Phyre^2

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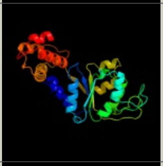
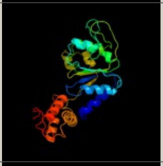
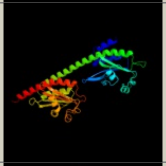
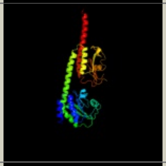
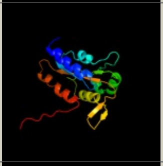
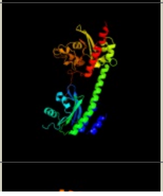
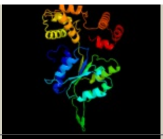
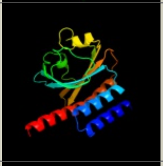
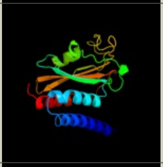
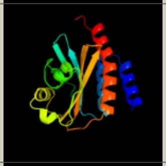
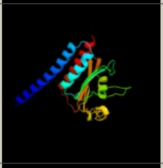
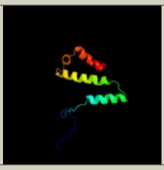
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1ny5A_	Alignment		100.0	42	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigm54 activator (aaa+ atpase) in the inactive2 state
2	c3dzdA_	Alignment		100.0	47	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4 in the inactive2 state
3	c2c99A_	Alignment		100.0	44	**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
4	d1ny5a2	Alignment		100.0	45	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
5	c1ojlF_	Alignment		100.0	51	**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
6	c3mf0A_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cgmp-specific 3',5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of pde5a gaf domain (89-518)
7	c3ibjB_	Alignment		100.0	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-dependent 3',5'-cyclic phosphodiesterase; **PDBTitle:** x-ray structure of pde2a
8	c1mc0A_	Alignment		100.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3',5'-cyclic nucleotide phosphodiesterase 2a; **PDBTitle:** regulatory segment of mouse 3',5'-cyclic nucleotide phosphodiesterase2 2a, containing the gaf a and gaf b domains
9	c1ykdB_	Alignment		100.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**adenylate cyclase; **PDBTitle:** crystal structure of the tandem gaf domains from a cyanobacterial2 adenylyl cyclase: novel modes of ligand-binding and dimerization
10	c3co5B_	Alignment		99.9	23	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**putative two-component system transcriptional response **PDBTitle:** crystal structure of sigma-54 interaction domain of putative2 transcriptional response regulator from neisseria gonorrhoeae
11	c2veaA_	Alignment		99.9	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phytochrome-like protein cph1; **PDBTitle:** the complete sensory module of the cyanobacterial2 phytochrome cph1 in the pr-state.
						PDB header:hydrolase

12	c3pfiB_	Alignment		99.9	14	**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
13	c3k2nB_	Alignment		99.8	21	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**sigma-54-dependent transcriptional regulator; **PDBTitle:** the crystal structure of sigma-54-dependent transcriptional2 regulator domain from chlorobium tepidum tls
14	c3p01C_	Alignment		99.8	15	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
15	c3ci6B_	Alignment		99.8	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** crystal structure of the gaf domain from acinetobacter2 phosphoenolpyruvate-protein phosphotransferase
16	c3oovA_	Alignment		99.8	14	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**methyl-accepting chemotaxis protein, putative; **PDBTitle:** crystal structure of a methyl-accepting chemotaxis protein, residues2 122 to 287
17	d2veaa1	Alignment		99.8	12	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
18	c3p01A_	Alignment		99.8	15	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**two-component response regulator; **PDBTitle:** crystal structure of two-component response regulator from nostoc sp.2 pcc 7120
19	c3trcA_	Alignment		99.8	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoenolpyruvate-protein phosphotransferase; **PDBTitle:** structure of the gaf domain from a phosphoenolpyruvate-protein2 phosphotransferase (ptsp) from coxiella burnetii
20	d2o9ca1	Alignment		99.8	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
21	d1r6bx3	Alignment	not modelled	99.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
22	c3c2wB_	Alignment	not modelled	99.8	12	**PDB header:**signaling protein **Chain:** B: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of the photosensory core domain of p.2 aeruginosa bacteriophytochrome pabphp in the pfr state
23	c2zmfA_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**camp and camp-inhibited cgmp 3',5'-cyclic phosphodiesterase **PDBTitle:** crystal structure of the c-terminal gaf domain of human2 phosphodiesterase 10a
24	c3mmhA_	Alignment	not modelled	99.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine-r-sulfoxide reductase; **PDBTitle:** x-ray structure of free methionine-r-sulfoxide reductase from2 neisseria meningitidis in complex with its substrate
25	d2oola1	Alignment	not modelled	99.8	10	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
26	c1in8A_	Alignment	not modelled	99.8	15	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**holliday junction dna helicase ruvb; **PDBTitle:** thermotoga maritima ruvb t158v
27	c1qvrB_	Alignment	not modelled	99.8	19	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
28	c3eeaB_	Alignment	not modelled	99.8	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**gaf domain/hd domain protein; **PDBTitle:** the crystal structure of the gaf domain/hd domain protein2 from geobacter sulfurreducens
						Fold:P-loop containing nucleoside triphosphate hydrolases

29	d1l8qa2	Alignment	not modelled	99.8	19	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
30	c3pxiB_	Alignment	not modelled	99.8	19	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
31	c1r6bX_	Alignment	not modelled	99.8	19	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa
32	d1qvra3	Alignment	not modelled	99.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
33	d1um8a_	Alignment	not modelled	99.7	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
34	c2vjwA_	Alignment	not modelled	99.7	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gaf family protein; **PDBTitle:** crystal structure of the second gaf domain of devs from2 mycobacterium smegmatis
35	c1vhmB_	Alignment	not modelled	99.7	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein yebr; **PDBTitle:** crystal structure of an hypothetical protein
36	c3nbxX_	Alignment	not modelled	99.7	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atpase rava; **PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
37	c3e0yA_	Alignment	not modelled	99.7	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved domain protein; **PDBTitle:** the crystal structure of a conserved domain from a protein of2 geobacter sulfurreducens pca
38	d1vhma_	Alignment	not modelled	99.7	12	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
39	c3pvsA_	Alignment	not modelled	99.7	20	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
40	d1mc0a1	Alignment	not modelled	99.7	15	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
41	c3dbaB_	Alignment	not modelled	99.7	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cone cgmp-specific 3',5'-cyclic phosphodiesterase subunit **PDBTitle:** crystal structure of the cgmp-bound gaf a domain from the2 photoreceptor phosphodiesterase 6c
42	c3o5yA_	Alignment	not modelled	99.7	17	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** the crystal structure of the gaf domain of a two-component sensor2 histidine kinase from bacillus halodurans to 2.45a
43	c2lb5A_	Alignment	not modelled	99.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sensor histidine kinase; **PDBTitle:** refined structural basis for the photoconversion of a phytochrome to2 the activated far-red light-absorbing form
44	c3hcyB_	Alignment	not modelled	99.7	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative two-component sensor histidine kinase protein; **PDBTitle:** the crystal structure of the domain of putative two-component sensor2 histidine kinase protein from sinorhizobium meliloti 1021
45	d2k2na1	Alignment	not modelled	99.7	13	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
46	c3k1jA_	Alignment	not modelled	99.7	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease lon; **PDBTitle:** crystal structure of lon protease from thermococcus onnurineus na1
47	c2w3gA_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**two component sensor histidine kinase devs (gaf **PDBTitle:** air-oxidized structure of the first gaf domain of2 mycobacterium tuberculosis doss
48	c2qybA_	Alignment	not modelled	99.7	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**membrane protein, putative; **PDBTitle:** crystal structure of the gaf domain region of putative membrane2 protein from geobacter sulfurreducens pca
49	c3ksiA_	Alignment	not modelled	99.7	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** structure of frmsr of staphylococcus aureus (complex with 2-propanol)
50	c2hcbC_	Alignment	not modelled	99.7	19	**PDB header:**replication **Chain:** C: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of amppcp-bound dnaa from aquifex aeolicus
51	d3c2wa1	Alignment	not modelled	99.6	12	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
52	c2z4rB_	Alignment	not modelled	99.6	17	**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
53	c1nsfA_	Alignment	not modelled	99.6	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive

						factor (nsf)
54	c3bosA_	Alignment	not modelled	99.6	15	**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
55	d1mc0a2	Alignment	not modelled	99.6	13	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
56	c2oolA_	Alignment	not modelled	99.6	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sensor protein; **PDBTitle:** crystal structure of the chromophore-binding domain of an unusual2 bacteriophytochrome rpbphp3 from r. palustris
57	c3hteC_	Alignment	not modelled	99.6	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
58	d1g8pa_	Alignment	not modelled	99.6	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
59	c1hqcB_	Alignment	not modelled	99.6	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ruvb; **PDBTitle:** structure of ruvb from thermus thermophilus hb8
60	c3e98B_	Alignment	not modelled	99.5	17	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**gaf domain of unknown function; **PDBTitle:** crystal structure of a gaf domain containing protein that belongs to2 pfam duf484 family (pa5279) from pseudomonas aeruginosa at 2.43 a3 resolution
61	c3f8tA_	Alignment	not modelled	99.5	20	**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
62	d1g41a_	Alignment	not modelled	99.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
63	c2o9bA_	Alignment	not modelled	99.5	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bacteriophytochrome; **PDBTitle:** crystal structure of bacteriophytochrome chromophore binding domain
64	d1ntca_	Alignment		99.5	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
65	d1f5ma_	Alignment	not modelled	99.5	12	**Fold:**Profilin-like **Superfamily:**GAF domain-like **Family:**GAF domain
66	c2k31A_	Alignment	not modelled	99.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphodiesterase 5a, cgmp-specific; **PDBTitle:** solution structure of cgmp-binding gaf domain of2 phosphodiesterase 5
67	c2c9oC_	Alignment	not modelled	99.5	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
68	c2r44A_	Alignment	not modelled	99.4	14	**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
69	d1in4a2	Alignment	not modelled	99.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
70	d1ixsb2	Alignment	not modelled	99.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
71	d1fnna2	Alignment	not modelled	99.4	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
72	d1ofha_	Alignment	not modelled	99.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
73	c2xssB_	Alignment	not modelled	99.4	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cgmp-specific 3', 5'-cyclic phosphodiesterase; **PDBTitle:** crystal structure of gafb from the human phosphodiesterase 5
74	d1sxjd2	Alignment	not modelled	99.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
75	d1etob_	Alignment	not modelled	99.4	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
76	d1d2na_	Alignment	not modelled	99.4	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
77	d1fipa_	Alignment	not modelled	99.4	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like

78	c3f9vA_	Alignment	not modelled	99.3	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
79	c2dhrC_	Alignment	not modelled	99.3	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ftsh; **PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
80	c2chgB_	Alignment	not modelled	99.3	22	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c domains 1 and 2
81	c3eihB_	Alignment	not modelled	99.2	21	**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
82	d1etxa_	Alignment	not modelled	99.2	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
83	d1njfa_	Alignment	not modelled	99.2	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
84	d1iqpa2	Alignment	not modelled	99.2	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
85	c1xwiA_	Alignment	not modelled	99.2	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**skd1 protein; **PDBTitle:** crystal structure of vps4b
86	c1xxhB_	Alignment	not modelled	99.2	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii subunit gamma; **PDBTitle:** atpgs bound e. coli clamp loader complex
87	c2ce7B_	Alignment	not modelled	99.2	23	**PDB header:**cell division protein **Chain:** B: **PDB Molecule:**cell division protein ftsh; **PDBTitle:** edta treated
88	d1umqa_	Alignment	not modelled	99.2	17	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
89	c1umqA_	Alignment	not modelled	99.2	17	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**photosynthetic apparatus regulatory protein; **PDBTitle:** solution structure and dna binding of the effector domain2 from the global regulator prra(rega) from r. sphaeroides:3 insights into dna binding specificity
90	c2kjqA_	Alignment	not modelled	99.2	21	**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.
91	c3e7lD_	Alignment	not modelled	99.2	22	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**transcriptional regulator (ntrc family); **PDBTitle:** crystal structure of sigma54 activator ntrc4's dna binding2 domain
92	c1fnnB_	Alignment	not modelled	99.1	11	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division control protein 6; **PDBTitle:** crystal structure of cdc6p from pyrobaculum aerophilum
93	c3b9pA_	Alignment	not modelled	99.1	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
94	d1g2ha_	Alignment	not modelled	99.1	27	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**FIS-like
95	c2r65A_	Alignment	not modelled	99.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cell division protease ftsh homolog; **PDBTitle:** crystal structure of helicobacter pylori atp dependent protease, ftsh2 adp complex
96	d1sxjc2	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
97	c3u5zM_	Alignment	not modelled	99.0	16	**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
98	d1sxjb2	Alignment	not modelled	99.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
99	d1w5sa2	Alignment	not modelled	99.0	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
100	d1qvra2	Alignment	not modelled	99.0	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
101	c1sxjD_	Alignment	not modelled	99.0	15	**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)
102	d2ce7a2	Alignment	not modelled	99.0	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain

103	c3h4mC_	Alignment	not modelled	99.0	21	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** aaa atpase domain of the proteasome- activating nucleotidase
104	c2p65A_	Alignment	not modelled	99.0	18	**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
105	c3d8bB_	Alignment	not modelled	99.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
106	c1sxjC_	Alignment	not modelled	99.0	18	**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)
107	c1sxjB_	Alignment	not modelled	99.0	15	**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)
108	c2qbyB_	Alignment	not modelled	98.9	19	**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)
109	c3cf1C_	Alignment	not modelled	98.9	22	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
110	c1iy2A_	Alignment	not modelled	98.9	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent metalloprotease ftsh; **PDBTitle:** crystal structure of the ftsh atpase domain from thermus2 thermophilus
111	c2zamA_	Alignment	not modelled	98.9	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form
112	c2chvE_	Alignment	not modelled	98.9	19	**PDB header:**dna-binding protein **Chain:** E: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c adpnp complex
113	d1r6bx2	Alignment	not modelled	98.9	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
114	c2qbyA_	Alignment	not modelled	98.9	10	**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)
115	c1iqpF_	Alignment	not modelled	98.9	21	**PDB header:**replication **Chain:** F: **PDB Molecule:**rfcs; **PDBTitle:** crystal structure of the clamp loader small subunit from2 pyrococcus furiosus
116	c2qz4A_	Alignment	not modelled	98.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**paraplegin; **PDBTitle:** human paraplegin, aaa domain in complex with adp
117	d1e32a2	Alignment	not modelled	98.9	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
118	c2v1uA_	Alignment	not modelled	98.9	15	**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
119	d1ixza_	Alignment	not modelled	98.9	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
120	d1sxja2	Alignment	not modelled	98.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain