Phyre^2

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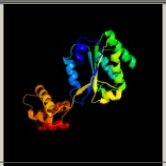
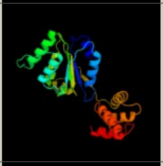
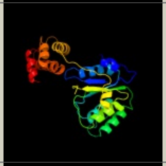
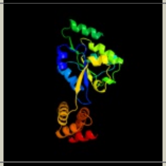
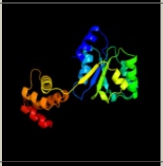
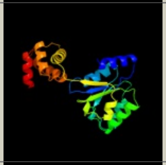
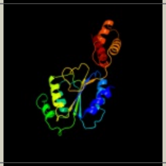
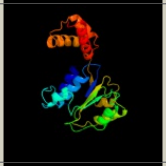
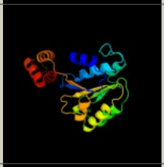
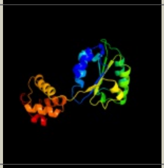
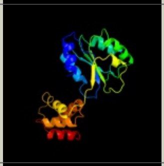
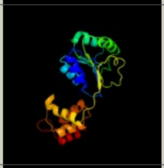
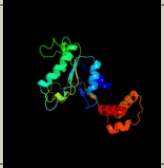
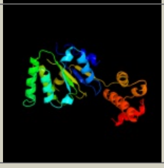
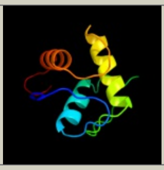
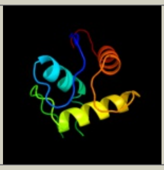
Description	P45756
Date	Thu Jan 5 12:03:32 GMT 2012
Unique Job ID	727a7bd9e889729f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1fnna2	Alignment		99.9	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
2	c3pfiB_	Alignment		99.8	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**holliday junction atp-dependent dna helicase ruvb; **PDBTitle:** 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
3	d1w5sa2	Alignment		99.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
4	c1fnnB_	Alignment		99.8	13	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division control protein 6; **PDBTitle:** crystal structure of cdc6p from pyrobaculum aerophilum
5	d1njfa_	Alignment		99.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
6	c2v1uA_	Alignment		99.7	12	**PDB header:**replication **Chain:** A: **PDB Molecule:**cell division control protein 6 homolog; **PDBTitle:** structure of the aeropyrum pernix orc1 protein in complex2 with dna
7	c2c9oC_	Alignment		99.7	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
8	c1in8A_	Alignment		99.7	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
9	d1in4a2	Alignment		99.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
10	c3te6A_	Alignment		99.7	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**regulatory protein sir3; **PDBTitle:** crystal structure of the s. cerevisiae sir3 aaa+ domain
11	d1sxjd2	Alignment		99.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain

12	c3pvsA_	Alignment		99.7	18	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
13	c1xxhB_	Alignment		99.7	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii subunit gamma; **PDBTitle:** atpgs bound e. coli clamp loader complex
14	d1a5ta2	Alignment		99.7	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
15	d1sxjc2	Alignment		99.7	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
16	d1ixsb2	Alignment		99.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
17	c1hqcB_	Alignment		99.7	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ruvb; **PDBTitle:** structure of ruvb from thermus thermophilus hb8
18	d2fnaa2	Alignment		99.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
19	c2chgB_	Alignment		99.7	14	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c domains 1 and 2
20	c2qbyA_	Alignment		99.7	14	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**cell division control protein 6 homolog 1; **PDBTitle:** crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
21	c1sxjC_	Alignment	not modelled	99.7	12	**PDB header:**replication **Chain:** C: **PDB Molecule:**activator 1 40 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
22	c1w5sB_	Alignment	not modelled	99.7	13	**PDB header:**replication **Chain:** B: **PDB Molecule:**origin recognition complex subunit 2 orc2; **PDBTitle:** structure of the aeropyrum pernix orc2 protein (adp form)
23	d1sxjb2	Alignment	not modelled	99.6	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
24	c3iytG_	Alignment	not modelled	99.6	16	**PDB header:**apoptosis **Chain:** G: **PDB Molecule:**apoptotic protease-activating factor 1; **PDBTitle:** structure of an apoptosome-procaspase-9 card complex
25	d1iqpa2	Alignment	not modelled	99.6	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
26	c1sxjA_	Alignment	not modelled	99.6	14	**PDB header:**replication **Chain:** A: **PDB Molecule:**activator 1 95 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
27	c2z4rB_	Alignment	not modelled	99.6	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** crystal structure of domain iii from the thermotoga2 maritima replication initiation protein dnaa
28	d1sxje2	Alignment	not modelled	99.6	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family: Extended AAA-ATPase domain
29	c2qbyB_	Alignment	not modelled	99.6	11	**PDB header:**replication/dna **Chain:** B: **PDB Molecule:**cell division control protein 6 homolog 3; **PDBTitle:** crystal structure of a heterodimer of cdc6/orc1 initiators2 bound to origin dna (from s. solfataricus)
30	c2fnaA_	Alignment	not modelled	99.6	14	**PDB header:**atp-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of an archaeal aaa+ atpase (sso1545) from sulfolobus2 solfataricus p2 at 2.00 a resolution
31	c2a5yB_	Alignment	not modelled	99.6	14	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**ced-4; **PDBTitle:** structure of a ced-4/ced-9 complex
32	d1sxja2	Alignment	not modelled	99.6	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
33	c1sxjE_	Alignment	not modelled	99.6	19	**PDB header:**replication **Chain:** E: **PDB Molecule:**activator 1 40 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
34	c1iqpF_	Alignment	not modelled	99.6	13	**PDB header:**replication **Chain:** F: **PDB Molecule:**rfcs; **PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
35	c1sxjB_	Alignment	not modelled	99.6	11	**PDB header:**replication **Chain:** B: **PDB Molecule:**activator 1 37 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
36	c2chvE_	Alignment	not modelled	99.6	14	**PDB header:**dna-binding protein **Chain:** E: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c adpnp complex
37	d1lbua1	Alignment		99.6	18	**Fold:**PGBD-like **Superfamily:**PGBD-like **Family:**Peptidoglycan binding domain, PGBD
38	c2qenA_	Alignment	not modelled	99.6	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**walker-type atpase; **PDBTitle:** the walker-type atpase paby2304 of pyrococcus abyssi
39	c3u5zM_	Alignment	not modelled	99.6	11	**PDB header:**dna binding protein/dna **Chain:** M: **PDB Molecule:**dna polymerase accessory protein 44; **PDBTitle:** structure of t4 bacteriophage clamp loader bound to the t4 clamp,2 primer-template dna, and atp analog
40	c3b9pA_	Alignment	not modelled	99.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
41	c1z6tC_	Alignment	not modelled	99.5	18	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**apoptotic protease activating factor 1; **PDBTitle:** structure of the apoptotic protease-activating factor 12 bound to adp
42	c2ce7B_	Alignment	not modelled	99.5	14	**PDB header:**cell division protein **Chain:** B: **PDB Molecule:**cell division protein ftsh; **PDBTitle:** edta treated
43	c2dhrC_	Alignment	not modelled	99.5	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ftsh; **PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
44	d2ce7a2	Alignment	not modelled	99.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
45	c1jr3E_	Alignment	not modelled	99.5	9	**PDB header:**transferase **Chain:** E: **PDB Molecule:**dna polymerase iii, delta' subunit; **PDBTitle:** crystal structure of the processivity clamp loader gamma2 complex of e. coli dna polymerase iii
46	c3h4mC_	Alignment	not modelled	99.5	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** aaa atpase domain of the proteasome- activating nucleotidase
47	c1sxjD_	Alignment	not modelled	99.5	14	**PDB header:**replication **Chain:** D: **PDB Molecule:**activator 1 41 kda subunit; **PDBTitle:** crystal structure of the eukaryotic clamp loader2 (replication factor c, rfc) bound to the dna sliding clamp3 (proliferating cell nuclear antigen, pcna)
48	d1r6bx2	Alignment	not modelled	99.5	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
49	c1iy2A_	Alignment	not modelled	99.5	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent metalloprotease ftsh; **PDBTitle:** crystal structure of the ftsh atpase domain from thermus2 thermophilus
50	c3hu2C_	Alignment	not modelled	99.5	16	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97 n-d1 r86a mutant in complex with atpgs
51	c1lbuA_	Alignment		99.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**muramoyl-pentapeptide carboxypeptidase; **PDBTitle:** hydrolase metallo (zn) dd-peptidase
						Fold:P-loop containing nucleoside triphosphate hydrolases

52	d1ixza_	Alignment	not modelled	99.5	16	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
53	c3d8bB_	Alignment	not modelled	99.5	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
54	c2x8aA_	Alignment	not modelled	99.5	14	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**nuclear valosin-containing protein-like; **PDBTitle:** human nuclear valosin containing protein like (nvl), c-2 terminal aaa-atpase domain
55	c3bkhA_	Alignment		99.4	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lytic transglycosylase; **PDBTitle:** crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
56	c1xwiA_	Alignment	not modelled	99.4	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**skd1 protein; **PDBTitle:** crystal structure of vps4b
57	c3bosA_	Alignment	not modelled	99.4	16	**PDB header:**hydrolase regulator,dna binding protein **Chain:** A: **PDB Molecule:**putative dna replication factor; **PDBTitle:** crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
58	c2zamA_	Alignment	not modelled	99.4	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form
59	c1s3sA_	Alignment	not modelled	99.4	16	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**transitional endoplasmic reticulum atpase (ter **PDBTitle:** crystal structure of aaa atpase p97/vcp nd1 in complex with2 p47 c
60	c3cf1C_	Alignment	not modelled	99.4	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
61	c3eihB_	Alignment	not modelled	99.4	11	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**vacuolar protein sorting-associated protein 4; **PDBTitle:** crystal structure of s.cerevisiae vps4 in the presence of atpgammas
62	c2r65A_	Alignment	not modelled	99.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell division protease ftsh homolog; **PDBTitle:** crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
63	c2qz4A_	Alignment	not modelled	99.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**paraplegin; **PDBTitle:** human paraplegin, aaa domain in complex with adp
64	d1ny5a2	Alignment	not modelled	99.3	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
65	d1lv7a_	Alignment	not modelled	99.3	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
66	d1l8qa2	Alignment	not modelled	99.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
67	d1r7ra3	Alignment	not modelled	99.2	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
68	d1e32a2	Alignment	not modelled	99.2	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
69	d2gnoa2	Alignment	not modelled	99.2	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
70	c2c99A_	Alignment	not modelled	99.2	15	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**psp operon transcriptional activator; **PDBTitle:** structural basis of the nucleotide driven conformational2 changes in the aaa domain of transcription activator pspf
71	c1ojlF_	Alignment	not modelled	99.2	16	**PDB header:**response regulator **Chain:** F: **PDB Molecule:**transcriptional regulatory protein zrar; **PDBTitle:** crystal structure of a sigma54-activator suggests the2 mechanism for the conformational switch necessary for3 sigma54 binding
72	d1qvra2	Alignment	not modelled	99.2	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
73	c3hteC_	Alignment	not modelled	99.2	18	**PDB header:**motor protein **Chain:** C: **PDB Molecule:**atp-dependent clp protease atp-binding subunit clpx; **PDBTitle:** crystal structure of nucleotide-free hexameric clpx
74	c1r6bX_	Alignment	not modelled	99.2	17	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa
75	d1r6bx3	Alignment	not modelled	99.1	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
						Fold:P-loop containing nucleoside triphosphate hydrolases

76	d1d2na_	Alignment	not modelled	99.1	18	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
77	d1g41a_	Alignment	not modelled	99.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
78	d1g8pa_	Alignment	not modelled	99.1	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
79	d1qvra3	Alignment	not modelled	99.1	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
80	c1qvrB_	Alignment	not modelled	99.1	19	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
81	c1ny5A_	Alignment	not modelled	99.1	17	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
82	c3k1jA_	Alignment	not modelled	99.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease lon; **PDBTitle:** crystal structure of lon protease from thermococcus onnurineus na1
83	d1um8a_	Alignment	not modelled	99.0	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
84	c1nsfA_	Alignment	not modelled	99.0	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
85	c3nbxX_	Alignment	not modelled	99.0	12	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atpase rava; **PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
86	c2hcbC_	Alignment	not modelled	99.0	15	**PDB header:**replication **Chain:** C: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of amppcp-bound dnaa from aquifex aeolicus
87	d1jbka_	Alignment	not modelled	98.9	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
88	c3pxiB_	Alignment	not modelled	98.9	15	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
89	c3pxgA_	Alignment	not modelled	98.9	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca121 and clpc1-485 complex
90	c3dzdA_	Alignment	not modelled	98.9	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
91	d1ofha_	Alignment	not modelled	98.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
92	c3b85A_	Alignment	not modelled	98.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphate starvation-inducible protein; **PDBTitle:** crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
93	c2r44A_	Alignment	not modelled	98.8	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
94	c3e1sA_	Alignment	not modelled	98.8	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease v, subunit recd; **PDBTitle:** structure of an n-terminal truncation of deinococcus radiodurans recd2
95	d1w36d1	Alignment	not modelled	98.8	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
96	c2kjqA_	Alignment	not modelled	98.8	14	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnaa-related protein; **PDBTitle:** solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
97	c1w36G_	Alignment	not modelled	98.7	16	**PDB header:**recombination **Chain:** G: **PDB Molecule:**exodeoxyribonuclease v alpha chain; **PDBTitle:** recbcd:dna complex
98	c2ja1A_	Alignment	not modelled	98.6	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
99	d1ye8a1	Alignment	not modelled	98.6	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
100	c2cnwF_	Alignment	not modelled	98.6	12	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
101	c2iy3A_	Alignment	not modelled	98.5	17	**PDB header:**rna-binding **Chain:** A: **PDB Molecule:**signal recognition particle protein ffh; **PDBTitle:** structure of the e. coli signal recognition particle2 bound to a translating ribosome

102	c2j7pA_	Alignment	not modelled	98.5	17	**PDB header:**signal recognition **Chain:** A: **PDB Molecule:**signal recognition particle protein; **PDBTitle:** gmppnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
103	c3dm5A_	Alignment	not modelled	98.5	15	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
104	d1x6va3	Alignment	not modelled	98.5	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Adenosine-5'phosphosulfate kinase (APS kinase)
105	c2wjyA_	Alignment	not modelled	98.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**regulator of nonsense transcripts 1; **PDBTitle:** crystal structure of the complex between human nonsense2 mediated decay factors upf1 and upf2 orthorhombic form
106	c2p65A_	Alignment	not modelled	98.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf08_0063; **PDBTitle:** crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
107	c3f8tA_	Alignment	not modelled	98.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted atpase involved in replication control, **PDBTitle:** crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri
108	d1oz4a3	Alignment	not modelled	98.5	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
109	c2yhsA_	Alignment	not modelled	98.5	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
110	c2xzlA_	Alignment	not modelled	98.5	17	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent helicase nam7; **PDBTitle:** upf1-rna complex
111	c2p5tD_	Alignment	not modelled	98.4	14	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**pezt; **PDBTitle:** molecular and structural characterization of the pezat chromosomal2 toxin-antitoxin system of the human pathogen streptococcus pneumoniae
112	c2vliB_	Alignment	not modelled	98.4	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**antibiotic resistance protein; **PDBTitle:** structure of deinococcus radiodurans tunicamycin resistance2 protein
113	c3dmdA_	Alignment	not modelled	98.4	14	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**signal recognition particle receptor; **PDBTitle:** structures and conformations in solution of the signal recognition2 particle receptor from the archaeon pyrococcus furiosus
114	c2bh7A_	Alignment	not modelled	98.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**n-acetylmuramoyl-l-alanine amidase; **PDBTitle:** crystal structure of a semet derivative of amid at 2.22 angstroms
115	c2qy9A_	Alignment	not modelled	98.3	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the ng+1 construct of the e. coli srp receptor2 ftsy
116	c2j37W_	Alignment	not modelled	98.3	12	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
117	c3b9qA_	Alignment	not modelled	98.3	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
118	c2v3cC_	Alignment	not modelled	98.3	19	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the srp54-srp19-7s.s srp rna complex2 of m. jannaschii
119	d1gvnb_	Alignment	not modelled	98.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Plasmid maintenance system epsilon/zeta, toxin zeta subunit
120	c1vmaA_	Alignment	not modelled	98.2	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** crystal structure of cell division protein ftsy (tm0570) from2 thermotoga maritima at 1.60 a resolution