Phyre^2

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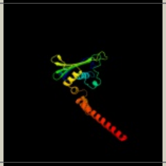
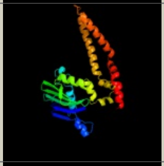
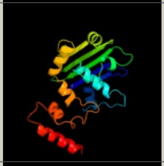
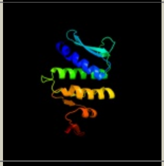
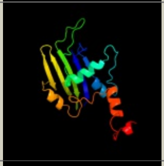
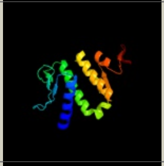
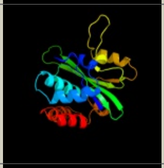
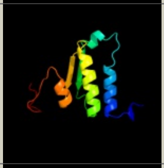
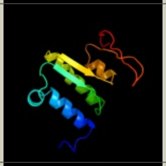
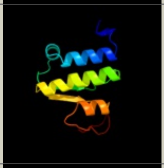
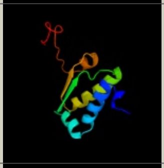
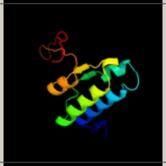
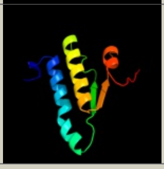
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3qg5A_	 Alignment		99.9	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rad50; **PDBTitle:** the mre11:rad50 complex forms an atp dependent molecular clamp in dna2 double-strand break repair
2	c1ii8A_	 Alignment		99.9	20	**PDB header:**replication **Chain:** A: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of the p. furiosus rad50 atpase domain
3	c1xexA_	 Alignment		99.9	19	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**smc protein; **PDBTitle:** structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
4	c3auyB_	 Alignment		99.9	22	**PDB header:**recombination **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** crystal structure of rad50 bound to adp
5	c3qkuB_	 Alignment		99.9	21	**PDB header:**replication **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** mre11 rad50 binding domain in complex with rad50 and amp-pnp
6	c1ii8B_	 Alignment		99.9	22	**PDB header:**replication **Chain:** B: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of the p. furiosus rad50 atpase domain
7	c1f2uD_	 Alignment		99.8	26	**PDB header:**replication **Chain:** D: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of rad50 abc-atpase
8	d1e69a_	 Alignment		99.8	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
9	c1us8A_	 Alignment		99.8	29	**PDB header:**dna repair **Chain:** A: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** the rad50 signature motif: essential to atp binding and2 biological function
10	c1xexB_	 Alignment		99.7	19	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**smc protein; **PDBTitle:** structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
11	d1w1wa_	 Alignment		99.7	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like

12	c2o5vA_	Alignment		99.6	26	**PDB header:**replication/recombination **Chain:** A: **PDB Molecule:**dna replication and repair protein recf; **PDBTitle:** recombination mediator recf
13	d1qhla_	Alignment		99.6	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
14	c3pihA_	Alignment		99.2	26	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
15	c3bk7A_	Alignment		99.2	25	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**abc transporter atp-binding protein; **PDBTitle:** structure of the complete abce1/rnaase-l inhibitor protein2 from pyrococcus abysii
16	c1yqtA_	Alignment		99.2	30	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
17	c2vf7B_	Alignment		99.2	24	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
18	c2ygrD_	Alignment		99.1	30	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** mycobacterium tuberculosis uvra
19	c3ozxA_	Alignment		99.0	20	**PDB header:**hydrolase, translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
20	c2pcjB_	Alignment		98.9	33	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipoprotein-releasing system atp-binding protein lold; **PDBTitle:** crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
21	c3dhwC_	Alignment	not modelled	98.9	35	**PDB header:**membrane protein/hydrolase **Chain:** C: **PDB Molecule:**methionine import atp-binding protein metn; **PDBTitle:** crystal structure of methionine importer metni
22	c2yl4A_	Alignment	not modelled	98.8	30	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**atp-binding cassette sub-family b member 10, **PDBTitle:** structure of the human mitochondrial abc transporter, abcb10
23	d1g6ha_	Alignment	not modelled	98.8	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
24	d1b0ua_	Alignment	not modelled	98.8	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
25	c2olkD_	Alignment	not modelled	98.8	25	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**amino acid abc transporter; **PDBTitle:** abc protein artp in complex with adp-beta-s
26	c2nq2C_	Alignment	not modelled	98.8	29	**PDB header:**metal transport **Chain:** C: **PDB Molecule:**hypothetical abc transporter atp-binding protein **PDBTitle:** an inward-facing conformation of a putative metal-chelate2 type abc transporter.
27	c1vciA_	Alignment	not modelled	98.8	23	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar-binding transport atp-binding protein; **PDBTitle:** crystal structure of the atp-binding cassette of multisugar2 transporter from pyrococcus horikoshii ot3 complexed with3 atp

28	c2iw3B_	Alignment	not modelled	98.8	24	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 3a; **PDBTitle:** elongation factor 3 in complex with adp
29	c2d62A_	Alignment	not modelled	98.8	26	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**multiple sugar-binding transport atp-binding **PDBTitle:** crystal structure of multiple sugar binding transport atp-2 binding protein
30	d1vpla_	Alignment	not modelled	98.8	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
31	c3fvqB_	Alignment	not modelled	98.8	32	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fe(3+) ions import atp-binding protein fbpc; **PDBTitle:** crystal structure of the nucleotide binding domain fbpc2 complexed with atp
32	c2yz2B_	Alignment	not modelled	98.8	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative abc transporter atp-binding protein tm_0222; **PDBTitle:** crystal structure of the abc transporter in the cobalt transport2 system
33	c1oxtB_	Alignment	not modelled	98.8	35	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, atp binding protein; **PDBTitle:** crystal structure of glcv, the abc-atpase of the glucose abc2 transporter from sulfolobus solfataricus
34	c2hydB_	Alignment	not modelled	98.8	28	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
35	d1l2ta_	Alignment	not modelled	98.7	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
36	d1v43a3	Alignment	not modelled	98.7	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
37	d2hyda1	Alignment	not modelled	98.7	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
38	c3eukC_	Alignment	not modelled	98.7	19	**PDB header:**cell cycle **Chain:** C: **PDB Molecule:**chromosome partition protein mukb, linker; **PDBTitle:** crystal structure of muke-mukf(residues 292-443)-mukb(head2 domain)-atpgammas complex, asymmetric dimer
39	d3dhwc1	Alignment	not modelled	98.7	35	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
40	c2pjzA_	Alignment	not modelled	98.7	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st1066; **PDBTitle:** the crystal structure of putative cobalt transport atp-2 binding protein (cbio-2), st1066
41	c2yyzA_	Alignment	not modelled	98.7	28	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar abc transporter, atp-binding protein; **PDBTitle:** crystal structure of sugar abc transporter, atp-binding protein
42	c3gfoA_	Alignment	not modelled	98.7	25	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**cobalt import atp-binding protein cbio 1; **PDBTitle:** structure of cbio1 from clostridium perfringens: part of2 the abc transporter complex cbionq.
43	c2d2fA_	Alignment	not modelled	98.7	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sufc protein; **PDBTitle:** crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
44	d1g2912	Alignment	not modelled	98.7	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
45	d3b60a1	Alignment	not modelled	98.7	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
46	d1jj7a_	Alignment	not modelled	98.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
47	d1ji0a_	Alignment	not modelled	98.7	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
48	d2pmka1	Alignment	not modelled	98.7	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
49	c1z47B_	Alignment	not modelled	98.7	26	**PDB header:**ligand binding protein **Chain:** B: **PDB Molecule:**putative abc-transporter atp-binding protein; **PDBTitle:** structure of the atpase subunit cysa of the putative2 sulfate atp-binding cassette (abc) transporter from3 alicyclobacillus acidocaldarius
50	c2it1B_	Alignment	not modelled	98.7	30	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**362aa long hypothetical maltose/maltodextrin **PDBTitle:** structure of ph0203 protein from pyrococcus horikoshii
51	c2r6fA_	Alignment	not modelled	98.7	31	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**excinuclease abc subunit a; **PDBTitle:** crystal structure of bacillus stearothermophilus uvra
						Fold:P-loop containing nucleoside triphosphate hydrolases

52	d1mv5a_	Alignment	not modelled	98.6	29	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
53	d3d31a2	Alignment	not modelled	98.6	36	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
54	c2cbzA_	Alignment	not modelled	98.6	24	**PDB header:**transport **Chain:** A: **PDB Molecule:**multidrug resistance-associated protein 1; **PDBTitle:** structure of the human multidrug resistance protein 12 nucleotide binding domain 1
55	d1oxxk2	Alignment	not modelled	98.6	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
56	d1r0wa_	Alignment	not modelled	98.6	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
57	c3g5uB_	Alignment	not modelled	98.6	32	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**multidrug resistance protein 1a; **PDBTitle:** structure of p-glycoprotein reveals a molecular basis for2 poly-specific drug binding
58	c3b5xB_	Alignment	not modelled	98.6	30	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of msba from vibrio cholerae
59	c3b5wE_	Alignment	not modelled	98.6	31	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of eschericia coli msba
60	c3d31B_	Alignment	not modelled	98.6	36	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**sulfate/molybdate abc transporter, atp-binding **PDBTitle:** modbc from methanosarcina acetivorans
61	c3nhaA_	Alignment	not modelled	98.6	25	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**atp-binding cassette sub-family b member 6, mitochondrial; **PDBTitle:** nucleotide binding domain of human abcb6 (adp mg bound structure)
62	d1xmia_	Alignment	not modelled	98.6	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
63	c2pzfB_	Alignment	not modelled	98.5	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**cystic fibrosis transmembrane conductance regulator; **PDBTitle:** minimal human cftr first nucleotide binding domain as a head-to-tail2 dimer with delta f508
64	d2onka1	Alignment	not modelled	98.5	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
65	d1l7vc_	Alignment	not modelled	98.5	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
66	c2d3wB_	Alignment	not modelled	98.5	20	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**probable atp-dependent transporter sufc; **PDBTitle:** crystal structure of escherichia coli sufc, an atpase2 compenent of the suf iron-sulfur cluster assembly machinery
67	c1q1bD_	Alignment	not modelled	98.5	22	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**maltose/maltodextrin transport atp-binding protein malk; **PDBTitle:** crystal structure of e. coli malk in the nucleotide-free form
68	d1pf4a1	Alignment	not modelled	98.4	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
69	c2ihyB_	Alignment	not modelled	98.3	29	**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
70	c3gd7C_	Alignment	not modelled	98.3	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fusion complex of cystic fibrosis transmembrane **PDBTitle:** crystal structure of human nbd2 complexed with n6-2 phenylethyl-atp (p-atp)
71	d1sgwa_	Alignment	not modelled	98.2	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
72	c2ghiD_	Alignment	not modelled	98.0	25	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**transport protein; **PDBTitle:** crystal structure of plasmodium yoelii multidrug resistance2 protein 2
73	d2awna2	Alignment	not modelled	97.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
74	d1vmaa2	Alignment	not modelled	97.7	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
75	d1np6a_	Alignment	not modelled	97.6	43	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
76	d2qy9a2	Alignment	not modelled	97.6	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family: Nitrogenase iron protein-like
77	d1okkd2	Alignment	not modelled	97.5	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
78	c2j41A_	Alignment	not modelled	97.5	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
79	c3tauB_	Alignment	not modelled	97.4	40	**PDB header:**transferase **Chain:** B: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of a putative guanylate monophosphaste kinase from2 listeria monocytogenes egd-e
80	d1ls1a2	Alignment	not modelled	97.4	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
81	c3a4mB_	Alignment	not modelled	97.3	35	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-seryl-trna(sec) kinase; **PDBTitle:** crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
82	d1qzxa3	Alignment	not modelled	97.1	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
83	d2i3ba1	Alignment	not modelled	97.0	47	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
84	d1ye8a1	Alignment	not modelled	97.0	53	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
85	d1cr2a_	Alignment	not modelled	96.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
86	d1ewqa2	Alignment	not modelled	96.9	41	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
87	d1znwa1	Alignment	not modelled	96.7	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
88	c1ewqA_	Alignment	not modelled	96.7	44	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure taq muts complexed with a heteroduplex2 dna at 2.2 a resolution
89	d1wb9a2	Alignment	not modelled	96.7	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
90	c2o8bA_	Alignment	not modelled	96.6	27	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**dna mismatch repair protein msh2; **PDBTitle:** human mutsalpha (msh2/msh6) bound to adp and a g t mispair
91	c2o8dB_	Alignment	not modelled	96.6	31	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**dna mismatch repair protein msh6; **PDBTitle:** human mutsalpha (msh2/msh6) bound to adp and a g du mispair
92	c3jvvA_	Alignment	not modelled	96.6	50	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
93	d1ki9a_	Alignment	not modelled	96.6	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
94	d1p9ra_	Alignment	not modelled	96.6	48	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
95	c2cnwF_	Alignment	not modelled	96.6	18	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
96	d1s96a_	Alignment	not modelled	96.6	40	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
97	c2j7pA_	Alignment	not modelled	96.5	24	**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
98	c2yhsA_	Alignment	not modelled	96.5	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
99	c3thxB_	Alignment	not modelled	96.5	31	**PDB header:**dna binding protein/dna **Chain:** B: **PDB Molecule:**dna mismatch repair protein msh3; **PDBTitle:** human mutsbeta complexed with an idl of 3 bases (loop3) and adp
100	c3b9qA_	Alignment	not modelled	96.5	30	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
101	c1u9iA_	Alignment	not modelled	96.5	19	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic; **PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
102	c3geiB_	Alignment	not modelled	96.5	44	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trna modification gtpase mnme;

102	c3geiB_	Alignment	not modelled	96.5	44	**PDBTitle:** crystal structure of mnme from chlorobium tepidum in complex2 with gcp
103	d1zp6a1	Alignment	not modelled	96.4	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Atu3015-like
104	c1wbdA_	Alignment	not modelled	96.4	31	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure of e. coli dna mismatch repair enzyme2 muts, e38q mutant, in complex with a g.t mismatch
105	c2og2A_	Alignment	not modelled	96.4	30	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
106	d1sxje2	Alignment	not modelled	96.4	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
107	c2f1rA_	Alignment	not modelled	96.4	35	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin-guanine dinucleotide biosynthesis **PDBTitle:** crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
108	c1ewrA_	Alignment	not modelled	96.4	44	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure of taq muts
109	c2qy9A_	Alignment	not modelled	96.4	18	**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
110	d1sxja2	Alignment	not modelled	96.4	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
111	d1yrba1	Alignment	not modelled	96.3	35	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
112	c1znyA_	Alignment	not modelled	96.3	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of mycobacterium tuberculosis guanylate kinase in2 complex with gdp
113	c2eyuA_	Alignment	not modelled	96.3	38	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**twitching motility protein pilt; **PDBTitle:** the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
114	c1wxqA_	Alignment	not modelled	96.3	26	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
115	c2gzaB_	Alignment	not modelled	96.2	39	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**type iv secretion system protein virb11; **PDBTitle:** crystal structure of the virb11 atpase from the brucella suis type iv2 secretion system in complex with sulphate
116	c1zu4A_	Alignment	not modelled	96.2	24	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
117	d1g6oa_	Alignment	not modelled	96.2	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
118	c3neyC_	Alignment	not modelled	96.2	20	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**55 kda erythrocyte membrane protein; **PDBTitle:** crystal structure of the kinase domain of mpp1/p55
119	c2gszE_	Alignment	not modelled	96.2	43	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**twitching motility protein pilt; **PDBTitle:** structure of a. aeolicus pilt with 6 monomers per2 asymmetric unit
120	c1vmaA_	Alignment	not modelled	96.1	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