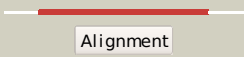

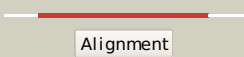

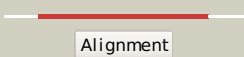

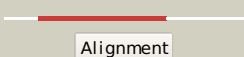

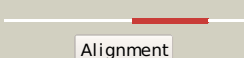

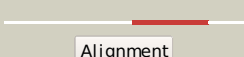

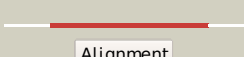

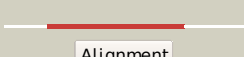

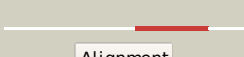
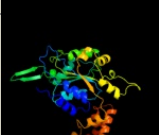



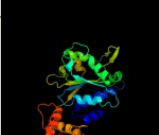


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1qvrB_</a>	 Alignment		100.0	55	<b>PDB header:</b> chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> crystal structure analysis of clpb
2	<a href="#">c3pxiB_</a>	 Alignment		100.0	50	<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
3	<a href="#">c1r6bX_</a>	 Alignment		100.0	44	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> clpa protein; <b>PDBTitle:</b> high resolution crystal structure of clpa
4	<a href="#">c3pxgA_</a>	 Alignment		100.0	44	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> negative regulator of genetic competence clpc/mecb; <b>PDBTitle:</b> structure of meca121 and clpc1-485 complex
5	<a href="#">d1qvra3</a>	 Alignment		100.0	63	<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
6	<a href="#">d1r6bx3</a>	 Alignment		100.0	45	<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
7	<a href="#">c3cf1C_</a>	 Alignment		100.0	24	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97/vcp in complex with adp/adp.alfx
8	<a href="#">d1qvra2</a>	 Alignment		100.0	59	<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
9	<a href="#">d1um8a_</a>	 Alignment		100.0	20	<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
10	<a href="#">d1g41a_</a>	 Alignment		100.0	21	<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
11	<a href="#">d1lofha_</a>	 Alignment		100.0	21	<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

12	<a href="#">dle94e_</a>	Alignment		100.0	22	<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
13	<a href="#">c3hteC_</a>	Alignment		100.0	20	<b>PDB header:</b> motor protein <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent clp protease atp-binding subunit clpx; <b>PDBTitle:</b> crystal structure of nucleotide-free hexameric clpx
14	<a href="#">d1r6bx2</a>	Alignment		100.0	53	<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
15	<a href="#">c2p65A_</a>	Alignment		100.0	67	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein pf08_0063; <b>PDBTitle:</b> crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
16	<a href="#">d1jbka_</a>	Alignment		100.0	99	<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
17	<a href="#">d1ny5a2</a>	Alignment		99.9	18	<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="#">c2c99A_</a>	Alignment		99.9	20	<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
19	<a href="#">c1ny5A_</a>	Alignment		99.9	20	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator (ntrc family); <b>PDBTitle:</b> crystal structure of sigma54 activator (aaa+ atpase) in the inactive2 state
20	<a href="#">c1xwiA_</a>	Alignment		99.9	22	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> skd1 protein; <b>PDBTitle:</b> crystal structure of vps4b
21	<a href="#">c1ojlF_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> response regulator <b>Chain:</b> F: <b>PDB Molecule:</b> transcriptional regulatory protein zrar; <b>PDBTitle:</b> crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding
22	<a href="#">c3dzdA_</a>	Alignment	not modelled	99.9	22	<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
23	<a href="#">c3eihB_</a>	Alignment	not modelled	99.9	21	<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
24	<a href="#">c3hu2C_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase; <b>PDBTitle:</b> structure of p97 n-d1 r86a mutant in complex with atpgs
25	<a href="#">c2zamA_</a>	Alignment	not modelled	99.9	22	<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
26	<a href="#">c3pfiB_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> hydrolase <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
27	<a href="#">c3m6aC_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> atp-dependent protease la 1; <b>PDBTitle:</b> crystal structure of bacillus subtilis lon c-terminal

						domain
28	<a href="#">c1s3sA</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> transitional endoplasmic reticulum atpase (ter <b>PDBTitle:</b> crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
29	<a href="#">c2r44A</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
30	<a href="#">c2dhrC</a>	Alignment	not modelled	99.9	22	<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 (g3991)
31	<a href="#">c3b9pA</a>	Alignment	not modelled	99.9	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cg5977-pa, isoform a; <b>PDBTitle:</b> spastin
32	<a href="#">c3d8bB</a>	Alignment	not modelled	99.9	19	<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
33	<a href="#">d1khya</a>	Alignment	not modelled	99.8	99	<b>Fold:</b> Double Clp-N motif <b>Superfamily:</b> Double Clp-N motif <b>Family:</b> Double Clp-N motif
34	<a href="#">c1nsfA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> n-ethylmaleimide sensitive factor; <b>PDBTitle:</b> d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
35	<a href="#">c2qz4A</a>	Alignment	not modelled	99.8	24	<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
36	<a href="#">c3fesB</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> atp binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent clp endopeptidase; <b>PDBTitle:</b> crystal structure of the atp-dependent clp protease clpc from2 clostridium difficile
37	<a href="#">c2k77A</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> chaperone, protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> negative regulator of genetic competence <b>PDBTitle:</b> nmr solution structure of the bacillus subtilis clpc n-2 domain
38	<a href="#">c3nbxX</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> X: <b>PDB Molecule:</b> atpase rava; <b>PDBTitle:</b> crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
39	<a href="#">c1in8A</a>	Alignment	not modelled	99.8	21	<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
40	<a href="#">d2ce7a2</a>	Alignment	not modelled	99.8	19	<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="#">d1d2na</a>	Alignment	not modelled	99.8	19	<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="#">c3pvsA</a>	Alignment	not modelled	99.8	21	<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
43	<a href="#">c3h4mC</a>	Alignment	not modelled	99.8	22	<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
44	<a href="#">c3fh2A</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable atp-dependent protease (heat shock protein); <b>PDBTitle:</b> the crystal structure of the probable atp-dependent protease (heat2 shock protein) from corynebacterium glutamicum
45	<a href="#">c2x8aA</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> nuclear protein <b>Chain:</b> A: <b>PDB Molecule:</b> nuclear valosin-containing protein-like; <b>PDBTitle:</b> human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
46	<a href="#">d1qvra1</a>	Alignment	not modelled	99.8	30	<b>Fold:</b> Double Clp-N motif <b>Superfamily:</b> Double Clp-N motif <b>Family:</b> Double Clp-N motif
47	<a href="#">d1ixza</a>	Alignment	not modelled	99.8	22	<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
48	<a href="#">c2ce7B</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> cell division protein <b>Chain:</b> B: <b>PDB Molecule:</b> cell division protein ftsh; <b>PDBTitle:</b> edta treated
49	<a href="#">c1iy2A</a>	Alignment	not modelled	99.8	20	<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
50	<a href="#">d1in4a2</a>	Alignment	not modelled	99.8	18	<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
51	<a href="#">d1e32a2</a>	Alignment	not modelled	99.8	19	<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
52	<a href="#">d1g8pa</a>	Alignment	not modelled	99.8	19	<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 <b>PDB header:</b> hydrolase

53	<a href="#">c2r65A_</a>	Alignment	not modelled	99.8	19	<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
54	<a href="#">c3zriA_</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> clpb protein; <b>PDBTitle:</b> n-domain of clpV from vibrio cholerae
55	<a href="#">c3kljA_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent protease lon; <b>PDBTitle:</b> crystal structure of lon protease from thermococcus onnurineus na1
56	<a href="#">d1r7ra3</a>	Alignment	not modelled	99.8	23	<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
57	<a href="#">d1ixsb2</a>	Alignment	not modelled	99.7	19	<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="#">d1k6ka_</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> Double Clp-N motif <b>Superfamily:</b> Double Clp-N motif <b>Family:</b> Double Clp-N motif
59	<a href="#">c3u5zM_</a>	Alignment	not modelled	99.7	17	<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
60	<a href="#">c2c9oC_</a>	Alignment	not modelled	99.7	19	<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 ruvbl1
61	<a href="#">c1hqcb_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ruvb; <b>PDBTitle:</b> structure of ruvb from thermus thermophilus hb8
62	<a href="#">c2chgB_</a>	Alignment	not modelled	99.7	21	<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
63	<a href="#">d1l8qa2</a>	Alignment	not modelled	99.7	20	<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="#">c1xxhB_</a>	Alignment	not modelled	99.7	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dna polymerase iii subunit gamma; <b>PDBTitle:</b> atpγs bound e. coli clamp loader complex
65	<a href="#">d1w5sa2</a>	Alignment	not modelled	99.7	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
66	<a href="#">c1sxjD_</a>	Alignment	not modelled	99.7	20	<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 loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
67	<a href="#">d1njfa_</a>	Alignment	not modelled	99.7	24	<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
68	<a href="#">c2hcbC_</a>	Alignment	not modelled	99.7	19	<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
69	<a href="#">d1fnna2</a>	Alignment	not modelled	99.7	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
70	<a href="#">d1iqpa2</a>	Alignment	not modelled	99.7	21	<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
71	<a href="#">c1sxjE_</a>	Alignment	not modelled	99.7	17	<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 loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
72	<a href="#">c1sxjA_</a>	Alignment	not modelled	99.6	17	<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 loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
73	<a href="#">d1lv7a_</a>	Alignment	not modelled	99.6	24	<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
74	<a href="#">d1sxje2</a>	Alignment	not modelled	99.6	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
75	<a href="#">c3te6A_</a>	Alignment	not modelled	99.6	13	<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
76	<a href="#">d1sxjb2</a>	Alignment	not modelled	99.6	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
77	<a href="#">d1sxja2</a>	Alignment	not modelled	99.6	17	<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
78	<a href="#">c3f8tA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> predicted atpase involved in replication control,

						<b>PDBTitle:</b> crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri
79	<a href="#">c1jr3E_</a>	Alignment	not modelled	99.6	16	<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 gamma2 complex of e. coli dna polymerase iii
80	<a href="#">d1sxd2</a>	Alignment	not modelled	99.6	19	<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
81	<a href="#">d1a5ta2</a>	Alignment	not modelled	99.6	17	<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
82	<a href="#">c1iqpF_</a>	Alignment	not modelled	99.6	23	<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
83	<a href="#">c1sxC_</a>	Alignment	not modelled	99.6	26	<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 loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
84	<a href="#">c2chvE_</a>	Alignment	not modelled	99.6	23	<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
85	<a href="#">c1sxB_</a>	Alignment	not modelled	99.6	13	<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 loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
86	<a href="#">d1sxc2</a>	Alignment	not modelled	99.6	24	<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="#">c3bosA_</a>	Alignment	not modelled	99.5	13	<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
88	<a href="#">c3qmzA_</a>	Alignment	not modelled	99.5	23	<b>PDB header:</b> motor protein <b>Chain:</b> A: <b>PDB Molecule:</b> cytoplasmic dynein heavy chain; <b>PDBTitle:</b> crystal structure of the cytoplasmic dynein heavy chain motor domain
89	<a href="#">d1gvnb_</a>	Alignment	not modelled	99.5	15	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Plasmid maintenance system epsilon/zeta, toxin zeta subunit
90	<a href="#">c1fnnB_</a>	Alignment	not modelled	99.5	18	<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
91	<a href="#">c2z4rB_</a>	Alignment	not modelled	99.4	22	<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
92	<a href="#">d1oz4a3</a>	Alignment	not modelled	99.4	19	<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
93	<a href="#">c1w5sB_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> replication <b>Chain:</b> B: <b>PDB Molecule:</b> origin recognition complex subunit 2 orc2; <b>PDBTitle:</b> structure of the aeropyrum pernix orc2 protein (adp form)
94	<a href="#">c2qbyB_</a>	Alignment	not modelled	99.3	25	<b>PDB header:</b> replication/dna <b>Chain:</b> B: <b>PDB Molecule:</b> cell division control protein 6 homolog 3; <b>PDBTitle:</b> crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
95	<a href="#">c2qbyA_</a>	Alignment	not modelled	99.3	19	<b>PDB header:</b> replication/dna <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 6 homolog 1; <b>PDBTitle:</b> crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
96	<a href="#">c3f9vA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> minichromosome maintenance protein mcm; <b>PDBTitle:</b> crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
97	<a href="#">d2gnoa2</a>	Alignment	not modelled	99.3	18	<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
98	<a href="#">c3ec2A_</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dna replication protein dnac; <b>PDBTitle:</b> crystal structure of the dnac helicase loader
99	<a href="#">c2kjqA_</a>	Alignment	not modelled	99.2	22	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> dnaa-related protein; <b>PDBTitle:</b> solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
100	<a href="#">c2v1uA_</a>	Alignment	not modelled	99.2	16	<b>PDB header:</b> replication <b>Chain:</b> A: <b>PDB Molecule:</b> cell division control protein 6 homolog; <b>PDBTitle:</b> structure of the aeropyrum pernix orc1 protein in complex2 with dna
101	<a href="#">c3co5B_</a>	Alignment	not modelled	99.2	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> B: <b>PDB Molecule:</b> putative two-component system transcriptional response <b>PDBTitle:</b> crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
						<b>PDB header:</b> hydrolase



102	<a href="#">c2w58B_</a>	Alignment	not modelled	99.1	17	<b>Chain:</b> B: <b>PDB Molecule:</b> primosome component (helicase loader); <b>PDBTitle:</b> crystal structure of the dnaI
103	<a href="#">c3cmvG_</a>	Alignment	not modelled	99.0	20	<b>PDB header:</b> recombination <b>Chain:</b> G: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
104	<a href="#">c2p5tD_</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> transcription regulator <b>Chain:</b> D: <b>PDB Molecule:</b> pez2; <b>PDBTitle:</b> molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
105	<a href="#">c2qgzA_</a>	Alignment	not modelled	98.7	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative primosome component; <b>PDBTitle:</b> crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58
106	<a href="#">c2fnaA_</a>	Alignment	not modelled	98.6	21	<b>PDB header:</b> atp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein; <b>PDBTitle:</b> crystal structure of an archaeal aaa+ atpase (sso1545) from sulfobolbus2 solfataricus p2 at 2.00 a resolution
107	<a href="#">d1svma_</a>	Alignment	not modelled	98.6	20	<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
108	<a href="#">c2qenA_</a>	Alignment	not modelled	98.5	14	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> walker-type atpase; <b>PDBTitle:</b> the walker-type atpase paby2304 of pyrococcus abyssi
109	<a href="#">d1qzma_</a>	Alignment	not modelled	98.5	25	<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
110	<a href="#">d2fnaa2</a>	Alignment	not modelled	98.4	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
111	<a href="#">c2qy9A_</a>	Alignment	not modelled	98.4	12	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the ng+1 construct of the e. coli srp receptor2 ftsy
112	<a href="#">d1ye8a1</a>	Alignment	not modelled	98.4	19	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> RecA protein-like (ATPase-domain)
113	<a href="#">d1tuea_</a>	Alignment	not modelled	98.4	17	<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
114	<a href="#">c2j7pA_</a>	Alignment	not modelled	98.4	13	<b>PDB header:</b> signal recognition <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein; <b>PDBTitle:</b> gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
115	<a href="#">c2og2A_</a>	Alignment	not modelled	98.4	13	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative signal recognition particle receptor; <b>PDBTitle:</b> crystal structure of chloroplast ftsy from arabidopsis2 thaliana
116	<a href="#">c2gnoA_</a>	Alignment	not modelled	98.4	16	<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
117	<a href="#">c1vmaA_</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution
118	<a href="#">c3b9qA_</a>	Alignment	not modelled	98.3	15	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> chloroplast srp receptor homolog, alpha subunit <b>PDBTitle:</b> the crystal structure of cpfts2y from arabidopsis thaliana
119	<a href="#">c1x37A_</a>	Alignment	not modelled	98.2	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent protease la 1; <b>PDBTitle:</b> structure of bacillus subtilis lon protease ssd domain
120	<a href="#">c2yhsA_</a>	Alignment	not modelled	98.2	12	<b>PDB header:</b> cell cycle <b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsy; <b>PDBTitle:</b> structure of the e. coli srp receptor ftsy