Phyre2

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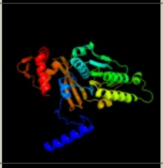
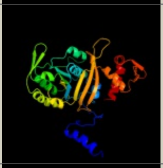
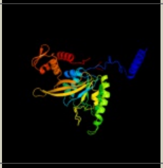
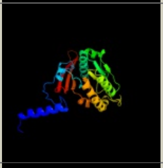
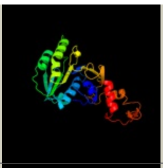
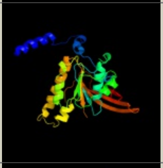
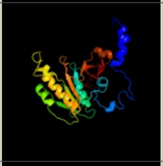
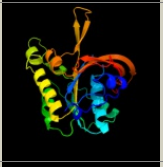
Description	P0A7G6
Date	Thu Jan 5 11:05:38 GMT 2012
Unique Job ID	e23e1f574178e204

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cmwA_	Alignment		100.0	99	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
2	c3hr8A_	Alignment		100.0	59	**PDB header:**recombination **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** crystal structure of thermotoga maritima reca
3	c2zroA_	Alignment		100.0	65	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** msreca adp form iv
4	c3cmvG_	Alignment		100.0	100	**PDB header:**recombination **Chain:** G: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
5	c2recB_	Alignment		100.0	100	**PDB header:**helicase **PDB COMPND:**
6	c3cmuA_	Alignment		100.0	99	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
7	c1xp8A_	Alignment		100.0	60	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"
8	d1mo6a1	Alignment		100.0	66	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
9	d1u94a1	Alignment		100.0	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
10	d1ubea1	Alignment		100.0	68	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
11	d1xp8a1	Alignment		100.0	64	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)

12	c3io5B_	Alignment		100.0	23	**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
13	c3ldaA_	Alignment		100.0	28	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** yeast rad51 h352y filament interface mutant
14	c1t4gA_	Alignment		100.0	24	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** atpase in complex with amp-pnp
15	c2dflA_	Alignment		100.0	29	**PDB header:**recombination **Chain:** A: **PDB Molecule:**dna repair and recombination protein rada; **PDBTitle:** crystal structure of left-handed rada filament
16	d1v5wa_	Alignment		100.0	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
17	d1szpa2	Alignment		100.0	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
18	d2i1qa2	Alignment		100.0	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
19	c1szpC_	Alignment		100.0	31	**PDB header:**dna binding protein **Chain:** C: **PDB Molecule:**dna repair protein rad51; **PDBTitle:** a crystal structure of the rad51 filament
20	c2zjbB_	Alignment		100.0	29	**PDB header:**recombination **Chain:** B: **PDB Molecule:**meiotic recombination protein dmc1/lim15 homolog; **PDBTitle:** crystal structure of the human dmc1-m200v polymorphic2 variant
21	d1n0wa_	Alignment	not modelled	100.0	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
22	d1pzna2	Alignment	not modelled	100.0	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
23	c2cvhB_	Alignment	not modelled	100.0	26	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna repair and recombination protein radb; **PDBTitle:** crystal structure of the radb recombinase
24	d1tf7a2	Alignment	not modelled	100.0	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
25	c2ztsB_	Alignment	not modelled	100.0	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
26	c1pznG_	Alignment	not modelled	100.0	23	**PDB header:**recombination **Chain:** G: **PDB Molecule:**dna repair and recombination protein rad51; **PDBTitle:** rad51 (rada)
27	d1tf7a1	Alignment	not modelled	100.0	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
28	c3bh0A_	Alignment	not modelled	100.0	14	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** atpase domain of g40p

29	c2q6tB_	Alignment	not modelled	100.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
30	c2w0mA_	Alignment	not modelled	100.0	28	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso2452; **PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus2 p2
31	c1u9iA_	Alignment	not modelled	100.0	20	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic; **PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
32	c3bgwD_	Alignment	not modelled	99.9	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
33	c2vyeA_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
34	c2dr3A_	Alignment	not modelled	99.9	20	**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
35	c1q57G_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
36	c3bs4A_	Alignment	not modelled	99.9	14	**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
37	d1nlfa_	Alignment	not modelled	99.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
38	d1cr2a_	Alignment	not modelled	99.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
39	d1u94a2	Alignment	not modelled	99.5	100	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
40	d1ubea2	Alignment	not modelled	99.5	47	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
41	d1mo6a2	Alignment	not modelled	99.5	51	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
42	d1xp8a2	Alignment	not modelled	99.5	38	**Fold:**Anti-LPS factor/recA domain **Superfamily:**RecA protein, C-terminal domain **Family:**RecA protein, C-terminal domain
43	c2cnwF_	Alignment	not modelled	98.8	18	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
44	d1skyb3	Alignment	not modelled	98.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
45	c3oaaC_	Alignment	not modelled	98.6	15	**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
46	c2qe7C_	Alignment	not modelled	98.6	16	**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
47	c3b9qA_	Alignment	not modelled	98.5	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
48	c2r9vA_	Alignment	not modelled	98.5	18	**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
49	d1skye3	Alignment	not modelled	98.5	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
50	d1fx0a3	Alignment	not modelled	98.5	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
51	d2jdia3	Alignment	not modelled	98.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
52	d2jdid3	Alignment	not modelled	98.4	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
53	c2og2A_	Alignment	not modelled	98.4	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
54	c1skyE_	Alignment	not modelled	98.4	18	**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

55	c2iy3A_	Alignment	not modelled	98.4	23	**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
56	c1w0jB_	Alignment	not modelled	98.4	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase alpha chain heart isoform, **PDBTitle:** beryllium fluoride inhibited bovine f1-atpase
57	d1qzxa3	Alignment	not modelled	98.4	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
58	c2w6fA_	Alignment	not modelled	98.4	15	**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.
59	c2j7pA_	Alignment	not modelled	98.3	23	**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
60	d1fx0b3	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)
61	c1fx0B_	Alignment	not modelled	98.3	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp synthase beta chain; **PDBTitle:** crystal structure of the chloroplast f1-atpase from spinach
62	c2yhsA_	Alignment	not modelled	98.3	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
63	c1vmaA_	Alignment	not modelled	98.3	17	**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
64	d1xpua3	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)
65	c3l0oB_	Alignment	not modelled	98.3	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**transcription termination factor rho; **PDBTitle:** structure of rna-free rho transcription termination factor from2 thermotoga maritima
66	c3hu2C_	Alignment	not modelled	98.3	21	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97 n-d1 r86a mutant in complex with atpgs
67	c2oblA_	Alignment	not modelled	98.3	18	**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
68	c3cf1C_	Alignment	not modelled	98.3	22	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
69	c1zu4A_	Alignment	not modelled	98.3	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
70	c2qy9A_	Alignment	not modelled	98.3	14	**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
71	c1s3sA_	Alignment	not modelled	98.3	20	**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
72	c2jizD_	Alignment	not modelled	98.3	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp synthase subunit beta; **PDBTitle:** the structure of f1-atpase inhibited by resveratrol.
73	c1kmhA_	Alignment	not modelled	98.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atpase alpha subunit; **PDBTitle:** crystal structure of spinach chloroplast f1-atpase2 complexed with tentoxin
74	c2w6jD_	Alignment	not modelled	98.3	19	**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.
75	c3dmdA_	Alignment	not modelled	98.2	15	**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
76	c2j37W_	Alignment	not modelled	98.2	18	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
77	c1xpuB_	Alignment	not modelled	98.2	19	**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)
78	d1vmaa2	Alignment	not modelled	98.2	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
79	c3a5dB_	Alignment	not modelled	98.2	17	**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
						PDB header:rna binding protein, transport protein

80	c3dm5A_	Alignment	not modelled	98.2	21	**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.
81	d1okkd2	Alignment	not modelled	98.2	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
82	c2c61A_	Alignment	not modelled	98.1	18	**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
83	c2dpyA_	Alignment	not modelled	98.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flagellum-specific atp synthase; **PDBTitle:** crystal structure of the flagellar type iii atpase flii
84	c1oftC_	Alignment	not modelled	98.1	17	**PDB header:**bacterial cell division inhibitor **Chain:** C: **PDB Molecule:**hypothetical protein pa3008; **PDBTitle:** crystal structure of sula from pseudomonas aeruginosa
85	c2dhrC_	Alignment	not modelled	98.1	16	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ftsh; **PDBTitle:** whole cytosolic region of atp-dependent metalloprotease2 ftsh (g399l)
86	d1ofux_	Alignment	not modelled	98.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Bacterial cell division inhibitor SulA
87	c3fkqA_	Alignment	not modelled	98.1	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**ntrc-like two-domain protein; **PDBTitle:** crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
88	c3b9pA_	Alignment	not modelled	98.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cg5977-pa, isoform a; **PDBTitle:** spastin
89	c1vdzA_	Alignment	not modelled	98.0	16	**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
90	d2qy9a2	Alignment	not modelled	98.0	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
91	d2ce7a2	Alignment	not modelled	98.0	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
92	c2ce7B_	Alignment	not modelled	98.0	19	**PDB header:**cell division protein **Chain:** B: **PDB Molecule:**cell division protein ftsh; **PDBTitle:** edta treated
93	c3h4mC_	Alignment	not modelled	98.0	20	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** aaa atpase domain of the proteasome- activating nucleotidase
94	c2kjqA_	Alignment	not modelled	98.0	22	**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.
95	c3a5dM_	Alignment	not modelled	98.0	18	**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
96	d1ls1a2	Alignment	not modelled	98.0	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
97	d1e32a2	Alignment	not modelled	98.0	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
98	c2ja1A_	Alignment	not modelled	97.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidine kinase; **PDBTitle:** thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
99	c2it1B_	Alignment	not modelled	97.9	20	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**362aa long hypothetical maltose/maltodextrin **PDBTitle:** structure of ph0203 protein from pyrococcus horikoshii
100	c3d8bB_	Alignment	not modelled	97.9	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
101	d1g2912	Alignment	not modelled	97.9	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
102	d2awna2	Alignment	not modelled	97.8	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
103	c1qzwC_	Alignment	not modelled	97.8	18	**PDB header:**signaling protein/rna **Chain:** C: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
104	d1ixza_	Alignment	not modelled	97.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
105	c1xwiA_	Alignment	not modelled	97.8	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**skd1 protein;

						PDBTitle: crystal structure of vps4b
106	d3d31a2	Alignment	not modelled	97.8	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
107	c2qmoA_	Alignment	not modelled	97.7	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
108	d1c9ka_	Alignment	not modelled	97.7	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
109	c1nsfA_	Alignment	not modelled	97.7	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
110	c2px0D_	Alignment	not modelled	97.7	23	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
111	d1v43a3	Alignment	not modelled	97.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
112	c2v1uA_	Alignment	not modelled	97.7	19	**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
113	d1r7ra3	Alignment	not modelled	97.7	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
114	c2w58B_	Alignment	not modelled	97.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**primosome component (helicase loader); **PDBTitle:** crystal structure of the dnai
115	c2iusB_	Alignment	not modelled	97.7	21	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**dna translocase ftsk; **PDBTitle:** e. coli ftsk motor domain
116	c1sxjA_	Alignment	not modelled	97.7	25	**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)
117	c2j289_	Alignment	not modelled	97.7	19	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
118	c1fnnB_	Alignment	not modelled	97.7	10	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cell division control protein 6; **PDBTitle:** crystal structure of cdc6p from pyrobaculum aerophilum
119	c2ihyB_	Alignment	not modelled	97.6	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**abc transporter, atp-binding protein; **PDBTitle:** structure of the staphylococcus aureus putative atpase subunit of an2 atp-binding cassette (abc) transporter
120	c2v3cC_	Alignment	not modelled	97.6	23	**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