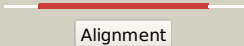
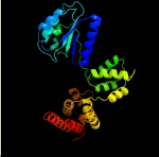
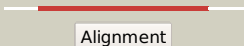
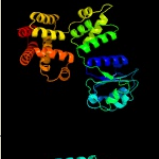
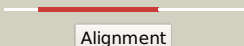


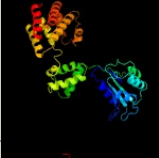

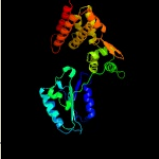







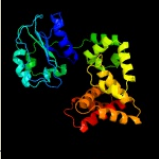












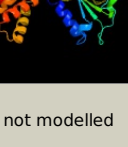


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2413c (- )_2710361_2711311
Date	Wed Aug 7 12:50:03 BST 2019
Unique Job ID	32f14fcabec622f2

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1xxiF_</a>	 Alignment		100.0	15	<b>PDB header:</b> transferase <b>Chain:</b> F: <b>PDB Molecule:</b> dna polymerase iii, delta subunit; <b>PDBTitle:</b> adp bound e. coli clamp loader complex
2	<a href="#">c3zh9B_</a>	 Alignment		100.0	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> delta; <b>PDBTitle:</b> bacillus subtilis dna clamp loader delta protein (yqen)
3	<a href="#">d1jr3d2</a>	 Alignment		100.0	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
4	<a href="#">c1xxhB_</a>	 Alignment		100.0	11	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase iii subunit gamma; <b>PDBTitle:</b> atpgs bound e. coli clamp loader complex
5	<a href="#">c1jr3E_</a>	 Alignment		99.9	11	<b>PDB header:</b> transferase <b>Chain:</b> E: <b>PDB Molecule:</b> dna polymerase iii, delta' subunit; <b>PDBTitle:</b> crystal structure of the processivity clamp loader gamma complex of e.2 coli dna polymerase iii
6	<a href="#">d1jr3d1</a>	 Alignment		99.9	15	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
7	<a href="#">d1jqlb_</a>	 Alignment		99.8	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
8	<a href="#">c1sxD_</a>	 Alignment		99.5	14	<b>PDB header:</b> replication <b>Chain:</b> D: <b>PDB Molecule:</b> activator 1 41 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
9	<a href="#">c2gnoA_</a>	 Alignment		99.5	11	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna polymerase iii, gamma subunit-related protein; <b>PDBTitle:</b> crystal structure of a dna polymerase iii, gamma subunit-related2 protein (tm0771) from thermotoga maritima msb8 at 2.00 a resolution
10	<a href="#">c1iqpF_</a>	 Alignment		99.4	15	<b>PDB header:</b> replication <b>Chain:</b> F: <b>PDB Molecule:</b> rfcs; <b>PDBTitle:</b> crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
11	<a href="#">c2chvE_</a>	 Alignment		99.4	14	<b>PDB header:</b> dna-binding protein <b>Chain:</b> E: <b>PDB Molecule:</b> replication factor c small subunit; <b>PDBTitle:</b> replication factor c adpnp complex

12	<a href="#">d1jr3a1</a>	Alignment		99.4	11	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
13	<a href="#">c1sxE</a>	Alignment		99.4	11	<b>PDB header:</b> replication <b>Chain:</b> E: <b>PDB Molecule:</b> activator 1 40 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
14	<a href="#">c3pvsA</a>	Alignment		99.3	12	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> replication-associated recombination protein a; <b>PDBTitle:</b> structure and biochemical activities of escherichia coli mgsa
15	<a href="#">c1sxC</a>	Alignment		99.3	12	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> activator 1 40 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
16	<a href="#">c1sxB</a>	Alignment		99.2	12	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> activator 1 37 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
17	<a href="#">d2gnoa2</a>	Alignment		99.0	13	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
18	<a href="#">c3u5zM</a>	Alignment		99.0	12	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> M: <b>PDB Molecule:</b> dna polymerase accessory protein 44; <b>PDBTitle:</b> structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
19	<a href="#">c6genX</a>	Alignment		98.9	10	<b>PDB header:</b> nuclear protein <b>Chain:</b> X: <b>PDB Molecule:</b> ruvb-like protein 1; <b>PDBTitle:</b> chromatin remodeller-nucleosome complex at 4.5 a resolution.
20	<a href="#">c2chgB</a>	Alignment		98.9	14	<b>PDB header:</b> dna-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> replication factor c small subunit; <b>PDBTitle:</b> replication factor c domains 1 and 2
21	<a href="#">d1sxC2</a>	Alignment	not modelled	98.7	9	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
22	<a href="#">c1sxA</a>	Alignment	not modelled	98.6	12	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> activator 1 95 kda subunit; <b>PDBTitle:</b> crystal structure of the eukaryotic clamp loader (replication factor2 c, rfc) bound to the dna sliding clamp (proliferating cell nuclear3 antigen, pcna)
23	<a href="#">d1iqa2</a>	Alignment	not modelled	98.6	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
24	<a href="#">d1sxB2</a>	Alignment	not modelled	98.6	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
25	<a href="#">d1njfa</a>	Alignment	not modelled	98.6	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
26	<a href="#">d1sxD2</a>	Alignment	not modelled	98.5	14	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
27	<a href="#">d1sxE2</a>	Alignment	not modelled	98.4	10	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
28	<a href="#">c5oafB</a>	Alignment	not modelled	98.4	9	<b>PDB header:</b> gene regulation <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> human rvb1/rvb2 heterohexamers in ino80 complex
						<b>PDB header:</b> hydrolase

29	<a href="#">c3pfiB</a>	Alignment	not modelled	98.3	15	<b>Chain:</b> B: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruvb; <b>PDBTitle:</b> 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
30	<a href="#">c3bosA</a>	Alignment	not modelled	98.2	9	<b>PDB header:</b> hydrolase regulator,dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna replication factor; <b>PDBTitle:</b> crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
31	<a href="#">c2c9oA</a>	Alignment	not modelled	98.2	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ruvb-like 1; <b>PDBTitle:</b> 3d structure of the human ruvb-like helicase ruvb1
32	<a href="#">c4ww4B</a>	Alignment	not modelled	98.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
33	<a href="#">d1in4a2</a>	Alignment	not modelled	98.0	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
34	<a href="#">d1sxja2</a>	Alignment	not modelled	97.9	8	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
35	<a href="#">c2z4rB</a>	Alignment	not modelled	97.8	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
36	<a href="#">c4ww4A</a>	Alignment	not modelled	97.8	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> ruvb-like 1; <b>PDBTitle:</b> double-heterohexameric rings of full-length rvb1(adp)/rvb2(adp)
37	<a href="#">c1in8A</a>	Alignment	not modelled	97.7	11	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction dna helicase ruvb; <b>PDBTitle:</b> thermotoga maritima ruvb t158v
38	<a href="#">c5ep0A</a>	Alignment	not modelled	97.6	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative repressor protein luxo; <b>PDBTitle:</b> quorum-sensing signal integrator luxo - receiver+catalytic domains
39	<a href="#">d1sxd1</a>	Alignment	not modelled	97.0	13	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
40	<a href="#">d1ixsb2</a>	Alignment	not modelled	96.9	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
41	<a href="#">d1a5ta2</a>	Alignment	not modelled	96.7	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
42	<a href="#">c5m7nA</a>	Alignment	not modelled	96.3	16	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> nitrogen assimilation regulatory protein; <b>PDBTitle:</b> crystal structure of ntrx from brucella abortus in complex with atp2 processed with the crystaldirect automated mounting and cryo-cooling3 technology
43	<a href="#">d1l8qa2</a>	Alignment	not modelled	96.2	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
44	<a href="#">c3dzdA</a>	Alignment	not modelled	95.8	14	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator ntrc4 in the inactive2 state
45	<a href="#">c3h4mC</a>	Alignment	not modelled	95.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> aaa atpase domain of the proteasome- activating nucleotidase
46	<a href="#">c1ny5A</a>	Alignment	not modelled	95.7	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
47	<a href="#">c2c9oC</a>	Alignment	not modelled	95.6	8	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ruvb-like 1; <b>PDBTitle:</b> 3d structure of the human ruvb-like helicase ruvb1
48	<a href="#">c6blbA</a>	Alignment	not modelled	95.6	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> holliday junction atp-dependent dna helicase ruvb; <b>PDBTitle:</b> 1.88 angstrom resolution crystal structure holliday junction atp-2 dependent dna helicase (ruvb) from pseudomonas aeruginosa in complex3 with adp
49	<a href="#">c4z8xC</a>	Alignment	not modelled	95.3	11	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent zinc metalloprotease ftsh; <b>PDBTitle:</b> truncated ftsh from a. aeolicus
50	<a href="#">c5gjqL</a>	Alignment	not modelled	94.9	9	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease regulatory subunit 10b; <b>PDBTitle:</b> structure of the human 26s proteasome bound to usp14-ubal
51	<a href="#">c4b4tL</a>	Alignment	not modelled	94.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease subunit rpt4; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
52	<a href="#">c5zr1A</a>	Alignment	not modelled	94.8	14	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> A: <b>PDB Molecule:</b> origin recognition complex subunit 1; <b>PDBTitle:</b> saccharomyces cerevisiae origin recognition complex bound to a 72-bp2 origin dna containing acs and b1 element
53	<a href="#">c3vfdA</a>	Alignment	not modelled	94.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> spastin; <b>PDBTitle:</b> human spastin aaa domain

54	<a href="#">dlixza_</a>	Alignment	not modelled	94.5	16	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
55	<a href="#">c2ce7B_</a>	Alignment	not modelled	94.5	15	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
56	<a href="#">dliqpa1</a>	Alignment	not modelled	94.4	15	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
57	<a href="#">d1ny5a2</a>	Alignment	not modelled	94.1	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
58	<a href="#">c1iy2A_</a>	Alignment	not modelled	93.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent metalloprotease ftsh; <b>PDBTitle:</b> crystal structure of the ftsh atpase domain from thermus2 thermophilus
59	<a href="#">c4b4tl_</a>	Alignment	not modelled	93.6	10	<b>PDB header:</b> hydrolase <b>Chain:</b> I: <b>PDB Molecule:</b> 26s protease regulatory subunit 4 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
60	<a href="#">c4b4tM_</a>	Alignment	not modelled	92.7	9	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> 26s protease regulatory subunit 6a; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
61	<a href="#">c2dhrC_</a>	Alignment	not modelled	92.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ftsh; <b>PDBTitle:</b> whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
62	<a href="#">c3sylB_</a>	Alignment	not modelled	92.3	12	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> protein cbbx; <b>PDBTitle:</b> crystal structure of the aaa+ protein cbbx, native structure
63	<a href="#">d1fnna2</a>	Alignment	not modelled	91.9	12	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
64	<a href="#">c5ubvB_</a>	Alignment	not modelled	91.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> atpase domain of i-aaa protease; <b>PDBTitle:</b> atpase domain of i-aaa protease from myceliophthora thermophila
65	<a href="#">c4b4tH_</a>	Alignment	not modelled	91.7	13	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> 26s protease regulatory subunit 7 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
66	<a href="#">c6f3tK_</a>	Alignment	not modelled	91.1	14	<b>PDB header:</b> transcription <b>Chain:</b> K: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 6; <b>PDBTitle:</b> crystal structure of the human taf5-taf6-taf9 complex
67	<a href="#">c6qj8E_</a>	Alignment	not modelled	91.0	10	<b>PDB header:</b> chaperone <b>Chain:</b> E: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> truncated human r2tp complex, structure 3 (adp-filled)
68	<a href="#">c5ep4A_</a>	Alignment	not modelled	90.7	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> putative repressor protein luxo; <b>PDBTitle:</b> structure, regulation, and inhibition of the quorum-sensing signal2 integrator luxo
69	<a href="#">c3te6A_</a>	Alignment	not modelled	90.4	11	<b>PDB header:</b> gene regulation <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein sir3; <b>PDBTitle:</b> crystal structure of the s. cerevisiae sir3 aaa+ domain
70	<a href="#">c2v6zM_</a>	Alignment	not modelled	90.2	13	<b>PDB header:</b> transferase <b>Chain:</b> M: <b>PDB Molecule:</b> dna polymerase epsilon subunit 2; <b>PDBTitle:</b> solution structure of amino-terminal domain of human dna polymerase2 epsilon subunit b
71	<a href="#">c5mpaL_</a>	Alignment	not modelled	90.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> L: <b>PDB Molecule:</b> 26s protease subunit rpt4; <b>PDBTitle:</b> 26s proteasome in presence of atp (s2)
72	<a href="#">c6azyA_</a>	Alignment	not modelled	90.0	17	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein hsp104; <b>PDBTitle:</b> crystal structure of hsp104 r328m/r757m mutant from calcarisporiella2 thermophila
73	<a href="#">c3b9pA_</a>	Alignment	not modelled	89.9	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
74	<a href="#">c6nyyA_</a>	Alignment	not modelled	89.8	11	<b>PDB header:</b> translocase <b>Chain:</b> A: <b>PDB Molecule:</b> afg3-like protein 2; <b>PDBTitle:</b> human m-aaa protease afg3l2, substrate-bound
75	<a href="#">c6epcJ_</a>	Alignment	not modelled	89.4	12	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 8; <b>PDBTitle:</b> ground state 26s proteasome (gs2)
76	<a href="#">c4b4tJ_</a>	Alignment	not modelled	88.8	9	<b>PDB header:</b> hydrolase <b>Chain:</b> J: <b>PDB Molecule:</b> 26s protease regulatory subunit 8 homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
77	<a href="#">d1tafb_</a>	Alignment	not modelled	88.4	10	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> TBP-associated factors, TAFs
78	<a href="#">c6hecH_</a>	Alignment	not modelled	87.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> proteasome-activating nucleotidase; <b>PDBTitle:</b> pan-proteasome in state 4
79	<a href="#">d1sxjc1</a>	Alignment	not modelled	87.1	11	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain

80	<a href="#">c2c99A</a>	Alignment	not modelled	86.9	14	<b>PDB header:</b> transcription regulation <b>Chain:</b> A: <b>PDB Molecule:</b> psp operon transcriptional activator; <b>PDBTitle:</b> structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
81	<a href="#">c3pxiB</a>	Alignment	not modelled	86.6	15	<b>PDB header:</b> protein binding <b>Chain:</b> B: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mecb; <b>PDBTitle:</b> structure of meca108:clpc
82	<a href="#">c1hqcB</a>	Alignment	not modelled	86.4	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb; <b>PDBTitle:</b> structure of ruvb from thermus thermophilus hb8
83	<a href="#">d1w5sa2</a>	Alignment	not modelled	86.3	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
84	<a href="#">c3uk6H</a>	Alignment	not modelled	85.7	9	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> ruvb-like 2; <b>PDBTitle:</b> crystal structure of the tip48 (tip49b) hexamer
85	<a href="#">c1qvrB</a>	Alignment	not modelled	85.1	13	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
86	<a href="#">d2ce7a2</a>	Alignment	not modelled	85.0	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
87	<a href="#">c5w0tA</a>	Alignment	not modelled	84.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> protein msp1; <b>PDBTitle:</b> crystal structure of monomeric msp1 from s. cerevisiae
88	<a href="#">c6epdM</a>	Alignment	not modelled	84.5	10	<b>PDB header:</b> hydrolase <b>Chain:</b> M: <b>PDB Molecule:</b> 26s proteasome regulatory subunit 6a; <b>PDBTitle:</b> substrate processing state 26s proteasome (sps1)
89	<a href="#">c1r6bX</a>	Alignment	not modelled	83.7	14	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
90	<a href="#">c6nyyC</a>	Alignment	not modelled	83.6	13	<b>PDB header:</b> translocase <b>Chain:</b> C: <b>PDB Molecule:</b> afg3-like protein 2; <b>PDBTitle:</b> human m-aaa protease afg3l2, substrate-bound
91	<a href="#">c2r65A</a>	Alignment	not modelled	83.6	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protease ftsh homolog; <b>PDBTitle:</b> crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
92	<a href="#">c5j1sA</a>	Alignment	not modelled	83.1	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> torsin-1a; <b>PDBTitle:</b> torsina-lull1 complex, h. sapiens, bound to vhh-bs2
93	<a href="#">d1sxb1</a>	Alignment	not modelled	83.1	11	<b>Fold:</b> post-AAA+ oligomerization domain-like <b>Superfamily:</b> post-AAA+ oligomerization domain-like <b>Family:</b> DNA polymerase III clamp loader subunits, C-terminal domain
94	<a href="#">c5d4wB</a>	Alignment	not modelled	82.6	17	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> putative heat shock protein; <b>PDBTitle:</b> crystal structure of hsp104
95	<a href="#">c6az0A</a>	Alignment	not modelled	81.2	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial inner membrane i-aaa protease supercomplex <b>PDBTitle:</b> mitochondrial atpase protease yme1
96	<a href="#">c4l16A</a>	Alignment	not modelled	79.0	9	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> figletin-like protein 1; <b>PDBTitle:</b> crystal structure of figl-1 aaa domain in complex with adp
97	<a href="#">c4b4tK</a>	Alignment	not modelled	77.9	11	<b>PDB header:</b> hydrolase <b>Chain:</b> K: <b>PDB Molecule:</b> 26s protease regulatory subunit 6b homolog; <b>PDBTitle:</b> near-atomic resolution structural model of the yeast 26s proteasome
98	<a href="#">d1id3b</a>	Alignment	not modelled	77.4	12	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
99	<a href="#">c2zamA</a>	Alignment	not modelled	77.2	12	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associating protein 4b; <b>PDBTitle:</b> crystal structure of mouse skd1/vps4b apo-form
100	<a href="#">c6hqaE</a>	Alignment	not modelled	76.4	13	<b>PDB header:</b> transcription <b>Chain:</b> E: <b>PDB Molecule:</b> subunit (60 kda) of tfiid and saga complexes; <b>PDBTitle:</b> molecular structure of promoter-bound yeast tfiid
101	<a href="#">c2hcbC</a>	Alignment	not modelled	76.3	12	<b>PDB header:</b> replication <b>Chain:</b> C: <b>PDB Molecule:</b> chromosomal replication initiator protein dnaa; <b>PDBTitle:</b> structure of amppcp-bound dnaa from aquifex aeolicus
102	<a href="#">d1hiod</a>	Alignment	not modelled	75.2	12	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
103	<a href="#">c4xguB</a>	Alignment	not modelled	74.5	7	<b>PDB header:</b> atp-binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative pachytene checkpoint protein 2; <b>PDBTitle:</b> structure of c. elegans pch-2
104	<a href="#">c3v9rC</a>	Alignment	not modelled	74.3	14	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein yol086w-a; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae mhf complex
105	<a href="#">d1e32a2</a>	Alignment	not modelled	72.9	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
106	<a href="#">c6e111</a>	Alignment	not modelled	71.7	16	<b>PDB header:</b> protein transport <b>Chain:</b> 1: <b>PDB Molecule:</b> heat shock protein 101; <b>PDBTitle:</b> ptex core complex in the resetting (compact) state

107	<a href="#">c5uj7C_</a>	Alignment	not modelled	70.8	8	<b>PDB header:</b> dna binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> origin recognition complex subunit 4; <b>PDBTitle:</b> structure of the active form of human origin recognition complex2 atpase motor module, complex subunits 1, 4, 5
108	<a href="#">c4d2qC_</a>	Alignment	not modelled	70.0	18	<b>PDB header:</b> chaperone <b>Chain:</b> C: <b>PDB Molecule:</b> clpb; <b>PDBTitle:</b> negative-stain electron microscopy of e. coli clpb mutant e432a (bap2 form bound to clpp)
109	<a href="#">d2huec1</a>	Alignment	not modelled	69.3	12	<b>Fold:</b> Histone-fold <b>Superfamily:</b> Histone-fold <b>Family:</b> Nucleosome core histones
110	<a href="#">d1lv7a_</a>	Alignment	not modelled	69.2	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Extended AAA-ATPase domain
111	<a href="#">c1fnnB_</a>	Alignment	not modelled	69.1	13	<b>PDB header:</b> cell cycle <b>Chain:</b> B: <b>PDB Molecule:</b> cell division control protein 6; <b>PDBTitle:</b> crystal structure of cdc6p from pyrobaculum aerophilum
112	<a href="#">c6mzml_</a>	Alignment	not modelled	66.3	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> I: <b>PDB Molecule:</b> transcription initiation factor tfiid subunit 6; <b>PDBTitle:</b> human tfiid bound to promoter dna and tfiia
113	<a href="#">c3vh5A_</a>	Alignment	not modelled	65.4	9	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cenp-s; <b>PDBTitle:</b> crystal structure of the chicken cenp-t histone fold/cenp-w/cenp-2 s/cenp-x heterotetrameric complex, crystal form i
114	<a href="#">c2qz4A_</a>	Alignment	not modelled	65.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> paraplegin; <b>PDBTitle:</b> human paraplegin, aaa domain in complex with adp
115	<a href="#">c6djuA_</a>	Alignment	not modelled	65.0	18	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> chaperone protein clpb; <b>PDBTitle:</b> mtb clpb in complex with atpgammas and casein, conformer 1
116	<a href="#">c3eihB_</a>	Alignment	not modelled	64.9	9	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4; <b>PDBTitle:</b> crystal structure of s.cerevisiae vps4 in the presence of atpgammas
117	<a href="#">c1xwiA_</a>	Alignment	not modelled	63.4	8	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
118	<a href="#">c3d8bB_</a>	Alignment	not modelled	63.3	10	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fidgetin-like protein 1; <b>PDBTitle:</b> crystal structure of human fidgetin-like protein 1 in complex with adp
119	<a href="#">c5t0gA_</a>	Alignment	not modelled	60.8	8	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 26s protease regulatory subunit 7; <b>PDBTitle:</b> structural basis for dynamic regulation of the human 26s proteasome
120	<a href="#">c5e7pA_</a>	Alignment	not modelled	60.1	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein cdc48; <b>PDBTitle:</b> crystal structure of msmeg_0858 (uniprot a0qqs4), a aaa atpase.