Phyre2

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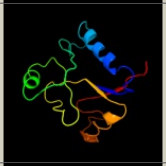
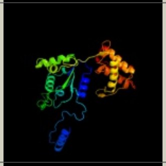
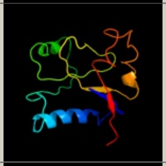
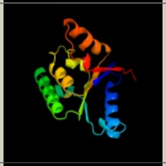
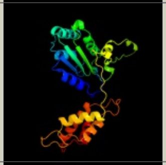
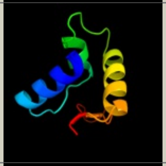
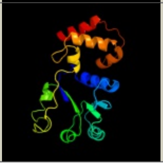
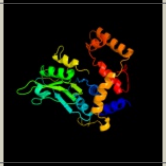
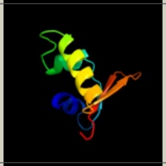
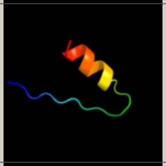
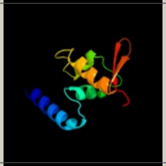
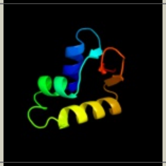
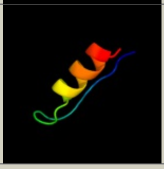
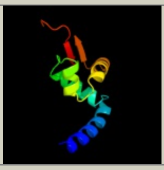
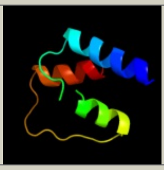
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f8tA_	Alignment		98.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**predicted atpase involved in replication control, **PDBTitle:** crystal structure analysis of a full-length mcm homolog2 from methanopyrus kandleri
2	c3f9vA_	Alignment		97.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**minichromosome maintenance protein mcm; **PDBTitle:** crystal structure of a near full-length archaeal mcm: functional2 insights for an aaa+ hexameric helicase
3	d1w5sa2	Alignment		97.3	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
4	c3pxgA_	Alignment		96.5	20	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca121 and clpc1-485 complex
5	c2p65A_	Alignment		96.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pf08_0063; **PDBTitle:** crystal structure of the first nucleotide binding domain of2 chaperone clpb1, putative, (pv089580) from plasmodium vivax
6	c3k1jA_	Alignment		95.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent protease lon; **PDBTitle:** crystal structure of lon protease from thermococcus onnurineus na1
7	c3pxiB_	Alignment		95.9	17	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
8	d1jbka_	Alignment		95.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
9	d1fnna2	Alignment		95.2	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
10	d1jhfa1	Alignment		95.0	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**LexA repressor, N-terminal DNA-binding domain
11	d1qvra2	Alignment		94.5	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain

12	c2qbyA_	Alignment		94.5	12	**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)
13	c3nbxX_	Alignment		93.3	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**atpase rava; **PDBTitle:** crystal structure of e. coli rava (regulatory atpase variant a) in2 complex with adp
14	d3ctaa1	Alignment		93.0	16	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
15	c2ccjA_	Alignment		92.4	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of s. aureus thymidylate kinase complexed2 with thymidine monophosphate
16	d2fbha1	Alignment		92.1	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
17	c2v1uA_	Alignment		91.5	13	**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
18	c3ctaA_	Alignment		91.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**riboflavin kinase; **PDBTitle:** crystal structure of riboflavin kinase from thermoplasma2 acidophilum
19	c2gxaA_	Alignment		91.4	20	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**replication protein e1; **PDBTitle:** crystal structure of papillomavirus e1 hexameric helicase2 with ssdna and mgadp
20	c2plrB_	Alignment		91.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable thymidylate kinase; **PDBTitle:** crystal structure of dtmp kinase (st1543) from sulfolobus tokodaii2 strain7
21	d2i3ba1	Alignment	not modelled	91.0	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
22	c3cjnA_	Alignment	not modelled	90.9	5	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of transcriptional regulator, marr family, from2 silicibacter pomeroyi
23	c2z0hA_	Alignment	not modelled	90.9	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of thymidylate kinase in complex with dtdp2 and adp from thermotoga maritima
24	d1g8pa_	Alignment	not modelled	90.9	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
25	c3k0lA_	Alignment		90.5	15	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**repressor protein; **PDBTitle:** crystal structure of putative marr family transcriptional2 regulator from acinetobacter sp. adp
26	c3tauB_	Alignment	not modelled	90.3	30	**PDB header:**transferase **Chain:** B: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of a putative guanylate monophosphaste kinase from2 listeria monocytogenes egd-e
27	c3a4mB_	Alignment	not modelled	90.0	31	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l-seryl-trna(sec) kinase; **PDBTitle:** crystal structure of archaeal o-phosphoseryl-trna(sec)2 kinase

28	d1ye8a1	Alignment	not modelled	90.0	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
29	d1y63a_	Alignment	not modelled	90.0	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
30	d1np6a_	Alignment	not modelled	89.8	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
31	c2gaaA_	Alignment	not modelled	89.8	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical 39.9 kda protein; **PDBTitle:** crystal structure of yfh7 from saccharomyces cerevisiae: a2 putative p-loop containing kinase with a circular3 permutation.
32	c3e6mD_	Alignment	not modelled	89.7	8	**PDB header:**transcription regulator **Chain:** D: **PDB Molecule:**marr family transcriptional regulator; **PDBTitle:** the crystal structure of a marr family transcriptional2 regulator from silicibacter pomeroyi dss.
33	c1znyA_	Alignment	not modelled	89.7	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of mycobacterium tuberculosis guanylate kinase in2 complex with gdp
34	c2j41A_	Alignment	not modelled	89.4	29	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
35	d1znwa1	Alignment	not modelled	89.4	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
36	d1ak2a1	Alignment	not modelled	89.2	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
37	d1p4xa2	Alignment	not modelled	88.9	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
38	d1okkd2	Alignment	not modelled	88.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
39	c1qvrB_	Alignment	not modelled	88.8	20	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**clpb protein; **PDBTitle:** crystal structure analysis of clpb
40	d2qy9a2	Alignment	not modelled	88.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
41	c2pbrB_	Alignment	not modelled	88.7	24	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of thymidylate kinase (aq_969) from aquifex aeolicus2 vf5
42	c2jatA_	Alignment	not modelled	88.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**deoxyguanosine kinase; **PDBTitle:** structure of deoxyadenosine kinase from m.mycoides with2 products dcmp and a flexible dcdp bound
43	c3qmzA_	Alignment	not modelled	88.6	17	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**cytoplasmic dynein heavy chain; **PDBTitle:** crystal structure of the cytoplasmic dynein heavy chain motor domain
44	c3eqxB_	Alignment	not modelled	88.4	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**fic domain containing transcriptional regulator; **PDBTitle:** crystal structure of a fic family protein (so_4266) from shewanella2 oneidensis at 1.6 a resolution
45	d1gkya_	Alignment	not modelled	88.2	35	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
46	d1kgda_	Alignment	not modelled	87.9	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
47	c2r44A_	Alignment		87.9	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative atpase (chu_0153) from cytophaga2 hutchinsonii atcc 33406 at 2.00 a resolution
48	d1qzxa3	Alignment	not modelled	87.8	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
49	d3broa1	Alignment	not modelled	87.8	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
50	d1zina1	Alignment	not modelled	87.7	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
51	c2f6rA_	Alignment	not modelled	87.7	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**bifunctional coenzyme a synthase; **PDBTitle:** crystal structure of bifunctional coenzyme a synthase (coa synthase):2 (18044849) from mus musculus at 1.70 a resolution
52	c2wwiC_	Alignment	not modelled	87.7	31	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidilate kinase, putative;

52	c2wwfC_	Alignment	not modelled	87.7	31	**PDBTitle:** plasmodium falciparum thymidylate kinase in complex with2 aztmp and adp
53	d1s3ga1	Alignment	not modelled	87.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
54	d1ls1a2	Alignment	not modelled	87.6	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
55	d1p4xa1	Alignment	not modelled	87.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
56	d1svma_	Alignment	not modelled	87.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
57	d1stza1	Alignment	not modelled	87.4	10	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Heat-inducible transcription repressor HrcA, N-terminal domain
58	d1e4va1	Alignment	not modelled	87.4	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
59	d1teva_	Alignment	not modelled	87.4	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
60	c3ld9D_	Alignment	not modelled	87.4	31	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of thymidylate kinase from ehrlichia chaffeensis at2 2.15a resolution
61	c2ak2A_	Alignment	not modelled	87.3	28	**PDB header:**phosphotransferase **Chain:** A: **PDB Molecule:**adenylate kinase isoenzyme-2; **PDBTitle:** adenylate kinase isoenzyme-2
62	d1rkba_	Alignment	not modelled	87.2	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
63	c3pfiB_	Alignment	not modelled	87.1	13	**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
64	d1p3ja1	Alignment	not modelled	87.1	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
65	d2ak3a1	Alignment	not modelled	87.1	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
66	c2qagB_	Alignment	not modelled	87.0	25	**PDB header:**cell cycle, structural protein **Chain:** B: **PDB Molecule:**septin-6; **PDBTitle:** crystal structure of human septin trimer 2/6/7
67	c3lv8A_	Alignment	not modelled	87.0	24	**PDB header:**transferase **Chain:** A: **PDB Molecule:**thymidylate kinase; **PDBTitle:** 1.8 angstrom resolution crystal structure of a thymidylate kinase2 (tmk) from vibrio cholerae o1 biovar eltor str. n16961 in complex3 with tmp, thymidine-5'-diphosphate and adp
68	c3bj6B_	Alignment	not modelled	87.0	6	**PDB header:**transcription regulator **Chain:** B: **PDB Molecule:**transcriptional regulator, marr family; **PDBTitle:** crystal structure of marr family transcription regulator sp03579
69	d1akya1	Alignment	not modelled	86.9	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
70	d1uf9a_	Alignment	not modelled	86.8	32	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
71	d2cdna1	Alignment	not modelled	86.8	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
72	c1r6bX_	Alignment	not modelled	86.6	18	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**clpa protein; **PDBTitle:** high resolution crystal structure of clpa
73	d1w1wa_	Alignment	not modelled	86.6	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
74	d3adka_	Alignment	not modelled	86.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
75	c3ch4B_	Alignment	not modelled	86.4	20	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphomevalonate kinase; **PDBTitle:** the crystal structure of human phosphomavelonate kinase at2 1.8 a resolution
76	c2w0sB_	Alignment	not modelled	86.4	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**thymidylate kinase; **PDBTitle:** crystal structure of vaccinia virus thymidylate kinase2 bound to brivudin-5'-monophosphate
77	d1jgsa_	Alignment	not modelled	86.4	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain

						Family: MarR-like transcriptional regulators
78	c3cm0A_	Alignment	not modelled	86.3	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase; **PDBTitle:** crystal structure of adenylate kinase from thermus2 thermophilus hb8
79	c1ly1A_	Alignment	not modelled	86.3	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide kinase; **PDBTitle:** structure and mechanism of t4 polynucleotide kinase
80	d1ly1a_	Alignment	not modelled	86.3	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
81	d1nn5a_	Alignment	not modelled	86.2	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
82	d1gsia_	Alignment	not modelled	86.1	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
83	c3neyC_	Alignment	not modelled	86.0	25	**PDB header:**membrane protein **Chain:** C: **PDB Molecule:**55 kda erythrocyte membrane protein; **PDBTitle:** crystal structure of the kinase domain of mpp1/p55
84	c3h0kA_	Alignment	not modelled	85.9	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0200 protein sso1041; **PDBTitle:** crystal structure of an adenylated kinase related protein from2 sulfolobus solfataricus to 3.25a
85	d1jjva_	Alignment	not modelled	85.8	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
86	c2grjH_	Alignment	not modelled	85.7	30	**PDB header:**transferase **Chain:** H: **PDB Molecule:**dephospho-coa kinase; **PDBTitle:** crystal structure of dephospho-coa kinase (ec 2.7.1.24)2 (dephosphocoenzyme a kinase) (tm1387) from thermotoga maritima at3 2.60 a resolution
87	d1vmaa2	Alignment	not modelled	85.7	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
88	c2if2C_	Alignment	not modelled	85.7	25	**PDB header:**transferase **Chain:** C: **PDB Molecule:**dephospho-coa kinase; **PDBTitle:** crystal structure of the putative dephospho-coa kinase from aquifex2 aeolicus, northeast structural genomics target qr72.
89	d1ki9a_	Alignment	not modelled	85.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
90	d2bdta1	Alignment	not modelled	85.7	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Atu3015-like
91	c2xb4A_	Alignment	not modelled	85.5	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase; **PDBTitle:** crystal structures of zinc containing adenylate kinase from2 desulfovibrio gigas
92	d1s96a_	Alignment	not modelled	85.5	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
93	c2bwjC_	Alignment	not modelled	85.5	19	**PDB header:**transferase **Chain:** C: **PDB Molecule:**adenylate kinase 5; **PDBTitle:** structure of adenylate kinase 5
94	c2yvuA_	Alignment	not modelled	85.5	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable adenylyl-sulfate kinase; **PDBTitle:** crystal structure of ape1195
95	d1vhta_	Alignment	not modelled	85.5	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
96	c2ar7A_	Alignment	not modelled	85.4	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase 4; **PDBTitle:** crystal structure of human adenylate kinase 4, ak4
97	d4tmka_	Alignment	not modelled	85.4	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
98	d1qf9a_	Alignment	not modelled	85.4	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
99	c3tlxA_	Alignment	not modelled	85.3	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase 2; **PDBTitle:** crystal structure of pf10_0086, adenylate kinase from plasmodium2 falciparum
100	c1z6gA_	Alignment	not modelled	85.3	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of guanylate kinase from plasmodium falciparum
101	d1tmka_	Alignment	not modelled	85.3	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
102	c2nq2C_	Alignment	not modelled	85.3	33	**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.
						Fold:P-loop containing nucleoside triphosphate hydrolases

103	d1e32a2	Alignment	not modelled	85.2	7	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
104	c2ak3B_	Alignment	not modelled	85.2	27	**PDB header:**transferase (phosphotransferase) **Chain:** B: **PDB Molecule:**adenylate kinase isoenzyme-3; **PDBTitle:** the three-dimensional structure of the complex between2 mitochondrial matrix adenylate kinase and its substrate3 amp at 1.85 angstroms resolution
105	d1zp6a1	Alignment	not modelled	85.2	30	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Atu3015-like
106	c1zakB_	Alignment	not modelled	85.2	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenylate kinase; **PDBTitle:** adenylate kinase from maize in complex with the inhibitor2 p1,p5-bis(adenosine-5'-)pentaphosphate (ap5a)
107	d1zaka1	Alignment	not modelled	85.1	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
108	d2etha1	Alignment	not modelled	85.0	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
109	d2fbia1	Alignment	not modelled	84.9	9	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
110	c2qa5A_	Alignment	not modelled	84.8	33	**PDB header:**cell cycle, structural protein **Chain:** A: **PDB Molecule:**septin-2; **PDBTitle:** crystal structure of sept2 g-domain
111	c3t5dC_	Alignment	not modelled	84.8	43	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**septin-7; **PDBTitle:** crystal structure of septin 7 in complex with gdp
112	c3jvvA_	Alignment	not modelled	84.5	21	**PDB header:**atp binding protein **Chain:** A: **PDB Molecule:**twitching mobility protein; **PDBTitle:** crystal structure of p. aeruginosa pilt with bound amp-pcp
113	c2rh5B_	Alignment	not modelled	84.5	36	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenylate kinase; **PDBTitle:** structure of apo adenylate kinase from aquifex aeolicus
114	d1ofha_	Alignment	not modelled	84.5	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Extended AAA-ATPase domain
115	c3c8uA_	Alignment	not modelled	84.4	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructokinase; **PDBTitle:** crystal structure of putative fructose transport system kinase2 (yp_612366.1) from silicibacter sp. tm1040 at 1.95 a resolution
116	d2onka1	Alignment	not modelled	84.4	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
117	d1qhxa_	Alignment	not modelled	84.3	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Chloramphenicol phosphotransferase
118	c3gmtB_	Alignment	not modelled	84.3	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**adenylate kinase; **PDBTitle:** crystal structure of adenylate kinase from burkholderia pseudomallei
119	d2a61a1	Alignment	not modelled	84.3	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**MarR-like transcriptional regulators
120	c1yqtA_	Alignment	not modelled	84.2	32	**PDB header:**hydrolyase/translation **Chain:** A: **PDB Molecule:**rnase l inhibitor; **PDBTitle:** rnase-l inhibitor