Phyre^2

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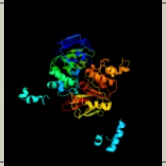
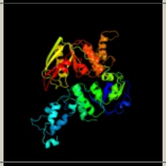
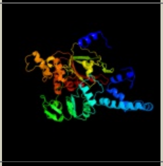
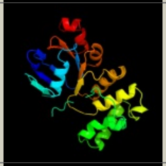
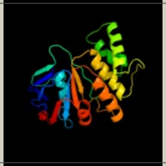
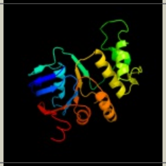
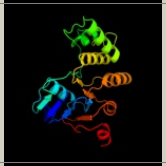
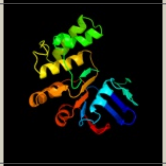
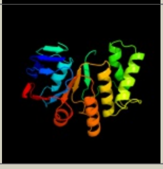
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2iw3B_	Alignment		100.0	31	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 3a; **PDBTitle:** elongation factor 3 in complex with adp
2	c1yqtA_	Alignment		100.0	25	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor
3	c3bk7A_	Alignment		100.0	23	**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
4	c3ozxA_	Alignment		100.0	19	**PDB header:**hydrolase, translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** crystal structure of abce1 of sulfolubus solfataricus (-fes domain)
5	c3g5uB_	Alignment		100.0	29	**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
6	c2ygrD_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** mycobacterium tuberculosis uvra
7	c3pihA_	Alignment		100.0	29	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein a; **PDBTitle:** t. maritima uvra in complex with fluorescein-modified dna
8	c2vf7B_	Alignment		100.0	22	**PDB header:**dna-binding protein **Chain:** B: **PDB Molecule:**excinuclease abc, subunit a.; **PDBTitle:** crystal structure of uvra2 from deinococcus radiodurans
9	c2r6fA_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**excinuclease abc subunit a; **PDBTitle:** crystal structure of bacillus stearothermophilus uvra
10	c2d62A_	Alignment		100.0	29	**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
11	c1oxtB_	Alignment		100.0	24	**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

12	c2olkD_	Alignment		100.0	28	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**amino acid abc transporter; **PDBTitle:** abc protein artp in complex with adp-beta-s
13	c3dhwC_	Alignment		100.0	31	**PDB header:**membrane protein/hydrolase **Chain:** C: **PDB Molecule:**methionine import atp-binding protein metn; **PDBTitle:** crystal structure of methionine importer metni
14	c2yyzA_	Alignment		100.0	29	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sugar abc transporter, atp-binding protein; **PDBTitle:** crystal structure of sugar abc transporter, atp-binding protein
15	d1g2912	Alignment		100.0	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
16	d1b0ua_	Alignment		100.0	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
17	d1g6ha_	Alignment		100.0	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
18	c3fvqB_	Alignment		100.0	28	**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
19	c2it1B_	Alignment		100.0	32	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**362aa long hypothetical maltose/maltodextrin **PDBTitle:** structure of ph0203 protein from pyrococcus horikoshii
20	c2pcjB_	Alignment		100.0	26	**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	d1oxxk2	Alignment	not modelled	100.0	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
22	c3gfoA_	Alignment	not modelled	100.0	22	**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.
23	c1z47B_	Alignment	not modelled	100.0	29	**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
24	d3dhwc1	Alignment	not modelled	100.0	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
25	d1ji0a_	Alignment	not modelled	100.0	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
26	c1q1bD_	Alignment	not modelled	100.0	20	**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
27	c1vciA_	Alignment	not modelled	100.0	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	d1vpla_	Alignment	not modelled	100.0	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
29	c2nq2C_	Alignment	not modelled	100.0	23	**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.
30	d1v43a3	Alignment	not modelled	100.0	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
31	c2yz2B_	Alignment	not modelled	100.0	25	**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
32	d3b60a1	Alignment	not modelled	100.0	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
33	d1jj7a_	Alignment	not modelled	100.0	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
34	d3d31a2	Alignment	not modelled	100.0	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
35	d1mv5a_	Alignment	not modelled	100.0	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
36	d1l2ta_	Alignment	not modelled	100.0	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
37	d2pmka1	Alignment	not modelled	100.0	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
38	c3d31B_	Alignment	not modelled	100.0	29	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**sulfate/molybdate abc transporter, atp-binding **PDBTitle:** modbc from methanosarcina acetivorans
39	c2d2fA_	Alignment	not modelled	100.0	21	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**sufc protein; **PDBTitle:** crystal structure of atypical cytoplasmic abc-atpase sufc from thermus2 thermophilus hb8
40	c2hydB_	Alignment	not modelled	100.0	26	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter homolog; **PDBTitle:** multidrug abc transporter sav1866
41	c2pzfB_	Alignment	not modelled	100.0	21	**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
42	c3nhaA_	Alignment	not modelled	100.0	24	**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)
43	c3gd7C_	Alignment	not modelled	100.0	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)
44	c2yl4A_	Alignment	not modelled	100.0	26	**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
45	c2pjzA_	Alignment	not modelled	100.0	21	**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
46	c2cbzA_	Alignment	not modelled	100.0	22	**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
47	d2hyda1	Alignment	not modelled	100.0	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
48	c2d3wB_	Alignment	not modelled	100.0	21	**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
49	d1r0wa_	Alignment	not modelled	100.0	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
50	c3b5wE_	Alignment	not modelled	100.0	25	**PDB header:**membrane protein **Chain:** E: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of eschericia coli msba
51	c2ihyB_	Alignment	not modelled	100.0	24	**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
52	d1xmia_	Alignment	not modelled	100.0	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
53	c3b5xB_	Alignment	not modelled	100.0	25	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**lipid a export atp-binding/permease protein msba; **PDBTitle:** crystal structure of msba from vibrio cholerae
54	d2onka1	Alignment	not modelled	100.0	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
55	d1pf4a1	Alignment	not modelled	100.0	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
56	d1sgwa_	Alignment	not modelled	100.0	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
57	c2ghiD_	Alignment	not modelled	100.0	27	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**transport protein; **PDBTitle:** crystal structure of plasmodium yoelii multidrug resistance2 protein 2
58	d2awna2	Alignment	not modelled	100.0	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
59	d1l7vc_	Alignment	not modelled	100.0	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
60	c1u9iA_	Alignment	not modelled	99.9	14	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic; **PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
61	d1cr2a_	Alignment	not modelled	99.9	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
62	d1w1wa_	Alignment	not modelled	99.9	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
63	c3tauB_	Alignment	not modelled	99.8	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of a putative guanylate monophosphaste kinase from2 listeria monocytogenes egd-e
64	c2j41A_	Alignment	not modelled	99.8	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
65	c1wxqA_	Alignment	not modelled	99.7	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**gtp-binding protein; **PDBTitle:** crystal structure of gtp binding protein from pyrococcus horikoshii2 ot3
66	c1xexB_	Alignment	not modelled	99.7	21	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**smc protein; **PDBTitle:** structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
67	c3a4mB_	Alignment	not modelled	99.7	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-seryl-trna(sec) kinase; **PDBTitle:** crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase
68	c2o5vA_	Alignment	not modelled	99.6	23	**PDB header:**replication/recombination **Chain:** A: **PDB Molecule:**dna replication and repair protein recf; **PDBTitle:** recombination mediator recf
69	c1f2uD_	Alignment	not modelled	99.6	37	**PDB header:**replication **Chain:** D: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of rad50 abc-atpase
70	c1ii8B_	Alignment	not modelled	99.5	38	**PDB header:**replication **Chain:** B: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of the p. furiosus rad50 atpase domain
71	d2qy9a2	Alignment	not modelled	99.5	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
72	d1ls1a2	Alignment	not modelled	99.4	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
73	d1ye8a1	Alignment	not modelled	99.4	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
74	d1vmaa2	Alignment	not modelled	99.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
75	c3geiB_	Alignment	not modelled	99.3	10	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**trna modification gtpase mnme; **PDBTitle:** crystal structure of mnme from chlorobium tepidum in complex2 with gcp
76	c3lncB_	Alignment	not modelled	99.2	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of guanylate kinase from anaplasma2 phagocytophilum
77	d1okkd2	Alignment	not modelled	99.2	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases

						Family: Nitrogenase iron protein-like
78	d1np6a_	Alignment	not modelled	99.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
79	d1e69a_	Alignment	not modelled	99.0	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
80	c3cmvG_	Alignment	not modelled	98.9	13	**PDB header:**recombination **Chain:** G: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
81	c1q57G_	Alignment	not modelled	98.8	13	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
82	c2w0mA_	Alignment	not modelled	98.8	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso2452; **PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus2 p2
83	d2i3ba1	Alignment	not modelled	98.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
84	c3auyB_	Alignment	not modelled	98.8	22	**PDB header:**recombination **Chain:** B: **PDB Molecule:**dna double-strand break repair rad50 atpase; **PDBTitle:** crystal structure of rad50 bound to adp
85	c2dr3A_	Alignment	not modelled	98.8	15	**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
86	d1qzxa3	Alignment	not modelled	98.6	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
87	c3thxB_	Alignment	not modelled	98.5	19	**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
88	d1ewqa2	Alignment	not modelled	98.4	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
89	c2o8bA_	Alignment	not modelled	98.4	22	**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
90	d1wb9a2	Alignment	not modelled	98.4	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
91	c1wbdA_	Alignment	not modelled	98.3	21	**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
92	c2o8dB_	Alignment	not modelled	98.3	19	**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
93	c1ewqA_	Alignment	not modelled	98.2	31	**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
94	d1nlfa_	Alignment	not modelled	98.1	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
95	c3cf1C_	Alignment	not modelled	98.1	19	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**transitional endoplasmic reticulum atpase; **PDBTitle:** structure of p97/vcp in complex with adp/adp.alfx
96	d1tf7a1	Alignment	not modelled	98.0	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
97	c1ewrA_	Alignment	not modelled	98.0	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna mismatch repair protein muts; **PDBTitle:** crystal structure of taq muts
98	c3qg5A_	Alignment	not modelled	98.0	32	**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
99	c3qkuB_	Alignment	not modelled	98.0	23	**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
100	c2hjgA_	Alignment	not modelled	98.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gtp-binding protein enga; **PDBTitle:** the crystal structure of the b. subtilis yphc gtpase in2 complex with gdp
101	d1tf7a2	Alignment	not modelled	98.0	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
102	c1mkyA_	Alignment	not modelled	97.9	23	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**probable gtp-binding protein enga; **PDBTitle:** structural analysis of the domain interactions in der, a2 switch protein containing two gtpase domains

103	c2recB_	Alignment	not modelled	97.8	22	**PDB header:**helicase **PDB COMPND:**
104	d1yrba1	Alignment	not modelled	97.8	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
105	c1pznG_	Alignment	not modelled	97.7	13	**PDB header:**recombination **Chain:** G: **PDB Molecule:**dna repair and recombination protein rad51; **PDBTitle:** rad51 (rada)
106	c2cnwF_	Alignment	not modelled	97.7	21	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
107	c2j7pA_	Alignment	not modelled	97.7	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
108	c3lxwA_	Alignment	not modelled	97.7	21	**PDB header:**immune system **Chain:** A: **PDB Molecule:**gtpase imap family member 1; **PDBTitle:** crystal structure of human gtpase imap family member 1
109	c1ii8A_	Alignment	not modelled	97.7	23	**PDB header:**replication **Chain:** A: **PDB Molecule:**rad50 abc-atpase; **PDBTitle:** crystal structure of the p. furiosus rad50 atpase domain
110	c3p1jC_	Alignment	not modelled	97.6	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**gtpase imap family member 2; **PDBTitle:** crystal structure of human gtpase imap family member 2 in the2 nucleotide-free state
111	c1us8A_	Alignment	not modelled	97.6	23	**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
112	d1zp6a1	Alignment	not modelled	97.6	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Atu3015-like
113	c2vyeA_	Alignment	not modelled	97.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
114	d1znwa1	Alignment	not modelled	97.5	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
115	c2cvhB_	Alignment	not modelled	97.5	20	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna repair and recombination protein radb; **PDBTitle:** crystal structure of the radb recombinase
116	c1xp8A_	Alignment	not modelled	97.5	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"
117	c2ztsB_	Alignment	not modelled	97.4	14	**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
118	c3b9qA_	Alignment	not modelled	97.4	23	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
119	d1qhla_	Alignment	not modelled	97.4	32	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
120	c1znyA_	Alignment	not modelled	97.3	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of mycobacterium tuberculosis guanylate kinase in2 complex with gdp