Phyre^2

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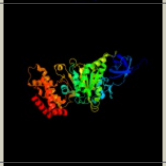
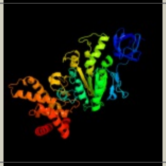
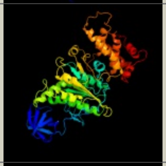
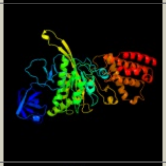
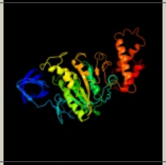
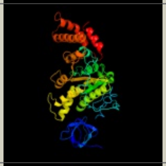
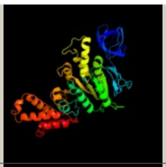
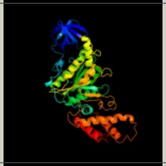
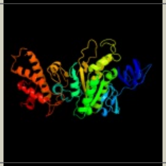
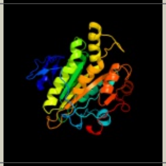
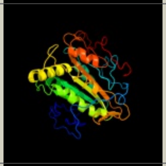
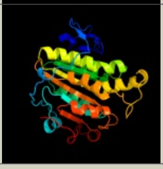
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3oaaC_	Alignment		100.0	100	**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
2	c2r9vA_	Alignment		100.0	56	**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
3	c2w6fA_	Alignment		100.0	60	**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.
4	c1kmhA_	Alignment		100.0	55	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atpase alpha subunit; **PDBTitle:** crystal structure of spinach chloroplast f1-atpase2 complexed with tentoxin
5	c1w0jB_	Alignment		100.0	60	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase alpha chain heart isoform, **PDBTitle:** beryllium fluoride inhibited bovine f1-atpase
6	c2qe7C_	Alignment		100.0	59	**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
7	c3a5dB_	Alignment		100.0	21	**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
8	c3a5dM_	Alignment		100.0	23	**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
9	c1fx0B_	Alignment		100.0	25	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase beta chain; **PDBTitle:** crystal structure of the chloroplast f1-atpase from spinach
10	c2dpyA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flagellum-specific atp synthase; **PDBTitle:** crystal structure of the flagellar type iii atpase flii
11	c2w6jD_	Alignment		100.0	24	**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.

12	c2jizD_	Alignment		100.0	24	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp synthase subunit beta; **PDBTitle:** the structure of f1-atpase inhibited by resveratrol.
13	c1skyE_	Alignment		100.0	26	**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
14	c2c61A_	Alignment		100.0	24	**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	21	**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	72	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
18	d1skyb3	Alignment		100.0	68	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
19	d1fx0a3	Alignment		100.0	66	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
20	d2jdid3	Alignment		100.0	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
21	d1skye3	Alignment	not modelled	100.0	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
22	d1fx0b3	Alignment	not modelled	100.0	28	**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	18	**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	16	**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	d1fx0a1	Alignment	not modelled	99.9	38	**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	d2jdia1	Alignment	not modelled	99.9	47	**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	d1skyb1	Alignment	not modelled	99.9	35	**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	d2f43a1	Alignment	not modelled	99.9	47	**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	d1skyb2	Alignment	not modelled	99.5	40	**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
31	d1maba2	Alignment		99.5	35	**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	d2jdia2	Alignment	not modelled	99.5	38	**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
33	d1fx0a2	Alignment	not modelled	99.4	46	**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
34	d1skye1	Alignment	not modelled	98.7	13	**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
35	c1u9iA_	Alignment	not modelled	98.7	14	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic; **PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
36	d1fx0b1	Alignment	not modelled	98.7	14	**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
37	d2jdid1	Alignment	not modelled	98.6	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
38	d1tf7a2	Alignment	not modelled	98.3	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
39	c2recB_	Alignment	not modelled	98.3	18	**PDB header:**helicase **PDB COMPND:**
40	d1tf7a1	Alignment	not modelled	98.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
41	d1xp8a1	Alignment	not modelled	98.2	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
42	c2zroA_	Alignment	not modelled	98.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** msreca adp form iv
43	c3hr8A_	Alignment	not modelled	98.2	19	**PDB header:**recombination **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** crystal structure of thermotoga maritima reca
44	d1mo6a1	Alignment	not modelled	98.1	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
45	c1xp8A_	Alignment	not modelled	98.1	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"
46	d1ubea1	Alignment	not modelled	98.1	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
47	c3ldaA_	Alignment	not modelled	98.0	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** yeast rad51 h352y filament interface mutant
48	c2dr3A_	Alignment	not modelled	98.0	19	**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
49	d2i1qa2	Alignment	not modelled	98.0	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
50	c2w0mA_	Alignment	not modelled	98.0	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso2452; **PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus2 p2
						Fold:P-loop containing nucleoside triphosphate hydrolases

51	d1n0wa_	Alignment	not modelled	97.9	17	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
52	d1u94a1	Alignment	not modelled	97.8	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
53	c2ztsB_	Alignment	not modelled	97.8	15	**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
54	c2dflA_	Alignment	not modelled	97.8	18	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** crystal structure of left-handed rada filament
55	c1t4gA_	Alignment	not modelled	97.8	18	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** atpase in complex with amp-pnp
56	d1v5wa_	Alignment	not modelled	97.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
57	d1pzna2	Alignment	not modelled	97.7	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
58	c3io5B_	Alignment	not modelled	97.7	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
59	d1szpa2	Alignment	not modelled	97.7	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
60	c1szpC_	Alignment	not modelled	97.6	18	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** a crystal structure of the rad51 filament
61	c2zjbB_	Alignment	not modelled	97.6	13	**PDB header:**recombination **Chain:** B: **PDB Molecule:**meiotic recombination protein dmc1/lim15 homolog; **PDBTitle:** crystal structure of the human dmc1-m200v polymorphic2 variant
62	c1pznG_	Alignment	not modelled	97.5	18	**PDB header:**recombination **Chain:** G: **PDB Molecule:**dna repair and recombination protein rad51; **PDBTitle:** rad51 (rada)
63	c2cvhB_	Alignment	not modelled	97.4	17	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna repair and recombination protein radb; **PDBTitle:** crystal structure of the radb recombinase
64	c3bh0A_	Alignment	not modelled	97.3	15	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** atpase domain of g40p
65	c3cmvG_	Alignment	not modelled	97.2	18	**PDB header:**recombination **Chain:** G: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
66	c2vyeA_	Alignment	not modelled	97.1	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
67	c3bs4A_	Alignment	not modelled	96.8	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
68	c1zu4A_	Alignment	not modelled	96.6	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
69	d2jdid2	Alignment	not modelled	96.6	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
70	c2q6tB_	Alignment	not modelled	96.6	27	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
71	d1cr2a_	Alignment	not modelled	96.5	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
72	d1skye2	Alignment	not modelled	96.5	25	**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
73	d1fx0b2	Alignment	not modelled	96.4	26	**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
74	c3bgwD_	Alignment	not modelled	96.4	23	**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	c2og2A_	Alignment	not modelled	96.4	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana

76	c3b9qA_	Alignment	not modelled	96.4	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
77	c2j7pA_	Alignment	not modelled	96.4	16	**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
78	c3dmdA_	Alignment	not modelled	96.4	13	**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
79	d1mabb2	Alignment	not modelled	96.3	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
80	c2cnwF_	Alignment	not modelled	96.2	20	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
81	c2a5yB_	Alignment	not modelled	96.1	12	**PDB header:**apoptosis **Chain:** B: **PDB Molecule:**ced-4; **PDBTitle:** structure of a ced-4/ced-9 complex
82	c1vmaA_	Alignment	not modelled	96.0	21	**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
83	c2qy9A_	Alignment	not modelled	95.8	19	**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
84	c3bosA_	Alignment	not modelled	95.8	14	**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
85	c3dm5A_	Alignment	not modelled	95.8	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.
86	d1nlfa_	Alignment	not modelled	95.6	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
87	c2iy3A_	Alignment	not modelled	95.6	16	**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
88	c3b85A_	Alignment	not modelled	95.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphate starvation-inducible protein; **PDBTitle:** crystal structure of predicted phosphate starvation-induced atpase2 phoh2 from corynebacterium glutamicum
89	c2kjqA_	Alignment	not modelled	95.5	15	**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.
90	c2j37W_	Alignment	not modelled	95.4	13	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
91	d1vmaa2	Alignment	not modelled	95.4	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
92	c2yhsA_	Alignment	not modelled	95.3	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
93	d1qzxa3	Alignment	not modelled	95.2	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
94	c1fnnB_	Alignment	not modelled	95.2	14	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division control protein 6; **PDBTitle:** crystal structure of cdc6p from pyrobaculum aerophilum
95	c3pvsA_	Alignment	not modelled	95.1	17	**PDB header:**recombination **Chain:** A: **PDB Molecule:**replication-associated recombination protein a; **PDBTitle:** structure and biochemical activities of escherichia coli mgsa
96	d1okkd2	Alignment	not modelled	95.1	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
97	c2qbyA_	Alignment	not modelled	94.9	18	**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)
98	c2zamA_	Alignment	not modelled	94.9	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**vacuolar protein sorting-associating protein 4b; **PDBTitle:** crystal structure of mouse skd1/vps4b apo-form
99	c3j04A_	Alignment	not modelled	94.7	22	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**myosin-11; **PDBTitle:** em structure of the heavy meromyosin subfragment of chick smooth2 muscle myosin with regulatory light chain in phosphorylated state
						PDB header:hydrolase

100	c2wjyA_	Alignment	not modelled	94.6	20	**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
101	d1fnna2	Alignment	not modelled	94.5	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
102	c1z6tC_	Alignment	not modelled	94.3	14	**PDB header:**apoptosis **Chain:** C: **PDB Molecule:**apoptotic protease activating factor 1; **PDBTitle:** structure of the apoptotic protease-activating factor 12 bound to adp
103	c3d8bB_	Alignment	not modelled	94.2	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
104	c3pfiB_	Alignment	not modelled	94.1	26	**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
105	d1qvra2	Alignment	not modelled	94.0	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
106	d1ls1a2	Alignment	not modelled	94.0	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
107	d1ye8a1	Alignment	not modelled	93.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
108	c2c9oC_	Alignment	not modelled	93.9	34	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ruvb-like 1; **PDBTitle:** 3d structure of the human ruvb-like helicase ruvbl1
109	c3lxwA_	Alignment	not modelled	93.9	20	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 1; **PDBTitle:** crystal structure of human gtpase imap family member 1
110	c3dtpA_	Alignment	not modelled	93.8	20	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**myosin 2 heavy chain chimera of smooth and **PDBTitle:** tarantula heavy meromyosin obtained by flexible docking to2 tarantula muscle thick filament cryo-em 3d-map
111	d1nn5a_	Alignment	not modelled	93.7	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
112	c1xwiA_	Alignment	not modelled	93.7	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**skd1 protein; **PDBTitle:** crystal structure of vps4b
113	d1tmka_	Alignment	not modelled	93.7	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
114	c1q57G_	Alignment	not modelled	93.7	7	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
115	c1nsfA_	Alignment	not modelled	93.7	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
116	c3iytG_	Alignment	not modelled	93.6	21	**PDB header:**apoptosis **Chain:** G: **PDB Molecule:**apoptotic protease-activating factor 1; **PDBTitle:** structure of an apoptosome-procaspase-9 card complex
117	c3e1sA_	Alignment	not modelled	93.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exodeoxyribonuclease v, subunit recd; **PDBTitle:** structure of an n-terminal truncation of deinococcus radiodurans recd2
118	c2xzlA_	Alignment	not modelled	93.5	22	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent helicase nam7; **PDBTitle:** upf1-rna complex
119	c2ce7B_	Alignment	not modelled	93.5	16	**PDB header:**cell division protein **Chain:** B: **PDB Molecule:**cell division protein ftsh; **PDBTitle:** edta treated
120	d1l8qa2	Alignment	not modelled	93.5	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain