~q
T 4CBH_B	28	ATDLTEMVKKITMNRGEFRQITLATGAGKTTTELPRSVIEEIGRHKRVLVLIPLRAAAES
T ss_dssp		---CHHHHHHHHTCCTTCEEEEC---CCTTHHHHHHHHCTTSCEEEESSHHHHH
T ss_pred		CcHHHHHHHHHHhCCEEEEECCCCCHhHHHHHHHHHHHCcCEEEEEcCHHHHHH
Q ss_pred		cCcchhccEEEEecCEEEEEECCEEEECCEEEECCEEEECCEEEEC-----ccceecEEEEc
Q Klein_Draft	68	RGPPTWSVIQSSKTNGRLSVSTSLCGAFGQVDFLPYGRGSA-----RGLIADLVILD
Q Consensus	68	~i~g~i~D
T Consensus	98	~i~T~L~V~I~D
T 4CBH_B	98	SIAFNLRIGEMKEGD-----MATGITYASYGYFCQMSQPKLRAAMVEYSFIFLD
T ss_dssp		TSCEEEESSCCTTC-----CCCSEEEEHHTTSCCHHHHHHHTTSCSEEEEC
T ss_pred		CCeEEeccccCCC-----CCeEEECcHHHHHHhCCHHHHHHhCCEEEEC
Q ss_pred		HHhhhhccc--CCeEEEEecc
Q Klein_Draft	130	GDIYPTVLTT--GGKIAAFGLL 149 (229)
Q Consensus	130	~l~i~tp 149 (229)
T Consensus	157	~l~i~LSaT~ 178 (516)
T 4CBH_B	157	AIMGKIHRFSENLRVAMTATP 178 (516)
T ss_dssp		HHHHHHHTTGGGCCCEEEEC--
T ss_pred		HHHHHHHHhCCEEEEEccC

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

Q ss_pred CHHHHHHHhhhhcccCeEEEEecc

Select all Forward Forward Query MSA

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

Q Klein_Draft 125 EPEVCGDITPTVLTIGKIAAFGLL 149 (229)

Q Consensus 125 ~~~~~~1~~~~~i~~~~tp 149 (229)

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

T Consensus 503 ~~~~~~1~~~~~--~1~1SATp 526 (780)

T 1GM5_A 503 GVKQREALMNKGKM-VDTLVMSATP 526 (780)

T ss_dssp ----CCCCSSSSC-CCEEEEESSC

T ss_pred CHHHHHHHHhCCC-CCEEEEECCC

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/5aga\)](#)☐ 95. [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: 98.33 E-value: 1.1E-7 Score: 81.33 Aligned Cols: 150 Identities: 13% Similarity

Q ss_pred CchHHHHHHH--HHhhCCeEEEEeCCCCCHHHHHHHHHhC---CC-eEEEEeCCHHHH

Q Klein_Draft 2 ELLAHQKLIH--ETIDNSSVSFAAPRQNGKTYAAVNYALRY---PG-RVLYFSRGFREA

Q Consensus 2 ~1~~~Q~~~~~i~~~~g~GKT~~~~~i~~~~~g~~~~~i

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

T Consensus 27 ~1~~~Q~~~~~i~~~~pTgsGKT~a~~~~i~~~~~vli~P~~~~l~

T 5AGA_A 27 KMFEWQAECLLLGQVLEGKNLVYSAPTSAGKTLVAELLILKRVLEMRKKALFILPFVSVA

T ss_dssp BCCHHHHHHHSSSTTTTCCCEEECCCTTSCCHHHHHHHHHHHHHTCCEEEEEESSHHH

T ss_pred ccCHHHHHHHhccccCCeEEEECCCCCHHHHHHHHHHHHHhCcEEEECCCHHHH

Q ss_pred HHcCcchhccEEEEeCCEEEEEeCCCCeEEEEeCCC-----CCCccceecEE

Q Klein_Draft 66 GDRGPGTWSVIQSSKTNGRLSVSTSLCGAFQGVDFLPYGR-----GSARGLIADLV

Q Consensus 66 ~~~~~~i~~~~~g~~~~~i

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

T Consensus 97 ~~~~~~V~~~~g~~~~~I~v~T~e~l~l~~~~~l~~~~~V

T 5AGA_A 97 FQEVGIKVDGYMGSTSPSRH-----FSSLDIAVCTIERANGLINRLIEENKMDLLGMV

T ss_dssp HGGGTCCEEEECTTCCSSC-----GGGCSEEEEEHHHHHHHHHHHTTCGGGEEEE

T ss_pred HHHhCCEEEEEeCCCCcc-----hhcCCEEEcHHHHHHHHHHHhchhhcCEE

Q ss_pred ----HHHHHHhhhh-----cccCeEEEEeccCHHHHHHHH

Q Klein_Draft 127 ----EVLGDIYPTV-----LTTGGKIAAFGLLHKQGLLAHV 158

Q Consensus 127 -----~1~~~~~i~~~~tp~~~~~ 158

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

T Consensus 160 ~~~~~~e~l~l~l~~~~~i~I~SATl~~~~~ 213

T 5AGA_A 160 SHRGYLLLELLTKICYITRKSASCQADLASSLSNAVQIVGMSATLPNLELVASW 213

T ss_dssp CSSTTHHHHHHHHHHHHTTGGGCC-----CCCCEEEEESCTTHHHHHHH

T ss_pred CCchHHHHHHHHHHHhchhchhhHHhccccCceEEEECCCCCHHHHHHHH

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/4q48\)](#)☐ 96. [4Q48 B \(http://pdb.rcsb.org/pdb/explore.do?structureId=4Q48\)](#) DNA helicase RecQ; DNA unwinding, h {Deinococcus radiodurans}

Probability: 98.32 E-value: 6.0E-9 Score: 84.34 Aligned Cols: 146 Identities: 14% Similarity

Q ss_pred CchHHHHHHHHhCCeEEEEeCCCCCHHHHHHHHHhCCeEEEEeCCHHHHHHHHH

Q Klein_Draft 2 ELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNYALRYPRVLYFSRGFREARCAFDL

Q Consensus 2 ~1~~~Q~~~~~i~~~~g~GKT~~~~~i~~~~~g~~~~~i

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

T Consensus 24 ~~~~~~Q~~~~i~~~~~l~~~~tG~GKTl~l~l~~~~~l~~~~~vi~P~~~~L~~~~~

T 4Q48_B 24 AFRGVQGEIVQQAEGGNALVLMPTGGGKSLCYQLPSLLRPGTGIVVSPLIALMKDQVDT

T ss_dssp SCCTTHHHHHHHHTTCCCEEECCSSSSCHHHHHHHHHSSSEEEECCHHHHHHHHH

T ss_pred ccCHHHHHHHHHhCCCCCEEECCCCCHHHHHHHHHhCCCEEEECCHHHHHHHHH

Q ss_pred hhccEEeCCEEEEEeCCCCeEEEEeCCC-----CCCccceCCEEEcCHHhC

Q Klein_Draft 72 TWSVIQSSKTNGRLSVSTSLCGAFQGVDFLPYGR-----GSARGLIADLVILDDADEV

Q Consensus	72	~~~~~i~~~~~g~~~~~ii~DE~~~~~
Select all	Forward	Forward Query MSA Color Segs Unwrap Segs
T Consensus	94	~~~~~i~tpe~l~~~~~ivideAh~~
T 4Q48_B	94	LNSTLLPHEAREVEDALL---RGDLDLLYVAPERLLMPRTL D L L E R A P V A L F A I D E A H C V
T ss_dssp		E C T T S C H H H H H H H H H H H H H H H H H H T T S C E E E E E C H H H H H H H H T S C E E E E E E T G G G G
T ss_pred		E C C C C H H H H H H H H H H H H H H H H H H C C C C E E E E E C H H H H
Q ss_pred		- H H H H H h h h h h c c c C C e E E E E e c c c h
Q Klein_Draft	127	- E V L G D I Y P T V L T T G G K I A A F G L L H K 151 (229)
Q Consensus	127	~~~~~l~~~~~i~~~~~tp~~ 151 (229)
		..+..+..... ..+..+++ +..
T Consensus	161	~~~l~~~l~~~~~l~lTAT~~~ 185 (525)
T 4Q48_B	161	Y Q Q L S V L A E R F P E - L P R V A L T A T A D E 185 (525)
T ss_dssp		G G G T T H H H H H C T T - S C E E E E E S C C C H
T ss_pred		H H H H H H H H H H C C C - C C E E E E E C C C C H

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/4q47\)](#)

☐ 97. [4Q47 A \(http://pdb.rcsb.org/pdb/explore.do?structureId=4Q47\)](#) DNA helicase RecQ; DNA unwinding, T HET: ADP; 2.899A {Deinococcus radiodurans}

Probability: 98.32 E-value: 6.0E-9 Score: 84.34 Aligned Cols: 146 Identities: 14% Similarity

Q ss_pred		CchHHHHHHHHhhcCCeEEEECCCCCHHHHHHHHHhCCCeEEEEeCCHHHHHHHHH
Q Klein_Draft	2	ELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNALRYPRVLYFSRGFREARCAFDL
Q Consensus	2	~l~~~Q~~~~~i~~~~~g~GKT~~~~~
		.+++ .+++..+..+++..+++ + .++..+..+..++++ ...+.+...
T Consensus	24	~~~~~Q~~~~i~~~~~lv~~~tG~GKTl~~~l~~~l~~~~~lv~P~~~L~~~~~
T 4Q47_A	24	A F R G V Q G E I V Q V A E G G N A L V L M P T G G G K S L C Y Q L P S L L R P G T G I V S P L I A L M K D Q V D T
T ss_dssp		S C C T T H H H H H H H H H T T C E E E E C C T T S C H H H H H H H H H S S E E E E E C S C H H H H H H H H H
T ss_pred		c c H H H H H H H H H H C C C E E E E C C C c c H 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
Q ss_pred		hhcEEEEecCEEEEEEEcCCCCEEEEEEcCC-----CCcceeecEEEEcCHHhc
Q Klein_Draft	72	TWSVIQSSKTNGRLSVSTSLCGAFGQVDFLPYGR-----GSARGLIADLVILDDADEV
Q Consensus	72	~~~~~i~~~~~g~~~~~ii~DE~~~~~
		+.....+..... ..+..+..+.....++++ + .+
T Consensus	94	~~~~~i~tpe~l~~~~~ivideAh~~
T 4Q47_A	94	LNSTLLPHEAREVEDALL---RGDLDLLYVAPERLLMPRTL D L L E R A P V A L F A I D E A H C V
T ss_dssp		E C T T S C H H H H H H H H H H H H H H H H H H T T H H H H H H T S C E E E E E S S G G G G
T ss_pred		E C C C C H H H H H H H H H H H H H H H H H H C C C C E E E E E C H H H H
Q ss_pred		- H H H H H h h h h h c c c C C e E E E E e c c c h
Q Klein_Draft	127	- E V L G D I Y P T V L T T G G K I A A F G L L H K 151 (229)
Q Consensus	127	~~~~~l~~~~~i~~~~~tp~~ 151 (229)
		..+..+..... ..+..+++ +..
T Consensus	161	~~~l~~~l~~~~~l~lTAT~~~ 185 (525)
T 4Q47_A	161	Y Q Q L S V L A E R F P E - L P R V A L T A T A D E 185 (525)
T ss_dssp		T T G G G H H H H H C T T - S C E E E E E S C C C T
T ss_pred		H H H H H H H H H H C C C - C C E E E E E C C C C H

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/3h1t\)](#)

☐ 98. [3H1T A \(http://pdb.rcsb.org/pdb/explore.do?structureId=3H1T\)](#) Type I site-specific restriction-modific. restriction enzyme hsdR, ATP-binding; 2.3A {Vibrio vulnificus}

Probability: 98.32 E-value: 2.9E-8 Score: 81.58 Aligned Cols: 144 Identities: 13% Similarity

Q ss_pred		CCchHHHHHHHHhhc-----CCeEEEECCCCCHHHHHHHHHhC-----CC-
Q Klein_Draft	1	MELLAHQKLIHETIDN-----SSVSFAAPRQNGKTYAAVNALRY-----PG-
Q Consensus	1	~l~~~Q~~~~~i~~~~~g~GKT~~~~~
		.. .++ .++++.+.+.+.+.+++ + .++..+...

```
T Consensus      177 ~~lr~~Q~~av~~~~l~~tGsgKT~~~  
Select all     Forward YSPRYTQQIAINRAVQSVLGGKRSLETHATGTGKTVVAQTISWKLWSARWNRTGDYRKP  
3H1T_A         177  
  
T ss_dssp       --CCHHHHHHHHHHHHHHTTCSEEEEEECTTSCHHHHHHHHHHHHHHTTCCSSCSSScc  
T ss_pred       CCCcHHHHHHHHHHHHHHHCcccEeeeeCCCCHHHHHHHHHHHHHHccccCCCCCCc  
  
Q ss_pred       HHHHHHHHHHHHHHCcchhccEEEEEecCEEEEEEEeCCCCcEEEEEECCCC-CCccc  
Q Klein_Draft   54    EARCAFDLAVKMGRDGPSTSVSIQSSKTINGRLSVSTSLCGAFGQVDFLPYGRG-SARGLI  
Q Consensus     54    ~~~~~~i~~~~~g~~~  
                .+.+.....+.+.....+. ..-.+.....  
  
T Consensus     247    l~q~~~~~i~nt~---~l~~~~~  
T 3H1T_A        247    LVDDPKDKFTFPFGDARHKIEGGKVKSREIFYAIY---QSIASDERRPGLYEFPQDF  
T ss_dssp       -----CCTTTCSSEEECCC--CCSCSEEEEG---GGC-----CCGGGSCTTS  
T ss_pred       hhcChhcccccccCcеееесCcссссссеЕЕЕЕе---hhhcCCCCcchhccCcc  
  
Q ss_pred       HcCHH---HHHHhhhccccCeEEEEecc  
Q Klein_Draft   123    EVEPE---VLGDIYPTVLTGGKIAAAGLL 149 (229)  
Q Consensus     123    ~~~~~~l~~~~~tp 149 (229)  
                .+... .+.+.+.+. .++.++|||  
  
T Consensus     313    ~~~~~~l~~~~~i~lTaTp 341 (590)  
T 3H1T_A        313    RGSARDNSNWREILEYFEP-AFIGMTATP 341 (590)  
T ss_dssp       -----CHHHHHHSTT-SEEEEEESSC  
T ss_pred       cccCCCCcchHHHHHHHccc-ceEEEECCCC
```

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(http://www.ebi.ac.uk/pdbe/entry/pdb/1t6n\)](http://www.ebi.ac.uk/pdbe/entry/pdb/1t6n)

99.

1T6N A (<http://pdb.rcsb.org/pdb/explore.do?structureId=1T6N>) Probable ATP-dependent RNA helicase processing protein; HET: FLC; 1.94A {Homo sapiens} SCOP: c.37.1.19

Probability: 98.32 E-value: 5.6E-7 Score: 64.42 Aligned Cols: 134 Identities: 16% Similarity

Q ss_pred		CchHHHHHHHHhhcCCeEEEECCCCCHHHHHHHHhc-----CC-eEEEeECCHHHH	
Q Klein_Draft	2	ELLAHQKLIHETIDNSSVSFAAPRQNGKTYAAVNYALRY----PG-RVLYFSRGFREA	
Q Consensus	2	~l~~~Q~~~~~i~~~~gGKT~~~~~ .+++ .+++.+..+.++++.++ + .++.+... .. .++++ +...+	
T Consensus	36	~~~~~Q~~~~~i~~~~GsGkt~~~~~liip~~~~~	
T 1T6N_A	36	HPSEVQHCEIPQAILGMDVLCQAkSGMGKTAVFVLATLQQLEPVTGQVSVLVMCHTRELA	
T ss_dssp		CCCHHHHHHHHHHTTCCEEEECCTTSCHHHHHHHHHHCCCCTTCCCEEEECSCHHHH	
T ss_pred		CCCHHHHHHHHHHCcCCeEEEECCCCCHHHHHHHHHhhcCcCeEEEEcCCHHHH	
Q ss_pred		HHcCchhccEEEEecCEEEEEEcCCCCc-----EIEEEcC-----	
Q Klein_Draft	66	GDRPGTWsvIQSSKTNGRLSVSTSLCGAFG-----QVDFLPYG-----	
Q Consensus	66	~~~~~+.+. .+.+.++.	
T Consensus	106	~~~~~v~~~~~i~vt~~~l~~~~~	
T 1T6N_A	106	SKYMPNVKVAVF-----FGGLSIKKDEEVLLKNCPHIVVGTPGRILALA	
T ss_dssp		TTTSTTCCEEEE-----SCCSCHHHHHHHHHSCSCEEEECHHHHHHHH	
T ss_pred		HhhCCcCeEEEE-----eCCCCCHHHHHHHHHCCCEEEECHHHHHHHH	
Q ss_pred		cEEEEcCHHHcCHHH----HHHhhhcccCCeEEEEeccch	
Q Klein_Draft	114	DLVILDDADEVEPEV----LGDIYPTVLTTGGKIAAFGLLHK	151 (229)
Q Consensus	114	~ii~dE~~~~~l~~~~~i~~~~tp~	151 (229)
		.++ + + .+. ... +.+.....++++ +..	
T Consensus	160	~liidE~~~~~lsat~~~	202 (220)
T 1T6N_A	160	KHFILDEC DKMLEQLDMRRDQEI FRMTPHEKQVM MF SATLSK	202 (220)
T ss_dssp		CEEEESHSHHHSSHSHHHHHHHHHTSCSSSEEEEEESCCT	
T ss_pred		CEEEeEChHHhhhhcCHHHHHHHHHCCCCeEEEEeCCCCH	

Template alignment | Template 3D structure | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/3i5x>)

