Phyre^2

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Description	P0ABB4
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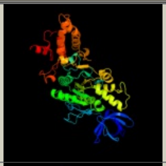
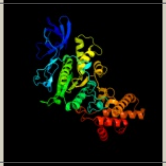
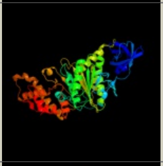
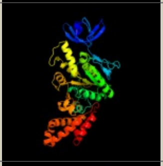
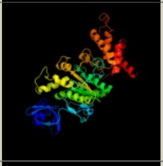
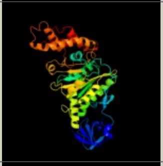
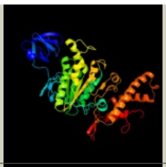
Unique Job ID	ea6bf3fd0cdc0638

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1skyE_	Alignment		100.0	68	**PDB header:**atp synthase **Chain:** E: **PDB Molecule:**f1-atpase; **PDBTitle:** crystal structure of the nucleotide free alpha3beta3 sub-complex of2 f1-atpase from the thermophilic bacillus ps3
2	c2w6jD_	Alignment		100.0	72	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp synthase subunit beta, mitochondrial; **PDBTitle:** low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 5.
3	c2jizD_	Alignment		100.0	72	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp synthase subunit beta; **PDBTitle:** the structure of f1-atpase inhibited by resveratrol.
4	c1fx0B_	Alignment		100.0	67	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase beta chain; **PDBTitle:** crystal structure of the chloroplast f1-atpase from spinach
5	c2r9vA_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** crystal structure of atp synthase subunit alpha (tm1612) from2 thermotoga maritima at 2.10 a resolution
6	c2w6fA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp synthase subunit alpha heart isoform, **PDBTitle:** low resolution structures of bovine mitochondrial f1-atpase2 during controlled dehydration: hydration state 2.
7	c2qe7C_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
8	c1kmhA_	Alignment		100.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atpase alpha subunit; **PDBTitle:** crystal structure of spinach chloroplast f1-atpase2 complexed with tentoxin
9	c1w0jB_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase alpha chain heart isoform, **PDBTitle:** beryllium fluoride inhibited bovine f1-atpase
10	c3oaaC_	Alignment		100.0	24	**PDB header:**hydrolase/transport protein **Chain:** C: **PDB Molecule:**atp synthase subunit alpha; **PDBTitle:** structure of the e.coli f1-atp synthase inhibited by subunit epsilon
11	c2dpyA_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flagellum-specific atp synthase; **PDBTitle:** crystal structure of the flagellar type iii atpase flii

12	c3a5dM_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** M: **PDB Molecule:**v-type atp synthase beta chain; **PDBTitle:** inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
13	c3a5dB_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**v-type atp synthase alpha chain; **PDBTitle:** inter-subunit interaction and quaternary rearrangement2 defined by the central stalk of prokaryotic v1-atpase
14	c2c61A_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**a-type atp synthase non-catalytic subunit b; **PDBTitle:** crystal structure of the non-catalytic b subunit of a-type2 atpase from m. mazei go1
15	c2oblA_	Alignment		100.0	27	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**escn; **PDBTitle:** structural and biochemical analysis of a prototypical atpase from the2 type iii secretion system of pathogenic bacteria
16	c1vdzA_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**a-type atpase subunit a; **PDBTitle:** crystal structure of a-type atpase catalytic subunit a from2 pyrococcus horikoshii ot3
17	d2jdia3	Alignment		100.0	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
18	d1skye3	Alignment		100.0	72	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
19	d2jdid3	Alignment		100.0	75	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
20	d1skyb3	Alignment		100.0	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
21	d1fx0b3	Alignment	not modelled	100.0	71	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
22	d1fx0a3	Alignment	not modelled	100.0	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
23	c3l0oB_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transcription termination factor rho; **PDBTitle:** structure of rna-free rho transcription termination factor from2 thermotoga maritima
24	c1xpuB_	Alignment	not modelled	100.0	17	**PDB header:**transcription/rna **Chain:** B: **PDB Molecule:**rho transcription termination factor; **PDBTitle:** structural mechanism of inhibition of the rho transcription2 termination factor by the antibiotic 5a-(3-formylphenylsulfanyl)-3 dihydrobicyclomycin (fpdb)
25	d1xpua3	Alignment	not modelled	100.0	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
26	d2jdid1	Alignment	not modelled	100.0	78	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
27	d1skye1	Alignment	not modelled	100.0	69	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
						Fold: Left-handed superhelix

28	d1fx0b1	Alignment	not modelled	99.9	72	**Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
29	d1fx0a1	Alignment	not modelled	99.3	17	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
30	d2jdia1	Alignment	not modelled	99.3	15	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
31	d1skye2	Alignment	not modelled	99.2	48	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
32	d1skyb1	Alignment	not modelled	99.2	19	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
33	d2f43a1	Alignment	not modelled	99.2	15	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
34	d2jdid2	Alignment	not modelled	99.0	57	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
35	d1mabb2	Alignment	not modelled	99.0	58	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
36	d1fx0b2	Alignment	not modelled	98.9	44	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
37	c1u9iA_	Alignment	not modelled	98.9	14	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic; **PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
38	d1tf7a1	Alignment	not modelled	98.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
39	d1skyb2	Alignment	not modelled	98.5	21	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
40	d2jdia2	Alignment	not modelled	98.5	19	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
41	d1tf7a2	Alignment	not modelled	98.4	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
42	c2recB_	Alignment	not modelled	98.4	18	**PDB header:**helicase **PDB COMPND:**
43	d1fx0a2	Alignment	not modelled	98.4	22	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
44	c3hr8A_	Alignment	not modelled	98.4	18	**PDB header:**recombination **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** crystal structure of thermotoga maritima reca
45	c2zroA_	Alignment	not modelled	98.3	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** msreca adp form iv
46	d1xp8a1	Alignment	not modelled	98.3	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
47	d1mo6a1	Alignment	not modelled	98.3	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
48	d2i1qa2	Alignment	not modelled	98.3	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
49	c2ztsB_	Alignment	not modelled	98.3	21	**PDB header:**atp-binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein ph0186; **PDBTitle:** crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
50	c2dr3A_	Alignment	not modelled	98.2	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0273 protein ph0284; **PDBTitle:** crystal structure of reca superfamily atpase ph0284 from pyrococcus2 horikoshii ot3
						PDB header:dna binding protein

51	c1xp8A_	Alignment	not modelled	98.2	20	**Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"
52	d1ubea1	Alignment	not modelled	98.2	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
53	d1n0wa_	Alignment	not modelled	98.2	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
54	c3ldaA_	Alignment	not modelled	98.2	20	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** yeast rad51 h352y filament interface mutant
55	d1maba2	Alignment	not modelled	98.1	19	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**N-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**N-terminal domain of alpha and beta subunits of F1 ATP synthase
56	c1t4gA_	Alignment	not modelled	98.1	15	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** atpase in complex with amp-pnp
57	c2w0mA_	Alignment	not modelled	98.1	17	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso2452; **PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus2 p2
58	c2dflA_	Alignment	not modelled	98.0	17	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** crystal structure of left-handed rada filament
59	c1szpC_	Alignment	not modelled	98.0	23	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** a crystal structure of the rad51 filament
60	d1v5wa_	Alignment	not modelled	98.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
61	d1szpa2	Alignment	not modelled	98.0	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
62	d1u94a1	Alignment	not modelled	98.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
63	d1pzna2	Alignment	not modelled	97.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
64	c2zjbB_	Alignment	not modelled	97.9	17	**PDB header:**recombination **Chain:** B: **PDB Molecule:**meiotic recombination protein dmc1/lim15 homolog; **PDBTitle:** crystal structure of the human dmc1-m200v polymorphic2 variant
65	c2cvhB_	Alignment	not modelled	97.9	18	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna repair and recombination protein radb; **PDBTitle:** crystal structure of the radb recombinase
66	c1pznG_	Alignment	not modelled	97.9	15	**PDB header:**recombination **Chain:** G: **PDB Molecule:**dna repair and recombination protein rad51; **PDBTitle:** rad51 (rada)
67	c2vyeA_	Alignment	not modelled	97.8	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
68	c3io5B_	Alignment	not modelled	97.8	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**recombination and repair protein; **PDBTitle:** crystal structure of a dimeric form of the uvsx recombinase core2 domain from enterobacteria phage t4
69	c2q6tB_	Alignment	not modelled	97.7	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
70	c3bh0A_	Alignment	not modelled	97.7	13	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** atpase domain of g40p
71	d1cr2a_	Alignment	not modelled	97.6	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
72	c3bs4A_	Alignment	not modelled	97.5	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein ph0321; **PDBTitle:** crystal structure of uncharacterized protein ph0321 from pyrococcus2 horikoshii in complex with an unknown peptide
73	c3cmvG_	Alignment	not modelled	97.5	16	**PDB header:**recombination **Chain:** G: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
74	c3bgwD_	Alignment	not modelled	97.0	15	**PDB header:**replication **Chain:** D: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** the structure of a dnab-like replicative helicase and its interactions2 with primase
75	c3pvsA_	Alignment	not modelled	96.7	30	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
76	c1fnnB_	Alignment	not modelled	96.7	16	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division control protein 6;

						PDBTitle: crystal structure of cdc6p from pyrobaculum aerophilum
77	c3b9qA_	Alignment	not modelled	96.6	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
78	c1zu4A_	Alignment	not modelled	96.6	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
79	c2a5yB_	Alignment	not modelled	96.5	13	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**ced-4; **PDBTitle:** structure of a ced-4/ced-9 complex
80	c3dmdA_	Alignment	not modelled	96.5	18	**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
81	c1q57G_	Alignment	not modelled	96.5	13	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
82	c2j7pA_	Alignment	not modelled	96.5	20	**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
83	c2og2A_	Alignment	not modelled	96.5	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
84	d2qy9a2	Alignment	not modelled	96.4	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
85	c2cnwF_	Alignment	not modelled	96.3	22	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
86	d1qvra2	Alignment	not modelled	96.3	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
87	d1vmaa2	Alignment	not modelled	96.3	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
88	c3ec2A_	Alignment	not modelled	96.3	13	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna replication protein dnac; **PDBTitle:** crystal structure of the dnac helicase loader
89	d1fnna2	Alignment	not modelled	96.2	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
90	d1nlfa_	Alignment	not modelled	96.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
91	d1okkd2	Alignment	not modelled	96.0	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
92	c3iytG_	Alignment	not modelled	95.9	19	**PDB header:**apoptosis **Chain:** G: **PDB Molecule:**apoptotic protease-activating factor 1; **PDBTitle:** structure of an apoptosome-procaspase-9 card complex
93	c3bosA_	Alignment	not modelled	95.9	8	**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
94	d1tmka_	Alignment	not modelled	95.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
95	c1z6tC_	Alignment	not modelled	95.8	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
96	c3d8bB_	Alignment	not modelled	95.8	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
97	c2wjyA_	Alignment	not modelled	95.7	35	**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
98	d1qzxa3	Alignment	not modelled	95.6	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
99	c1yqtA_	Alignment	not modelled	95.6	27	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
100	d1ls1a2	Alignment	not modelled	95.6	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
101	d1ye8a1	Alignment	not modelled	95.6	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family: RecA protein-like (ATPase-domain)
102	c2qgzA_	Alignment	not modelled	95.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative primosome component; **PDBTitle:** crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58
103	c2zamA_	Alignment	not modelled	95.5	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form
104	c2rhmD_	Alignment	not modelled	95.4	12	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** crystal structure of a putative kinase (caur_3907) from chloroflexus2 aurantiacus j-10-fl at 1.70 a resolution
105	d2ak3a1	Alignment	not modelled	95.4	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
106	c1vmaA_	Alignment	not modelled	95.3	15	**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
107	d2qm8a1	Alignment	not modelled	95.3	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
108	c1nsfA_	Alignment	not modelled	95.3	21	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
109	d2i3ba1	Alignment	not modelled	95.3	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
110	c2kjqA_	Alignment	not modelled	95.3	17	**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.
111	d1x6va3	Alignment	not modelled	95.2	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Adenosine-5'phosphosulfate kinase (APS kinase)
112	c2yhsA_	Alignment	not modelled	95.1	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
113	d1ixsb2	Alignment	not modelled	95.1	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
114	c2z4rB_	Alignment	not modelled	95.1	18	**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
115	c3dm5A_	Alignment	not modelled	95.1	17	**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.
116	c2x8aA_	Alignment	not modelled	95.0	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
117	c1xxhB_	Alignment	not modelled	95.0	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii subunit gamma; **PDBTitle:** atpgs bound e. coli clamp loader complex
118	d2ce7a2	Alignment	not modelled	95.0	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
119	c3b85A_	Alignment	not modelled	94.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphate starvation-inducible protein; **PDBTitle:** crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
120	d2awna2	Alignment	not modelled	94.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like