



HHpred

Created: Jul 20, 2017 3:36 PM

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

Input Parameters Results (/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)

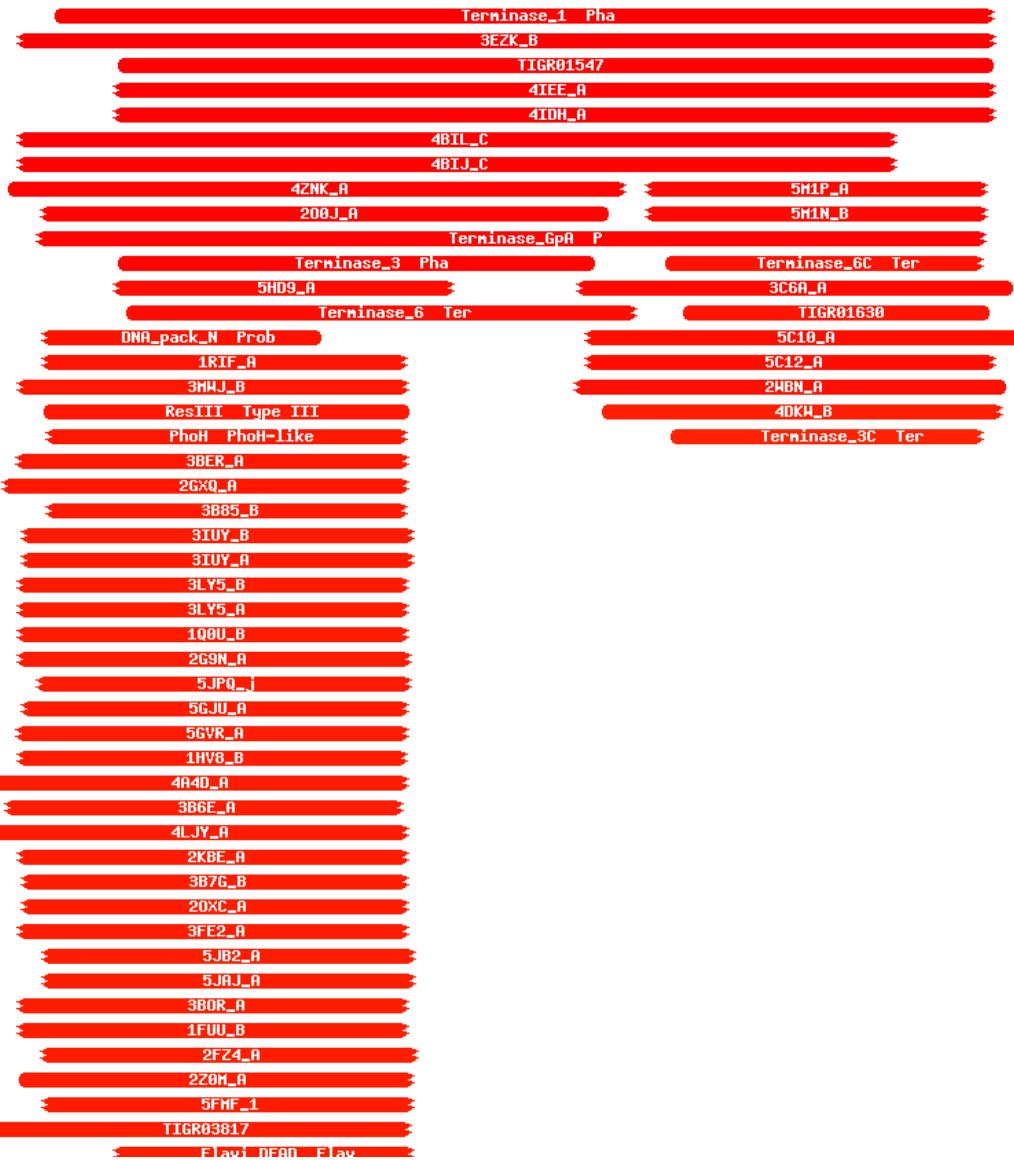
Query Template MSA (/api/job/result/1419573/hhpred/Query Template MSA) **Visualization**

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

[Resubmit section](#)

35

480



<u>Vis</u>	<u>Hits</u>	<u>Aln</u>	<u>Select all</u>	<u>Forward</u>	<u>Forward Query MSA</u>	<u>Color Seqs</u>	<u>Unwrap Seqs</u>
			2J8U_R				
			5SUP_B				
			1W36_D				
			TIGR04095				
			3DKP_A				
			2PL3_A				
			1VEC_B				
			5IVL_B				
			3PEY_A				
			5LD2_D				
			4R4Z_A				
			3O1Y_B				
			3FHT_B				
			1Z63_B				
			5SUQ_C				
			4CT4_B				
			TIGR00643				
			1Z6A_A				
			3TBK_A				
			2DB3_A				
			5JC3_B				
			3LLM_A				
			5JC3_A				
			4W7S_B				
			4W7S_A				
			3P4X_B				
			4XGT_A				
			5DZR_A				
			4D26_A				
			4D25_A				
			TIGR00580				
			2EYQ_A				
			5AGA_A				
			1S2H_A				
			4C9B_A				
			2ZJB_A				
			3G0H_A				
			2P6R_A				
			2FWR_A				
			TIGR00603				
			1GM5_A				
			2XGJ_A				
			2I4T_A				
			TIGR04121				
			3FH0_B				
			4R36_B				
			1WP9_A				
			1WP9_E				
			4U4C_A				
			TIGR00348				
			1T6N_A				
			5DTU_A				
			3SQH_A				
			5XDR_A				
			400H_A				
			400H_G				
			4TYN_A				
			5FFJ_A				
			5FFJ_B				
			3DMQ_A				
			TIGR02621				
			3H1T_A				
			2VA8_B				
			Helicase_RecD_H				
			3I5X_A				
			DEAD_DEAD/DEAH				
			2Z83_A				
			4NHO_A				
			TIGR01447				
			5LJ5_Q				
			5W5G_e				
			5GH6_Y				
			5LOH_O				
			1Z3T_X				
			TIGR01448				
			5HQF_q				
			4CBH_B				
			2JLU_B				
			4DDV_B				
			4ODU_A				
			5AO8_A				

Vis	Hits	Aln	Select all	3E1S_C	Forward	Forward Query MSA	<u>Color Seqs</u>	<u>Unwrap Seqs</u>
				4F91_B				
				5HZR_A				
				4XJK_A				
				4Q2D_A				
				4Q2C_A				
				2H74_B				
				4F91_B				
				5DCA_A				
				4XQK_A				
				4Q47_A				
				4Q48_B				
				1OYH_A				
				5JWH_A				
				5DCA_A				
				5H59_E				
				5H59_G				
				TIGR00614				
				3HWY_H				
				1HRB_A				
				5H59_E				
				5H59_G				
				5JXR_A				
				TIGR03714				
				TIGR04397				
				AAA_19 AAA donai				
				4CBL_A				
				TIGR01389				
				5EAN_A				
				TIGR04221				
				1GL9_B				
				3O8B_B				
				2ZPA_B				
				AAA_34 P-Loop co				
				TIGR01054				
				TIGR01587				
				TIGR00963				
				1GKU_B				
				TIGR02562				
				1YKS_A				
				3UPU_A				
				AAA_11 AAA donai				
				5B7I_A				
				3JB9_X				
				2FSF_B				
				UTP25 Utp25, U3				
				5XBX_O				
				4PJ3_A				
				TIGR01967				
				4NL4_H				
				2VDA_A				
				3KQN_A				
				1H74_A				
				3JUX_A				
				4UHQ_A				
				4YSB_A				
				TIGR01970				
				2XZL_A				
				SecA_DEAD SecA				
				2IPC_A				
				2IPC_D				
				2WIX_A				
				2VBC_A				
				3BXZ_B				
				5LTJ_A				
				5D8U_A				
				TIGR02768				
				3VKH_A				
				2XZ0_A				
				2XZP_A				
				TIGR00376				
				UvrD-helicase_U:				
				1TF5_A				
				AAA_30 AAA donai				
				4NON_A				
				5MZN_A				
				3RC8_A				
				3RC3_A				
				4B3F_X				
				SNF2_N SNF2_fan				
				1NKT_A				
				4NL2_O				



Hitlist

Show 25 entries

Nr	Hit	Name	Probability
1	<input type="checkbox"/> PF03354.14 (http://pfam.xfam.org/family/PF03354.14#tabview=tab0)	; Terminase_1 ; Phage Terminase	100
2	<input type="checkbox"/> 3EZK_B (http://pdb.rcsb.org/pdb/explore.do?structureId=3EZK)	DNA packaging protein Gp17; pentameric motor, DNA packaging, Alternative; 34.0A {Bacteriophage T4}	99.95
3	<input type="checkbox"/> 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.	99.95
4	<input type="checkbox"/> 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}	99.94

<u>Vis</u>	<u>Hits</u>	<u>AlnNr</u>	<u>Hits</u>	<u>Select all</u>	<u>Forward</u>	<u>Forward Query MSA</u>	<u>Color Seqs</u>	<u>Name</u>	<u>Unwrap Seqs</u>	<u>Probability</u>
								DNA helicase		
							uvsW;			
							Bacteriophage, T4,			
							Helicase, UvsW,			
							RecG; 2.0A		98.33	
							{Enterobacteria			
							phage T4} SCOP:			
							c.37.1.23			
							psIM2_ORF9;			
							phage			
							uncharacterized			
							protein (putative			
							large terminase),			
							C-terminal			
							domain. This			
							model represents			
							the C-terminal			
							region of a set of		98.33	
							phage proteins			
							typically about			
							400-500 amino			
							acids in length,			
							although some			
							members are			
							considerably			
							shorter.			
							Heat resistant RNA			
							dependent			
							ATPase; RNA			
							HELICASE,			
							RIBOSOME			
							BIOGENESIS,			
							THERMOPHILIC;			
							HET: SO4; 1.4A			
							{Thermus			
							thermophilus}			
							;			
							ResIII ; Type III			
							restriction			
							enzyme, res		97.98	
							subunit			

Showing 1 to 25 of 250 entries

Previous 1 2 3 4 5 ... 10

[Next](#)

Alignments

<input type="checkbox"/>	1.	Template alignment CDD (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrvcgi?uid=pfam03354)
		PF03354.14 (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 HHHHHHHHHhccChhHhhccCccchh----hhheeEeeEEecCCCCHHHHHHHHHHHHHH
		Q Klein_Draft 35 PWQELCLHEALKESDELVQLESGAWVK----KWAASSFGLVVSQNGKGSILEALELAGL
		Q Consensus 35 ~~Q~~~~~g~~~~~-~~~~~rg~GKT~~~~~

Vis	Hits	Aln	Select all	Forward	Forward Query MSA	Color Segs	Unwrap Segs
			T Consensus	...++...+. ~ ~	+ +. +++.+++.+ + +++.+++.+		
			T PF03354.14	1 PWQVFRHGSVF-----	GWKREGSGVRRFRSTYHQVGKKNGKTTDAVPMFLTQ		
			T ss_pred	CcceeEEEeh-----	eeEecCCCCeEEEEEEecccCCCCCcHHHHHHHHHHHH		
			Q ss_pred	EEECCCHHHHHHHHHHHHHHHcc-cchhhceccCCceEEecCCCCcEEEEEECCCC			
			Q Klein_Draft	99 IHSAHEFKTAVNQMERLESIAKS-GLKYKAKQAHGAESIEILDGPNGARVIFQTRTD			
			Q Consensus	99 ~i~~t~~~a~~~~~l~~~~~i~~~~~g~~i~~~~~	+++++.++++.++..+++. .+..+. .+..+. .+ +. .+.+++..		
			T Consensus	59 ~~~~t~~~~~i~~~~~i~~~~~g~~i~~~~~	~~~~~t~~~~~i~~~~~i~~~~~g~~i~~~~~		
			T PF03354.14	59 FCAATTRDQAGLLFKEVGRIVKRSPVLCRMMQ--TMRHEIVTP--RVDGVIKCLSRDGD			
			T ss_pred	EEEeCCHHHHHHHHHHHHHhCHHHHHHHH-hcccEEEec---CCCCeEEEeeCCCC			
			Q ss_pred	EEecHHhcCH-HHHHHHHhhcCCCCCEEEEecCCCC-CCcchchHHHHHHHHHHH			
			Q Klein_Draft	168 IFDEAMTITP-GSLKALLPTVSSRPNPQIVYTGTADQR-TQPYCHTFGGVRYALEQLR			
			Q Consensus	168 ~iDE~~~~~l~~~~~i~~stp~~~~~	++ +++. ++.++.++...+....++ .++..+ ..+++.+.		
			T Consensus	124 ~~DE~~~~~stp~~~~~	~~DE~~~~~stp~~~~~		
			T PF03354.14	124 ARDEMHRWTDLRELAETIVESMIARAQPIDWITTAGHDHS--LCGELR---GYAEGVL			
			T ss_pred	EEechHhCCCCHHHHHHHHccccCCeEEEEeCCCCCCC--hhHHHH---HHHHHH			
			Q ss_pred	EEEEeCCCCCcCcCCCHHHHHHHCCCCCCHHHHHHHH----HHHHHcHHhhHHH			
			Q Klein_Draft	234 FLEWSAPDDLPEEKFGDPQYWAMANPGLGYRQTEEKILDEY---EEMWANLRDFGVDR			
			Q Consensus	234 ~~~~~~nP~~~~~e1~~~~~f~~~	.+.+++.+...++..+..+++.+ ... ++.. .++		
			T Consensus	188 ~~~~~~np~~~~~e1~~~~~	~~~~~np~~~~~e1~~~~~		
			T PF03354.14	188 GFVAEPPAD---CDPLDPAFWPMGNPNLGVSKPIGKMHEAASKAAIAA--SMPNFKRFH			
			T ss_pred	hheecCCCC---CCCCChhhcCCCCCCCCCHHHHHHHHHhchh--hcchhh			
			Q ss_pred	CCCCCCCHHHHHhCCCCCc----CCCeEEEEEEeCCCCcEEEEEEeCCCCEEEE			
			Q Klein_Draft	299 AGISEIPLDKWRLDNPEPDL---AGARALILYRTPEGPWAIVGSQRCTDGRIGHVEV			
			Q Consensus	299 ~~~~~~f~~~~~p~~~~~g~D~a~~~d~tai~~~~~g~~v~~	+.+++.++..+.....+ ...++ + +.++ .+++++. .++.++..		
			T Consensus	251 --f~~~~~g~D~a~~~D~~~i~~~~~v~~	--f~~~~~g~D~a~~~D~~~i~~~~~v~~		
			T PF03354.14	251 --QMWIARESWDQGAADAPFDPRMLYGRDAWGVVDLSNKIDTTAIVVAVP-LDGLIYLIA			
			T ss_pred	--CceecHHHHHhccccCCCCCHHHHCCEEeeeeCCCCcEEEeCCCCeEEEE			
			Q ss_pred	-----CCHHHHHHHHHHHHHHHCCCEEeCccHHHH			
			Q Klein_Draft	359 -----DPVDRVVDKFIQAITAWGPEEILVGRGGAAEV			
			Q Consensus	359 -----i~~~~~i~id~~g~g~~	.+++++. ..++..++.. ++ .++..+		
			T Consensus	318 ~~~~~~y~~~~~i~~~~~i~~~~~i~~~~~i~~~~~	~~~~~y~~~~~i~~~~~i~~~~~i~~~~~i~~~~~		
			T PF03354.14	318 FIVRAQKEKREYVAWRDQGWLEVHTGAIdeaQIEARIGWIAKTFAVQEIAYPWGMKYM			
			T ss_pred	hHhhhhhhHhHHHHHHCCCEEeCCCCcCHHHHHHHHHHHhCCeEEecccHHH			
			Q ss_pred	EeCCCCHHHHHHHHhHHHHHHhCCCCceeeCCcHHHHHHHcEEEECCCCecccC-			
			Q Klein_Draft	401 VYSPNQSEEAQACGGFLNDALVPENPLLSHGHNQHSLNAISRAVKRDLPSSGFVWDCI-			
			Q Consensus	401 ~~~~~~l~~~~~g~i~~~~~l~~~l~~~~~	+.++....++.. .+..++..++ ++..++.. . .++..++..++..++		
			T Consensus	388 ~~~~~~l~~~~~g~i~~~~~l~~~l~~~~~	~~~~~l~~~~~g~i~~~~~l~~~l~~~~~		
			T PF03354.14	388 MVEHRQGFASMSN--PMKRVEEELVAQNRLRHGGNPVLAWQVGNVRDDEAAENIKPNKKR			
			T ss_pred	eEEecCCchhcCh--HHHHHHHHHHCCCcCCChhHHHhccEEecCCCCCcCCCC			
			Q ss_pred	HHHHHHHHHHc			
			Q Klein_Draft	470 VTLGRWALLKH 480 (510)			
			Q Consensus	470 ~~~a~~~~~ 480 (510)			
				+++ ++..++..			
			T Consensus	456 ~~~a~~~~~ 466 (467)			

Vis Hits Aln | PF03354.14 456 MIMAVGRAAG 466 (467) Select all Forward Forward Query MSA Color Seqs Unwrap Seqs

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

2. [3EZK B](http://pdb.rcsb.org/pdb/explore.do?structureId=3EZK) (<http://pdb.rcsb.org/pdb/explore.do?structureId=3EZK>) DNA packaging protein Gp17; pentamer
Alternative: 34.0A {Bacteriophage T4}

Probability: 99.95 E-value: 7.0E-29 Score: 259.6 Aligned Cols: 404 Identities: 14% Similarity:

Q ss_pred		CHHHHHHHHHHHHHHHHHCCeEEEEcCCHHHHHHHHHHHHHHcc-cchhceccCCc
Q Klein_Draft	77	GKGSILEALELAGLILFGERLIIHSAHEFKTAVNGMERLESLIAKS-GLKYAKQAHGAE
Q Consensus	77	GKT~~~~~i~i~~t~~~a~~~~~l~~~~~ ++++..++ .+.+. +.++++++.++++.++..+.+++. .+.....+..
T Consensus	165	GKT~~~~~1~~~~~p~~~i~i~a~t~~~a~~~~~i~~~i~~~p~~~~~
T 3EZK_B	165	GKTTVVAIFLAHFVCFNKDKAvgIHLHKGSMSAeVLDRTKQAIELLPDFLQPGeWNKG
T ss_pred		CHHHHHHHHHHHHHHHHHCCeEEEEcCcHHHHHHHHHHHHHHCcHHhCCceccCC

Q ss_pred		CcEEEEEECCCCCcccccceeEEEEecHHhcCH--HHHHHHHHhhcCCCCCEEEEecCCC
Q Klein_Draft	146	GARVIFQRTDRSGLGLTADRVIFDEAMITP--GSLKALLPTVSSRPNPQIVYTGTAAAD
Q Consensus	146	g~~~i~~~~~G~~~~~v~iDE~~~~~l~~~~~i~~stp~~ +. .+..+..++ .++++++ +++. +. +.++..+...+....++ . +
T Consensus	231	Gs~i~~~~~rG~~~~~iiIDE~~~~~l~~~l~~~~~ii~~stp~~
T 3EZK_B	231	GSSIGAYASSPDAVRGNSFAMUYIDECAFIPNFHDSWLAIQPVISSGRRSKIIITTPNG
T ss_pred		CCEEEEEECCCCCcccccceeEEEEecHHhcHHHCCCCHHHHHHhhcCCCCCEEEEecCCC

Q ss_pred		HHHHHHHHHHHcCCCCEEEEEECCCCCCCcCCHHHHHHHCcccccccCHHHHH--
Q Klein_Draft	214	GGVRYRALEQLRTGERKRLCFLEWSAPDDLPEEKFGDPQYWAMANPGLGYRQTEEKIL--
Q Consensus	214	~~~~~nP~~~~~e1~~~
		+ +.+.+....+. . +.+.+.... .+. +.+.++.+.+
T Consensus	295	~~~~~e~~~~~
T 3EZK_B	295	Y---DIWTAAVEGK-SGFEPYPTAIWNSV-----KERLYNDEDIFDDGQWQS
T ss_pred		H---HHHHHHHcCC-CCcEEEeecccc-----CcccCCCCccccCCCCHHH

Q ss_pred		HHhhHHHHCCCCCCCCCCCCCCCCCHHHHhcC-----CCCCccCCCeEEEE
Q Klein_Draft	281	LRDFGVDRLLGIGDWQPQFGAGISEIPLDKWRRLD-----NPEPDLAGARALIL
Q Consensus	281	~~~f~~e~~g~~~~~f~~~~~p~~~~~g~ +. .+ ++ .+. +..++...+. .+..++ +
T Consensus	345	~~~f~~ey~~~~~g~vf~~~i~~~~~p~~~~~vigm
T 3EZK_B	345	LAQFRQEHTAA--FEGTS--GTLISGMKLAVMDFIEVTPDDHGFHQFKKPEPDRKYIATL
T ss_pred		HHHHHHHHHhc---cccc--CCCCcHHHHhbceeeeerCCCCCeeFeeCCCCCcEEEEEE

0 ss pred ----eFeCCCHHHHHHbCCCCCCeeCCchHHHHHHHccFFFFCeeee

<u>Vis</u>	<u>Hits</u>	<u>Aln</u>	<u>Q Klein_Draft</u>	<u>400</u>	<u>----TVYSPNQSEEAQACGGFLNDALVDPENPLLSHGNQHSLNAAISRAVKRDLPSSGFV</u>
			<u>Select all</u>	<u>Forward</u>	<u>Forward Query MSA</u>
			<u>Q Consensus</u>	<u>400</u>	<u>Color Seas</u>
					<u>Unwrap Seas</u>
					<u>++.+.+....++..</u>
					<u>++.+.+....++ ++..++.</u>
					<u>+. .+ .++.++..</u>
			<u>T Consensus</u>	<u>481</u>	<u>~~~~~k~~~~~i~~l~~~i~~g~i~i~~~l~~e~~~~~k</u>
			<u>T 3EZK_B</u>	<u>481</u>	<u>CDSYTDLGMKQTKRTKAV--GCSTLKDIEKDKLIHH-RATIQEFRTFSEKG-----VS</u>
			<u>T ss_pred</u>		<u>cccccccccCCcCCHHh--HHHHHHHHHhCCeeeCC-HHHHHHHHHhCc-----CC</u>
			<u>Q ss_pred</u>		<u>HHHHHHHHHHHHHHHcc</u>
			<u>Q Klein_Draft</u>	<u>466</u>	<u>QLMGVTLGRWALLKHA 481 (510)</u>
			<u>Q Consensus</u>	<u>466</u>	<u>~~dA~~~a~~~~~ 481 (510)</u>
					<u>.+ +++ ++.+....</u>
			<u>T Consensus</u>	<u>543</u>	<u>~~DA1a~~a~~~~~ 558 (577)</u>
			<u>T 3EZK_B</u>	<u>543</u>	<u>LVMSLVIFGWLSTQSK 558 (577)</u>
			<u>T ss_pred</u>		<u>HHHHHHHHHHHHHHhhcc</u>

Template alignment

3. [TIGR01547](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR01547) (<http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR01547>) phage_term_2; phage_PBSX family. This model detects members of a highly divergent family of the large subunit of phage terminase.

Q ss_pred		eeEeeEeccccchhhhhhhhhhhhhhhhhccEeeEEEccchhhh-hhhhhhhhhhhhhcc
Q Klein_Draft	65	ASSFGLVVSQRQNGKGSILEALELAGLILFGERLIHSAAHEFKTA-VNGMERLESIAKSG
Q Consensus	65	~~~~~rg~GKT~~~~~i~i~~t~~a~~~~~ +++++.+ + +++.+++.+++.++++++.++ +.++..++.++..+
T Consensus	1	~~~~~rg~GKT~~~~~
T TIGR01547	1	HEEIIAKGGRGSGKTFIAKLVEKAARNKPQNILCARKVQNSIRDSVFKDIEDLLSIEG
T ss_pred		CceEEEEeccccchhhhhhhhhhhhhhhhhccEeeEEEccchhhh-hhhhhhhhhhhhhcc

Q ss_pred		CceEEEcCCCC-CcEEEEEC--CCCCCccccc-eEEEEecHHhcCHHHHHHHHHhhcC
Q Klein_Draft	134	AESIEILDGPNP-GARVIFQTR--TDRSGLGLTA-DRVIFDEAMITPGSLKALLPTVSS
Q Consensus	134	~~~i~~~~~-g~~i~~~~~-G~~~~~v~iDE~~~~~l~~ ...+.+. + .+ .+.+. +.++ +.++ + +.+++.+.+.++.+
T Consensus	71	~~~i~~~~~-g~~i~~~~~-G~~~~~i~DE~~~~~l~~~~~
T TIGR01547	71	SMEIKIL---NTGKKFIFKGLNKPNKLKGAGIAIWFFEEASQLTKEDIKELIPRLRE
T ss_pred		cceFFFFc---CCCCFFFFFFecCCCCccccccCcceFFFFeChhhCCHHHHHHHHHhhcC

Q ss_pred		HHHHHHHHHHHHHHcHHhhHHhhCCCCCCCC-CCCCCCCCHHHHhcCCCCCcCCCCeEE
Q Klein_Draft	267	EKILDEYEEMWANLRDFGVDRLGIGDWPQF-GAGISEIPLDKWRRLDNPEPDLAGARAL
Q Consensus	267	~e~1~~~~~f~~~g~~~~~f~~~~~p~~~~~.+++++++.++. .+...+ .+ +.+...+.+...+.++
T Consensus	175	~~~~~f~~~~~.~~~~~
T TIGR01547	175	EVTIQEIEELKRRDPALYRRIWLGE--WVSALG--GILYKKLDVKAAYIK-ESPNHPIDF
T ss_pred		HHHHHHHHHHHHcCCCCHHHHHHhCC-ccbbhcc-cccccHHHHhccCCCCCCCC

Q ss_pred	EEEEEEEEEccccCCCC-----CHHHHHHHHHHHHHHHCCCEEeCcHH
Q Klein_Draft	336 WAIVGSQRCTDGR-IHVEVGYAGMD-----PVDRVVDFKIQAITAWGPEEILVGRGGAA
Q Consensus	336 tai~~~~~g~~~~v~~~~~i~~~~~i~~~~~i~iD~~~g~g +++++.+++.+++.++... .+++.++... .+..++... .+..++... .+
T Consensus	240 ~a~~~~~v~~~~~i~~~~~ie~~~~

Vis	Hits	Aln	T TIGR01547	240	SASVVLGIEHGKKIYVAEYYYYSNAIEQVKDAVLEYAIEIKQFLN---VKQLIYADSGD		
			Select all	Forward	Forward Query MSA	Color Segs Unwrap Segs	
			F ss_pred				
			Q ss_pred		-----CCCeEeCCCCHHHHHHHHhhHHHHHHhCCCCCceeeCC--cHHHHHHHHc-cEEEE		
			Q Klein_Draft	397	-----AGFTVYSPNQSEEAQACGGFLNDALVDPENPLLSHGN--QHSLNAAISR-AVKRD		
			Q Consensus	397	-----g~~~~~l~~~~~g~i~~~~~l~~~l~~~~~.+++.++..++ +++.++ .+. ++ .+.++..		
			T Consensus	306	~~~~~k~~~i~~~~~i~~~~~l~~~~~y~~~		
			T TIGR01547	306	EHQFYQDVAAIKAQGAKLAVRD--RIEVFRDLLASRKLKFLKEPCNTYKKDIYNEYVWDD		
			T ss_pred		HHHhhcccccCCCCCHHH--HHHHHHHHHHcCCEECCChhHHHHHHhccccC		
			Q ss_pred		CCCCcHHHHHHHHHHHHHHHHc		
			Q Klein_Draft	459	IEQSTYAQLMGVTLGRWALLKA 481 (510)		
			Q Consensus	459	~~~~~D~~dA~~~a~~~~~ 481 (510)		
					+... +. .+ +++++.++..+		
			T Consensus	372	~~~~~dd~~Da~y~~~~~ 394 (394)		
			T TIGR01547	372	PVDLHDHAFDALRYAVLAFLRKM 394 (394)		
			T ss_pred		CCCCCCHHHHHHHHHHHhCc		

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

4. [4IEE_A \(<http://pdb.rcsb.org/pdb/explore.do?structureId=4IEE>\) Gene 2 protein; DNA packaging, terminase; AGS; 1.89A {Shigella phage Sf6}](#)

Probability: 99.94 E-value: 2.8E-27 Score: 242.96 Aligned Cols: 369 Identities: 14% Similar

Q ss_pred		heeEeeEEecCCCCHHHHHHHHHHHHHHhCcEEEEEcCCHHHH-HHHHHHHHHHHHHc
Q Klein_Draft	64	AASSFGLVVSQRNGKGSILEALELAGLILFGERLIIHSAEFKTA-VNGMERLESLIAMS
Q Consensus	64	~~~~~rg~GKT~~~~~i~~~~~t~~~a~~~~~.+++.++ + +++.++..+... .+++++++.+++.++..+..++..
T Consensus	34	~~r~~~~~rg~GKT~~~~~p~~~i~~~a~~~t~~~a~~~~~i~~~i~~~
T 4IEE_A	34	AHRYKVAKGGRRGGSKSWAIARLLVEAARRQP-VRILCARELQNSISDSVIRLLEDТИЕРЕ
T ss_dssp		CCSEEEEEECTTSSHHHHHHHHHHHHHTSC-CEEEEEECCSSGGGSTHHHHHHHHHHHH
T ss_pred		cCCEEEEEEeCCCCCHHHHHHHHHHHHHhCc-ceEEEEEcHHHHHHHHHHHHHHHHHHc
Q ss_pred		CCceEE-EecCCCCCcEEEEEECC--CCCCcccc-eeEEEEEcHHhCCHHHHHHHHHhCc
Q Klein_Draft	133	GAESIE-ILDGPNP GARVIFQTRT--DRSGLGLT-ADR VIFDEAMTITPGSLKALLPTVS
Q Consensus	133	~~~~i~~~~~g~~i~~~~~G~~~v~iDE~~~~~l~+...+.+.+ +. +.+.+ ..++ +.++ +..+++. ...+.++..
T Consensus	101	~~~i~~~~~ngs~i~~~~~G~~~g~~~ii~DE~~~~~i~~~l~
T 4IEE_A	101	QRSMIRHLG---TNAEFMFYGIKNNPTKIKSLEGIDICWEEAEAVTKESWDILIPTIR
T ss_dssp		ETTEEEETT---TCCEEEEEEETTCHHHHHCCCCCEEEECGGGCCHHHHHHGGGCC
T ss_pred		ccceEEEcC---CCCEEEEEEccCChhhcccCCCCEEEeEcchhCCHHHHHHHHHhCc
Q ss_pred		ecCCCCCCCchhchHHHHHHHHHHhCCCCCCCCCCeCCCCCccccCCHHHHHHHHC
Q Klein_Draft	199	GTAADQRTQPYCFTFGGVRYRALEQLRTGERKRLCFLEWSAPDDLPEEKFGDPQYWAMAN
Q Consensus	199	stp~~~~~n +.++ + ++ +.+.+++.+.+.+ .+
T Consensus	166	sTP~~~~~n
T 4IEE_A	166	FNPKNILD--D---TY---QRFVV---NPPDDICLLTVNY-----TDN
T ss_dssp		ECCCBTTS--H---HH---CCCC--SCCSSEEEEEEcg-----GGC
T ss_pred		eCCCCCCC--h---HH---Hheee--CCCCeEEEeEc-----ccc
Q ss_pred		HHHHHHHHHHhHHhhHHHHCCCCCCCCCCCCCCCCHHHHhCCC---CCcccCcE
Q Klein_Draft	269	KILDEYEEMWANLRDFGVDRLGIGDWQPQFGAGISEIPLDKWRLLDNP---EPDLAGARA
Q Consensus	269	~l~~~~~f~~~e~~~g~~~~~f~~~~~p~~~~~.+++++.++..+... ...+ ++ +.++ +..++..+... .+....++
T Consensus	204	~~~~~f~~~e~~~g~~~~~f~~~~~i~~~~~
T 4IEE_A	204	LRLEMEECKRNPTLYRHIWLGE--PVSAS-DMAIIKREWLEATDAHKLGWKAKGAVV

Vis	Hits	Aln	T_ss_dssp Select all	Forward	Forward Query MSA	Color Segs	Unwrap Segs
			T_ss_pred				
			Q_ss_pred	CcEEEEEEeCCCEEEEcccCCCCHHHHHHHHHHHHCCEEEEeCcHH-HHHH			
			Q_Klein_Draft	334 GPWAIVGSQRCTDGRIHVEVGYAGMDPVDRVVDKFIFIQAITAWGPEEILVGGRGAA-EVIP			
			Q_Consensus	334 d~tai~~~~~g~~~v~~~~~i~~~~~i~iD~g~g~~~ .+++++.+.++.+++. .++++. +++. .+ . .++			
			T_Consensus	271 D~tv~v~~~~~v~~~~~e~~~i~~~~~i~iD~G~G~v~~~			
			T_4IEE_A	271 DAKGYASRH---GSVVKRIAEGL-LMDINEGADWATS LAIEDGADHYLWDGDGVGAGLRR			
			T_ss_dssp	CCEEEEEE---TTEEEEEEc-SCCHHHHHHHHHHHHTCSEEEECSTTTCHH			
			T_ss_pred	CCceEEEEe---CceEEEEecC-CCCHHHHHHHHHHHCCCEECCCCCCchHHHH			
			Q_ss_pred	CeEeCCCHHHH-----HHhhHHHHHhcCCCC			
			Q_Klein_Draft	399 FTVYSPNQSEEA-----QACGGFLNDALVPEN			
			Q_Consensus	399 ~~~~~~-----~~~~~1~~~~~ .++..+....++.++..+....			
			T_Consensus	337 ~~~~~~n~r~e-----1~~~			
			T_4IEE_A	337 ITATMFKGSESPFDEDAPYQAGAWADEVVQGDNVRTIGDFRKNRAQ--FYYALADRLYL			
			T_ss_dssp	CEEEECTSCTTTSBCCC-----CCCBHHHHBSSH----HHHHHHHHHHH			
			T_ss_pred	cEEEEecCCCCCCCCCCCCccccCCCCccccCCCCccchHHHHHHHHHHH--HHHHHHHHHHH			
			Q_ss_pred	-----eeeCCchHHHHHHHccEEEECCCCCeeeeC-----CCccHHHHH			
			Q_Klein_Draft	429 -----LSHGNQHSLNAISRAVKRDLPSGGFVWDCI-----EQSTYAQLM			
			Q_Consensus	429 -----i~~~~~l~~~l~~~~~-----D~~~d .++.. ++.+++.++. .+++.+ ... +.+			
			T_Consensus	405 ~~~~~~1~~~eL~~~~~g~~~~~K~~~k~~~g~~~spD~~~d			
			T_4IEE_A	405 ADPDDMLSFDKEAIGEKMLEKLFAELTQIQRKFNNNGKLELMTKVEMKQKLGIPSPNLAD			
			T_ss_dssp	CGGGGCCEEHHHHCHHHHHHHHHHTCBBCCTTSCBCBCHHHHHHCCCCCHHHH			
			T_ss_pred	CCHhceeeCHHHhCHHHHHHHHHHHhCcCeEeeCCCCCEEeChHHHHHHCCCCcHHHH			
			Q_ss_pred	Hcc			
			Q_Klein_Draft	479 KHA 481 (510)			
			Q_Consensus	479 ~~~ 481 (510) ..+			
			T_Consensus	475 ~~~ 477 (490)			
			T_4IEE_A	475 LVR 477 (490)			
			T_ss_dssp	BCC			
			T_ss_pred	ccc			

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

5. [4IDH A](http://pdb.rcsb.org/pdb/explore.do?structureId=4IDH) Gene 2 protein; DNA packaging, terminal {Shigella phage Sf6}

Probability: 99.94 E-value: 2.8E-27 Score: 242.96 Aligned Cols: 369 Identities: 14% Similar

Q ss_pred		heeEeeEEecCCCCHHHHHHHHHHHHHHHHCCeEEEcCCHHHH-HHHHHHHHHHHHc
Q Klein_Draft	64	AASSFGLVSVRQNGKGSILEALELAGLILFGERLIIHSACHEFKTA-VNGMERLESLIAKS
Q Consensus	64	~~~~~rg~GKT~~~~~i~i~~t~~a~~~~~..+....++ ++ +++.+++.++ .+++++++.++ +.++..+..+++.+
T Consensus	34	~~r~~~~~rg~GKT~~~~~p~~i~~a~~~a~~~~~i~~~i~~~
T 4IDH_A	34	AHYRKVAKGGRGSGKSWAIARLLVEAARRQP-VRILCARELQNSISDSVIRLLEDTIER
T ss_dssp		CCSEEEECCCTCCHHHHHHHHHHHHTTSC-CEEEEEESCSSGGGSSHHHHHHHHHH
T ss_pred		cCCEEEEeCCCCHHHHHHHHHHHHHHHHCC-ceEEEEEcCCHHHHHHHHHHHHHHHHc

Vis	Hits	Aln						
			T Consensus	101	~~~i~~~~~ngs~i~~~~~G~~g~~ii~DE~~~~~i~~~l			
		Select all	Forward	101	QRSMINHGL---TNAFLMIFYGIKNNPTKIRSKLEGIDICWELAATKESWDILIPTIR	Color Seas	Unwrap Seas	
			T 4IDH_A		ETTEEEETT---TCCEEEEETTTCHHHHHCCCCCEECSGGGCCHHHHHGGGCC			
			T ss_dssp		ccceEEEcC---CCCEEEEccCChhhcccCCCIEEEechhCCHHHHHHHHHhc			
			T ss_pred		ecCCCCCCCchchHHHHHHHHhCCCCEEEEeCCCCCccccCCHHHHHHHHC			
			Q Klein_Draft	199	GTAADQRTQPYCHTFGGVRYRALEQLRTGERKRLCFLEWSAPDDLPEEKFGDPQYWAMAN			
			Q Consensus	199	stp~~~~~n .++ + ++ +.+. .+. .++.+. .+			
			T Consensus	166	sTP~~~~~n			
			T 4IDH_A	166	FNPKNILD--D--TY---QRFVV---NPPDDICLLTVNY-----TDN			
			T ss_dssp		ECCCBTTS--H--HH---CCCC--SCCSSEEECCG-----GGC			
			T ss_pred		eCCCCCCC--h--HH---Hheee---CCCCeEEEeec-----ccc			
			Q ss_pred		HHHHHHHHHHHHcHHhhHHHHhCCCCCCCCCCCCCCCCCHHHHHhCCC---CCcccCCcE			
			Q Klein_Draft	269	KILDEYEEMWANLRDFGVDRIGIGDWQPQFGAGISEIPLDKWRRLDNP---EPDLAGARA			
			Q Consensus	269	~l~~~~~f~~e~~g~~~~~f~~~~~p~~~~~+++++.+.++.. .+++++ ++. +...+...+.+.++			
			T Consensus	204	~~~~~f~~e~~g~~~~~f~~~~~i~~~~~			
			T 4IDH_A	204	LRLEMEECKRNPTLYRHIWLGE--PVSAS-DMAIIKREWLEAATDAKKLGWAKGAVV			
			T ss_dssp		HHHHHHHHHHHHCHHHHHHHHSCC---CBCCC-TTBSSCHHHHHHBTHHHHTCCCSCEE			
			T ss_pred		HHHHHHHHHHhCHHHHHHHHHhCc---ccccC-CcceeCHHHHHHHHHhchhcCCCCCCCfEE			
			Q ss_pred		CcEEEEEEeCCCCEEEEcccCCCCHHHHHHHHHHHHCCEEEeCcHH-HHHH			
			Q Klein_Draft	334	GPWAIVGSQRCTDGRIHVVEGYAGMDPVDRVVDKFIFIQAITAWGPEEILVGRGAA-EVIP			
			Q Consensus	334	d~tai~~~~~g~~~v~~~~~i~~~~~i~id~~g~~~ .++++.. .+.++.... . .+++.++.. .+++.++.. .++.. .+ . . .++			
			T Consensus	271	D~tv~v~~~~~v~~~~~e~~~i~~~~~i~id~~G~v~~			
			T 4IDH_A	271	DAKGYASRH--GSVVKRIAEGL-LMDINEGADWATSLAIEDGADHYLWDGDGVGAGLRR			
			T ss_dssp		CCEEEEEE---TTEEEEEE-SCCHHHHHHHHHHHHTCSEEEECSSGGGGCHH			
			T ss_pred		CCceEEEEe---CceEEEeecC-CCCHHHHHHHHHHHhCCCEEEeCCCCChHHH			
			Q ss_pred		CeEeCCCHHHHH-----HHhhHHHHHHhCC			
			Q Klein_Draft	399	FTVYSPNQSEEA-----QACGGFLNDALVPDEN			
			Q Consensus	399	~~~~~1~~~~~+.+.+.+.++. ++.+.++.+++			
			T Consensus	337	~~~~~n~r~e-----1~~			
			T 4IDH_A	337	ITATMFKGSESPFDEDAPYQAGAWADEVVGQGDNVRTIGDVRNKRAQ--FYYALADRYL			
			T ss_dssp		CEEEEEECCTTSCTTTSBCCC-----CCBHHHHBSSH----HHHHHHHHHH			
			T ss_pred		cEEEEecCCCCCCCCCCCCccccCCCCccccCCCCchHHHHHHHHHHHHHHHHHHHHHHHHHHHH			
			Q ss_pred		-----eeeCCcHHHHHHHHhCCEEECCCCCeeeeecC-----CCcccHHHHH			
			Q Klein_Draft	429	-----LSHGNQHSLNAAISRAVKRDLPSGGFWDCI-----EQSTYALQM			
			Q Consensus	429	-----i~~~~~1~~~1~~~~~D~~~d+. .+.+++.++. .++..+ ... +.+			
			T Consensus	405	~~~~~1~~~eL~~~~~g~~~~~K~~~k~~~g~~~spD~~~d			
			T 4IDH_A	405	ADPDDMLSFKDKEAIGEKMELKLFIAELTQIQRKFNNNGKLEMTKVEMKQKLGIPSPNLAD			
			T ss_dssp		CGGGGCCEEHHHHCHHHHHHHHHHTCBCCCTTSCBCBCHHHHHHHCCCCCHHHH			
			T ss_pred		CCHHhceeeCHHHhCHHHHHHHHHhCeEeCCCCCEEeChHHHHHHCCCCchHHH			
			Q ss_pred		Hcc			
			Q Klein_Draft	479	KHA 481 (510)			
			Q Consensus	479	~~~ 481 (510)			
					..+			
			T Consensus	475	~~~ 477 (490)			
			T 4IDH_A	475	LVR 477 (490)			
			T ss_dssp		BCC			
			T ss_pred		ccc			

Vis	Hits	Aln	Select all	Forward	Forward Query MSA	Color Seqs	Unwrap Seqs
					Template alignment Template 3D structure PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4bil)		
	6.				4BIL_C (http://pdb.rcsb.org/pdb/explore.do?structureId=4BIL) DNA MATURASE B; HYDROLASE, PACKAGEN, 29.0A {ENTEROBACTERIA PHAGE T7}	DNA MATURASE B; HYDROLASE, PACKAGEN, 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 hHHHHHHHH-HHcC---CCCHHHHHHHHHhccChhHhhccCcchhhheeEeeEEe Q Klein_Draft 18 AGQEAIIDLAAACG---LILDPWQELCLHEALKESDELVQLESGAWVKWAASSFGLVV Q Consensus 18 ~~~~~~l~~~Q~~~~~g~~~~~ +...+. +..+++.+. +. .+.+.+.... .+...+.+ T Consensus 15 ~~~d~~~f~~~~~Q~~~~~ T 4BIL_C 15 LKGDFVAFLVLWKALNLPVPTKCQIDMAKVLANGD-----NKKFILQA T ss_dssp HHHHHTCCCCBTTBSCCCCCCHHHHHHHHHSSSS-----CSEEEEC T ss_pred HHhcHHHHHHHHHHhCCCCCHHHHHHHHHhCC-----CCeEEEEe		
					Q ss_pred HHHHHHHHHHHhCCeeEEEecCCHHHHHHHHHHHHHHHHHcccchhceec--cCcEEEEE Q Klein_Draft 83 EAELAGLILFGERLIIHSASHEFKTAVNGMERLESЛИAKSGLKYKAKQA--HGAESIEIL Q Consensus 83 ~~~~~~i~~~t~~~a~~~~~l~~~~~i~~~ +...++.+. +...+++.+++++.++...+.++...+.++...+.+...+.+. T Consensus 69 ~~~~~~p~~~i~~~s~t~~~a~~~~~i~~~~~ T 4BIL_C 69 CAFVVWSLWRDPQLKILIVSASKERADANSIFIKNIIDLPPFLSELKPRPGQRDSVISFD T ss_dssp HHHHHHHHHHTSSCCEEEECSTSHTHHHHHHHHHHHTSCTTCCCSBCSTSCSCBS T ss_pred HHHHHHHHHhCCCCEEeeCCHHHHHHHHHHHHHhCCHHHHHHCCCCCCCCCeeEee		
					Q ss_pred --CcEEEEECCCCCCcceeEEEecHHcC-----HHHHHHHHh--hcCCCC Q Klein_Draft 146 --GARVIFQTRTDRLGLLTADRVLFEAMTIT-----PGSLKALLP--TVSSRPN Q Consensus 146 --g~~i~~~~~G~~~v~iDE~~~~~l~~~~~ +. .+...+.++ .+++++++ . +.+++.++...+.+...+.+...+.+...+.+ T Consensus 135 ~~g~~i~~~~~G~~~v~DE~~~~~ T 4BIL_C 135 DHSPSVKSVGITG-QLTGSRADIIIADDVEIPSNSATMGAREKLWLVQEFAALLKPLPS T ss_dssp EEEEEECTTTTHH-HHHCSSEEEEEEETTSCTTHHHHHHHHHHHSSHHHHHTTCCC T ss_pred CCCcEEEEecCC-ccccCcCEEeeCCCCcccCCCHHHHHHHHHHHHHhCCCCC		
					Q ss_pred CCCCCccccchHHHHHHHHHHhCCCCCEEeeCCC----- Q Klein_Draft 203 DQRTQPYCHTFGGVRYRALEQLRTGERKRLCFLEWSAPD----- Q Consensus 203 ~~~~~~+...++++...+.++...+. ...++.. T Consensus 204 ~~~~~~ T 4BIL_C 204 TEMT--L---YK---ELEDN-----RGYTTIIPALYPRTREONLYYSQRLAPMLRAE T ss_dssp TTSH--H---HH---HHHHH----HTTCCCCCCTTSGGGBCTTSCBCTTHHHHH T ss_pred CcCC--H---HH---HHHhc-----CCceEEEecccCCCCchhchccccchHHHHHH		
					Q ss_pred ccccCCHHHHHHHCCCCccccchHHHHHHHHHHhCCCCCCCCCCCCCCCC Q Klein_Draft 245 EEKFGDPQYWAMANPGLGYRQTEEKILDEYEEMWANLRDFGVDRIGDWQFGAGISEI Q Consensus 245 ~~~~~~nP~~~~~e~l~~~~~f~~e~~g~~~~~f+.+++.+++++++.++...+.++ ++...+.+ T Consensus 257 -----e~l~~~~~f~~ey~~~~~f T 4BIL_C 257 -----AGTPTDPVRFDRDLRERELEY-GKAGFTLQFMLN--PNLSD--AEKY T ss_dssp -----THHHHTTCCCTTSBSSCHH--HHTTCCCCCCC--CSSSE--EESS T ss_pred -----CCCCCCCCccccchHHHHHHHHHHh--ccccchHHHHHHhCC--CCCC--cccc		
					Q ss_pred -----HHHHHhcCCC-----CCcccCCeEEEEEcCCC Q Klein_Draft 306 -----LDKWRRLDNP-----EPDLAGARALILYRTPEG Q Consensus 306 -----p~~~~~g~D~a~~~ +...+..... .+...+.++ + ...+.+ T Consensus 310 ~~~~~~g~D~a~~~ T 4BIL_C 310 ALDLEKAPMHYQWLPNRQNIIEDLPNVGLKGDDLHTYHDCSNNSGQQKILVIDPSGRG T ss_dssp EEBCCSSTSCEEEEEECSSSSEEEEEEESCCSSSSHHHHHHHHHTSCCCCC		

<u>Vis</u>	<u>Hits</u>	<u>Aln</u>	<u>T ss_pred</u>	<u>cCCCCCCCCeEEeCCCCchhhcCCCCCCCCCCCCccccccCccCcCcCcCcceeEEEEeCCCC</u>			
			<u>Select all</u>	<u>Forward</u>	<u>Forward Query MSA</u>	<u>Color Seqs</u>	<u>Unwrap Seqs</u>
			<u>Q ss_pred</u>	eCC			
			<u>Q Klein_Draft</u>	344 CTDGRIHVEVGYAG-MDPVDRVVDKFIQAITAWGPEEILVGRGGAA-EVIPQIEA-----			
			<u>Q Consensus</u>	344 ~~~g~~~v~~~~~i~~~~~i~~~~~i~~~~~i~~~~~i~~~~~i~~~~~l~~~~~			
				...+++.+++.+++.+++.+++.+++.+++.+++.+++.+++.+++.+++.+++.+++.+++			
			<u>T Consensus</u>	380 ~~~~~v~~~~~i~~~~~i~~~~~i~~~~~i~~~~~i~~~~~i~~~~~l~~~~~			
			<u>T 4BIL_C</u>	380 TLNGIYLMEAGGFRDGYSDKTLELLAKAKQWGVQTVVYESNFGDGFMGFKVFSPILLKH			
			<u>T ss_dssp</u>	HTSSSSSSCCSCEECSSSSCSSECCSTHHHHHHHHHHHHHHHTTSEECCSHHHHHHTT			
			<u>T ss_pred</u>	EeCCCCCCCCeCcCCCCchhh			
			<u>Q ss_pred</u>	HHHHHHHHHHHH-HhhCCCCCeeeCCc			
			<u>Q Klein_Draft</u>	407 SEEAQACGGFLN-DALVDPENPLLSHGMQ 434 (510)			
			<u>Q Consensus</u>	407 ~~~~~~l~~~~~g~~~~~i~~~~~ 434 (510)			
				++..+ .. ++.+++.+++.++..			
			<u>T Consensus</u>	449 ~~~~K~~~~ri~~~~l~~~~~g~~~~~i~~~~~ 475 (476)			
			<u>T 4BIL_C</u>	449 ARGMKEM--RICDTLEPVMQTHRLVIRDE 475 (476)			
			<u>T ss_dssp</u>	ECTTCCC--HHHHHHHHHHHHHHSGGGTT			
			<u>T ss_pred</u>	cCCcHHH--HHHHchHHHHhcCcEEEecc			

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

7. [4BIJ](http://pdb.rcsb.org/pdb/explore.do?structureId=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		HHHHHHHHHHhCCeeEEEeCCHHHHHHHHHHHHHHHccchhceec--cCcCeEEe
Q Klein_Draft	83	EALELAGLILFGERLIIHSAHEFKTAVNGMERLESIAKSGLKYAKQAA-HGAESIEIL
Q Consensus	83	~~~~~i~~~t~~~a~~~~~l~~~~~i~~~ +..+++.+.+. +.+++++++.++++..+.+.++...+.+.+.+.+.+
T Consensus	69	~~~~~p~~~i~~~s~t~~~a~~~~~i~~~~~
T 4BIJ_C	69	CAFVVWSLWRDPQLKILIVSASKERADANSIFIKNIIDLLPFLSELKPRPGQRDSVISFD
T ss_dssp		HHHHHHHHHTSSSCEEEEECSSSTHHHHHHHHHHHHHTSCTTCCCCSCBTTSCSCBS
T ss_pred		HHHHHHHHHHhCCCEEEEeCCHHHHHHHHHHHHHHHccHHHHHHCCCCCCCCCeeEee

Q ss_pred		--CcEEEEEECCCCCcccccEEEEEecHHhcC-----HHHHHHHHH--hhcCCCC
Q Klein_Draft	146	--GARVIFQTRTDRLGLTADRVIFDEAMTIT-----PGSLKALLP---TVSSRPN
Q Consensus	146	--g~~i~~~~~G~~~~v~iDE~~~~~ +.+.+.++ .++++++ +.+++.++.++...+
T Consensus	135	~~g~~i~~~~~G~~~~v~DE~~~~~
T 4BIJ_C	135	DHSPSVKSVGITG-QLTGSRADIIADDVEIPSNSATMGAREKLWTLVQEFAALLKPLPS
T ss_dssp		EEEEEC TT TTHH-HHHCSSEEEETTSCTTHHHHHHHHHHHSSHHHHHTTCC
T ss_pred		CCCCCcEEEecCC-ccccCCcCEEEecCCCCcccccCCCCHHHHHHHHHHHHHHHHHHCCCC

[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

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(<http://www.ebi.ac.uk/pdbe/entry/pdb/2o0j>\)](http://www.ebi.ac.uk/pdbe/entry/pdb/2o0j)

9. [200j A](http://pdb.rcsb.org/pdb/explore.do?structureId=200j) (<http://pdb.rcsb.org/pdb/explore.do?structureId=200j>) DNA packaging protein Gp17; nucleotide HET: ADP; 1.8 Å {Enterobacteria phage T4}

Probability: 99.65 E-value: 6.2E-17 Score: 159.33 Aligned Cols: 220 Identities: 14% Similar

cCCCCCCCCHHHHHHHHHHHbcccChbHhbccCccbbhbbeeFeeEEecCCCCCHHHHHHHHHHHHH

CGLTLDPWQELCIEHALKESDELVOLESQAWVKKAASSEGILVVSRONKGSTLFALELA

R_KICIN_D4VE 29 CQEELD. WQECLCERAEKRESDEEVQLEESGAVVKKRASSI. GEVVSQRQNGRSKILLAEELA

Q consensus 25 100% Q consensus

Consensus 160 ~~~~1~p~Q~eii~~1~~~~~r~~~i1~~gRq~GK1~t~~a~~~1~

I 200J_A 160 IKVQLRDYQRDMLKIMSS-----KRMTVCNLSRQLGKIVVAIPLAH

T ss_pred eccCCCCHHHHHHHHHHcc-----CCeEEEEEcCCCCCChhHHHHHHHHHH

O ss pred EEEcCCHHHHHHHHHHHHHHHHHHcccc-hhhceccccCcEEEcCCCCCCCcEEEEEECCCC

O Klein Draft 99 IHSAAHEFKTAVNGMERLESIAKSGL-KYKAKOAHGAESIEILDGPNPGARVIFOTRDP

0. Consensus 99 ~i~~~t~~~a~~~~~l-~~~~~i~~~~~g~~i~~~~~

Q consensus 99 100 100 100 100 100 100 100 100

T. Consensus 212 liis+caelae+iaelpa+ca+inf+pcg+T+ca

1 2005_A 212 GILAHKGMSAELDRIKQAEELLPDFLQPGIVEWNKGSIELD---NGSS1GAYASSPD

T ss_dssp EEEEESSHHHHHHHHHHHHHHHHHHHHHSCTTSCCEEECSSEEEET---TSCEEESEECSSH

T ss_pred EEEeCChhHHHHHHHHHHHHHHHHHHCCCHhCcCcEEEeC- - -CCCEEEEeCCCC

Q ss_pred EEEecHHhcCH--HHHHHHHHhhcCCCCCEEEEEecCCCCCCCcchhchHHHHHHHHHHHH

Vis	Hits	Aln						
			T Consensus	265	~~W~~~~p~~~~~g~~~~~l~~p~~~~~i~~~~~a~~~~~f~n~L			
		Select all	Forward	265	RGFWVTNLDAQRNRRRT-SADGLLCFRSGREARQWREAQELWEETEQSEA-GLVGFFNGKA	Color Segs	Unwrap Segs	
			T ss_pred		CceccccCCCCeEEEEeeccCCCHHHHHHHHHHHHHcCCHH-HhhheeCCC			
			Q ss_pred		CCC--CCCHHHHHhCC----CCCccCCCeEEEEEcCCCCcEEEEEEeCCCCEE			
			Q Klein_Draft	300	GIS--EIPLDKWRRLDN----PEPDLAGARALILYRTPEGGPWAIVGSQRCTDGRHV			
			Q Consensus	300	~~~~~f~~~~~p~~~~~g~D~a~~~d~tai~~~~~g~~~v+++.+.+.+.+ + ++.. .+++.+.+.++			
			T Consensus	331	~~~~~i~~~~~p~~~~~GvD~q~~~~~v~~~~~			
			T PF05876.11	331	LSGEPPIEIKTLAARRRKGWKLGTVPAGVKVIVITDVQAN--RFECAAVGYGDGLECWV			
			T ss_pred		cCCCCCCCHHHHHHHhCCccCCCCCcEEEEEEeEc--EEEEEEEeCcEEE			
			Q ss_pred		-----CCHHHHHHHHHHHHHH-----HCCEEeCc-cHH-HHHHHHHHC			
			Q Klein_Draft	359	-----DPVDRVVDKFQAITA-----WGPEEILVGRG-GAA-EVIPQIEAA			
			Q Consensus	359	-----i~~~~~i~~~~~i~~~~~iD~~~g~g~~~~~l~~~+.+. .+++. .+++.+ .. .+.+.++.			
			T Consensus	399	~g~~~~~l~~~~~g~~~~~i~~~~~iD~g~~~~~v~~~~~			
			T PF05876.11	399	DGLTSVQPLRYREHWAALLPLFSRDWPLADARGESDLVTGFWHLC			
			T ss_pred		CCCCCCcccHHHHHHHHHHhCCcccCCCCCcEEEEEECCCCcHHHHHHHHH			
			Q ss_pred		-----CCeEeCCCHHHHHHHhHHHHHHHHhCC-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		EEEecCCCCCceeeecccccccCCCcccCCeEEEc-hHHHHHH--HHHHhCCCCC			
			Q ss_pred		cHHHHHHHHcEEEECCCCeccccCCCcHHHHHHHHHHHH			
			Q Klein_Draft	434	QHSLNAAISRAVKRDLPSGGFWWDCIEQSTYAQLMGVTLGRWA 476 (510)			
			Q Consensus	434	~~~l~~~D~~~dA~~~a~~~ 476 (510)+.+. .+-+. +. +.+. .+ .+ +.+ ...			
			T Consensus	536	~~~qltae~~~g~~~W~~~nh~~~d~~~ya~~~ 572 (578)			
			T PF05876.11	536	RELHFDELTAEEKQD---GK--WKKIR-PRNETLDMVMSYAA 572 (578)			
			T ss_pred		CHHHHHHheeeEeeC---Cc--eeeCC-CChHHHHHHHHHHHH			

<input type="checkbox"/>	11.	Template alignment CDD (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrvcgi?uid=pfam04466)
		PF04466.12 (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% Similarit
		Q ss_pred eeEeeEecCCCCHHHHHHHHHHHHHHh---CCeEEEEeCCHHHHH-HHHHHHHHHHH
		Q Klein_Draft 65 ASSFGLVVSRQNGKGSILEALELAGLILF---GERLIIHSHEFKTAV-NGMERLESLIA
		Q Consensus 65 ~~~~~rg~GKT~~~~~i~~~~~t~~~~a~~~~~ .++.++.++ + +++.+++.+. +. +++++ +.+++.+++.++.
		T Consensus 1 ~~~~~g~GKT~~~~~
		T PF04466.12 1 HLTEVWYGGASSGKSHGVVKVLKSLQHWNVPR-KVLWLKVDRTVKNSIFTDVTCLS
		T ss_pred CcEEEEeccccchHHHHHHHHHHHHhCCccc-eEEEEeccccchHHHHHHHHHHHH
		Q ss_pred ccCCceEEEEeccccCCCCcEEEEEC-CCCCccc-ceeEEEEeccccHHhCCHHHHHHHHHH
		Q Klein_Draft 131 AHGAESIEILDGPNGPGRVIFQTRT-DRSGLGL-TADRVI FDEAMTITPGSLKALLPTVS
		Q Consensus 131 ~~~~~i~~~~~g~~~i~~~~~G~~~v~iDE~~~~~l~~~+.+. + +.+.+. .+++. .+++++ +.+++.+++.++.
		T Consensus 70 ~~~~~g~~~i~~~~~g~~~i~~~~~DE~~~~~l~~~
		T PF04466.12 70 NRSDKTIVLP---NGAIFLFQGMDDPEKIKSIKGSLDVDVMEASEFNHNDYTQLTLRLR
		T ss_pred eCCCCEEECC---CCCEEEEeccccCCCCccccCCCCccccCCCC
		Q ss_pred EEecCCCCCCCCccccHHhCCHHHHHHHHHHhCCccc-EEEEeccccCCCCccccCCCC

Template alignment Template 3D structure PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/3c6a)						
3C6A A (http://pdb.rcsb.org/pdb/explore.do?structureId=3C6A) Terminase large subunit; terminase nI {Enterobacteria phage RB49}						
Probability: 99.21	E-value: 1.3E-12	Score: 120.96	Aligned Cols: 194	Identities: 10%	Similar	
Q ss_pred		hhHHHhCCCCCCCCCCCCCCCCHHHHhCCCC-----CccCCCeEEEEEEcCc				
Q Klein_Draft	284	FGVDRRLGIGDWPQFGAGISEIPLDKWRRLDNPE-----PDLAGARALILYRTP				
Q Consensus	284	f~~~e~~g~~~~~f~~~~~p~~~~~g~D~a ..+++ + .+.+ +.+ +.+++.+. . .+.++ + +. .				
T Consensus	14	~~~~~g~~~f~~~~~i~~~~~p~~~~~g~D~a				
T 3C6A_A	14	LVPRGSHM--LEDPM--GTLIRATTLSRLSFIDVVNDNGFYQFEKPKEGRKYVATLDCSE				
T ss_dssp		-----CBSSCHHHHHCCCCCCCCCTTEESSCCCTTCCEECCCC				
T ss_pred		ccccceEe--eeCCC--CCccCHHHHhCcceeCCceEEEEecCCCCcEEEECCCC				
Q ss_pred		EEEEeCCCIEEEEcCcC-CCCHHHHHHHHHHHHHCCIEEEeCcHH-HHHHHHHH				
Q Klein_Draft	340	GSQRCTDGRIHVEVGYAG-MDPVDRVVDKFQAITAWGPPEILVGRGGAA-EVIPQIEAA				
Q Consensus	340	~~~~~g~~~v~~~~~i~~~~~i~iD~g~g-~~~l~~~++.. .+.+++.+. . .+.+++. .++ .++. .++. .++ .+				
T Consensus	80	v~~~~~v~~~~~i~l~~~~~i~iD~g~g~G~~~~~L~~~				
T 3C6A_A	80	IIDI-TEFPYKQVAVYHSNTTSFILPDIVFKYLMYNECPVYIELNSTGVSIAKSLAMD				
T ss_dssp		EEEC-SSSEEEEEEEESCCCTTTHHHHHHHHHHTSCCEEBCSHHHHHHHHHHHT				
T ss_pred		EEEc-CCCCcEEEEEEecCCCChhHHHHHHHHHHhCCCCEEEecCCCChhHHHHHHHHH				
Q ss_pred		--eCCCHHHHHHHhHHHHHHhCcCCCCceeCCchHHHHHHhCcEEEECCCCeeee				
Q Klein_Draft	402	--YSPNQSEEAQACGGFLNDALVDPENPLLShGNQHSLNAISRAVKRDLPSGGFWVDC				
Q Consensus	402	-----l~~~~~g~i~~~~~l~~~l~~~~~.+.++ .. ++..+....++ ++..++ ++. .+..++ + .++ .+				
T Consensus	149	~~~~~K~~~~~l~~~i~~~g~i~i~~~l~~~el~~~~~				
T 3C6A_A	149	FIDLGMKQSRSKAM--GCSALKDLIEKDQLIIN-HKGTIQELRTFSEK---G-VSWAA				
T ss_dssp		TTBSSBCCHHHHHH--HHHHHHHHHHHTCEECC-CHHHHHHHHHCBSC---C-----				
T ss_pred		ccccccccCCCCcHHH--HHHHHHHHHHCCeEc-ChHHHHHHHHhcc---C-CCccc				
Q ss_pred		HHHHHHHHHHhccccCCCCCc				
Q Klein_Draft	469	GTVLGRWALLKHAINAAPPTPI 490 (510)				
Q Consensus	469	A~~~a~~~~~ 490 (510) +++ ++.....+....+....+				
T Consensus	211	a~a~a~~~~~ 232 (232)				
T 3C6A_A	211	SLVIFGWLTQEKFAEYAGKDE 232 (232)				
T ss_dssp		HHHHHHHHHTSGGGGTSSCCCC				
T ss_pred		HHHHHHHHHHhHHHHHHhCCCC				

Vis Hits Aln 13. | [Template alignment](#) | [Template 3D structure](#) | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/5m1p>)
Select all Forward Forward Query MSA Color Segs Unwrap Segs

[SM1P_A](#) (<http://pdb.rcsb.org/pdb/explore.do?structureId=5M1P>) Large terminase large subunit; large terminase

Hydrolase; 1.1A {Thermus phage G20c}

Probability: 99.13 E-value: 2.1E-11 Score: 109.18 Aligned Cols: 157 Identities: 9% Similarit

Q ss_pred CccCCeEEEEEcCCCCcEEEEEEeCCCCEEEEccccccccHHHHHHHHHHHHHHHHHH

Q Klein_Draft 317 PDLAGARALILYRTPEGGPWAIVGSQRCTDGRIHVEVGYAGMDPVDRVVDKFIQAITAWG

Q Consensus 317 p~~~~~g~D~a~~~d~tai~~~~~g~~v~~~~~i~~~~~| .+...++| +| .++| .+++++.... ..+...+.+++.+++.++.++.++

T Consensus 31 ~~~~~~g~D~A~~~D~tai~~~v~~~~~v~~~~~i~~~~~l~~~~~

T 5M1P_A 31 YRPDHLYCIGADFGKNQDYSVFSVLSDLT--GAIACLERMNGATWSDQVARLKALSEDYG

T ss_dssp CCTTSCEEEEEECCSSSEEEEEEETTT--TEEEEEEEEESCCHHHHHHHHHHHHHHTT

T ss_pred CCCCceEEEEEEeCCCCc eEEEEEcCC--CeEEEEEEccccHHHHHHHHHHHHHHhC

Q ss_pred HH-HHHHHHHHCCeEeCCCH-HHHHHHhHHHHHhcCCCCc eCcHHHHHHHHCC

Q Klein_Draft 387 AA-EVIPQIEAAAGFTVYSPNQ-SEEAQACGGFLNDALVPENPLSHGNQHSLNAAISRA

Q Consensus 387 ~g~~~~~1~~~g~~~~~1~~~~~g~i~~~~~1~~~1~~~. | .+..| ++.+.... +...+... +...+| ++.+...+| ..|| .++

T Consensus 99 ~g~~~~~L~~~~~k~~~~~1~~~~~g~i~~~~~1~~~e1~~~

T 5M1P_A 99 VGDAIAEELDAQGINYTPLPVKSSSVKEQ--LISNLALLMEKGQVAVPNDKTILDELRF

T ss_dssp CCHHHHHHHHHHTCCEECCCSHHHHH--HHHHHHHHHHHTCCEECCHHHHHHHTE

T ss_pred CChHHHHHHHHCCCc eCcHHHHH--HHHHHHHHHHhCCCCCCCCCHHHHHHHhC

Q ss_pred eeeCCCcHHHHHHHHHHHHHH

Q Klein_Draft 455 VWDCIEQSTYAQLMGVTLGRWAL 477 (510)

Q Consensus 455 ~~~~~~D~~~dA~~~a~~~ 477 (510)

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

T Consensus 167 ~~~~~~dD~~~da~~~a~~~ 189 (191)

T 5M1P_A 167 VMRAYGRGHDDIVMSLALAYSOY 189 (191)

T ss_dssp EEEESTTCCCHHHHHHHHHHTC

T ss_pred EEecCCCCChHHHHHHHHHHHHh

[Template alignment](#) | [Template 3D structure](#) | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/5m1n>)

14. [5M1N_B](#) (<http://pdb.rcsb.org/pdb/explore.do?structureId=5M1N>) Large terminase protein; large terminase HET: SO4, BTB; 1.2A {Thermus phage G20c}

Probability: 99.13 E-value: 2.1E-11 Score: 109.18 Aligned Cols: 157 Identities: 9% Similarit

Q ss_pred CccCCeEEEEEcCCCCcEEEEEEeCCCCEEEEccccccccHHHHHHHHHHHHHHHH

Q Klein_Draft 317 PDLAGARALILYRTPEGGPWAIVGSQRCTDGRIHVEVGYAGMDPVDRVVDKFIQAITAWG

Q Consensus 317 p~~~~~g~D~a~~~d~tai~~~~~g~~v~~~~~i~~~~~| .+...++| +| .++| .+++++.... ..+...+.+++.+++.++.++

T Consensus 31 ~~~~~~g~D~A~~~D~tai~~~v~~~~~v~~~~~i~~~~~l~~~~~

T 5M1N_B 31 YRPDHLYCIGADFGKNQDYSVFSVLSDLT--GAIACLERMNGATWSDQVARLKALSEDYG

T ss_dssp CCTTSCEEEEEECCCTSSEEEEEEETTT--TEEEEEEEEESCCHHHHHHHHHHHHTT

T ss_pred CCCCceEEEEEEeCCCCc eEEEEEcCC--CeEEEEEEccccHHHHHHHHHHHHhC

Q ss_pred HH-HHHHHHHHCCeEeCCCH-HHHHHHhHHHHHhcCCCCc eCcHHHHHHHHCC

Q Klein_Draft 387 AA-EVIPQIEAAAGFTVYSPNQ-SEEAQACGGFLNDALVPENPLSHGNQHSLNAAISRA

Q Consensus 387 ~g~~~~~1~~~g~~~~~1~~~~~g~i~~~~~1~~~1~~~. | .+..| ++.+.... +...+... +...+| ++.+...+| ..|| .++

T Consensus 99 ~g~~~~~L~~~~~k~~~~~1~~~~~g~i~~~~~1~~~e1~~~

T 5M1N_B 99 VGDAIAEELDAQGINYTPLPVKSSSVKEQ--LISNLALLMEKGQVAVPNDKTILDELRF

T ss_dssp SSSHHHHHHHHHTCCEECCCSHHHHH--HHHHHHHHHHHTCCEECCHHHHHHHTE

T ss_pred CChHHHHHHHHCCCc eCcHHHHH--HHHHHHHHHHhCCCCCCCCCHHHHHHHhC

Q ss_pred eeeCCCcHHHHHHHHHHHH

Q Klein_Draft 455 VWDCIEQSTYAQLMGVTLGRWAL 477 (510)

Q Consensus 455 ~~~~~~D~~~dA~~~a~~~ 477 (510)

Vis	Hits	Aln	Select all	Forward	+++.+.+ +.+ +++ +..+	Forward Query MSA	Color Segs	Unwrap Seqs
			P consensus	167		189 (191)		
			T 5M1N_B	167	VMRAYGRGHDDIVMSLALAYSQY	189 (191)		
			T ss_dssp		EEEEESTTCCCHHHHHHHHHHTTC			
			T ss_pred		EEecCCCCChHHHHHHHHHHHH			
<hr/>								
			Template alignment CDD (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrvc.cgi?uid=pfam03237)					
		15.	PF03237.14 (http://pfam.xfam.org/family/PF03237.14#tabview=tab0) ; Terminase_6 ; Terminase-like far					
			Probability: 98.89	E-value: 5.7E-12	Score: 116.38	Aligned Cols: 200	Identities: 9%	Similarit
			Q ss_pred		eEEecCCCCHHHHHHHHHHHHHHhCeeEEEeCCHHHHH-HHHH--HHHHHHHcccc			
			Q Klein_Draft	69	GLVVSQRNGKGSILEALELAGLILFGERLIIHSAHEFKTAV-NGME--RLESIAKSGL			
			Q Consensus	69	~~~~~rg~GKT~~~~~i~i~~t~~a~~~~~1 ++.+ + +++.+++.+++.+++++++.++++ .++. .+.+++.++			
			T Consensus	1	~~~~~r~GKT~~~~~			
			T PF03237.14	1	IIEIPPPQHGKSTVITETFPAYYLMRHPDSLVMVVSYSKELFQKFGRKNRKFRFLFSQDF			
			T ss_pred		CcccCCCCCHHHHHHHHHHHHHhhCcccEEEEeCCHHHHHHHHHHHHHhchHHH			
			Q ss_pred		ceEEEecCCCCCcE-EEEECC---CCCCccceEEEEEeHHhcCHHHHHHHHHhcc			
			Q Klein_Draft	135	ESIEILDGPNGAR-VIFQTRT---DRSGLGLTADRVIFDEAMTITPGSLKALLPTVSS			
			Q Consensus	135	~i~~~~~g~~~i~~~~~G~~~~~v~iDE~~~~~1~ ..+.+. + +. .+.+ ..++ .++++++ +..+.+.+.++..			
			T Consensus	67	~~~~~g~~~i~~~~~G~~~~~i~DE~~~~~			
			T PF03237.14	67	ETSSVS---EWGVEGHLGSLYSTSILGGATGRGARLLKEQTLPEEIKIPAIAEDDD-----			
			T ss_pred		ccccccc---cccccccccEEEEEeCCCCcccCCCCCEECCCCCCChHHhcCHHHHHHH			
			Q ss_pred		cCCCCCCcccHHchHHHHHHHHHHHHhCC-----CCCEEEEEEeC---CCCCCccc			
			Q Klein_Draft	200	TAADQRTQPYCHTFGGVRYRALEQLRTGE-----RKRLCFLEWSA---PDDLPEEK			
			Q Consensus	200	tp~~~~~ ...+ + ++ +.....++...+... . .+ .+ +. . .			
			T Consensus	132	tp~~~~~			
			T PF03237.14	132	RLTADA---S---VI---VIMTRWHEDDLAGRLLKEQTLPEEIKIPAIAEDDD-----			
			T ss_pred		CCCC---e---EE---EEccccCcCHHHHHhcccCCCCcEEEEecccCcc---			
			Q ss_pred		CcccccccCHHHHHHHHHHHHHhCHHhhHHHHCCCCCCC-----CCCCCCCCCHH			
			Q Klein_Draft	258	NPGLGYRQTEEKILDEYEEMWANLRDFGVDRLGIGDWQP-----FGAGISEIPLD			
			Q Consensus	258	nP~~~~~e1~~~~~f~~e~~g~~~~~f~~~ .+. ++++++++.+ ++.. +++++ + .. .+ .+ +. .			
			T Consensus	179	~~~~~g~~~g~~~~~g~~~~~g~~~~~g~~~~~g~~~~~g~~~~~g~~~~~g~~~~~g~~~~~f~~~			
			T PF03237.14	179	GRKP---GEALAPEIGKDE--EWAAKTKAVTGS--RGWAALYQQRPTPAG--GNIFKRS			
			T ss_pred		CCCC---CCCCCcccCCHH--HHHHHHHHHHhCh--HHHHHHCCCCCCCC--CCCCCHH			
			Template alignment Template 3D structure PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/5hd9)					
		16.	5HD9_A (http://pdb.rcsb.org/pdb/explore.do?structureId=5HD9) Encapsidation protein; ASCE fold, VIR {Bacillus phage phi29}					
			Probability: 98.86	E-value: 1.8E-10	Score: 102.84	Aligned Cols: 143	Identities: 11%	Similar
			Q ss_pred		heeEeeEEecCCCCHHHHHHHHHHHHHHhCeeEEEeCCHHHHHHHHHHHHHccc			
			Q Klein_Draft	64	AASSFGLVVSRQNGKGSILEALELAGLILFGERLIIHSAHEFKTAVNGMERLESIAKSG			
			Q Consensus	64	~~~~~rg~GKT~~~~~i~i~~t~~a~~~~~1 ..+.++. + + .+++.+++.+++. +.+++++++.+++.+.++.++.			
			T Consensus	13	~~~~~ggrgsGKT~~~~~l~~~~~i~r~t~~~l~~~~~l~~~~~			
			T 5HD9_A	13	DRILNFVIGARGIGKSAMYKVPINRFIKY-GEQFIYVRRYKPELAKV-SNYFNDVAQEF			
			T ss_dssp		CCSEEEECSCCSSHHHHHHHHHHHHHHHH-CCEEEEEESEGGGGTTG-GGGGGGTGGGC			
			T ss_pred		CCEEEEEECCCCChhHHhhHHHHHHHHh-CCeEEEEeCCHHHHHHHHHHHHHhC			

Vis	Hits	Aln	Q ss_pred Select all	CceEEEEecCCCCCcEEEEEECC-CCCcccc--e-eEEEecHHhcC---H---HH
			Q Klein_Draft 134 AESIIEEDGPNPAGARVITQTRT-DRSGLGT-A-DRVTLDEAMTFIT-P---GSL	Forward Query MSA
			Q Consensus 134 ~~~i~~~~~g~~i~~~~~G~~~`~~~~~iDE~~~~~	Color Seqs
				...+.+. + +. .+..+ ..++ .+ . +++++ +..++ . +.+
			T Consensus 79 ~~~i~~~~~g~~I~f~~~~~lrG~~~~~iDEa~~~~~	Unwrap Seqs
			T 5HD9_A 79 GRRFYID---GKLAGWAIPLSVWQSEKSNAYPNVSTIVFDEFIREKDNSNYIPNEVSAL	
			T ss_dssp TTEEEET---TEEEEEEEGGGHHHHTSCSSEEEEEETSCCSSCCCCCTTHHHHH	
			T ss_pred CcEEEEC---CeEEEEEEeCCChHHhcccCCcccEEEEecceccccCCCCChhHHHHHH	
			Q ss_pred CCCCEEEE-----EecCCCCCCCchhhchHHHHHHHHHH	
			Q Klein_Draft 190 RPNPQIVY-----TGTAAQRTQPYCHTFGGVRYRALEQ 223 (510)	
			Q Consensus 190 ~~~~i~~~~~stp~~~~~ 223 (510)	
				.+.+++. ++ .+... ++ .+.+
			T Consensus 145 ~~~~i~~~g~~~~~NP~~~~~ 175 (194)	
			T 5HD9_A 145 RERVRCICLNSAVSVNPYFLFF--N---LV---PDVNK 175 (194)	
			T ss_dssp STTCEEEECSCCSSSHHHHH--T---CC---CCTTC	
			T ss_pred CCCcEEEecCCcccCchHHh--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://pdb.rcsb.org/pdb/explore.do?structureId=5C10) (<http://pdb.rcsb.org/pdb/explore.do?structureId=5C10>) Gene 2 protein; nuclease domain, meta-Enterobacteria phage Sf6

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

Q ss_pred		HhCCCCCCCCCCCCCCCCCHHHHhcCCC---CCcCCCeEEEEEcCCCCcEEEEEEE
Q Klein_Draft	288	RLGIGDWPQFGAGISEIPLDKWRRLDNP---EPDLAGARALILYRTPEGGPWAIVGSQR
Q Consensus	288	~~g~~~~~f~~~~~p~~~~~g~D~a~~d~tai~~~ .+ +.+ +.+++. + +....++ + +.+++.+++++.+++++. .
T Consensus	12	~~~~~f~~~f~~~i~~a~~~~~GvDvA~~G~D~svi~v~~
T 5C10_A	12	SGLV--PRGSH--MAIKREWLEATDAHKKLGWKAKGAVVSAHDPSDTGPDAKGYASRH
T ss_dssp		- - - - - -CBSSCHHHHHHHBTHHHHHTCCCSCEEEEECCSSSCEEEEEEE
T ss_pred		CCcC---CCCCC---cceeeHHHHHHHHHHhhccccCCCEEEEEecCCCCCCCCCEE

Q ss_pred		cccCCCCHHHHHHHHHHHHHHHHCCCEEeCccHH-HHHHHHHHC---CCeEeCCCHH
Q Klein_Draft	354	GYAGMDPVDRVVKFIQAITAWGPEEILVGRGGAA-EVIPQIEAA---GFTVYSPNQSE
Q Consensus	354	~~~~~i~~~~~i~~~~~i~D~~g~g~~~~l~~~~~g~~~~~ .+. ..++..+++.++..++.. ++..+..+ .+ . .+. ++. ++..+..+.
T Consensus	76	~~~~~a~~i~~l~~~~~i~D~~GvG~g~v~d~L~~~~~
T 5C10_A	76	EGL-LMDINEGADWATSLAIEDGADHYLWDGDGVAGLRRQTTEAFSGKKITATMFKGSE
T ss_dssp		EEC-SCCHHHHHHHHHHHHHHHHTCSEEEECCSGGGGCHHHHHHTTSCEEEEETTS
T ss_pred		Eec-CCCHHHHHHHHHHHHHHHHHCCCEECCCCChHHHHHHHHHcCCCeEEEEEccCC

Vis	Hits	Aln	Select all	Forward	Forward Query MSA	Color Seqs	Unwrap Seqs
					Template alignment Template 3D structure PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/5c12)		
	18.				5C12_A (http://pdb.rcsb.org/pdb/explore.do?structureId=5C12) Gene 2 protein; nuclease domain, metallocproteinase {Enterobacteria phage Sf6}		
					Probability: 98.81 E-value: 5.2E-10 Score: 105.55 Aligned Cols: 186 Identities: 11% Similarity:		
					Q ss_pred HhCCCCCCCCCCCCCCCCCCCCHHHHhCCCC---CCcCCeEEEEEEcCCCCcEEEEEE Q Klein_Draft 288 RLGIGDWPQFGAGISEIPLDKWRLDNP---PDLAGARALILYRTPEGGPWAIVGSQR Q Consensus 288 ~g~~~~~f~~~~~p~~~~~g~D~a~~~d~tai~~~ .+ .+...+ .+.+ .+++. +.+.++ + + .++++.++++.. T Consensus 11 ~~~~~~i~a~~~~~iGvDvA~~G~D~svi~v~~ T 5C12_A 11 SSGL--VPRGS-HMAIIKREWLEATDAHKLGWKAKGAVVSAHDPSDTGPDAKGYASRH T ss_dssp -----CBSSCHHHHHHHBTHHHHHTCCCSCEEEECCSSSSCEEEE T ss_pred ccCc--cCCCC-CcceeHHHHHHHHHHHHhCCCCCEEecCCCCCeeEEEe Q ss_pred ccccCCCCHHHHHHHHHHHHHHCCCEEeCcHH-HHHHHHHHC---CCeEeCCCHHH Q Klein_Draft 354 GYAGMDPVDRVVDFKIQAITAWGPEEILVGRGGAA-EVIPQIEAA---GFTVYSPNQSE Q Consensus 354 ~~~~~~i~~~~~i~~~~~i~~~~~g~~~~~l~~~~~g~~~~~.+. .+++.+++.+.+++. .+ .+++. ++. ++.+.+.+. T Consensus 76 ~~~~~~a~~~l~~~~~i~~~~~i~~~~~GvG~gv~d~L~~~~~ T 5C12_A 76 EGL-LMDINEGADWATS LAIEDGADHYLWDGDGVGAGLRRQTTEAFSGKKITATMFKGSE T ss_dssp EEC-SCCHHHHHHHHHHHHHHTCSEEEECSSTTTCHHHHHHTTSCEEEECTTS T ss_pred ecc-CCCHHHHHHHHHHHHHHHhCCCEECCCCChhHHHHHHHHhCCCCcEEEecCCC Q ss_pred -----HHHHhHHHHHHhCCCCc----- Q Klein_Draft 409 -----EAQACGGFLNDALVDOPENPL----- Q Consensus 409 -----l~~~~~g~~~~~.+.+.+...+++. T Consensus 145 ~~~~~~f~n~Kae~~~l~~~l~~~~~p~~~~~ T 5C12_A 145 AGAWADEVVQGDNVRTIDVFRNKRAQ--FYYALADRILTYRAVHVGEYADPDDMLSFD T ss_dssp C-----CCBHHHHBSSHHHH--HHHHHHHHHHHHHHCCCCGGGCCEC T ss_pred cCCCCCCCCcccchHhHHHHHHH--HHHHHHHHHHhccceecCCCCChhhcccc Q ss_pred HHHHHHHccEEECCCCCeeeeC-----CCcHHHHHHHHHHHHHHHcc Q Klein_Draft 436 SLNAAlSRAVKRDLPSGGFVWDCI-----EQSTYAQLMGVTLGRWALLKHA 481 (Q Consensus 436 ~1~~~l~~~~~D~~~dA~~~a~~~~~. .+ .+++.+++.+++. .+ .+ .+++.++. T Consensus 213 ~1~~~EL~~~~~g~~~i~~~k~~~g~~~spD~~~dA1~1a~~~~~ 265 (T 5C12_A 213 KLFAELTQIQRKFNNNGKLELMTALEMKQKLGIPSPNLADALMMCMHCPALVR 265 (T ss_dssp HHHHHHTTCBBCCTTSBCBCCHHHHHHHCCCCCHHHHHHTTCCCC-- T ss_pred HHHHHHhcCeEEECCCCCEEeeHHHHHHHHCCCCChHHHHHHHHhCcchhc Template alignment Template 3D structure PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2wbn) 19. 2WBN_A (http://pdb.rcsb.org/pdb/explore.do?structureId=2WBN) TERMINASE LARGE SUBUNIT; LARGE PROTEIN; 1.9A {BACILLUS PHAGE SPP1} Probability: 98.68 E-value: 2.8E-9 Score: 97.24 Aligned Cols: 193 Identities: 8% Similarity: Q ss_pred hhHHhCCCCCCCCCCCCCCCCHHHHhCCCC--CccCCeEEEEEEcCCCCcEEEEEE Q Klein_Draft 283 DFGVDRLGIGDWPQFGAGISEIPLDKWRLDNPE---PDLAGARALILYRTPEGGPWAIVG Q Consensus 283 ~f~~e~~g~~~~~f~~~~~p~~~~~g~D~a~~~d~tai~~~. +++++. ...+ +.+ +....+.... .+.+.++ + + .+.+.++++ T Consensus 13 ~~~~~~G~~~~~G~v~f~~~f~~~~~v~~~~~g~D~G~~~~~p~a~~~ T 2WBN_A 13 GLVPRGSHM--ALGSG--VVPFENLQIEEGIITDAEVARFDNIRQGLDFGYGPDPЛАFVR T ss_dssp -----CCSCTEEECTCSCHHHHHCCCEECCCBTTBCEEEE T ss_pred Ccccccccc--cccc--ceecCCeEecCCCCHHhcccCCeEEEeCCCCCCCCcEEEE		

Vis	Hits	Aln	Q ss_pred	EEEEcccC-CCCHHHHHHHHHHHHHHHCCCCEEEeCcHHHHHHHHHHH-CCe-EeCCCH
		Select all	Q Klein_Draft	350 HVEVGYAG-MDPVDRVVDKTIQAITANGPEELGRGGAAVLVIPQIEA-TAGFT-VYSPNQ
		Forward	Q Consensus	350 ~v~~~~~i~~~~~i~~~~~i~D~g~g~~~~l~~~g~~~~~
		Forward	T Consensus	79 ~~~~e~~~~~i~~~~~D~~~~~l~~~g~~~~~
		Query MSA	T 2WBN_A	79 YAIDELVDHKVSLKRTADFVRKNK--YESARIADSSEP-RSIDALKLEHGINRIEGAKK
		Color Segs	T ss_dssp	EEEEEEESSCCHHHHHHHHHTT--CTTSCEEECTTCH-HHHHCCCCCTCCTTEEECCS
		Unwrap Segs	T ss_pred	EEEEecccCCCCHHHHHHHHhCC--CcCcEEEcCCCH-HHHHHHHHHhCccccccCCC
			Q ss_pred	HHHhhcCCCCceeeC-CcHHHHHHHccEEEECCCCCeeeeCCCcHHHHHHHHHHH
			Q Klein_Draft	417 LNDALVPENPLLSHG-NQHSLNAAISRAVKRDLPSGGFVWDCIEQSTYAQLMGVTLGRW
			Q Consensus	417 ~~l~~~~g~i~~~~~l~~~l~~~~~D~~dA~~a~~
			T Consensus	144 i~~~~~l~i~~~c~~~i~e~~~y~~~~~p~~~dH~~Da~rY~~~
			T 2WBN_A	144 ERWLDE--LDAVIDPLRTPNIAREFENIDYQTDKNGDP-IPRLEDKDNTIDATRYAFE
			T ss_dssp	HHHHHT--SSEEECTTCHHHHHHHHCCCEEETTCCE-EEECSSCHHHHHHHHHTG
			T ss_pred	HHHHHh--CCeEEECCCCCHHHHHHHhcccCcCCCCC-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

[Template alignment | CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrvcgi?uid=pfam02500\)](#)

20. [PF02500.14 \(http://pfam.xfam.org/family/PF02500.14#tabview=tab0\)](#); DNA_pack_N ; Probable DNA packer

Probability: 98.53 E-value: 1.5E-8 Score: 94.3 Aligned Cols: 116 Identities: 16% Similarity:

Q ss_pred	CCCCCHHHHHHHHccChhHhhccCc---ch-----
Q Klein_Draft	30 GLILDWPQECLCLHEALKESDELVQLESGA---WV-----
Q Consensus	30 ~~l~~~Q~~~~~g~~~~~
T Consensus	122 ~~LepfQk~il~~~~~f~~~~~f~~~~~
T PF02500.14	122 VHWLEPFQQQLVMHTF-----FFLVSIKAPQTKHQLFGLFKQYFGLFETPNSV
T ss_pred	CccCHHHHHHHHHH-----HHHhhccCchhhHHHHHHHHCCCCCCCC
Q ss_pred	EEecCCCCHHHHHHHHHHHHHHCCeeEEEEeCCCHHHHHHHHHHHHHccccch--h
Q Klein_Draft	70 LVVSRQNGKGSILEALELAGLILFGERLIIHSAHEFKTAVNGMERLESIAKGLKY--K
Q Consensus	70 ~~~rg~GKT~~~~~i~i~~t~~a~~~~~l~~~
T Consensus	180 i~v~RqnGKT~l~aa~l~~~g~~~v~A~t~~QA~~v~f~~i~~~p~~~
T PF02500.14	180 FLIPRRHGKTWIVVAIISMLLASVENINIGYVAHQKHVANSVFAEIKTLCRWFPPKNLN
T ss_pred	EEeCCCCChHHHHHHHHHHhCCceEEEEeCCCHHHHHHHHHHHHHCCCC
Q ss_pred	EEecCCCC--cEEEEEC-CCCCcc
Q Klein_Draft	138 EILDGPNG--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---GGRSSSLMCATCFNKNIRG 272 (272)
T ss_pred	EeC---CCeEEEEeCCCCccCC

[Template alignment | CDD \(http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrvcgi?uid=pfam17289\)](#)

Vis Hits Aln 21. PF17289.1 (<http://pfam.xfam.org/family/PF17289.1#tabview=tab0>) ; Terminase_6C ; Terminase RNaseH
Select all Forward Forward Query MSA Color Segs Unwrap Segs Aligned Cols: 141 Identities: 6% Similarity: -
Probability: 98.4 E-value: 1.8E-8 Score: 87.19

Q ss_pred	EEEEEcCCCCcEEEEEEEeCCCEEEEcccC-CCCHHHHHHHHHHHHHHHCCEEEE
Q Klein_Draft	325 LILYRTPEGGPWAIVGSRCTGRIHVEVGYAG-MDPVDRVVDKFIQAITAWGPPEEILVG
Q Consensus	325 ~g~D~a~~~d~tai~~~~~g~~~v~~~~~i~~~~~i~d + + ++ +.+++.++++.+++.++..+++.++..++..++
T Consensus	1 ~g~D~g~~~d~~~~~i~~~~~i~d
T PF17289.1	1 IGIDLGFDPNAIACVAWDPEKDYYLYDERSESGETLGMHADAIYLKGHHQIPVVPHD
T ss_pred	CceeCCCCCcEEEEEeCCCCEEeeEcCCCCHHHHHHhccccCCeEEecC
Q ss_pred	-HHHHHHHHCC-CeEeCCCHH-----HHHHhhHHHHhccC---CCCceeeC-Cch
Q Klein_Draft	389 -EVIPQIEAAG-FTVYSPNQSE-----EAQACGGFLNDALVDP---ENPLLSHG-NQH
Q Consensus	389 -~~~~~l~~~g~~~~~g~~~~~l~~~~~g~i~~~~~ .++. +++.+++.++.... .+.. ++...++ +++++.++ . +
T Consensus	71 ~~~~~l~~~~~k~~~~~i~~~~~
T PF17289.1	71 RRFVDLLKDDHNLNVYEPFSNPPGPDGKHGGNS--VEFGVNWMLTRMENGDLKFNTCT
T ss_pred	hHHHHHHHHcCcEEEcCCCCCCCCCCCCCc--hhHHHHHHHHhccCcEEcccc
Q ss_pred	EEECCCCCeEEecCCCcHHHHHHHHHHHH
Q Klein_Draft	446 KRDLPSSGFVWDCIEQSTYAQLMGVTLGRW 475 (510)
Q Consensus	446 ~~~~~~D~~~dA~~~a~~~ 475 (510) +... .+... .+ +++++
T Consensus	139 ~~~~~~dD~~~Da~~~~~ 160 (161)
T PF17289.1	139 RKDG-----KIIDRNDDMISATRYALL 160 (161)
T ss_pred	eeCC-----CCCCCcHHHHHHHH

Template alignment | Template 3D structure | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/1rif>)
22. 1RIF_A (<http://pdb.rcsb.org/pdb/explore.do?structureId=1RIF>) DNA helicase uvsW; Bacteriophage, T4, {Enterobacteria phage T4} SCOP: c.37.1.23

Probability: 98.33 E-value: 5.1E-8 Score: 93.34 Aligned Cols: 148 Identities: 13% Similarity

Q ss_pred	CCCCCHHHHHHHHHhccChhHhhccCcchhhheeEeeEEecCCCCHHHHHHHHHHHH
Q Klein_Draft	30 GLILD PWQELCLHEALKESDELVQLES GAWVKKWAASSFGLVVS RQNGKGSILEALELAG
Q Consensus	30 ~~~l~~~Q~~~~~g~~~~~rg~GKT~~~~~ .++ +++.+++.++...++..++ + .++. .++..
T Consensus	111 ~~~l~~~Q~~av~~~~~i~~~GsGKT~~~~~
T 1RIF_A	111 RIEPHWYQKDAVFEGLV-----NRRRI LNLPTSAGRSLIQA-LLARY
T ss_dssp	ECCCCHHHHHHHHHHHH-----HSEEECCCTSCHHHHH-HHHHH
T ss_pred	CCCCCHHHHHHHHHHHh-----CCCeEEecCCCCCHHHHH-HHHHH

Q ss_pred	EECCCCHHHHHHHHHHHHHHcccchhceecCCeEEecCCCCcEEEEEC---
Q Klein_Draft	100 HSAHEFKTAVNGMERLES LIAKSGLK YKAK QAHGAESIEILDGPNGARVIFQTRT---
Q Consensus	100 i~~~t~~~a~~~~~l~~~~~i~~~~~g~~~i~~~~~ ++ +...+.++...+.....+...+. .+.. .+..
T Consensus	162 iv~p~~~l~~q~~~~~i~~~i~t~~~l~~
T 1RIF_A	162 IIIVPTTALTTQMADD FVDYRLFSHAMI K KIGGGASKDDKYK---NDAPVVGTWQTVVK
T ss_dssp	EECSSHHHHHHHHHHHHHTSCCGGGEEC STCS TTCCC---TTCSEEECHHHHTT
T ss_pred	EEeCCHHHHHHHHHHHHHcccCcEEEEEecCCCCchhh---cCCCEEEeCHHHHHc

Q ss_pred	EEEEEcHHhcCHHHHHHHHHhhcCCCCEEEecC
Q Klein_Draft	166 RVIFDEAMTITPGSLK ALLPTVSSRPNPQIVYTGT A 201 (510)
Q Consensus	166 ~v~iDE~~~~~l~~~~~i~~~stp 201 (510) ++ + ++..+.++..+...+. .++..++
T Consensus	228 ~vIVDEah~~~~~l~~~~~lt~Tp 262 (282)
T 1RIF_A	228 MMMNDECHLATGKSISSIISGLNNC-MFKFGLGSGL 262 (282)
T ss_dssp	EEEEETGGGCCHHHHHHHHTTCTC-CEEEEECSSC
T ss_pred	EEEEeChhhCCcccHHHHHHhccC-cEEEEEcCc

Vis	Hits	Aln	T ss_pred Select all	Forward	Forward Query MSA	<u>Color Seqs</u>	<u>Unwrap Seqs</u>
			Q ss_pred	HHHHHHHHHcCCCCChHHHHhHHHHHhC-----CCCEECCCCCH			
			Q Klein_Draft	89 GLILFG-----ERLIIHS AHEFKTAVNGMERLES LIAKS -GLKYKAKQAHGAESIEIL			
			Q Consensus	89 ~~~~~i~i~~t~~~a~~~~~l~~~~~i~~~.+.+.+...+....			
			T Consensus	81 ~~~~~liip~~~~~			
			T 3IUY_B	81 HLDSQPISREQRNGPGMLVLTPRELALHVEAECSKYSYKGLKSICIYGRNRNGQIEDI			
			T ss_dssp	HHTC-----CCCSEEECSSHHHHHHHHHHHHHCCTCCEECC-----			
			T ss_pred	HHhcCCc hhcc CCCcEEEEeCCHHHHHHHHHHHhhccCCeEEEEcCCchHHHHHH			
			Q ss_pred	EEECC-----CCCCcccc eeEEEecHHhcCH---HHHHHHHhhccCCCCCEE EEE			
			Q Klein_Draft	151 FQTRT-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRPNPQIVYTG			
			Q Consensus	151 ~~~~~G~~~~~v~iDE~~~~~l~~~~~i~~~.+.+.+...+.+++. ++			
			T Consensus	148 v~t~~~~~iiDE~~~~~i~~~.+.+.+...+.+++. ++			
			T 3IUY_B	148 IATPGRLNDLQMNNNSVNLSITYLVIDEADKMLDMEFEPQIRKILLDVRP--DRQTVMTS			
			T ss_dssp	EECHHHHHHHHHHTCSCCTTCCEECCHHHHHTTCHHHHHHHHSCS--SCEEEE			
			T ss_pred	EECHHHHHHHHHhCCcccccc EEEEeCHHHHhcccHHHHHHHhCC--cCeEEEE			

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

31. [3IUY_A](#) (<http://pdb.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	HHHHHHHHHcCC-CCCHHHHHHHHHhccChhHhhccCCchhhheeEeeEecCCCC
Q Klein_Draft	20 QEAIDLAAACGL-ILDPWQELCLHEALKESDELVQLESGAWVKWAASSFGLVVS RQNGK
Q Consensus	20 ~~~~~~l~~~~~Q~~~~~g~~~~~rg~GK .++.+.+++. +++.+... .+++.+++. ++
T Consensus	29 ~~~~~~Q~~~~~li~~~g~GK
T 3IUY_A	29 PDLLKSIIRVGILKPTPIQSQA万里Q-----GIDLIVVAQTGTGK
T ss_dssp	HHHHHHHHHHHTCCSCCHHHHHHHHH-----TCCEECCCTTSCH
T ss_pred	HHHHHHHHHcCCCCChHHHHhHHHHhC-----CCeEEEECCCC

Q ss_pred	HHHHhC-----CeeEEEecCCHHHHHHHHHHHHHHcc-cchhceccCCeEEE
Q Klein_Draft	89 GLILFG-----ERLIIHS AHEFKTAVNGMERLES LIAKS -GLKYKAKQAHGAESIEIL
Q Consensus	89 ~~~~~i~i~~t~~~a~~~~~l~~~~~i~~~.+.+.+...+....
T Consensus	81 ~~~~~liip~~~~~
T 3IUY_A	81 HLDSQPISREQRNGPGMLVLTPRELALHVEAECSKYSYKGLKSICIYGRNRNGQIEDI
T ss_dssp	HHC-----CCCSEEECSSHHHHHHHHHHHHHCCTCCEECC-----CHHHH
T ss_pred	HHhcCCc hhcc CCCcEEEEeCCHHHHHHHHHHHhhccCCeEEEEcCCchHHHHHH

Q ss_pred	EEECC-----CCCCcccc eeEEEecHHhcCH---HHHHHHHhhccCCCCCEE EEE
Q Klein_Draft	151 FQTRT-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRPNPQIVYTG
Q Consensus	151 ~~~~~G~~~~~v~iDE~~~~~l~~~~~i~~~.+.+.+...+.+++. ++
T Consensus	148 v~t~~~~~iiDE~~~~~i~~~.+.+.+...+.+++. ++
T 3IUY_A	148 IATPGRLNDLQMNNNSVNLSITYLVIDEADKMLDMEFEPQIRKILLDVRP--DRQTVMTS
T ss_dssp	EECHHHHHHHHHHTCCCTTCCEECCHHHHHTTCHHHHHHHHSCS--SCEEEE
T ss_pred	EECHHHHHHHHHhCCcccccc EEEEeCHHHHhcccHHHHHHHhCC--cCeEEEE

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

32. [3LY5_B](#) (<http://pdb.rcsb.org/pdb/explore.do?structureId=3LY5>) ATP-dependent RNA helicase DDX18 {E. Structural Genomics, Structural Genomics; 2.8A {Homo sapiens}}

Probability: 97.79 E-value: 7.3E-6 Score: 77.48 Aligned Cols: 163 Identities: 12% Similarity:

Vis	Hits	Aln	Select all	Forward	Forward Query MSA	Color Segs	Unwrap Segs
			Q_ss_pred	hHHHHHHHHHHHHCCCCC	QConsensus	hHHHHHHHHHHHHCCCCC	EeeEeEcCCCC
			Q Klein_Draft	18	AGQEAIIDLAAACGL-ILD PWQELCLHEALKESDELVQLES GAWVKKWAASSFGLVVSRQN		
			Q Consensus	18	~~~~~+~~~~~1~~~~Q~~~~~g~~~~~rg~	+.....+...+++. +++/+.+.+..	...+++.+++ +
			T Consensus	61	~~~~~1~~~~~Q~~~~~	- - - - -	~~~~~1~~~~~Gs
			T 3LY5_B	61	VNENTLKAIAKEMGFTNMTEIQHKSIRPLE-----	- - - - -	GRDLAAAKTGS
			T ss_dssp		CCHHHHHHHHTTCBCCHHHHHHHHHHHHH	- - - - -	TCCCEEECCCTTS
			T ss_pred		cCHHHHHHHHHhCCCCCCCHHHHHHHHHHC	- - - - -	CCcEEEEcccccc
			Q ss_pred		HHHHHH----hCCeeEEEecCCHHHHHHHHHHHHHcc--cchhcceccCcceeEE		
			Q Klein_Draft	87	LAGLIL----FGERLIIHSAHEFKTAVNGMERLESLIAKS--GLKYKAKQAHGAESIEI		
			Q Consensus	87	~~~~~+~~~~~i~i~~t~~~a~~~~~	...+.. .+....++++ +...+.+....+....	~~~~~i~~
			T Consensus	113	~~~~~1iv~p~~~l~~~~~		
			T 3LY5_B	113	VELIVKLRFMPRNGTGVLILSPTRELAMQTFGVLKELMTHHVHTYGLIMGGSNRSAEAQK		
			T ss_dssp		HHHHHHHTCTTCCCEECSHHHHHHHHHHHHTTCCCCEECSSSCHHHHHHH		
			T ss_pred		HHHHHHhcccCCCCceEEEEecCCHHHHHHHHHHHhccCCeEEEEecCCCHHHHHHH		
			Q ss_pred		EEEECC----CCCCcccccEEEEEecHHhcCH---HHHHHHHhhcCCCCCEE		
			Q Klein_Draft	150	IFQTRT----DRSGLGLTADRVIFDEAMITP---GSLKALLPTVSSRPNPQIVY		
			Q Consensus	150	~~~~~+~~~~~G~~~~~v~iDE~~~~~	.+.+.+...++ + +++.+. .+..+.+... .++.	~~~~~i~~
			T Consensus	180	iv~t~~~l~~~~~vIiDE~h~~~~~		~~~~~i~~~v~l
			T 3LY5_B	180	IVATPGRLLDHMQNTPGFMYKNLQCLVIDEADRILDVGFEEELKQI KLLPTR-RQTMLF		
			T ss_dssp		EEECHHHHHHHHHCTTCCCTCCEECSHHHHHHTTCHHHHHHHHSCSS-SEEEEEE		
			T ss_pred		EEEecHHHHHHHHhhCCCcHhhccEEEEecHHHHhccCCHHHHHHHHHCCCC-CEEEEEE		

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

33. [3LY5 A](http://pdb.rcsb.org/pdb/explore.do?structureId=3LY5) (<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 hHHHHHHHHHHhCC-CCCHHHHHHHHHhccChhHhhccCCCChhhhheeEeeEEecCCC

O Klein Draft 18 AGOEAATDI AACGIL - TLDPWQELCI HEALKESDELVOL ESGAWVKKWAASSEGLIVVSRON

Q_RIGID_BIOMECH_100_Q_ELASTICITY_RIGIDITY_Q_ISOTROPY_ANISOTROPY_SEPARATION

Q consensus 18

T Consensus 61 ~~~~~1~~~~~1~~Q~~~~1~~~~-~~~~1~~~~G~

T 3LY5_A 61 VNENTLKA~~I~~KEMGFTNMTEI~~Q~~HKSIRPLLE-----GRDL~~L~~A~~A~~AKTGS

T ss pred cCHHHHHHHHHcCCCCCCCCHHHHHHHHHHC-----CCcEEEEEcCCCC

Q ss_pred HHHHHH----hCeeEEEcCCHHHHHHHHHHHHHHHHHc--cchhcceccCCceEEE

Q Klein Draft 87 LAGLIL-----FGERLIIHSAHEFKTAVNGMERLESIAKS--GLKYKAKOQAHGAESIEI

Q Consensus 87 ~~~~~----i~i~~~t~~~a~~~~~-----]~~~~~i~~

Q. CONCERNING THE PRACTICE OF THE CHURCHES IN THE STATE OF ILLINOIS.

..... 112 113 114 115 116 117 118 119 120

Consensus 113 ~~~~~~VIV~p~~~1~~~~~

T ss_dssp HHHHHHTCCGGGCCCEEECSSLHHHHHHHHHHHHHHHTTCCSCEEEECSSSCHHHHHHH

T ss pred HHHHHHhccCCCCCcEEEeCCHHHHHHHHHHHHHhbCCCeEEEEEcCCCHHHHHHH

Q ss_pred EEEECC-----CCCCccccceeEEEEecHHhcCH---HHHHHHHHhhcCCCCCEEEE

Q Klein_Draft 150 IFQTRT-----DRSGLGLTADRVIFDEAMTTIP---GSLKALLPTVSSRPNPQIVY

Q Consensus 150 ~~~~~----G~~~~~v~iDE~~~~~----l~~~~~i~~

$$\ldots + \ldots + \ldots \quad \ldots \ldots \ldots + + + + | + + + + \ldots \ldots + + + +$$

Vis	Hits	Aln	T ss_pred <u>Select all</u>	Forward	EEEcHHHHHHHHhCCCCcHhCCEE Template alignment Template 3D structure PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/1q0u)	Forward Query MSA	<u>Color Seqs</u>	<u>Unwrap Seqs</u>
		34.			1Q0U_B (http://pdb.rcsb.org/pdb/explore.do?structureId=1Q0U) BstDEAD; DEAD PROTEIN, RNA BINDII steathermophilus} 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		hHHHHHHHHHHhCCC-CCHHHHHHHHHhccChhHhcCcchhhheeEeeEEecCCC			
			Q Klein_Draft	18	AGQEAIIDLAAACGL-IIDPWQELCLHEALKESDELVQLEGAWVKWAASSFGLVVSQRN			
			Q Consensus	18	~~~~~l~~~Q~~~~~g~~~~~rg~ +....+.+.++.. .+++. .+.+...+.. .+++.++ +			
			T Consensus	11	~~~~~Q~~~~~i~~~G~			
			T 1Q0U_B	11	FQPFIIIEAIKTLRFYKPTIQLERIIPGALR-----GESMVGQSQTGT			
			T ss_dssp		CCHHHHHHHHHHTTCCSCCHHHHHHHHHHT-----TCCEEECCCSH			
			T ss_pred		CCHHHHHHHHHhCCCCCCCCHHHhHHHHHHhC-----CceEEEEecCCCC			
			Q ss_pred		HHHHHHhC-CeeEEEEcCCHHHHHHHHHHHHHHHHHhC-----ccchhhcecccCcceeEEE			
			Q Klein_Draft	87	LAGLILFG-ERLIHSASHFKTAVNGMERLESIAK-----SGLKYAKQAHGAESIEI			
			Q Consensus	87	~~~~~i~~~t~~~a~~~~~l~~~~~i~~~ ...+...+ ...++++ +...+.++...+.....			
			T Consensus	63	~~~~~l~v~p~~~~~			
			T 1Q0U_B	63	MEKIKPERAEVQAVITAPRELATQIYHETLKITKFCPKDRMIVARCLIGGTDQKALEK			
			T ss_dssp		HHHCCTTSCSCCEECSHBBBBBBBBBBHTSCGGGCCCEECCSHHHHHH			
			T ss_pred		HHHHhhccCcceEEeCcHHHHHHHHHHHHhccCCCCceEEEEecCcHHHHHHHH			
			Q ss_pred		EEEECC-----CCCCccccEEEEEecHHhcCH---HHHHHHHHhccCCCCCEE			
			Q Klein_Draft	150	IFQTRT-----DRSGLGLTADRVIDFDEAMTITP---GSLKALLPTVSSRPNPQIVYT			
			Q Consensus	150	~~~~~G~~~~~v~iDE~~~~~l~~~~~i~~~ .+.+.+...++++ + +.+. .+.+.+...+... .+++			
			T Consensus	130	~v~t~~~~~i~~~iiDE~~~~~i~~~			
			T 1Q0U_B	130	VIGTPGRINDFIREQALDVTAHILVVDEADMIDMGFITDVDQIAARMPKD-LQMLVFS			
			T ss_dssp		EEECHHHHHHHHTTSCCCTTCCEECSHBBBBBBHTSCGGGCCCEECCSHHHHHH			
			T ss_pred		EEECHHHHHHHHHhCCCCchccCCEEEeCHHHHccCcHHHHHHHHhCCc-eeEEEE			
			Q ss_pred		HHHHHHhC-CeeEEEEcCCHHHHHHHHHHHHHHHhccchhhcecccCcceeCCC			
		35.	Q Klein_Draft	18	AGQEAIIDLAAACGLI-LDPWQELCLHEALKESDELVQLEGAWVKWAASSFGLVVSQRN			
			Q Consensus	18	~~~~~l~~~Q~~~~~g~~~~~rg~ +....+-.+.++.. .+++. .+.+...+.. .+++.++ +			
			T Consensus	22	~~~~~Q~~~~~i~~~G~			
			T 2G9N_A	22	LSESLLRGIYAGFEKPSAIQQRAILPCIK-----GYDVIQAQSGT			
			T ss_dssp		CCHHHHHHHHHHTTCCSCCHHHHHHHHH-----TCCEEECCCTS			
			T ss_pred		CCHHHHHHHHHCCCCCCCCHHHHHHHHHhC-----CCcEEEECCCC			
			Q ss_pred		HHHHHHhC-CeeEEEEcCCHHHHHHHHHHHHHHHhccchhhcecccCcceeCCC			
			Q Klein_Draft	87	LAGLILFG-ERLIHSASHFKTAVNGMERLESIAKSGLYAKQAHGAESIEILDGPNP			
			Q Consensus	87	~~~~~i~~~t~~~a~~~~~l~~~~~i~~~ ...+...+ ...++++ +...+.++...+.....+.....			
			T Consensus	74	~~~~~li~~~p~~~~~			
			T 2G9N_A	74	LQIQLDLKATQALVLAPTRLAQQIQKVVMALGDYMGASCHACIGGTVNRAEVQKLQME			
			T ss_dssp		HHHCCTTCCSCCEECSHBBBBBBHTTTCCCEECC--CCCTTTSSSSC			
			T ss_pred		HHHHHHhccCcceEEeCCHHHHHHHHHHHHHHHhCcEEEEEecCCCCHHHHHHHH			

Vis	Hits	Aln		T Consensus	62	~~~~~1~~~~p~~~~~	Color Segs	Unwrap Segs
		Select all	Forward	Forward Query MSA	62	NLDPELKAPQLELAVPTRLAIVQVAEAMTDSKHMRCGVNVVALYGGQRDVQLRAL--R		
		T ss_dssp				TSCCTCCSCEEECCSSHHHHHHHHHHHHHHHTTSTCCEECC-----CHHHHH--H		
		T ss_pred				HchhhCCCCeEEEEeCCHHHHHHHHHHHHHHHccCCCCEECCcHHHHHHHH--h		
		Q ss_pred				C-----CCCCcccEEEEEecHHhcCH---HHHHHHHhhcCCCCCEECCeCC		
		Q Klein_Draft	155			T-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRPNPQIVYGTAA		
		Q Consensus	155			~~~~~G~~~~~v~iDE~~~~~1~~~~~i~~stp~		
		T Consensus	129		+ ++.. .+.+.+.+. .+++.+ +. .		
		T 5GJU_A	129			~1~~~~~li~DE~~~~~i~sat~~		
		T ss_dssp				GRLLDHLKRGTLDLSKLGLVLDEADEMLRMGFIEDVETIMAQIPEG-HQTALFSATMP		
		T ss_pred				HHHHHHHHHTSSCCTTCCEEESHHHHHHHTCSS-CEEEECCSSCC		
						HHHHHHHHhCCCCHHccEEEEeCHHHHHhCcHHHHHHHHhCCCC-CEEEECCCCC		

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

38. [5GVR A \(<http://pdb.rcsb.org/pdb/explore.do?structureId=5GVR>\) 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	chHHHHHHHHHHhCC-CCCHHHHHHHHHhccChhHhccCcchhhheeEEEecCC
Q Klein_Draft	17 SAGQEAIIDLAAACGL-TLDPWQECLCLHEALKESDELVQLESQAWKKWAASSFGLVSRQ
Q Consensus	17 ~~~~~~1~~~~Q~~~~~g~~~~~rg
T Consensus	.+++++.+++.++ .+++. +.++...+.
T 5GVR_A	19 ~~~~~~1~~~~~Q~~~~~li~~~g
T ss_dssp	KFPAAILRGLKKKGIIHHPPTPIQGIPTILS-----GRDMIGIAFTG
T ss_pred	TCCHHHHHHHHHTCCSCCHHHHHHHHHHT-----TCCEEEECCCTT
	CCCHHHHHHHHHhCCCCcHHHHhHHHHHHhCC-----CCcEEEEeCCC

Q ss_pred	HHHHHHHh-----CCeeEEEEeCCHHHHHHHHHHHHHHHh-----ccchhhc
Q Klein_Draft	86 ELAGLILF-----GERLIIHSAHEFKTAVGMERLESLIAK-----SGLKYKA
Q Consensus	86 ~~~~~~i~i~~t~~~a~~~~~1~~~~~
T Consensus	+++.+... .+++++ +...+.++...+....
T 5GVR_A	71 ~~~~~~li~p~~~~~
T ss_dssp	VIMFCLEQEKRLPFSKREGPYGLIICPSRELARQTHGILEYYCRLQEDSSPLLCALCI
T ss_pred	HHHHHHHHHHHSCCTCCSEECSCHHHHHHHHHHHHHHTSCCCCEEE

Q ss_pred	EecCCCCCcEEEEEC-----CCCCcccEEEEEecHHhcCH---HHHHHHHHh
Q Klein_Draft	139 ILDGPNPGARVIFQTRT-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTV
Q Consensus	139 ~~~~~~g~~~i~~~~~G~~~~~v~iDE~~~~~1~~~~~
T Consensus+.. .+++++ +...+.++...+....
T 5GVR_A	141 ~~~~~~i~v~t~~~1~~~~~viiDE~~~~~i~~~
T ss_dssp	TI---RHGVHMMVATPGRLMDLLQKMKVSLDICRYLALDEADMIDMGFEGDIRTIFSYF
T ss_pred	HH---HTCCSEECHHHHHHHHTSSCCTTCCEEESHHHHHHHTCHHHHHHHHTC

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

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(<http://www.ebi.ac.uk/pdbe/entry/pdb/1hv8>\)](#)

Vis	Hits	Aln	39.	1HV8_B (http://pdb.rcsb.org/pdb/explore.do?structureId=1HV8) DEAD BOX HELICASE; Helicase, RNA-bi	DEAD BOX HELICASE; Helicase, RNA-bi				
				Select all	Forward	Forward	Query MSA	Color Seqs	Unwrap Seqs
				HEV_594_3.0A {Methanocaldococcus jannaschii} SCOP: c.37_19					
				Probability: 97.59	E-value: 1.5E-5	Score: 78.78	Aligned Cols: 162	Identities: 12%	Similarity
				Q ss_pred	hHHHHHHHHHHhCC-CCHHHHHHHHHHHhCCChhHhcCCcchhhheeEeeEeC				
				Q Klein_Draft	18 AGQEAIIDLAAACGL-ILD PWQELCLHEALKESDELVQLES GAWVKKWAASSFGLVVSRQ				
				Q Consensus	18 ~~~~~~1~~~Q~~~~~g~~~~~rg~+.....++..++ . +++ .+.+.+..				
				T Consensus	13 ~~~~~~1~~~~~Q~~~~~				
				T 1HV8_B	13 LSDNILNAIRNKGFEKPTDIQMKVPIPLFN-----DEYNIVAQARTGS				
				T ss_dssp	CCHHHHHHHHHHTCCSCCHHHHHHHHHHH-----TCSEEEECSSS				
				T ss_pred	CCHHHHHHHHHCCCCCCCChHHHHhHhHHhc-----CCCcEEEEeCCCC				
				Q ss_pred	HHHHHHhCCeeEEEeCCHHHHHHHHHHHHHHHhCC--cchhcecccCCceEEEeC				
				Q Klein_Draft	87 LAGLILFGERLIIHSAHEFKTAVNGMERLESLI AKS--GLKYKAKQAHGAESIEILDGP				
				Q Consensus	87 ~~~~~~i~i~~t~~a~~~~~l~~~~~i~~~~~...+....+....++ +...+.+....+....				
				T Consensus	66 ~~~~~~liv~p~~~l~~~~~				
				T 1HV8_B	66 IELVNENNGIEAII LTPTRELAIQVADEIESLKGKNKNLKI AKIYGGKAIYPQIKAL-----				
				T ss_dssp	HHHSCSSSSC EEECSCHHHHHHHHHHHHCSSCC EEEECTTSCHHHHHHH-----				
				T ss_pred	HHHHHHhCCcEEEEeCCHHHHHHHHHHHHHhCCCCceEEEEeCCCCcHHHHHHH-----				
				Q ss_pred	C-----CCCCcccc eeEEEeC HHhCC-----HHHHHHHHhCCCCCC EEEEEEeC				
				Q Klein_Draft	155 T-----DRSGLGLTADR VIFDEAMTITP---GSLKALLPTVSSRPNPQIVYGT A				
				Q Consensus	155 ~~~~~~G~~~~~v~iDE~~~~~l~~~~~i~~stp . ..+....++ + +...+.+....+....+....				
				T Consensus	132 ~1~~~~~viDE~h~~~~~i~~sat~				
				T 1HV8_B	132 GRILDHINRGTLNLKNVKYFILDEADEMLNMGMFIKDV EKILNACNKD-KRILLFSATM				
				T ss_dssp	HHHHHHHHHTSSCGGGC EEEETHHHHHTTTHHHHHHHTCSS-CEEEEEE SSSC				
				T ss_pred	HHHHHHHHhCCCChccc EEEeC HHHHHHhcccHHHHHHHHhCCCC-cEEEEEEEccc				

Vis	Hits	Aln	T Consensus	157	~~~~~i~v~t~~~l~~~~~iiIDE~~~~~
		Select all	Forward	157	GPQIRDL---ERGVEIATPGRLLDPLECGTINLRRTTYLVLDEADRMEDEMGFEPQIRK
			T ss_dssp		HHHHHHH---HTCCSEEECHHHHHHHHTTCSSSCCEECSHHHHHHHTCBBBBB
			T ss_pred		hHHHHH---hCCCCEEEchHHHHHHHcCCCChhcCCEEEeEchHHHHHhcCCCC
			Q ss_pred		CEEEEecCC
			Q Klein_Draft	193	PQIVYTGTAA 202 (510)
			Q Consensus	193	~~i~~stp~ 202 (510)
					..++++ +.
			T Consensus	223	~i~s~t~~ 232 (253)
			T 4A4D_A	223	QTLMWSATWP 232 (253)
			T ss_dssp		EEEEEEESCCC
			T ss_pred		EEEEEECCCC

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

41. [3B6E A \(<http://pdb.rcsb.org/pdb/explore.do?structureId=3B6E>\)](#) Interferon-induced helicase C domain-DExD/H RNA-binding helicase, innate; 1.6A {Homo sapiens}

Probability: 97.57 E-value: 1.3E-5 Score: 72.8 Aligned Cols: 167 Identities: 13% Similarity:

Q ss_pred	CCCCCchHHHHHHHH-HhCCCCHHHHHHHHHHhccChhHhhccCccchhhheeEeeE
Q Klein_Draft	PEANSAGQEADILA-AACGLILDWPQELCLHEALKESDELVQLESQAWVKWAASSFGL
Q Consensus	~~~~~i~~~~~l~~~~~Q~~~~~g~~~~~.++..... .+ +++...+. .+...+
T Consensus	~~~~~l~~~Q~~~~~-----
T 3B6E_A	TMGSDSDEENVAARASPEPELQLRPYQMEVAQPALE-----GKNIII
T ss_dssp	-----CHHHHHHHHTCCSCCCCCCHHHHHHHHHHT-----TCCEE
T ss_pred	ccCCCCchhhhhhcCCCCCCCCCHHHHHHHHHhcc-----CCCEE

Q ss_pred	HHHHHHHHHHHHh---CCeeEEEEcCCHHHHHHHHHHHHHcc--cchhhcecccc
Q Klein_Draft	IILEALELAGLILF---GERLIIHSAHEFKTAVGMERLESLIAKS--GLKYKAKQAHGA
Q Consensus	~~~~~i~~~~~l~~~~~a~~~~~.++.... +...++....+.... .+....
T Consensus	~~~~~ili~~~p~~~~~
T 3B6E_A	VAVYIAKDHDKKKASEPGKVIVLVNKLLVEQLFRKEFQFLKKWYRIGLSGDTQLK
T ss_dssp	HHHHHHHHHHHHHHHTCCSCCCCCCHHHHHHHCCCHHHHTTSCEECCC--CC
T ss_pred	HHHHHHHHHHHhccCCCCCeEEEEechHHHHHHHHHHhccCceEEEEecCCccc

Q ss_pred	CCcEEEEEECCCC-----CcccccEEEEecHHhcCHH-HHHHHHHhhccc
Q Klein_Draft	PGARVIFQTRTDRS-----GLGLTADRVIFDEAMTITPG-SLKALLPTVSSR
Q Consensus	~g~~i~~~~~G~~~~~v~iDE~~~~~l~~~.++ .+ ++ +.+.+....
T Consensus	~~~~~i~v~t~~~~~v~iDE~h~~~~~
T 3B6E_A	KSCDIIISTAQILENSLLNLENGEDAGVQLSDFSLIIIDECHTNKEAVYNNIMRHLYLMQ
T ss_dssp	HHCSEEEEEEHHHHHHHHC-----CCGGGCSEEEETTC-----CHHHHHHHHHHH
T ss_pred	hcCCEEEEEEchHHHHHHHHhccCCCCccccccccCCCCccccccccCCCCcccc

Q ss_pred	-----CCEEEEe
Q Klein_Draft	-----NPQIVYTG 199 (510)
Q Consensus	-----i~~~s 199 (510)
	..+++.++
T Consensus	~~~~~s 214 (216)
T 3B6E_A	NKPVIPLPQILGLT 214 (216)
T ss_dssp	TCCCCCCCEE
T ss_pred	CCCCCCCCCcccc

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

Vis	Hits	Aln	42.	4LJY A (http://pdb.rcsb.org/pdb/explore.do?structureId=4LJY) Pre-mRNA-processing ATP-dependent R box, RNA-splicing, HELT, MRD, ADP, 1.95A {Saccharomyces cerevisiae}	Color Seqs	Unwrap Seqs
				Probability: 97.57 E-value: 1.8E-5 Score: 82.43 Aligned Cols: 179 Identities: 13% Similarity		
				Q ss_pred CCCCCcEEeCCCCCcHhhHHHHHHHHCC-CCCHHHHHHHHHhccChhHhccCCcch		
				Q Klein_Draft 2 GVPQPRIWLSPEANSSAGQEAIIDLAAACGL-ILDPWQELCLHEALKESDELVQLESGAWV		
				Q Consensus 2 ~~~~~~1~~~Q~~~~~g~~~+....+...+++. +++.+++.++..		
				T Consensus 42 ~~~~~~f~~~~~1~~~~~1~~~Q~~~i~~~-		
				T 4LJY_A 42 GTGCPKPVTKWSQLGLSTDMVLITEKLHFGLTPIQSQALPAIMS-----		
				T ss_dssp SCCCCCCCAGGGSCCCHHHHCCCCSCCCSCHHHHHHHHT-----		
				T ss_pred cCCCCCCCcHHhCCCHHHHHHHhCCCCCCHHHHHHHHC-----		
				Q ss_pred EecCCCCHHHHHHHHHHHHHHhC-----CeeEEEEcCCHHHHHHHHHHHHHHHc-		
				Q Klein_Draft 71 VVSQRNGKGSILEALELAGLILFG-----ERLIIHSAHEFKTAVNGMERLESIAKS-		
				Q Consensus 71 ~~~rg~GKT~~~~~i~~~t~~~a~~~~~.+++ + .++...++...+....+....		
				T Consensus 94 ~~~tGsGKT~~~~~lil~P~~~1~~q~~~~~		
				T 4LJY_A 94 ISKTGSGKTISYLLPLLRQVKAQRPLSKHETGPMGLILAPRELALQIHEEVTKFTEADT		
				T ss_dssp ECCTTSCHHHHHHHHHHHHHHTSCCCCTCCCSSEEECSSHHHHHHHHHHHHHTCT		
				T ss_pred EcCCCCcHHHHhHHHHHHHHhCCccCCCCCeEEEECcHHHHHHHHHHhCC		
				Q ss_pred cCCCcEEEecCCCCcEEEEEC-----CCCCcccEEEEEecHHc---C		
				Q Klein_Draft 131 AHGAESIEILDGPNGARVIFQTRT-----DRSGLGLTADRVIFDEAMTI---T		
				Q Consensus 131 ~~~~~i~~~~~g~~~i~~~~~G~~~~~v~ide~~~~~.++.. .+..+.+....+.... + +++.+..		
				T Consensus 164 ~~~~~~i~~~T~~~1~~~~~iViDeah~~~~~		
				T 4LJY_A 164 SEMKKQITDL---KRGTEIVVATPGRFIDILTNDGKLLSTKRITFVVMDEARLFDLGF		
				T ss_dssp SCTHHHHHHH---TTCCSEEECHHHHHHHHTSSCSTTCCEEETTHHHHHHTTC		
				T ss_pred cchHHHHHHH---HhCCcEEEECHHHHHHHhCCCCecccCCceEEEECcCHHHhCC		
				Q ss_pred hcCCCCCEEEEEEccC		
				Q Klein_Draft 187 VSSRPNPQIVYTGTAA 202 (510)		
				Q Consensus 187 l~~~~~i~~~stp~ 202 (510)		
				+.... ...++++ +.		
				T Consensus 231 ~~~~~~i~~~SaT~~ 245 (493)		
				T 4LJY_A 231 VRPD-KQCVLFSATFP 245 (493)		
				T ss_dssp SCTT-CEEEEEECCCC		
				T ss_pred CCCC-CEEEEEECCCC		

	43.	2KBE A (http://pdb.rcsb.org/pdb/explore.do?structureId=2KBE) ATP-dependent RNA helicase DBP5 (E. Helicase, Hydrolase, Membrane; NMR {Saccharomyces cerevisiae}	Template alignment Template 3D structure PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2kbe)
			Probability: 97.56 E-value: 4.0E-5 Score: 70.15 Aligned Cols: 161 Identities: 14% Similarity
			Q ss_pred hHHHHHHHHhCC-CCCHHHHHHHHHccChhHhccCcchhhhe--EeeeEEecC
			Q Klein_Draft 18 AGQEAIDLAACGL-ILDPWQELCLHEALKESDELVQLESGAWVKWAA--SSFLVVSR
			Q Consensus 18 ~~~~~~1~~~Q~~~~~g~~~~~r+....+....++ .++++ .+..+..+.. . .+++.+++
			T Consensus 29 ~~~~~~Q~~~~~i~~~~~
			T 2KBE_A 29 LAPELLKGIVAMKFQKPSKIQERALPLLLH-----NPPRNMIAQSQS
			T ss_dssp SCHHHHHHHHSSSSCCCSHHHHHHHHSSC-----CCSCEEEEESST
			T ss_pred CCHHHHHHHhCCCCCCCCHHHHHHHHHh-----CCCCcEEEEcccC
			Q ss_pred HHHHHHHhC-CeeEEEEcCCHHHHHHHHHHHHHHHccchhcecccCcEEEecCC
			Q Klein_Draft 85 LELAGLILFG-ERLIIHSAHEFKTAVNGMERLESIAKSLKYKAKQAHGAESIEILDGP
			Q Consensus 85 ~~~~~~i~~~t~~~a~~~~~l~~~~~i~~~~~.++....+ ...++++ +....+....+....

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(<http://www.ebi.ac.uk/pdbe/entry/pdb/3b7g>\)](http://www.ebi.ac.uk/pdbe/entry/pdb/3b7g)

44. [3B7G B](http://pdb.rcsb.org/pdb/explore.do?structureId=3B7G) (<http://pdb.rcsb.org/pdb/explore.do?structureId=3B7G>) Probable ATP-dependent RNA helicase CONSERVED DOMAIN; HET: ANP; 1.9A {Homo sapiens}

Probability: 97.55 E-value: 5.3E-5 Score: 69.5 Aligned Cols: 160 Identities: 12% Similarity:

Q ss_pred		HHHHHC-CeeEEEEcCCHHHHHHHHHHHHHHHH--cccchhcceccCCceEEEcCCC
Q Klein_Draft	89	GLILFG-ERLIIHSASHFKTAVNGMERLESLIA---KSGLKYKAKQAHGAESIEILDGPN
Q Consensus	89	~~~~~i~i~~t~~a~~~~~l~~~~~i~~~~~.+. +++++ +.+.+.+.+.....
T Consensus	85	~~~~~l~~~p~~~~~
T 3B7G_B	85	SLVLENLSTQIYLAPRTREIAVQIHSVITAIGIKMEGLECHVFIGGTPLSQDKTRL---
T ss_dssp		HCCTTCSCCEEECSSHHHHHHHHHHHHGGGSTTCCEEETTSCHHHHHHHT---
T ss_pred		HHHhcCCCCcEEEEeCCHHHHHHHHHHHHHHHhhcccCCeEEEECCCCChHHHHHH---

Q ss_pred		C-----CCCCccccEEEEEecHHhc----CHHHHHHHHHhcCCCCCEEeeeEcCC
Q Klein_Draft	155	T-----DRSGLGLTADRVLVFDEAMTI----TPGSLKALLPTVSSRPNPQIVYTGTAA
Q Consensus	155	~~~~~G~~~~~v~iDE~~~~~l~~~~~i~~~stp~ .
T Consensus	151	~~l~~~~~iDE~~~~~l~~~~~i~~sat~~
T 3B7G_B	151	GRIKQLIELDYLNPGSIRLFILDEADKLLEEGSFQEIQINWIYSSLPAS-KQMLAVSATYP
T ss_dssp		HHHHHHHHHTSSCGGGCEEEETHHHHHSTTSSHHHHHHHHSCSS-CEEEEEECS
T ss_pred		HHHHHHHHhCCcCccccCcEEEEecHHHHhhcCChHHHHHHHHhCCCC-CeEEEEEcCC

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

45. [2OXC A](http://pdb.rcsb.org/pdb/explore.do?structureId=2OXC) (<http://pdb.rcsb.org/pdb/explore.do?structureId=2OXC>) Probable ATP-dependent RNA helicase
STRUCTURAL GENOMICS; HET: ADP; 1.3A {Homo sapiens}

Probability: 97.55 E-value: 5.3E-5 Score: 69.5 Aligned Cols: 160 Identities: 12% Similarity:

Q ss_pred		HHHHHHHHhCC-CCCHHHHHHHHHhCcChhHhcCCcchhhheeEeeEeeCCCCC
Q Klein_Draft	20	QEAIIDLAAACGL-ILDWPQECLHEALKESDELVQLESGAWVKWAASSFGLVVSQRNGK
Q Consensus	20	~~~~~1~~~~Q~~~~~g~~~~~rg~GK++..+++.++ .+..++.. .+..++..++ +
T Consensus	33	~~~~~1~~~~~Q~~~~~-----i~~~g~GK
T 20XC_A	33	RPVLEGLRLAAGFERPSPVOLKAIPLGRG-----GLDLIVQAKSGTGK

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(<http://www.ebi.ac.uk/pdbe/entry/pdb/3fe2>\)](http://www.ebi.ac.uk/pdbe/entry/pdb/3fe2)

46. [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

Q ss_pred		hhhhhhhhhhCcCC-CCHHHHHHHHhCChhHhcCCcchhhheeeEeeEcCC
Q Klein_Draft	18	AGQEAIIDLAAACGLI-LDPWQELCLHEALKESDELVQLESQAWKKWAASSFGLVVSQRQN
Q Consensus	18	~~~~~1~~~Q~~~~~g~~~~~rg~ +....+...+++.+++ .+..+.. .++.++ ++ +
T Consensus	36	~~~~~Q~~~~~-~~~~il~~~g~
T 3FE2_A	36	FPANVMDFVIARQNFTEPTAIQAQGPVALS-----GLDMVGVAQTGS
T ss_dssp		CCHHHHHHHHTTCCSCCHHHHHHHHH-----TCCEEECTTS
T ss_pred		CCHHHHHHHHHCCCCCcHHHHhHHHHHC-----CCCEEECCCCC

Q ss_pred		HHHHHHhC----CeeEEEECcCHHHHHHHHHHHHHHHcc--cchhhceccCCceEE
Q Klein_Draft	87	LAGLILFG-----ERLIIHSAHEFKTAVNGMERLESLIAKS--GLKYKAKQAHGAESIE
Q Consensus	87	~~~~~i~~~~~i~~~~~a~~~~~l~~~~~i~ ...+....+ ...+++++ +.+.+.+.+.
T Consensus	88	~~~~~lii~p~~~~~
T 3FE2_A	88	IVHINHQPFLERGDPICLVLAPTRELAQVQQVAEYCRACLRKLSTCIYGGAPKGQPQIR
T ss_dssp		HHHHHTSCCCCTTCCCSEEECSSHHHHHHHHHHHHHHHHHHHTCCEEETTSCHHHHHH
T ss_pred		HHHHHcccccccCCCCeEEEEeCCHHHHHHHHHHHHHHHHHhCCeEEEECCCCchHHHH

Q ss_pred		EEEEEC-----CCCCcccEEEEEecHHhcCH---HHHHHHHhhcCCCCEEEE
Q Klein_Draft	149	VIFQTRT-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRNPQIVY
Q Consensus	149	i~~~~~-----~G~~~~~v~iDE~~~~~l~~~~~i~~ +.+.+.+..++ +++.+. ...+.+.+. ...++
T Consensus	155	i~v~t~~~l~~~~~iiiDE~~~~~i~~
T 3FE2_A	155	ICIATPGRLIDFLECGTKNLRRRTYLVLDREADRMLDMGFEPQIRKIVDQIRPD-RQTLMW
T ss_dssp		EEEECHHHHHHHHHHTSCCCTCCEEETTHHHHHHTTCCHHHHHHTCSS-CEEEEE
T ss_pred		EEEeCHHHHHHHHHHHCCCChhCCEEEEecHHHHhhCcHHHHHHHHhCcC-CEEEEE

Template alignment | Template 3D structure | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/5i2b>)

47. SJB2 A (<http://pdb.rcsb.org/pdb/explore.do?structureId=5JB2>) LGP2/RNA Complex; Innate immune pa
HET: ADP, GTP; 2.2A {*Gallus gallus*}

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

48. [5JA1](http://pdb.rcsb.org/pdb/explore.do?structureId=5JA1) A (<http://pdb.rcsb.org/pdb/explore.do?structureId=5JA1>) LGP2/RNA Complex; Innate immune path ADP, EDO; 1.5A {Gallus gallus}

Probability: 97.53 E-value: 1.4E-5 Score: 87.23 Aligned Cols: 155 Identities: 10% Similarity

0 ss pred CCCCCCHHHHHHHHHHhccCbbHhhccCCcchhhheeFeeEEecCCCCHHHHHHHHHHHH

GLTIDPWHQELGLHEALKESDELVOLESQAHVVKHAASSSEGIVVSPONGKGTLEALELAC

Q KIEIN_DIACT 38 GEIILDFWQECLCEILAEKESDDELVQLESGAWVRKWAASSTI GEVVSQRQNKGRSILLALLEAG

Q Consensus 30 ~~~T~~~Q~~~~g~~~~rg~GK~T~~~~~

$$+ \dots | \dots + | \dots + \dots + \dots \qquad \qquad \qquad . + \dots + \dots + \dots | + | | | \dots + \dots + \dots$$

T 5JAJ_A 7 GSELHGYQLEAVAPALR-----GRNSIVWLPTGAGKTRAAVHVCCRHH

T ss_dssp -- CCCHHHHHHHHHHHHHT ----- TCCEEEECCTSCHHHHHHHHHHHHH

Q ss_pred EEcCCHHHHHHHHHHHHHHHHHHc-cchhhceeccCcEEEcCCCCCcEEEEEECCCC-

O Klein Draft 100 HSAHEFKTAVNGMERLESLIAKS-GLKYKAKOAHGAESIEILDGPNPGARVIEFOTRDR-

⁹ Consensus = 100 $\frac{\text{number of responses in category}}{\text{total number of responses}}$

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

| Consensus 59 ~~11VP~~~~1~~q~~~~~V~~~~g~~~~~1V1~!~~~1~~

T 5JAJ_A 59 VLVNKVHLVQQHLEKFHVLRDAFKVTAVSGDSSHKCFFGQL -- AKGSDVVICTAQILQ

T ss_dssp EEESSHHHHHHHHHTGGGGGGTSCEEECTTTTSSCHHHH--HHTCSEEEEHHHHH

T ss_pred EEEcCChHHHHHHHHHHHhhccCcEEEEeCCCCccccchHH---hhCCCEEEECHHHHH

Q ss_pred CCccccceEEEEEcHHhcCHHHH-HHHHHhh-----cCCCCCEEEEEecCCCCC

Q Klein_Draft 158 SGLGLTADRVIFDEAMTITPGSL-KALLPTV-----SSRPNPQIVYTGTAAQR 20

Q Consensus 158 ~~~G~~~~~V~iDE~~~~~l-----~~~~~i~~~stp~~~ 20

Vis Hits Aln ss_dssp Select all Forward Forward Query MSA Color Segs Unwrap Segs

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

49. [3BOR A](http://pdb.rcsb.org/pdb/explore.do?structureId=3BOR) (<http://pdb.rcsb.org/pdb/explore.do?structureId=3BOR>) Human initiation factor 4A-II (E.C.3.6. DEAD box, structural; 1.85A {Homo sapiens})

Probability: 97.53 E-value: 3.0E-5 Score: 72.22 Aligned Cols: 166 Identities: 13% Similarity

Q ss_pred		-----CCCCccccEEEEEecHHhcCH---HHHHHHHhhcCCCCCEEEEEecCC
Q Klein_Draft	156	-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRPNPQIVYTGTAA
Q Consensus	156	-----~~~~~G~~~~~v~iDE~~~~~l~~~~~i~~stp~+++++ +++.+. .+.+.+.+. .+.+++++ +.
T Consensus	159	~1~~~~~1iiDEah~~~~~i~~saT~~
T 3BOR_A	159	RVFDMLNRRYLSPKWIKMFLVLEADEMLSRGFKDQIYEIFQKLNTS-IQVVLLSATMP
T ss_dssp		HHHHHHHTTSSCSTTCIEEEESHHHHHHHTCBBBBBBBBBBSCTT-CEEEECCSSCC
T ss_pred		HHHHHHHcCCCChhhCCEEEEeCHHHHHhcCcHHHHHHHHhCCCC-CEEEEeCCCC

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

50. [1FUU_B](http://pdb.rcsb.org/pdb/explore.do?structureId=1FUU) (<http://pdb.rcsb.org/pdb/explore.do?structureId=1FUU>) INITIATION FACTOR 4A; IF4A, HELICASE TRANSLATION; 2.5A {*Saccharomyces cerevisiae*} SCOP: c.37.1.19

Probability: 97.52 E-value: 4.0E-5 Score: 76.93 Aligned Cols: 162 Identities: 12% Similarity

Vis	Hits	Aln	Select all	Forward	Forward Query MSA	Color Seqs	Unwrap Seqs
			Q ss_pred	CC-----CCCCccccceEEEEEchHHhcCH---	HHHHHHHHhhcCCCCCEEEEEecCC		
			Q Klein_Draft	RT-----DRSGLGLTADRVIFDEAMTITP---	GSLKALLPTVSSRPNPQIVYTGTAA		
			Q Consensus	154 ~~~~~~G~~~~~v~iDE~~~~~1~~~~~i~~~stp~	.. .+++++ +++.+. .+.+.+. .+.+++= .		
			T Consensus	146 ~~~1~~~~~vivDE~h~~~~~i~~~sat~~			
			T 2FUU_B	146 PGRVFDNIQRRRFRTDKIKMFILDEAEMLSSGFKEQIYQIFTLLPP-TQVVLSSATMP			
			T ss_dssp	HHHHHHHHHTSSCCTTCCEEETTHHHHHHTTCHHHHHHHTSCTT-CEEEECSSCC			
			T ss_pred	HHHHHHHHHhCCCCCCCcEEEEeCHHHhhCcHHHHHHhCCCC-cEEEEeCCCC			

[Template alignment](#) | [Template 3D structure](#) | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/2fz4>)

51. **2FZ4_A (<http://pdb.rcsb.org/pdb/explore.do?structureId=2FZ4>) DNA repair protein RAD25; RecA-like dc recognition; 2.4A {Archaeoglobus fulgidus} SCOP: c.37.1.19**

Probability: 97.5 E-value: 3.3E-5 Score: 72.08 Aligned Cols: 140 Identities: 16% Similarity:

Q ss_pred	cCCCCCHHHHHHHHHhccChhHhccCCchhhheeEeeEEecCCCCHHHHHHHHHHHH
Q Klein_Draft	29 CGLILDPWQELCLHEALKESDELVQLESAGAWVKWAASSFGLVVSQRNGKGSILEALELA
Q Consensus	29 ~~~1~~~Q~~~~g~~~~rg~GKT~~~~~.+. +++= .++=+..
T Consensus	90 ~~~1~~~Q~~~i~~~~1~~~~~1~~~GsGKT~~~~~i~~~
T 2FZ4_A	90 AEISLRDYQEKALEWRWLV-----DKRGICVLPTGSGKTHVAMAAINE
T ss_dssp	CCCCCCHHHHHHHHHHTT-----TSEEEESSSTTHHHHHHHHHHH
T ss_pred	CCCCCCHHHHHHHHHh-----CCCEEEeCCCCCHHHHHHHHHHHHH
Q ss_pred	EEEcCCHHHHHHHHHHHHHHHcccchhceeccCCcEEEecCCCCcEEEEEC---
Q Klein_Draft	99 IHSAHFKTAVNGMERLESLIAKSGLKYKAKQAHGAESIEILDGPNGARVIFQTRT---
Q Consensus	99 ~i~~~t~~~a~~~~l~~~~~i~~~~~g~~i~~~~~.+++= .++=+..
T Consensus	137 lii~p~~~1~~~~~i~~~v~t~~~1~~~
T 2FZ4_A	137 LIVVPTLALAEQWKERLGFGEYVGEGSGRIK-----ELKPLTVSTYDSAY
T ss_dssp	EEEEEHHHHHHHHGGCGGGEEESSSCB-----CCSEEEEEEHHHH
T ss_pred	EEEEECHHHHHHHHHHHHHhChhhcEEecCcc-----ccCCEEEeHHHH
Q ss_pred	eEEEEecHHcCHHHHHHHHHhhcCCCCCEEEEecCCCCC
Q Klein_Draft	165 DRVIFDEAMTITPGSLKALLPTVSSRPNPQIVYTGTAAADQRT 206 (510)
Q Consensus	165 ~~~v~iDE~~~~~1~~~~~i~~~stp~~~~~ 206 (510)
T Consensus	194 ~~iiIDEah~l~~~~~i~lsat~~~~~ 233 (237)
T 2FZ4_A	194 MLLIFDEVHHLPAESYVQIAQMSIA--PFRGLTATFEREDG 233 (237)
T ss_dssp	SEEEEEECCSCTTTHHHHHHTCCC--SEEEEEEESCC---
T ss_pred	cEEEEChhhCCchHHHHHHhCC--CeEEEEeCCCCCCC

[Template alignment](#) | [Template 3D structure](#) | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/2z0m>)

52. **2Z0M_A (<http://pdb.rcsb.org/pdb/explore.do?structureId=2Z0M>) 337aa long hypothetical ATP-depende Hydrolase, Nucleotide-binding, RNA; 1.9A {Sulfolobus tokodaii}**

Probability: 97.5 E-value: 3.1E-5 Score: 75.29 Aligned Cols: 160 Identities: 11% Similarity:

Q ss_pred	hHHHHHHHHHHhCC-CCCHHHHHHHHHhccChhHhccCCchhhheeEeeEEecCCC
Q Klein_Draft	18 AGQEAIIDLAAACGL-ILDPWQELCLHEALKESDELVQLESAGAWVKWAASSFGLVVSQRNQ
Q Consensus	18 ~~~~~~1~~~Q~~~~g~~~~rg~GKT~~~~~.+. +++= .++=+..
T Consensus	1 l~~~~~1~~~i~~~
T 2Z0M_A	1 MNEKIEQAIREMGFKNFTEVQSKTIPLMLQ-----GKNVVVRAKTGS
T ss_dssp	CCHHHHHHHHTCCSCCHHHHHHHHHHT-----TCCEEEECCTTS
T ss_pred	CCHHHHHHHHHCCCCCCCCHHHHHHHHHHC-----CCeEEEEeCCCC

54. [Template alignment](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR03817)
[TIGR03817](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR03817) (<http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrv.cgi?uid=TIGR03817>) DECH_helic; helicase putative DEAH-box helicase. A conserved gene neighborhood widely spread in the Actinobacteria contains DEAH-box family helicase encoded convergently towards an operon of genes for protein homologous to formation proteins.

Vis	Hits	Aln	Q ss_pred Select all Q Klein_Draft	Forward	Forward Query MSA	Color Segs	Unwrap Segs
			Q Consensus	5	CccEEECCCCCchHHHHHHHHhCC-CCHHHHHHHHHHHhccChhHhcCcchhh	EPRINWSEANSAGQALIDLAACGELDPWELCLHEALKESDEEVLES GAWVKKW	
			T Consensus	8	~~~~~+....+....+....+.... + . +++.+.+.+..	g~~~~~	
			T TIGR03817	8	PARAGRTAPWPWAHPDVVAALEAAGIHRPWQHQARAAELAHA-----		
			T ss_pred		CCCccccCCCCccCCHHHHHHHHHCCCCCCCCHHHHHHHHHHHH	c-----	
			Q ss_pred		CCCCHHHHHHHHHHHHHHHHCCeEEEEEcCCHHHHHHHHHHHHHcccchhceccC		
			Q Klein_Draft	74	RQNGKGSILEALELAGLILFGERLIIHSAHEFKTAVNGMERLESIAKSGLKYKAKQAHG		
			Q Consensus	74	rg~GKT~~~~~i~~~t~~~a~~~~~l~~~~~	+ + .++...++...++..++ +.+.+.+.+.+.+	
			T Consensus	60	tGsGKT~~~l~il~~~~~Lii~P~aL~~~~~l~~~~~v~~~~~g~~~~~		
			T TIGR03817	60	TASGKSLAYQLPVL SALADDPRATALY LAPTKALAADQLRAVRELT LRGVRPAT YDGDT P		
			T ss_pred		CCCCHHHHHHHHHHHHhCCCCeEEEEeCcHHHHHHHHHHHHccCCCCeEEEeCCCC		
			Q ss_pred		CCCCEEEEEC--CCCCccc-----ceeEEEEEchHhcCH---HHHHHHHHhhc-		
			Q Klein_Draft	144	NPGARVIFQTRT--DRSGLGL-----TADRVIFDEAMTITP---GSLKALLPTVS-		
			Q Consensus	144	~g~~i~~~~~G~~~~~v~iDE~~~~~l~~~.+.+.+ ..-+. +++++ + +.+. ..+.+.++.		
			T Consensus	127	~~~~~i~i~Tp~~~l~~~l~~~~~l~~~~~iViDE~H~~~~~g~~~~~l~~~l~~~		
			T TIGR03817	127	REHARYVLTNPDMHLRGILP SHARWARFLRRLRYVVIDECHSYRGVFGSHVALV RRR RR		
			T ss_pred		HHcCCEEECHHHHHccccchHHHHHHhccCEE EEChhhccCCchHHHHHHHHHH		
			Q ss_pred		EEEEEEecCCC		
			Q Klein_Draft	194	QIVYTGT AAD 203 (510)		
			Q Consensus	194	~i~~~stp~~ 203 (510)	.+.++ +..	
			T Consensus	197	~i~1SAT~~~ 206 (742)		
			T TIGR03817	197	FVLASATTAD 206 (742)		
			T ss_pred		EEEEEEcCCCC		

			Template alignment CDD (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrvcgi?uid=pfam07652)					
		55.	PF07652.13 (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	heeEeeEEecCCCCHHHHHHHHHHHHHHHHCCeEEEEEcCCHHHHHHHHHHHHHHH				
			Q Klein_Draft	AASSFGLVVSRQNGKGSILEALELAGLILFGERLIIHSAHEFKTAVNGMERLESIAKSG				
			Q Consensus	~~~~~rg~GKT~~~~~i~~~t~~~a~~~~~l~~~~~.+.++. ++ + ++...++...+ ..+..++ +...+.+.+.+				
			T Consensus	3	~~~~~G~GKT~~~~~			
			T PF07652.13	KKQLIVLDPHPGAGKTRKVLPEFIRQAVE-RRLWTLALAPTRVVAE MAEALNGLPVRYL				
			T ss_pred	CCcEEEEeCCCCCHHHHHHHHHHHHH-CCeEEEEEchHHHHHHHHccCCCC				
			Q ss_pred	CceEEEEECCCCCcEEEEEECCCCCcceeEEEEEchHhcCHHHHH--HHHHhhcCCC				
			Q Klein_Draft	AESIEILDGPNP GARVIFQTRTDRSGLGLTADRVIFDEAMTITPGSLK--ALLPTVSSRP				
			Q Consensus	~~~i~~~~~g~~i~~~~~G~~~~~v~iDE~~~~~l~~~.+.+.+.....+...+.....				
			T Consensus	72	~~~~~i~i~Tp~~~l~~~l~~~~~iViDE~~~~~			
			T PF07652.13	KEIVDLM---CHATFTMRLLS--GGRVPN YNM FIMDEAHFTDPSSIAARGYISTKVDMG				
			T ss_pred	CceEEEEE----EechHHHHHhc--CCcCCCCeEEchHhcCcchhhHhHHheeeCC				
			Q ss_pred	CCCC				
			Q Klein_Draft	AADQ 204 (510)				
			Q Consensus	p~~~ 204 (510)				
			T Consensus	...				
			T Consensus	136 ~~~~ 139 (148)				

Vis Hits Aln | PF07652.13 136 PPGS 139 (148)
Select all FSS_pred Forward CCGE Forward Query MSA Color Seqs Unwrap Seqs

Aln | PF07652.13 136 PPGS 139 (148)
Select all Forward ccce Forward Query MSA
ss_pred

Color Segs

Unwrap Segs

Template alignment | Template 3D structure | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/2j0u>)

56. 2J0U A (<http://pdb.rcsb.org/pdb/explore.do?structureId=2J0U>) ATP-DEPENDENT RNA HELICASE DDX48, BINDING, DNA-BINDING, NUCLEAR PROTEIN; 3.0A {HOMO SAPIENS}

Probability: 97.48 E-value: 3.0E-5 Score: 76.81 Aligned Cols: 163 Identities: 16% Similarity:

Q ss_pred		hHHHHHHHHHHhCC-CCCHHHHHHHhCCChHhhcCCcchhhheeEeeEEecCCC
Q Klein_Draft	18	AGQEAIIDLAAACGL-ILDPWQEELCLHEALKESDELVQLESGAWVKKWAASSFGLVVSRQN
Q Consensus	18	~~~~~1~~~Q~~~~~g~~~~~rg~ +.....-+-..+++. +++. +++.+.. .+....++ + +
T Consensus	8	1~~~~~Q~~~~~-----~~~~~1~~~~~G~
T 2J0U_A	8	LREDLLRGIYAYGFEKPSAIQQRAIKQIIK-----GRDVIAQSQSGT
T ss_dssp		CCHHHHHHHHHHTCCSCCHHHHHHHHH-----TCCEEEDCSST
T ss_pred		CCHHHHHHHHHhCCCCCCHHHHHHHHH-----CCcEEECCCCC

Q ss_pred		CC-----CCCCccccEEEEEcHHhcCH---HHHHHHHhhcCCCCCEEEEecCC
Q Klein_Draft	154	RT-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRPNPQIVYTGTAA
Q Consensus	154	~~~~~G~~~~~v~iDE~~~~~l~~~~~i~~stp~
+++++ +++.++.. ..+.++.+.+. .++.+++++ . .
T Consensus	127	~~~~~iiiDE~h~~~~~i~~sat~~
T 2J0U_A	127	PGRVFDMIRRSLRTRAIKMLVLDEADEMLNKGFKEQIYDVYRLPPA-TQVVLISATLP
T ss_dssp		HHHHHHHHHTSCCCTTCCEEETTHHHHHTTCHHHHHHHHTSCTT-CEEEEESCCC
T ss_pred		HHHHHHHHhCCcCcCCCCeEEEEeCHHHHHHHhchHHHHHHHHhCCcCc-CEEEEeCCCC

Template alignment | Template 3D structure | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/4bu1>)

57. [4BUJ_A](http://pdb.rcsb.org/pdb/explore.do?structureId=4BUJ) (<http://pdb.rcsb.org/pdb/explore.do?structureId=4BUJ>) ANTIVIRAL HELICASE SKI2 (E.C.3.6.4.13)
DEXH BOX HELICASE, RNA; HET: SO4: 3.7A {SACCHAROMYCES CEREVISIAE}

Probability: 97.46 E-value: 4.6E-5 Score: 87.23 Aligned Cols: 171 Identities: 12% Similarity

Q ss_pred		ecCCCCHHHHHHHHHHHHHHHHcCeeEEEeCCHHHHHHHHHHHHHHHccchhhceec
Q Klein_Draft	72	VSRQNKGKSLALELAGLILFGERLIIHSAHEFKTAVNGMERLESIAKSGLKYKAKQA
Q Consensus	72	~~rg~GKT~~~~~i~i~~t~~a~~~~~l~~~~~ +++ + +++...+++.+. . .++ ++ +.+.+.+.+.+.+.+.+.+
T Consensus	355	a~TGSGKT~va~~ai~~~~~kvl~v~P~kaLa~q~~~~~Vg~~~gd~
T 4BUJ_A	355	AHTSAGKTVVAEYAIAMAHRR--MTKTIYTSPIKALSNQKFRDFKETFDVNIGLITGDV
T ss_dssp		CCTTSSCHHHHHHHHHHHHHHT--TCEEEEEESSHHHHHHHHHHHHHCSSCCEECCSSC
T ss_pred		cCCCCCCCCHHHHHHHHHHHHHHHc--CCeFFFFeCcHHHHHHHHHHHHHHHHccccFFFeCCC

Vis	Hits	Aln	Select all	Forward	Forward Query MSA	Color Segs	Unwrap Segs
			Q ss_pred	CCCCCcEEEEEECC-----	CCCCccccceEEEEEchHhcCH----	HHHHHHHHhhccc	
			Q Klein_Draft	142 GPNPGARVIFQTRT-----	DRSGLGLTADRVIFDEAMITP---	GSLKALLPTVSSR	
			Q Consensus	142 ~~~~g~~~i~~~~~	G~~~~~v~iDE~~~~~	~l~~~	
			T Consensus	416 .+.+.-+++ + .+..	...+.+.+.+	
			T 4BUJ_A	416 ---PDANCLIMTTEILRSMLYRGADLIRDVEFVIFDEVHYNDQDRGVVWEVIIMLPQH	---TTCSEEEEEHHHHHHHHHTCGGGGSEEEEEESGGTTCTTHHHHHHHHSBTT		
			T ss_dssp				
			T ss_pred		---CCCCEEEchHHHHHHHHhCChHHhcCCEEEEeHHHCCCCccHHHHHHHHCCCC		
			Q ss_pred	CCC			
			Q Klein_Draft	201 AAD 203 (510)			
			Q Consensus	201 p~ 203 (510)			
			T Consensus	482 ~n 484 (1044)			
			T 4BUJ_A	482 VPN 484 (1044)			
			T ss_dssp	CSC			
			T ss_pred	CCC			

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

58. [5SUP_B \(<http://pdb.rcsb.org/pdb/explore.do?structureId=5SUP>\) ATP-dependent RNA helicase SUB2, YR HYDROLASE-RNA complex; HET: BEF, ADP; 2.6A {Saccharomyces cerevisiae}](#)
- Probability: 97.45 E-value: 8.7E-5 Score: 74.33 Aligned Cols: 163 Identities: 10% Similarity

Q ss_pred	hHHHHHHHHHHhCC-C	CCCHHHHHHHHHhccChhHhcCcchhhheeEeeEEecCCC
Q Klein_Draft	18 AGQEAI	DLAACGL-I
Q Consensus	18 ~~~~~	LDPWQELCLHEALKESDELVQLEGAWVKWAASSFGLVSRQN
T Consensus	13 l~~~~~	Q~~~~~g~~~~~rg~
T 5SUP_B	13 LKPELSRAI	IDCGFEHPSEVQQHTIPQSIH-----GTDVLCQAKSGL
T ss_dssp	CCHHHHHHHHHHTCCSCCHHHHHHHHHHT-----	TCCEECCCTS
T ss_pred	CCHHHHHHHHHCCCCCCCCHHHHHHHHHhC-----	CCcEEEEeCCCC

Q ss_pred	HHHHHHhC-CeeEEE	cCCHHHHHHHHHHHHHHHHHcccchhceccCcEE----E
Q Klein_Draft	87 LAGLILFG-ERLIIHSAHEFKTAVNGMERLES	LSIAKSGLKYKAKQAHGAESIE----I
Q Consensus	87 ~~~~~~i~i~t~~~a~~~~~	1~~~~~i~~~~~
T Consensus	65 ~~~~~~liv~p~~~l~q~~~~~	~~~~~.~~~~~
T 5SUP_B	65 LQLDPVPGEAVVVICNARELAYQIRNEYLRF	SKYMPDVKTAVFYGGTPISKDAELLKN
T ss_dssp	HHCCCCCTCCCEECSH	HHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHHH
T ss_pred	HHhCCCCCceeEEEEeCh	HHHHHHHHHHHHhCCCCCCeEEEECCCCcchHHHHHhC

Q ss_pred	EEEECC-----	CCCCccccceEEEEEchHhcCH----	HHHHHHHHhhcCCCCCEE
Q Klein_Draft	150 IFQTRT-----	DRSGLGLTADRVIFDEAMITP---	GSLKALLPTVSSRPNPQIVY
Q Consensus	150 ~~~~~~G~~~~~v~iDE~~~~~	~l~~~~~i~~~	
T Consensus	132 ii~t~~~l~~~~~	.+.+. .-+++ + +++.+.+.+.+.++
T 5SUP_B	132 VVATPGR	LKALVREKYIDL	SHVKNFVIDECDKVLEELDMRRDVQEIFRATPRD-KQVMMF
T ss_dssp	EEEEEHHHHHHHHHTSSCCTTC	EEEETHHHHHHHHHHHHHHH	HHHHHHHHHHHHTCSS-SEEEE
T ss_pred	EEEEEHHHHHHHHhCC	CCCCchhCcEEEEeCHHHHHHHhCC	HHHHHHHHHHhCCCC-EEEE

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

59. [1W36_D \(<http://pdb.rcsb.org/pdb/explore.do?structureId=1W36>\) EXODEOXYRIBONUCLEASE V BETA CH RECOMBINATION, HELICASE, NUCLEASE, HYDROLASE, DNA; 3.1A {ESCHERICHIA COLI} SCOP: c.37.1.19](#)
- Probability: 97.45 E-value: 3.5E-5 Score: 82.89 Aligned Cols: 148 Identities: 19% Similarity

Vis	Hits	Aln	Q ss_pred Select all Q Klein_Draft	Forward	Forward Query MSA	Color Seas	Unwrap Seas
				32	CCCHHHHHHHHHHhccChhHhcCCcchhheeEeeEEecCCCCHHHHHHHHHHHHHHHH		
			Q Consensus	32	ILIDPWQELCLHEALKESDELVQLESQAWVKWAASSFGLVSRQNGKGSILEALELAGI		
			T Consensus	149	~1~~~Q~~~~g~~~~rg~GKT~~~~~	.++ +.++..+..	.++ +.++ + +++.++....
			T 1W36_D	149	DEINWQKAAVALT-----RRISVISGGPGTGKTTVAKLLAALIQ		
			T ss_pred		CCCHHHHHHHHHHh-----CCEEEEECCCCCHHHHHHHHHHHHHHHHH		
			Q ss_pred		EEcCCHHHHHHHHHHHHHHHcccchhceccC	EEecCCCCcEEEEEC	CCCC
			Q Klein_Draft	100	HSAHEFKTAVNGMERLESLIAKSGLKYKAKQAHGAESIEILDGPNGARVIFQTRTDRS	G	G
			Q Consensus	100	i~~~t~~~a~~~~l~~~~~i~~~~~g~~i~~~~~	+++ ...+.++..+....+.....+...+.....	
			T Consensus	201	~apT~~aa~~l~~~~Ti~~~l~~~~~		
			T 1W36_D	201	LAAPTGKAAARLTESLGKALRQLPLTDEQKKRIPEDASTLHR--LLGAQPGSQRLRHAG		
			T ss_pred		EEcCCHHHHHHHHHHHHHhCCCCHHHHhCCcccchHHH--HhcCCCCccccccc		
			Q ss_pred		eCHHhcCHHHHHHHHHhccCCC	EEEec	
			Q Klein_Draft	170	DEAMTITPGSLKALLPTVSSRPNPQIVYTGT	201 (510)	
			Q Consensus	170	DE~~~~~l~~~~~i~~~stp	201 (510)	
			T Consensus	269	DEasmv~~~~~l~l~~~r1IlvGD~	298 (608)	
			T 1W36_D	269	DEASMIDLPMMMSRLIDALPD--HARVIFLGRD	298 (608)	
			T ss_pred		eCcccCCHHHHHHHHHCCC--CcEEEEeCh		

					Template alignment			
60.					TIGR04095 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrvcgi?uid=TIGR04095) dnd_restrict_1; DN restriction enzyme. The DNA phosphorothioate modification system dnd (DNA instability during electrophoresis) 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		CCCCCHHHHHHHHhccChhHhcCCcchhheeEeeEEecCCCCHHHHHHHHHHHHH			
			Q Klein_Draft	30	GLIDPWQELCLHEALKESDELVQLESQAWVKWAASSFGLVSRQNGKGSILEALELAG			
			Q Consensus	30	~~~l~~~Q~~~~g~~~~rg~GKT~~~~~	.++ ...+.++..+....+.....+...+.....		
			T Consensus	6	~~~l~~~Q~~~~~l~~~~~i~~~~~G~GKT~~~~~			
			T TIGR04095	6	TFELRDYQKEAIRAWFK-----NNRGILKMATGTGKTLTAAASKL			
			T ss_pred		CCCCCHHHHHHHHHh-----hCCCEEeCCCCHHHHHHHHHHHH			
			Q ss_pred		EEcCCHHHHHHHHHHHHH-----HHcccchhceccC	EEecCCC		
			Q Klein_Draft	100	HSAHEFKTAVNGMERLES-----IAKSGLKYKAKQAHGAESIEILDGP	N		
			Q Consensus	100	i~~~t~~~a~~~~~l~~~~~i~~~~~	++ ...+.++..+....+.....+...+.....		
			T Consensus	59	vi~P~~~l~~q~~~~~i~~~~~			
			T TIGR04095	59	VVCPTYQHLVDQWAREAEKFGLNPTLCYESVSNWQSELSTGLYNLNSGNQFLAIT---			
			T ss_pred		EEechHHHHHHHHHHHHCCCCeEEEeCCCCccchHhhHhHhhccCCCCeEEE----			
			Q ss_pred		CCCCCccceeEEEeCHHhcCHHHHHHHHHhCC	CCCC		
			Q Klein_Draft	155	TDRSGLGLTADRVIFDEAMTITPGSLKALLPTVSSRPNPQIVYTGT	201 (510)		
			Q Consensus	155	~~~~~G~~~~~iDE~~~~~l~~~~~i~~~stp	201 (510)		
			T Consensus	125	~~~~~iViDE~h~~~~~l~~~~~l~lsaTp	168 (451)		
			T TIGR04095	125	QSQRRLRFPKGKTLIGDEAHNLGAPRIRESLPDNI---GFRGLSATP	168 (451)		
			T ss_pred		HHHHhhCCCCeEEEeCHHhcCHHHhCCcC---ceEEEeCC			

[Template alignment](#) | [Template 3D structure](#) | [PDBe \(<http://www.ebi.ac.uk/pdbe/entry/pdb/4a4z>\)](http://www.ebi.ac.uk/pdbe/entry/pdb/4a4z)

67. [4A4Z A](http://pdb.rcsb.org/pdb/explore.do?structureId=4A4Z) (<http://pdb.rcsb.org/pdb/explore.do?structureId=4A4Z>) ANTIVIRAL HELICASE SKI2 (E.C.3.6.4.13)
DEGRADATION, EXOSOME; HET: ANP, EDO; 2.4A {SACCHAROMYCES CEREVISIAE}
Probability: 97.38 E-value: 5.0E-5 Score: 86.45 Aligned Cols: 167 Identities: 13% Similarity

Probability: 97.38 E-value: 5.0E-5 Score: 86.45 Aligned Cols: 167 Identities: 13% Similarity

Q ss_pred		CcEEeCCCCCChHHHHHHHHCCCCCHHHHHHHHhccChhCcCcchhhhe
Q Klein_Draft	6	PRIWLSPPEANSSAGQEAIIDLAAACGLILDPWQEFLCLHEALKESDELVQLESGAWVKKWA
Q Consensus	6	~~~~~l~~~Q~~~~~g~~~~~ .+.+.+.+.+.+.++ . +++ .+++.+.+..
T Consensus	13	~~~~~f~Ld~fQ~~ai~~~- - - - -
T 4A4Z_A	13	AHVVDLNHKIENFDELI PNPARSWP FELDTFQKEAVYHLEQ- - - - -G
T ss_dssp		EEECCCTCCCTHHHCSSCSCCCCSCCHHHHHHHHHHT- - - - -T
T ss_pred		eEEecCccccccHHHHCCcchhhCCCCCCCCHHHHHHHHHHHhcc- - - - -C

Q ss_pred		CCHHHHHHHHHHHHHHHCCeeEEEeCCHHHHHHHHHHHHHHHcccccHHceecCCc
Q Klein_Draft	76	NGKGSILEALELAGLILFGERLIIHSAHEFKTAVNGMERLESIAKSGLKYAKQAHGAE
Q Consensus	76	~GKT~~~~~i~i~~~t~~~a~~~~~l~~~~~+ .++.+.+.+.+.+.+.+.+.~.~.
T Consensus	65	sGKT~~~ai~~~~~vl~i~P~kaL~~q~~~~~vg-----tG
T 4A4Z_A	65	AGKTVVAEYAIAMAHR--NMTKTIYTSPIKALSNQKFDFKETFDVNIG----LITG
T ss_dssp		SCSHHHHHHHHHHHHH--TTCEEEEEEESCGGGHHHHHHHHHTTC--CCEE----EECS
T ss_pred		CCHHHHHHHHHHHHHh--CCCEEEEEEccHHHHHHHHHHHHHHccCCEEE----EEEc

Q ss_pred	CcEEEEEECC-----CCCCccccceEEEeCHhCCH---HHHHHHHhhcCCCCC
Q Klein_Draft	146 GARVIFQTRT-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRPNPQ
Q Consensus	146 g~~~i~~~~~-----~~~~~~G~~~~~v~iDE~~~~~-----~~~~~~1~~~~~++.+..-+++- + +++.+. .. +.+.++.... ...
T Consensus	123 ~~~ilV~T~e~l~~~l~~~~~l~~~l~~VI~DEaH~l~d~~~~~e~~i~l~~~~~i
T 4A4Z_A	123 DANCLIMTTEILRSMLYRGADLIRDVEFVIFDEVHYVNDQDRGVVWEEVIIMLPQH-VKF
T ss_dssp	TSSEEEEEEHHHHHHHHHTCSGGGEEEEECCTCCCTTCTCCHHHHHSCTT-CEE
T ss_pred	CCCeEEEeHHHHHHHHhCcCbbhhCcFFFFEChhhCcCcCcHHHHHHHHhCcC-CEE

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

68. [Template alignment](#) | [Template 3D structure](#) | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/3OYI>)
3OYI_B (<http://pdb.rcsb.org/pdb/explore.do?structureId=3OYI>) reverse gyrase helicase domain; TOPOI
SUPERCOILING, ARCHAEA, HELICASE; 2.35A {Thermotoga maritima}
Probability: 0.7325 E-value: 1.65E-05 Score: 77.42 Alignments: 163 Identification: 141 Similarity: 0.9999999999999999

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

Vis	Hits	Aln	Q ss_pred Select all Q Klein_Draft	Forward	Forward Query MSA	Color Segs	Unwrap Segs
			Q Consensus	20	HHHHHHHH-HHCCCCCHHHHHHHHHhccChhHhhccCCcchhhhheeEeeEEecCCCC QEAIQDLA-TACQIILEDWQELCLHEALKESDELVQLESGAWVKWAASSFGLVVSQRNGK		
			T Consensus	8	~~~~~1~~~Q~~~~~g~~~~~rg~GK ..+..+. .+++. + +.+.+.+. .+...+.++ +		
			T 30IY_B	8	EDFRSFFKKFKGKDLTGYQRLWAKRIVQ-----GKSFTMVAPTGVGK		
			T ss_dssp		HHHHHHHHHHHHSSCCCHHHHHHHHHHTT-----TCCEECCSSCTTH		
			T ss_pred		HHHHHHHHHHHHCCCCCHHHHHHHHHhcc-----CCcEEEEeCCCCCCH		
			Q ss_pred		HHHHhCCeeEEEecCCHHHHHHHHHHHHHHHhcc-cchhhcecccCcEEE----ecC		
			Q Klein_Draft	89	GLILFGERLIIHSAHEFKTAvgMERLESIAKS-GLKYKAKQAHGAESIEI----LDG		
			Q Consensus	89	~~~~~i~i~~t~~~a~~~~~l~~~~~i~~~~~ ... +...+++. +...+.+.+.+. .+.....+ ..		
			T Consensus	60	~~~~~liv~P~~~l~~q~~~~~		
			T 30IY_B	60	LAR--KGKKSALVFPTVTLVQTLERLQKLADEKVKIFGFYSSMKKEEKFEKSFEE--		
			T ss_dssp		HHT--TTCCEEEESSHHHHHHHHHHHCCSCCEECCTSCHHHHHHHHHHHH--		
			T ss_pred		HHH--cCCCEEeCcHHHHHHHHHHHHhccCCCeEEEeCCCCHHHHHHHHHhh--		
			Q ss_pred		ECC----CCCCccceEEEEEecHHhcCH-----HHHHHHHhhc---		
			Q Klein_Draft	153	TRT----DRSGLGLTADRVI FDEAMTITP-----GSLKALLPTVS---		
			Q Consensus	153	~~~~~G~~~~~v~iD E~~~~~ +...+.++ + +.+.+. .+...+.+		
			T Consensus	124	t~~~l~~~~~ViD Eah~~~~~		
			T 30IY_B	124	STQFVSKNREKLSQKRDFVFDVDAVLKASRNIDTLLMMVGIPPEIIRKAFSTIKQGK EHHHHHHChHHHTCCSEEEESHHHHHTSHHHHHHHHHHTCCHHHHHHHHHHHTC		
			T ss_dssp		cHHHHhChHHhccCCEEEeCHHHHHHHhccHHHHHHhccCCCCHHHHHHHhcc		
			T ss_pred		cEEEEeCCCCcccc		

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

69. [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: 97.37 E-value: 1.5E-4 Score: 73.44 Aligned Cols: 163 Identities: 11% Similarity

Q ss_pred		hHHHHHHHHHHhCC-CCCHHHHHHHHHhccChhHhhccCCcchhhhhe--eEeeEEecC
Q Klein_Draft	18	AGQEAIIDLAAACGL-ILDPWQELCLHEALKESDELVQLESGAWVKWAAS-SFGLVVSR
Q Consensus	18	~~~~~1~~~Q~~~~~g~~~~~r +....+.++ .++ +.++.+. .+...+.++ +
T Consensus	32	1~~~~~1~~~~~Q~~~~~il~~~
T 3FHT_B	32	LKPQLLQGVYAMGFNRPSKIQENALPLMLA-----EPPQNLIAQS
T ss_dssp		CCHHHHHHHHHHTCCSCCHHHHHHHHHHTS-----SSCCCEECC
T ss_pred		CCHHHHHHHHHCCCCCCCCHHHHHHHHhcc-----CCcEEEeCCC
Q ss_pred		HHHHHHHHhC-CeeEEEecCCHHHHHHHHHHHHHccchhcecccCcEEEecCC
Q Klein_Draft	85	LELAGLILFG-ERLIIHSAHEFKTAvgMERLESIAKSGLYKAKQAHGAESIEILDGP
Q Consensus	85	~~~~~i~i~~t~~~a~~~~~i~~~~~ .++..+...+ ...+++. +...+.+.+.+. .+.....+ ..
T Consensus	84	~~~~~l~~~i~~~p~~~l~~~q~~~~~
T 3FHT_B	84	AMLSQVEPANKYPQCLCLSPTYELALQTGKVICQMGKFYPELKLAYAVRGNKLERGQ--
T ss_dssp		HHHHHCCTTS CSCCEECSHHHHHHHHHHHHHTTCTCCEEECTCC-----
T ss_pred		HHHHhccCCCeEEEeCcHHHHHHHHHHHHHHhccCceEEEeCCCchhcc--

Vis	Hits	Aln	Select all	Forward	Forward Query MSA	Color Segs	Unwrap Segs
			Q ss_pred	CC-----CCCCccccEEEecHHhcCH---	HHHHHHHHhhcCCCCEEEEec		
			Q Klein_Draft	RT-----DRSGLGLTADRVIFDEAMTITP	----GSLKALLPTVSSRPNPQIVYTG		
			Q Consensus	154 ~~~~~~G~~~~~iDE~~~~~l~~~~~i~~st	.. .+...++ + +++.+. .+...+... .+....		
			T Consensus	151 ~~~l~~~~~iIDe~h~~~~~i~~~Sat	.. .+...++ + +++.+. .+...+... .+....		
			T 3FHT_B	151 PGTVLWDWCSKLKFIDPKKIKVFLDEADVMIA	TQGHQDQSIRIQRMLPRN-CQMLLFSAT		
			T ss_dssp	HHHHHHHHHTTSCSCGGGCCEEETHHHHHSTTT	HHHHHHHHHTTSCTT-CEEEEEEESC		
			T ss_pred	HHHHHHHHHHhCCCCChhC	CEEEEEEeCHHHHHhccccCHHHHHHHHHCCCC-CEEEEEECC		

[Template alignment](#) | [Template 3D structure](#) | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/1z63>)

70. [1Z63_B](#) (<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 cCCCCCHHHHHHHHHhccChhHhccCCchhhheeEeeEEecCCCCHHHHHHHHHHHH

Q Klein_Draft 29 CGLILDPWQELCLHEALKESDELVQLES

Q Consensus 29 AWVKKWAASSFGLVVSQRNGKGSILEALELA ~~~l~~Q~~~~g~~~~rg~GKT~~~~~

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

T Consensus 34 ~~~l~~Q~~~~-----1~~~~tG~GKT~~~~~

T 1Z63_B 34 IKANLRPYQIKGFSWMRFMNKL -----GFGICLADDMLGKTLQTIAVFS

T ss_dssp CSSCCCHHHHHHHHHHHHHH-----TCCEECCCTSCHHHHHHHHHH

T ss_pred ccccChHHHHHHHHHHHHHHHH-----CCCEEEdCCCCCHHHHHHHHHHHHH

Q ss_pred EEEcCCHHHHHHHHHHHHHHccchhhceeccCCcEEEecCCCCcEEEEEC---

Q Klein_Draft 99 IHSAHFKTAVNGMERLESLIAKSGLKYKAKQAHGAESIEILDGPNGARVIFQTRT---

Q Consensus 99 ~i~~t~~a~~~~~l~~~~~i~~~~~g~~i~~~~~

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

T Consensus 90 lvv~p~~~l~q~~~~~i~~v~t~~~

T 1Z63_B 90 LVICP-LSVLKNWEELSFKAPHRLFA---VFHEDRSKIKL---EDYDIILTTYAVLL

T ss_dssp EEEEC-STTHHHHHHHHHHHCTTSEE---ECSSTTSCCG---GGSSEEEHHHHT

T ss_pred EEEe-HHHHHHHHHHHHHCcCeEE---EECCCCcccc---hhCCEEEdCHHHH

Q ss_pred eEEEecHHcCHHHHHHHHHhhcCCCCEEEecCCCC

Q Klein_Draft 165 DRVIFDEAMTITPGSLKALLPTVSSRNPQIVYTGTAAQR 205 (510)

Q Consensus 165 ~~~v~iDE~~~~~l~~~~~i~~stp~~~ 205 (510)

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

T Consensus 151 ~~ViDE~H~~~~~l~~~~~1~1TaTp~~~ 191 (500)

T 1Z63_B 151 KYIVIDEAQNIKNPQTKIFKAVKELSKYRIALTGTPIENK 191 (500)

T ss_dssp EEEEEEETGGGSCTTSHHHHHHTSCEEEEECSSCSTTC

T ss_pred cEEEEECHHHccChHHHHHHHHhCCCCeCCCCCCC

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

71. [5SUQ_C](#) (<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 hHHHHHHHHHHhCC-CCCHHHHHHHHHhccChhHhccCCchhhheeEeeEEecCCC

Q Klein_Draft 18 AGQEAIIDLAAACGL-IIDPWQELCLHEALKESDELVQLES

Q Consensus 18 AWVKKWAASSFGLVVSQRNGKGSILEALELA ~~~~l~~Q~~~~g~~~~rg~

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

T Consensus 69 l~~~l~~~l~~~~~Q~~~i~~~~~il~~~tGs

T 5SUQ_C 69 LKPELSRAIIDCGFEHPSEVQQHTIPQSIH-----GTDVLCQAKSGL

T ss_dssp CCHHHHHHHHHHTTCCSCCCHHHHHHHHHHTT-----TCCEECCCTS

T ss_pred CCHHHHHHHHHCCCCCCCCCHHHHHHHHHhCCCC-CCeEEEEeCCCC

[Template alignment](#) | [Template 3D structure](#) | PDBe (<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		EECC-----CCCCccccEEEEEecHHHhcCHHHHHHHHHhhcC--CCCCEEeeEcC
Q Klein_Draft	152	QTRT-----DRSGLGLTADRVIFDEAMTITPGSLKALLPTVSS--RPNPQIVYGTAA
Q Consensus	152	~~~~~G~~~~~v~iDE~~~~~l~~~~~i~~stp .+. ++++++ +++.+. . . . +. ++++++ +
T Consensus	130	~t~~~~~iiide~h~~~~~i~~sat~
T 4CT4_B	130	ATPGRILDLIKKGVAKVDHQVMIVLDEADKLLSQDFVQIMEDIILTPKNRQLLYSATF
T ss_dssp		ECHHHHHHHHHHTSSCCTTCEEEEESHHHTSTTHHHHHHHHTSCTCEEEEEESCC
T ss_pred		ECHHHHHHHHHCcCCCCccccEEEEEeCHHHHcChhHHHHHHHHHHCCCCCEEeeeeECC

[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; 2.02A {Enterobacteria phage P22}

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

Q ss_pred CCCCCCCCCCCCCHHHHhCCCCCcc -CCCeEEEEEEcCCCCcEEEEEEEEEeCC -CCCC
Q Klein Draft 295 POFGAGISEIPLDKWRRLDNPEPDL -AGARALIYRTPEGGPWAIVGSORCTD -GRIHVE

Vis	Hits	Aln	Q Consensus <u>Select all</u>	295	~~~~~f~~~~~p~~~g~D~a~~~d~t~i~~~~~g~~~v~ Forward + .+ Forward Query MSA + .+ Color Seqs + .+ Unwrap Seqs + .+ .++++
			T Consensus	1	~~~~~G~vy~~f~~~~~g~D~G~~~p~a~~~~~i~i~
			T 4DKW_B	1	TMGS--GRIFQIPEETIKCQPFECPDHFYVIDAQDFGN-HPQAHIQLWWDKDADVFYLA
			T ss_dssp		CCBT--EESCCSCHHHHEECCCCCTSEEEEEECSS-SCEEEEEEEETTTTEEEE
			T ss_pred		CCCC--ccccCCCCchhccccCCCCCcEeEEEecCCC-CCeEEEEEEeCCCCEEEE
			Q ss_pred		HHHHHHHHHHHHHHCCCEEeeCc-----HH-HHHHHHHHCCeEcC-----CCHH
			Q Klein_Draft	362	DRVVDKFIQAITAWGPPEILVGRGG-----AA-EVIPQIEAGFTVYS-----PNQSE
			Q Consensus	362	~~~~~i~~~~~i~~~~~i~id~~g-----g~~~l~~~g~~~~~.++++.+.+++.++.... .+++. +.+ .+ .+. ++. +.+..
			T Consensus	68	~~~~~i~~~~~D~~~~~.1~~~G~~~~~
			T 4DKW_B	68	VQAWGAVKSWA--NKIPVAWPHDGHQHEKGGEQLKTQYADAGFSMLPDHATFPDGGS
			T ss_dssp		HHHHHHHHHHH---TTCEECCSSSSSSCHHHHHHHHTCEECSSCCCTTSCCC
			T ss_pred		HHHHHHHHHHh---CCCcEcCCccccCCCCchhHHHHHHHCCccccccccCCCCCc
			Q ss_pred		HhhCCCCCeeeCCcHHHHHHHccEEEECCCCCeeeeCCCCcHHHHHHHHHHHHHH
			Q Klein_Draft	419	DALVDPENPLSHGNQHSLNAAISRAVKRDLPSGGFWDCIEQSTYALMGVTLGRWALL
			Q Consensus	419	~l~~~~~g~i~~~~~l~~~l~~~~~.~~~~~D~~~dA~~~a~~~~~.+.+++. +.++ .+++.++...+ .+...++ .+. +.++....
			T Consensus	135	~l~~~~~l~v~~~c~~~i~el~y~~~~~p~~~dH~~~Da~rY~~~~~
			T 4DKW_B	135	LML--EGRFKVNTCEPFFEFRLYHRDENG-----KIVKTNDVLDATRYGYMMRR
			T ss_dssp		HHH---TTCEEETTCHHHHHHHCEECTTS-----CBCCSSCHHHHHHHHHHTGG
			T ss_pred		HHh---cCCEEeCCCHHHHHHHhCeeCCCC-----CCCCCCcHHHHHHHHHHHHhh

<input type="checkbox"/>	74.	Template alignment
		TIGR00643 (http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrvcgi?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 HHHHHHHHcCCCCCHHHHHHHHHhccChhHhccCCchhhh----eeEeeEEecC
		Q Klein_Draft 21 EAIDLAAACGLLIDPWQELCLHEALKESDELVQLESQAWKKWA----ASSFGLVVSR
		Q Consensus 21 ~~~~~~l~~~Q~~~~~g~~~~~.~~~~~r....++...+++. ++ .+++.+.++....
		T Consensus 224 ~~~~~~l~~~Q~~~i~~~i~~~~~.~~~~~li~~~t
		T TIGR00643 224 LLTKFLASLPFKLTRAQKRVVKEIL-----QDLKSDVPMNRLLQGDV
		T ss_pred HHHHHHHhCCCCCHHHHHHHHH-----HHccCCCCCcEEEeeCC
		Q ss_pred HHHHHHHhCeeEEEecCCHHHHHHHHHHHHHccchhhceeccCCeEEE----
		Q Klein_Draft 85 LELAGLILFGERLIIHSAHEFKTAVNGMERLESIAKSLKYKAKQAHGAESIEI----
		Q Consensus 85 ~~~~~~i~i~~~t~~~a~~~~~.~~~~~i~~~.+.++.... .+...+++. +.++...+.+....+....-.....
		T Consensus 276 ~~~~~~l~~~i~P~~~l~~~q~~~~~v~~~~~
		T TIGR00643 276 AMLAAIEA--GYQVALMAPTEILAEQHYNSLRNLLAPLGIEVALLTGS LKGKRRKELLET
		T ss_pred HHHHHHHC--CcEEECCCHHHHHHHHHHHHHhhCcEEEeeCCChHHHHHHHH
		Q ss_pred EEEEEECC--CCCCccccEEEEEecHHhcCHHHHHHHHHhccCC-CCCEEEEecC
		Q Klein_Draft 148 RVIFQTRT--DRSGLGLTADRVIFDEAMTITPGSLKALLPTVSSR-PNPQIVYTGT A 2
		Q Consensus 148 ~i~~~~~G~~~~~i~DE~~~~~l~~~i~~~stp 2 .. .+...+.+++. + +.+.+....+.... .+....+++.
		T Consensus 340 ~iii~T~~~l~~~~~iViDEah~~~~~i~lSaTp 3
		T TIGR00643 340 HL VVGTHALI QEKF KRL ALVI DEQH RFGVEQRKKLREKG QGGFTPHVLVMSATP 3
		T ss_pred cEEEeechhhhhccccEEEEEccccccHHHHHHHHhccCCCCeEEEeeCC

Vis	Hits	Aln	75.	1Z6A_A (http://pdb.rcsb.org/pdb/explore.do?structureId=1Z6A) Helicase of the snf2/rad54 family; HYDROLYASE-RECOMBINATION COMPLEX, YET_1047, 30A {Sulfobiosolipid A} SCOP: c.37.1.19	Color Segs	Unwrap Segs
Select all				Forward	Forward	Query MSA
Probability: 97.34	E-value: 6.2E-5	Score: 78.66	Aligned Cols: 154	Identities: 16%	Similarity	
Q ss_pred	cCCCCCHHHHHHHHHccChhHhcCcchhhheeEeeEEecCCCCHHHHHHHHHH					
Q Klein_Draft	29 CGLIILDWPQELCLHEALKESDELVQLESQAWVKWAASSFGLVVSQRNGKGSILEALELA					
Q Consensus	29 ~~~~l~~~Q~~~~~g~~~~~rg~GKT~~~~~					
T Consensus	34 ~~~~l~~~Q~~~~~li~~~tG~GKT~~~~~					
T 1Z6A_A	34 IKANLRPYQIKGFSWMRFMNKL-----GFGICLADDMLGLKTLQTIAVFSD					
T ss_dssp	CSSCCCHHHHHHHHHHHHHHT-----TCCEECCCTTSCHHHHHHHHHHH					
T ss_pred	ccccChHHHHHHHHHHHHHHH-----CCCEEeCCCCCHHHHHHHHHHH					
Q ss_pred	EEEecCCHHHHHHHHHHHHHHHHHccchhceccCCceEEEecCCCCcEEEEEC---					
Q Klein_Draft	99 IHSAHEFKTAVNGMERLESIAKSGLKYKAKQAHGAESIEILDGPNPQARVIFQTRT---					
Q Consensus	99 ~i~~~t~~~a~~~~~l~~~~~i~~~~~g~~i~~~~~					
T Consensus	90 liv~p~~~l~q~~~~~i~v~t~~~					
T 1Z6A_A	90 LVICP-LSVLKNWEEELSKFAPHLRFA---VFHEDRSKIKL---EDYDIILTTYAVLL					
T ss_dssp	EEECC-HHHHHHHHHHHHHCTTSCEE---ECCSSCCSCCG---GGSSEEECSHHHH					
T ss_pred	EEEEe-HHHHHHHHHHHHHCcCeEE---EEecCCCCch---hhCxEEeHHHHH					
Q ss_pred	eEEEEeHHhcCHHHHHHHHhhcCCCCEEEEeC					
Q Klein_Draft	165 DRVIFDEAMTITPGSLKALLPTVSSRPNPQIVYTGTADQR 205 (510)					
Q Consensus	165 ~~v~iDE~~~~~l~~~~~i~~stp~~~ 205 (510)					
T Consensus	151 ~~v~IvDE~H~~~~~l~~~~~l~1TaTp~~~ 191 (500)					
T 1Z6A_A	151 KYIVIDEAQNIKNPQTKIFKAVKELKSKYRIALTGTPIENK 191 (500)					
T ss_dssp	SEEEECSCCSCCSHHHHHTTSCCEEEECSCCTT					
T ss_pred	cEEEEeCHHHccChHHHHHHHhcCCCCeEEEeCCCCCCC					

Vis	Hits	Aln	T_ss_dssp Select all T_ss_pred	Forward	CCEEEESSTHHHHHCCCCCHHHHTTSCEECCSSCHHH--HHHCSEEEE CEEEELCCHHHHHHHHHHHHCCCELECCCCCCHHH--HhhCCEEEE	Forward Query MSA	Color Segs	Unwrap Segs
			Q_ss_pred		C----CCccccEEEEEecHHhcCHHHH-HHHHhhhcC-----CCCCE			
			Q_Klein_Draft	157	R----SGLGLTADRVIFDEAMTITPGSL-KALLPTVSS-----RPNPQ			
			Q_Consensus	157	~~~~~G~~~~~V~iD~E~~~~~l~~~~~.~~~~~+ + ++.....			
			T_Consensus	124	~~~~~l~iI~D~H~~~~~i~~~l~~~~~.~~~~~i			
			T_5JC3_B	124	ATEEDESVRLSDFLSIIIDQCHHTQKEGVVNIMRRYLKEKIKNRKQAKENKPLIPQPQI			
			T_ss_dssp		SCCC--CCCGGCSEEEETGGCSTTCHHHHHHHHHHHHHHHHHHC---CCCCCEE			
			T_ss_pred		CCCCCCCCChhhceEEEEEecHHHhcccHhHHHHHHHHHHHHchhhhcCCCCCCCCeE			
			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>)
 79. [3LLM A](http://pdbs.rcsb.org/pdb/explore.do?structureId=3LLM) (<http://pdbs.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		hHHHHHHHHHHhCC-CCCHHHHHHHHHhccChhHhhccCcchhhheeEeeEEecCCC
Q_Klein_Draft	18	AGQEAIIDLAAACGL-ILDPWQELCLHEALKESDELVQLEGAWVKWAASSFGLVVSQRN
Q_Consensus	18	~~~~~l~~~Q~~~~~g~~~~~rg~+....+....++ .++++ .+++...+..
T_Consensus	46	~~~~~Q~~~~~gs
T_3LLM_A	46	QDHDLQAILQERELLPVKKFESEILEAISQ-----NSVVIIRGATGC
T_ss_dssp		HCHHHHHHHHHHTSGGGGGHHHHHHHH-----CSEEEECCTS
T_ss_pred		cCHHHHHHHHHhccCCHHHHHHHHHHH-----CCEEEEcCCCC
Q_ss_pred		HHHHH---hCCeeEEEEecCCHHHHHHHHHHHHHHccchhceeccCCceEEEcCC
Q_Klein_Draft	87	LAGLIL---FGERLIIHSAHEFKTAVNGMERLESIAKSLKYKAKQAHGAESIEILDGP
Q_Consensus	87	~~~~~i~t~~~a~~~~~l~~~~~i~~~.+.++ +.+.+....
T_Consensus	98	~~~~~vlii~p~~~~~
T_3LLM_A	98	LDDFIQNDRAACNCIVVTQPRISAVSVAERFAERGEPKSCGYSVRFESILPR---
T_ss_dssp		HHHHHHTCGGGCEEEESSHHHHHHHHHHHTTCCTSSEEEETTEEECCC----
T_ss_pred		HHHHHhCCCCCEEEEcCHHHHHHHHHHHHHCCCCCCCCccccceehhhccCCC----
Q_ss_pred		CCCCCc---ccceeEEEEEecHHhcCHHH----HHHHHhhcCCCCCEEecCC
Q_Klein_Draft	154	RTDRSGL---GLTADRVIFDEAMTITPGS-----LKALLPTVSSRNPQIVYGTAA
Q_Consensus	154	~~~~~G~~~~~V~iD~E~~~~~l~~~~~i~~~stp~.----.++ + ++.....
T_Consensus	163	~~~l~~~~~i~D~H~~~~~i~~~sat~~
T_3LLM_A	163	VGVLRLKLEAGIRGISHVIVDEIHERDINTDFLLVLRDVQAYPE--VRIVLMSATID
T_ss_dssp		HHHHHHHHHHCCCTCCEEECCTTSCCHHHHHHHHHHHHHCTT--SEEEECSSC
T_ss_pred		HHHHHHHHHhccCCCCccccChhHHHHHHHHHHHHCCCC--CEEEEcCCCC

Template alignment | Template 3D structure | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/5jc3>)
 80. [5JC3 A](http://pdbs.rcsb.org/pdb/explore.do?structureId=5JC3) (<http://pdbs.rcsb.org/pdb/explore.do?structureId=5JC3>) LGP2/RNA Complex; Innate immune pa1 HET: ADP; 2.6A {Gallus gallus}

Vis	Hits	Aln	Probability: 97.31	E-value: 5.2E-5	Score: 83.09	Aligned Cols: 155	Identities: 12%	Similarity
			<u>Select all</u>	<u>Forward</u>	<u>Forward Query MSA</u>	<u>Color Seqs</u>	<u>Unwrap Seqs</u>	
			Q ss_pred	CCCCCHHHHHHHHHhhcChhHhcCCchhhheeEEEecCCCCHHHHHHHHHHHHH				
			Q Klein_Draft	30 GLILD PWQELCLHEALKESDELVQLES GAWVKKWAASSFGLVSRQNGKGSILEALELAG				
			Q Consensus	30 ~~~1~~~Q~~~~~g~~~~~rg~GKT~~~~~.+. +++ .+++.+.+..				
			T Consensus	5 ~~~1~~~yQ~e~~~~~i~~~tGsGKT~~a~~~i~~~.+++.+++.+ .+.+..				
			T 5JC3_A	5 DLTLDYQMEVAKPALN-----GENIICLPTGSGKTRVAVYITKDH				
			T ss_dssp	CCCCCHHHHHHHHHHHHT-----TCCEECCCTSCHHHHHHHHHHHHH				
			T ss_pred	ccCchHHHHHHHHHHhC-----CCcEEEEeCCCCCHHHHHHHHHHHHH				
			Q ss_pred	eeEEEEcCCHHHHHHHHHHHHHHHHc--ccchhceeccCcEEEecCCCCcEEEEEE				
			Q Klein_Draft	96 RLIIHSAHEFKTAVNGMERLESLIAK--SGLKYAKQAHGAE SIEILDGPNPGRVIFQT				
			Q Consensus	96 ~~i~~~t~~~a~~~~~l~~~~~i~~~~~g~~i~~~.+++++.+++.+.+..				
			T Consensus	57 ~~~livvP~~~l~~~q~~~~~v~~~~~Iii~T				
			T 5JC3_A	57 GKIVLVNKVPLVEQHLKEFNPFLKH WYQVIGLSGDSELKISFPEV--VKRYDVIICT				
			T ss_dssp	CCEEEESSTHHHHHCCCCCHHHHTTSCEE ECSSCSSCHHH--HHHCSEEEE				
			T ss_pred	CEEEEEEeCChHHHHHHHHHHhCCeEEEEeCCcccCCChHH--HhcCCEEEE				
			Q ss_pred	C----CCccccEEEEEecHHhcCHHHH-HHHHhhcC-----CCCE				
			Q Klein_Draft	157 R----SGLGLTADRVIFDEAMTITPGSL-KALLPTVSS-----RPNPQ				
			Q Consensus	157 ~~~~~G~~~~~v~iDE~~~~~l~~~~~.+++++.+++.+.+..				
			T Consensus	124 ~~~~~l~iI~DE~H~~~~~i~~~l~~~~~i~~~~~.~~~~~				
			T 5JC3_A	124 ATEEDESVRLSDFLSIIIDQCHHTQKEGVYNNIMRRYLKEKIKNRQAKENKPLIPQPQI				
			T ss_dssp	SCCC--CCGGGCSEEEETGGGCSTTCHHHHHHHHHHHHHHHHHHHHC---CCCCCE				
			T ss_pred	CCCCCCcChhceEEEecHHhcccHhHHHHHHHHHHhchhhhcCCCCCCCCeE				
			Q ss_pred	C				
			Q Klein_Draft	205 R 205 (510)				
			Q Consensus	205 ~ 205 (510)				
			T Consensus	194 ~ 194 (701)				
			T 5JC3_A	194 G 194 (701)				
			T ss_dssp	T				
			T ss_pred	C				

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

81. **4W7S_B (<http://pdb.rcsb.org/pdb/explore.do?structureId=4W7S>) S.cerevisiae Prp28 (127-588 aa); splicir ATPase; HET: MSE, ANP, P6G; 2.542A {Saccharomyces cerevisiae}**

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

Q ss_pred	CCCCCcEEeCCCCCcHHHHHHHH-HHhcC-CCHHHHHHHHHhccChhHhcCCCC
Q Klein_Draft	2 GVQEPRWLSPPEANSSAGQEAI DLA-AACGL-ILDPWQELCLHEALKESDELVQLES GAW
Q Consensus	2 ~~~~~rg~GKT~~~~~.~~~~~i~~~t~~~a~~~~~.+++++.+++.+.+..
T Consensus	39 ~~~~~Q~~~~~i~~~~~.~~~~~
T 4W7S_B	39 GGTVENPLRNWEELNIIPRDLLRVIQELRFPSPPTPIQRITIPNVNCNMKQ-----
T ss_dssp	SSSCCCCCSSSSTTCCSCHHHHCCCCSCCCSCCHHHHHHHHHHCTTT-----
T ss_pred	CCCCCCCCCHHcCCCCHHHHHHhcccc-----
Q ss_pred	EEecCCCCCHHHHHHHHHHHHHHHHc-----CeeEEEEeCCHHHHHHHHHHHHHHH
Q Klein_Draft	70 LVVSRQNGKGSILEALELAGLILFG-----ERLIIHSAHEFKTAVNGMERLES I
Q Consensus	70 ~~~rg~GKT~~~~~.~~~~~i~~~t~~~a~~~~~.+++++.+++.+.+..
T Consensus	94 i~~~tGsGKT~~~~~.~~~~~l~iI~P~~~l~~~q~~~~~
T 4W7S_B	94 GVASTGSGKTLAFVIPILIKMSRPPRPPSLKIIDGPKALILAPTR ELVQQIQKETQKV T

Vis	Hits	Aln	T ss_dssp Select all T ss_pred	Forward	Forward Query MSA	Color Segs	Unwrap Segs
					EECCSCTTHHHHHHHHHHHHHHTSCCCCCHHHHHHCCSEEECSSHHHHHHHHHHHHHH		
					EECCCCCCHHHHHHHHHHHHHHccCCCCCCCCCCCCCCCCCCCCHHHHHHHHHHHHHH		
			Q ss_pred		cchhhceeccCCceEEEecCCCCcEEEEEC-----CCCCccccEEEEEecHHh		
			Q Klein_Draft	122	SGLKYKAKQAHGAESIEILDGPNGPGRVIFQTRT-----DRSGLGLTADRVIFDEAMT		
			Q Consensus	122	~~l~~~~~i~~~~~g~~i~~~~~G~~~~v~iDE~~~		
			T Consensus	164+..... ..+.+.+..-....++ ++ ++.		
			T 4W7S_B	164	CKVISIVGGHSLEEISFSL---SEGCDILVATPGRILIDSLENHLLVMKQVETLVLDEADK		
			T ss_dssp		CCEEEECTTSCHHHHHHG---GCCSEEECHHHHHHHHTCCCTCCEECSHH		
			T ss_pred		cEEEEeCCCCHHHHHHHH---hcCcEEEECHHHHHHHhCcCCCCCCEEEEeCHH		
			Q ss_pred		HhhcCC-----CCCEEEEec		
			Q Klein_Draft	184	LPTVSSR-----PNPQIVYTGT 200 (510)		
			Q Consensus	184	~~~l~~~~~i~~st 200 (510)		
			T Consensus	231+... ...++++.+.		
			T 4W7S_B	231	TNILTKVDINADSAVNQTLMTA 254 (463)		
			T ss_dssp		HHHHHHHHHSCTTCCEEEEES		
			T ss_pred		HHHHHhCCcCCCCcCCEEEEEC		

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

82. [4W7S_A \(<http://pdbe.rcsb.org/pdb/explore.do?structureId=4W7S>\) 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		CCCCCcEEeCCCCCcHHHHHHHH-HHcCC-CCCHHHHHHHHHhccChhHhccCCCC
Q Klein_Draft	2	GVQEPRWLSPPEANSSAGQEADLA-AACGL-IIDPWQELCLHEALKESDELVQLESGAW
Q Consensus	2	~~~~~l~~~~~i~~~~~Q~~~~~g~~~
T Consensus	39	+....+....+....+....-+ ..+++. ++ .+++.+....
T 4W7S_A	39	~~~~~Q~~~~~i~~~~~
T ss_dssp		GGTVENPLRNWEELNIIPRDLLRVIQELRFPSPPTPIQRITIPNVNCNMKQ-----
T ss_pred		SSSSCCCCSSSSTTCSCHHHHCCCCCTCCSSCCHHHHHHHHHSCTTC-----
		CCCCCCCCCCCCHHhCCCCHHHHHHHHhCCCCCCCCHHHHHHHHhcccc-----
Q ss_pred		EEecCCCCHHHHHHHHHHHHHHhC-----CeeEEEecCCHHHHHHHHHHHHHHH
Q Klein_Draft	70	LVVSQRNGKGSILEALELAGLILFG-----ERLIIHSAAHEFKTAVNGMERLESILI
Q Consensus	70	~~~rg~GKT~~~~~i~~~~~t~~~a~~~~~
T Consensus	94	+....+ ..+....+....+ ..+++. +.+.++....+..
T 4W7S_A	94	i~~~tGsGKT~~~~~lii~P~~~l~~q~~~~~
T ss_dssp		GVASTGSGKTLAFVIPILIKMSRSPRPPSLKIIDGPKAIIAPRELVQQIQKETQKV
T ss_pred		EECCTSSHHHHHHHHHHHHHHHTSCCCCHHHHHHHCCSEEECSSHHHHHHHHHHHH
		EECC
Q ss_pred		cchhhceeccCCceEEEecCCCCcEEEEEC-----CCCCccccEEEEEecHHh
Q Klein_Draft	122	SGLKYKAKQAHGAESIEILDGPNGPGRVIFQTRT-----DRSGLGLTADRVIFDEAMT
Q Consensus	122	~~l~~~~~i~~~~~g~~i~~~~~G~~~~v~iDE~~~
T Consensus	164+..... ..+.+.+..-....++ ++ ++.
T 4W7S_A	164	CKVISIVGGHSLEEISFSL---SEGCDILVATPGRILIDSLENHLLVMKQVETLVLDEADK
T ss_dssp		CCEEEECTTCCCHHHHHHH---TTCCSEEECHHHHHHHHTCCC-CCCCEEETTHHH
T ss_pred		cEEEEeCCCCHHHHHHHH---hcCcEEEECHHHHHHHhCcCCCCCCEEEEeCHH
Q ss_pred		HhhcCC-----CCCEEEEec
Q Klein_Draft	184	LPTVSSR-----PNPQIVYTGT 200 (510)
Q Consensus	184	~~~l~~~~~i~~st 200 (510)
	+... ...++++.+.

Vis	Hits	Aln	T ss_dssp Select all T ss_pred	Forward	Forward Query MSA	Color Seas	Unwrap Seas
				TTCCCCHHHHHHHHHHHT-----	-----TCEEEECCGGGCTHHHHHHHHHH		
				CCCECCHHHHHHHHHH	-----CCCEEECCCCHHHHHHHHHH		
			Q ss_pred	EEECCCHHHHHHHHHHHHHHccchhhceeccCCceEEEecCCCCcEEEEEC---			
			Q Klein_Draft	99 IHSHEFKTAVNGMERLESLIAKSGLKYKAKQAHGAESIEILDGPNGARVIFQTRT---			
			Q Consensus	99 ~i~~~t~~~a~~~~~l~~~~~g~~i~~~~~			
			T Consensus	114 l~~v~P~~aL~~q~~~~~v~i~~~~~tg~d~~~~~ili~T~e~L~			
			T 4XGT_A	114 IYTSPIKALSNQKYRDFQAEFGDVGML-----TGDVTIN---PTASCLVMTTEILR			
			T ss_dssp	EEEEECHHHHHHHHHHHHHHSCEEE-----CSSCEEC---TTCSEEEEEEHHHH			
			T ss_pred	EEEEECCHHHHHHHHHHHHHcccee-----ccccccc---CCCCEEEeHHHH			
			Q ss_pred	cceeEEEecHHhcCH---HHHHHHHhhcCCCCCEEecCCC			
			Q Klein_Draft	162 LTADRVIFDEAMITIP---GSLKALLPTVSSRPNPQIVYGTAAAD 203 (510)			
			Q Consensus	162 ~~~~v~iDE~~~~~l~~~~~i~~~st~p~~ 203 (510)			
			T Consensus	172 ~~~~VI~DEaH~i~~~r~~~e~~~i~~~l~~~iv~lSAT~~n 216 (993)			
			T 4XGT_A	172 REVAVVFDEIHMRDKIRGVVWEETIILPDK-VRYVFLSATIPN 216 (993)			
			T ss_dssp	HHEEEEEEESCGGGGGCTTHHHHHHHHTSCTT-SEEEEEEESCCTT			
			T ss_pred	HheeEEEecHHccccccHHHHHHHHCCCC-CEEEEEEecCCCC			

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

85. **5DZR A (<http://pdb.rcsb.org/pdb/explore.do?structureId=5DZR>) FRQ-interacting RNA helicase; helicas 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	cCCCCCHHHHHHHHccChhHhccCCchhhheeEeeEEecCCCCHHHHHHHHHH
Q Klein_Draft	29 CGLILDWPQECLHEALKESDELVQLESQAWVKWAASSFGLVVSQRNGKGSILEALELA
Q Consensus	29 ~~~~l~~~Q~~~~~g~~~~~rg~GKT~~~~~
T Consensus	64 ~~~~l~~~Q~~~i~~~~~v~l~v~a~TGsGKT1~~~~~i~~
T 5DZR_A	64 YSFKLDPFQALSVASIER-----EESVLVSAHTSAGKTVVAEYAIAQ
T ss_dssp	TTCCCCHHHHHHHHHHT-----TCCEEEECCGGGCTHHHHHHHHH
T ss_pred	CCCCCCHHHHHHHHHc-----CEEEEEEecCCCCHHHHHHHHHH
Q ss_pred	EEECCCHHHHHHHHHHHHHHccchhhceeccCCceEEEecCCCCcEEEEEC---
Q Klein_Draft	99 IHSHEFKTAVNGMERLESLIAKSGLKYKAKQAHGAESIEILDGPNGARVIFQTRT---
Q Consensus	99 ~i~~~t~~~a~~~~~l~~~~~g~~i~~~~~
T Consensus	114 l~~v~P~~aL~~q~~~~~tg~d~~~~~ili~T~e~L~
T 5DZR_A	114 IYTSPIKALSNQKYRDFQAEFGDVGML-----TGDVTIN---PTASCLVMTTEILR
T ss_dssp	EEEEECHHHHHHHHHHSCEEE-----CSSCBCC---TTSSEEEEEEHHHH
T ss_pred	EEEEECCHHHHHHHHHcccee-----ccccccc---CCCCEEEeHHHH
Q ss_pred	cceeEEEecHHhcCH---HHHHHHHhhcCCCCCEEecCCC
Q Klein_Draft	162 LTADRVIFDEAMITIP---GSLKALLPTVSSRPNPQIVYGTAAAD 203 (510)
Q Consensus	162 ~~~~v~iDE~~~~~l~~~~~i~~~st~p~~ 203 (510)
T Consensus	172 ~~~~VI~DEaH~i~~~r~~~e~~~i~~~l~~~iv~lSAT~~n 216 (993)
T 5DZR_A	172 REVAVVFDEIHMRDKIRGVVWEETIILPDK-VRYVFLSATIPN 216 (993)
T ss_dssp	GSEEEEEEESCGGGGGCTTHHHHHHHHTSCTT-CEEEEEEESCCTT
T ss_pred	HheeEEEecHHccccccHHHHHHHHCCCC-CEEEEEEecCCCC

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

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

Vis	Hits	Aln	Probability: 97.28	E-value: 6.7E-5	Score: 76.51	Aligned Cols: 164	Identities: 9%	Similarity:
			<u>Select all</u>	<u>Forward</u>	<u>Forward Query MSA</u>	<u>Color Seqs</u>	<u>Unwrap Seqs</u>	
			Q ss_pred		hHHHHHHHHHHCCC-CCHHHHHHHHHhccChhHhccCcchhhhheeEeeEecCCC			
			Q Klein_Draft	18	AGQEAIIDLAAACGL-IIDPWQELCLHEALKESDELVQLESGAWVKWAASSFGLVVSQRN			
			Q Consensus	18	~~~~~l~~~Q~~~~~g~~~~~rg~ +.....-+....++ . +++ .+++.+. .+...+.++ +....+....+....+....			
			T Consensus	57	l~~~l~~~l~~~~Q~~~~~i~~~~~li~~~tGs			
			T 4D26_A	57	LRKYVLDNVLKAGYRKPTPIQKNAIPIIMS-----GRDLMGCAQTGS			
			T ss_dssp		CCHHHHHHHHHHTTCCSCCHHHHHHHHHHT-----TCCEEECCTTS			
			T ss_pred		CCHHHHHHHHHCCCCCCCCHHHHHHHHHHC-----CCeEEEECCCC			
			Q ss_pred		HHHHHHhC-----CeeEEEEcCCHHHHHHHHHHHHHHHhcc--chhhcecccc			
			Q Klein_Draft	87	LAGLILFG-----ERLIIHSAHEFKTAVNGMERLESIAKS--GLKYKAKQAHGA			
			Q Consensus	87	~~~~~i~~~~~t~~~~~a~~~~~l~~~~~ +...+...+ ..++ ++ +...+.+....+.... .+...+....			
			T Consensus	109	~~~~~liv~p~~~l~~~q~~~~~			
			T 4D26_A	109	INMLLQDPKDLISENGCAQPQVIIVSPTRELTQIFNEARKFSYGSVLKVAVAYGGTAVR			
			T ss_dssp		HHHHHHSCCCCCETTEECSEEECSSHHHHHHHHHHHTTSSCEEECTTSCHH			
			T ss_pred		HHHHhCChHHcccCCCCCCCcEEEEeCCHHHHHHHHHHHhCCcEEEEEECCCC			
			Q ss_pred		CCcEEEEEECC-----CCCCcccceeEEEEecHHhcCHHH-HHHHhhcC----C			
			Q Klein_Draft	145	PGARVIFQTRT-----DRSGLGLTADRVIFDEAMTITPGSL-KALLPTVSS-----R			
			Q Consensus	145	~g~~~i~~~~~G~~~~~v~iDE~~~~~l~~~~~ .+. .+.+.+ ..-..++ ++ +...+.+....+....+....+....			
			T Consensus	176	~~~~~i~v~t~~~l~~~~~liiDE~h~~~~~			
			T 4D26_A	176	RGCHILVATPGRLLHDVERNRVSFGSVRFVVLQADCMDFMPSIEKMLHPTMVETT			
			T ss_dssp		TCCSEEECHHHHHHHHTTSBCCTTCCEEETHHHTSTTTHHHHHHHTCTSCGG			
			T ss_pred		hCCCEEEEchHHHHHHhCCcCcCcCcEEEeCHHHHHhCCCHHHHHhCCcCCCC			
			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			

<input type="checkbox"/>	87.	Template alignment Template 3D structure PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/4d25) 4D25_A (http://pdb.rcsb.org/pdb/explore.do?structureId=4D25) BMVLG PROTEIN; HYDROLASE, PIRNA, TRANSPOSON; HET: ANP; 1.9A {BOMBYX MORI}	Probability: 97.28	E-value: 6.7E-5	Score: 76.51	Aligned Cols: 164	Identities: 9%	Similarity:
			Q ss_pred		hHHHHHHHHHHCCC-CCHHHHHHHHHhccChhHhccCcchhhhheeEeeEecCCC			
			Q Klein_Draft	18	AGQEAIIDLAAACGL-IIDPWQELCLHEALKESDELVQLESGAWVKWAASSFGLVVSQRN			
			Q Consensus	18	~~~~~l~~~Q~~~~~g~~~~~rg~ +.....-+....++ . +++ .+++.+. .+...+.++ +....+....+....			
			T Consensus	57	l~~~l~~~l~~~~Q~~~~~i~~~~~li~~~tGs			
			T 4D25_A	57	LRKYVLDNVLKAGYRKPTPIQKNAIPIIMS-----GRDLMGCAQTGS			
			T ss_dssp		CCHHHHHHHHHHTTCCSCCHHHHHHHHHHT-----TCCEEECCTTS			
			T ss_pred		CCHHHHHHHHHCCCCCCCCHHHHHHHHHHC-----CCeEEEECCCC			
			Q ss_pred		HHHHHHhC-----CeeEEEEcCCHHHHHHHHHhcc--chhhcecccc			
			Q Klein_Draft	87	LAGLILFG-----ERLIIHSAHEFKTAVNGMERLESIAKS--GLKYKAKQAHGA			
			Q Consensus	87	~~~~~i~~~~~t~~~~~a~~~~~l~~~~~ +...+...+ ..++ ++ +...+.+....+....+....+....			
			T Consensus	109	~~~~~liv~p~~~l~~~q~~~~~			
			T 4D25_A	109	INMLLQDPKDLISENGCAQPQVIIVSPTRELTQIFNEARKFSYGSVLKVAVAYGGTAVR			

Template alignment

88. [TIGR00580](http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrvc.cgi?uid=TIGR00580) (<http://www.ncbi.nlm.nih.gov/Structure/cdd/cddsrvc.cgi?uid=TIGR00580>) mfd; transcription
All proteins in this family for which functions are known are DNA-dependent ATPases that function in coupled DNA repair in which the repair of the transcribed strand of actively transcribed genes is repaired by repair of non-transcribed regions of the genome and than the non-transcribed strand of the same gene.
Probability: 97.28 E-value: 1.5E-4 Score: 82.28 Aligned Cols: 161 Identities: 11% Similarity:

Probability: 97.28 E-value: 1.5E-4 Score: 82.28 Aligned Cols: 161 Identities: 11% Similarity

Q ss_pred		HHHHHHHHHHHHHHHHCCeEEEEEccCCHHHHHHHHHHHHHHccccchhcceecccc---
Q Klein_Draft	78	KGSILEALELAGLILFGERLIIHSASHEFKAVNGMERLESIAKSGLKAKQAHGA---
Q Consensus	78	KT~~~~~i~i~~~t~~~a~~~~~l~~~~~ .++....++..+... ..+++++ +.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+.+
T Consensus	485	KT~~~l~~~~~vlii~Pt~~~L~~q~~~l~~~~~v~~~~~
T TIGR00580	485	KTEVAMRAAFKAVLDG--KQVALVPTTLAQQHFETFKERFANFPVTIELLSRFRSAKE
T ss_pred		HHHHHHHHHHHHHHCC--CEEEEEcchHHHHHHHHHHHHcccccccccccccccccccccccc

Q ss_pred		ecCCCCCcEEEEEECC--CCCCccceeeEEEecHHhcCHHHHHHHHhhccccCCCCCEE
Q Klein_Draft	140	LDGPNGARVIFQTRT--DRSGLGLTADRVIFDEAMTITPGSLKALLPTVSSRPNPQIVY
Q Consensus	140	~~~~~g~~~i~~~~~G~~~~~V~iDE~~~~~l~~~~~i~~+..+...-+++++ + +++.+.....+..... ...+.+
T Consensus	553	-----iiI~T~~~l~~~~~l~1iIiDEaH~~~~~l~~~~~l~1l
T TIGR00580	553	-----GKIDILIGTHKLQLQKDVFKFDLGLLIIDEQRFGVQKKEKLERTS--VDVLT
T ss_pred		----CCCCEEEeHHHhcCCCCccccCCCCFEEecHHhcCccHHHHHHHhcCC--CcEEE

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

2EYQ A (<http://pdb.rcsb.org/pdb/explore.do?structureId=2EYQ>) Transcription-repair coupling factor; I

WEB-ELP-352A (Escherichia coli) SCGP-C.57.1.15, B35418.1, Q51511

[Template alignment](#) | [Template 3D structure](#) | PDBe (<http://www.ebi.ac.uk/pdbe/entry/pdb/2zj8>)

93. [2Z8 A](http://pdb.rcsb.org/pdb/explore.do?structureId=2Z8) (<http://pdb.rcsb.org/pdb/explore.do?structureId=2Z8>) Putative ski2-type helicase (E.C.3.6.1.-); I Helicase, Hydrolase; 2.0A {Pyrococcus furiosus}

Probability: 97.25 E-value: 2.0E-4 Score: 78.88 Aligned Cols: 162 Identities: 15% Similarity

Q ss_pred		-----CCCCccccEEEEEcHHhcCH---HHHHHHHhhccCCCCCEEEEecCCC
Q Klein_Draft	156	-----DRSGLGLTADRVIFDEAMTITP---GSLKALLPTVSSRPNPQIVYTGAAD
Q Consensus	156	-----~G~~~~~v~iDE~~~~~l~~~~~i~~~stp~~-+++++ +++.++... .++.+.++... .+.+++/+..
T Consensus	125	1~~~~~iIiDE~H~~~~~le~~~~~i~1SaT~~~
T 2ZJ8_A	125	FDSLLRHGSSWIKDVKILVADEIHLIGS RDRGATLEVILA HMLGK-AQIIGLSATIGN
T ss_dssp		HHHHHHHHCTTGGGEEEEEETGGGGCTTHHHHHHHHHHHBT-BEEEEEECCCS
T ss_pred		HHHHHHhcCchHhhcCEEEEeHhcCCCCchHHHHHHHHHHhc-CeEEEeCCCCC

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

94. [3G0H A](http://pdb.rcsb.org/pdb/explore.do?structureId=3G0H) (<http://pdb.rcsb.org/pdb/explore.do?structureId=3G0H>) ATP-dependent RNA helicase DDX19B RNA COMPLEX, DBP5, Structural Genomics; HET: ANP; 2.7A {Homo sapiens}

Probability: 97.25 E-value: 3.1E-4 Score: 71.51 Aligned Cols: 163 Identities: 11% Similarity

Q ss_pred hHHHHHHHHHcCC-CCCHHHHHHHHHhCChhHhhccCcchhhhe--EeeeEEecC
Q Klein_Draft 18 AGQEAIIDLAAACGL-ILDPWQELCLHEALKESDELVQLESAGAWKKWAAS-SFGLVVSR

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

95. [2P6R A](http://pdb.rcsb.org/pdb/explore.do?structureId=2P6R) (<http://pdb.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

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

Q ss_pred chHHHHHHHHHHCCCC-CCCHHHHHHHHHhccChhHhhccccCcchhhheeEeeEEecCC

Q Klein Draft 17 SAGOEAIIDLAAACGL-ILDPWOELCLHEALKESDELVOLESAGAWVKKWAASSFGLVVSRQ

| Consensus 9 ~~~~~T~~~~~g~~~~Q~~~~~-----~~~~~lvapIG

T 2P6R_A 9 SISSYAVGILKEEGIEELFPPQAEAVEKVFS-----GKNLLLAMPTA

T ss_dssp HHHHHHHHHHHCC---CCCCCCCBBBBBTT-----CSCEEECSSH

T ss_pred hcCHHHHHHHHHCCCCcCCCCHHHHHHHHHhc-----CCcEEEECCCCC

SEARCHED SERIALIZED INDEXED FILED 11/11/2005 5555 5555 5555

Q ss_pred HHHHHHHhCcEEEEECCCCHHHHHHHHHHHHHHHHHHHccccchhhceeeccccccccc

Q Klein_Draft 86 ELAGLILFGERLIIHSAHEFKTAVNGMERLESIAKSGLKYKAKQAHGAESEIEILDGPNP

Q Consensus 86 ~~~~~i~i~~t~~a~~~~l~~~~i~~~~

T Consensus 61 i1~~~~~l1~v~P~L~q~~~~~v~~~~g~~~~~- - -

T_2P6R_A 61 MVRATK--GGKSIVYVPIRALAGEKYSEKKWEK-TGIRGTGSTGDYESRDEHLI----G

1 ss_dssp

ss_pred HHHHHHh--cCeEEEcChHHHHHHHHHHHHHHHH-ccCeEEEcCCCCccccHHH---c

O ss pred -----CCCCccccccEEEEEecHHhcCH-----HHHHHHHHhhcCCCCCCEEEEEEecC

O Klein Draft 156 -----DRSGIQLTADRVTFEAMTTTP-----GSLKALLPTVSSRPNPOTVYGTAA

Q RICIN_DRAVE 156 DRSEGGETADKIVBEAHTW... QSERALEPFLVSDRKNQIVVSTGA...

Q Consensus 156 -----G-----V-----I-----D-----E-----P-----I-----T-----I-----S-----P-----

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

T Consensus 124 ~1~~~~~liIvDE~H~i~~~r~~~e~~~~l~~~~~ii~1SAT~

T 2P6R_A 124 KADSLIRNRASWIKAWSCLVVDEIHLLDSEKRGATLEILVTKMRRMNKA-LRVIGLSATA

Vis	Hits	Aln	<u>Select</u>	Forward	HHH Forward	Query MSA	<u>Color Seqs</u>	<u>Unwrap Seqs</u>
			Q Klein_Draft	466	QLMGVTLGRW	475 (510)		
			Q Consensus	466	~~dA~~~a~~	475 (510)	.+ +.++.	
			T Consensus	133	~~Da~rY~~~	142 (143)		
			T PF17288.1	133	TLSAIWYALD	142 (143)		
			T ss_pred		HHHHHHHHhc			
<hr/>								
Template alignment Template 3D structure PDBe (http://www.ebi.ac.uk/pdbe/entry/pdb/2xgj)								
100. 2XGJ_A (http://pdb.rcsb.org/pdb/explore.do?structureId=2XGJ) ATP-DEPENDENT RNA HELICASE DOB1 (COMPLEX, HYDROLASE, TRAMP, EXOSOME; HET: ADP; 2.9A {SACCHAROMYCES CEREVISIAE})								
Probability: 97.21 E-value: 1.4E-4 Score: 83.17 Aligned Cols: 143 Identities: 17% Similarity								
<p>Q ss_pred HccccccHHHHHHHHhhCcChhHhccCccchhhheeEeeEcCCCCHHHHHHHHHHHH</p> <p>Q Klein_Draft 28 ACGLILDPWQECLHEALKESDELVQLESQAWVKWAASSFGLVVSQRNGKGSILEALEL</p> <p>Q Consensus 28 ~~~~~l~~~Q~~~~~g~~~~~rg~GKT~~~~~</p> <p> .+++. +++ .+...+.. .+...++..++ + .++....++</p> <p>T Consensus 82 ~~~~~l~~~Q~~ai~~l~~~~~ll~a~tGsGKT1~~~~~i~</p> <p>T 2XGJ_A 82 TYPFTLDPFQDTAISCDR-----GESVLVSAHTSAGKTVVAEYAI</p> <p>T ss_dssp 82 CCSSCCCHHHHHHHHHHH-----TCEEEECCCTSCHHHHHHHHH</p> <p>T ss_pred 82 hCCCCCCHHHHHHHHHHH-----CCcEEEEecCCCCCHHHHHHHHHHH</p> <p>Q ss_pred EEEEcCCHHHHHHHHHHHHHHHHHcccchhceccCcceEEEcCCCCcEEEEEC--</p> <p>Q Klein_Draft 98 IIHSAHEFKTAVNGMERLESLIAKSGLKYAKQAHGAESIEILDGPNGARVIFQRTT--</p> <p>Q Consensus 98 i~i~~~t~~~a~~~~~l~~~~~i~~~~~g~~i~~~~~</p> <p> ++ ++ +...+.+....+....+. + .+.++</p> <p>T Consensus 132 ~l~v~P~~aL~~Q~~~~~v~~~~~g~~~~~ilV~T~e~l</p> <p>T 2XGJ_A 132 VIYTSPIKALSNQKYRELLAEFGDVGLM-----TGEDITIN----PDAGCLVMTTEIL</p> <p>T ss_dssp 132 EEEESSHHHHHHHHHHHHHSCEE-----CSSCEEC---TTCSEEEEHHHH</p> <p>T ss_pred 132 EEEEcCcHHHHHHHHHHHHHCCceee-----ecCccCC---CCCCEEeHHHH</p> <p>Q ss_pred ccceeEEEecHHhcCH----HHHHHHHHhhCcCCCCCEEeeEcCCC</p> <p>Q Klein_Draft 161 GLTADRVIFDEAMTITP---GSLKALLPTVSSRPNPQIVYTGTAAAD 203 (510)</p> <p>Q Consensus 161 G~~~~~v~iDE~~~~~l~~~~~i~~~stp~~ 203 (510)</p> <p> -.++. + ++.+.+ ..+++.+....+... ...+++++ +..</p> <p>T Consensus 190 ~~~~~v~DEaH~l~d~~rg~~e~~i~~l~~~~~v~1SATi~n 235 (1010)</p> <p>T 2XGJ_A 190 MREVAWVIFDEVHYMRDKERGVVWEETIILLPDK-VRVVFSLATIPN 235 (1010)</p> <p>T ss_dssp 190 GGEEEEEEETGGGGCTTTHHHHHHHHSCTT-CEEEEEECCCTT</p> <p>T ss_pred 190 HHheeEEEecccccCcccccHHHHHHhCCCC-CEEEEEEcccc</p>								

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References

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The MPI bioinformatics Toolkit as an integrative platform for advanced protein sequence and structure analysis.

Alva V, Nam SZ, Söding J, Lupas AN. *Nucleic Acids Res.* 2016 Jul 8;44(W1):W410-5 ([//academic.oup.com/nar/article-lookup/doi/10.1093/nar/gkw348](http://academic.oup.com/nar/article-lookup/doi/10.1093/nar/gkw348)).

And one or more of the following:

Protein homology detection by HMM-HMM comparison.

Söding J. *Bioinformatics*. 2005 Apr 1;21(7):951-60 ([//academic.oup.com/bioinformatics/article-lookup/doi/10.1093/bioinformatics/bti125](http://academic.oup.com/bioinformatics/article-lookup/doi/10.1093/bioinformatics/bti125)),

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Fast and accurate automatic structure prediction with HHpred.
Aln Hildebrand A, Rehmert M, Biegert A, Söding J. *Proteins*. 2009; *75 Suppl 1*:28-32.
<https://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
<https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1004343>.

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