Phyre^2

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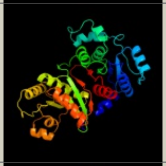
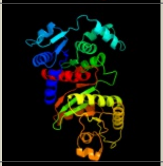
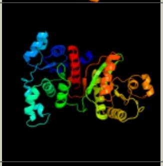
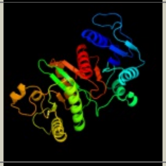
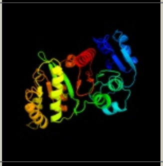
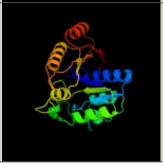
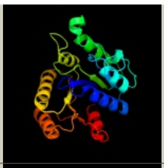
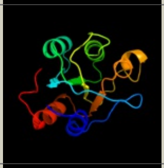
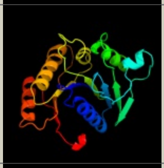
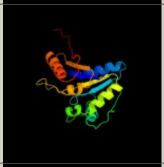
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1vmia_	Alignment		100.0	37	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
2	c1vmiA_	Alignment		100.0	37	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative phosphate acetyltransferase; **PDBTitle:** crystal structure of putative phosphate acetyltransferase2 (np_416953.1) from escherichia coli k12 at 2.32 a resolution
3	d1xcoa_	Alignment		100.0	44	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
4	d2af4c1	Alignment		100.0	45	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
5	d1r5ja_	Alignment		100.0	43	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**Phosphotransacetylase
6	c3tngA_	Alignment		100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lmo1369 protein; **PDBTitle:** the crystal structure of a possible phosphate acetyl/butaryl2 transferase from listeria monocytogenes egd-e.
7	c1ycoA_	Alignment		100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**branched-chain phosphotransacylase; **PDBTitle:** crystal structure of a branched-chain phosphotransacylase from2 enterococcus faecalis v583
8	d1vi1a_	Alignment		100.0	15	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
9	d1u7na_	Alignment		100.0	24	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PlsX-like
10	c3fmfA_	Alignment		99.9	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
11	d1byia_	Alignment		99.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like

12	c3of5A_	Alignment		99.9	14	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
13	c2qmoA_	Alignment		99.9	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
14	d2ioja1	Alignment		99.9	25	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**DRTGG domain
15	d1ptma_	Alignment		99.8	17	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
16	c2ph1A_	Alignment		99.8	10	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**nucleotide-binding protein; **PDBTitle:** crystal structure of nucleotide-binding protein af2382 from2 archaeoglobus fulgidus, northeast structural genomics target gr165
17	c3la6P_	Alignment		99.8	14	**PDB header:**transferase **Chain:** P: **PDB Molecule:**tyrosine-protein kinase wzc; **PDBTitle:** octameric kinase domain of the e. coli tyrosine kinase wzc with bound2 adp
18	d2afhe1	Alignment		99.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
19	c3cioA_	Alignment		99.8	10	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase etk; **PDBTitle:** the kinase domain of escherichia coli tyrosine kinase etk
20	d1iona_	Alignment		99.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
21	d1g3qa_	Alignment	not modelled	99.8	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
22	d1cp2a_	Alignment	not modelled	99.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
23	c2vedA_	Alignment	not modelled	99.7	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane protein capa1, protein tyrosine kinase; **PDBTitle:** crystal structure of the chimerical mutant capabk55m2 protein
24	c1hyqA_	Alignment	not modelled	99.7	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division inhibitor (mind-1); **PDBTitle:** mind bacterial cell division regulator from a. fulgidus
25	d1hyqa_	Alignment	not modelled	99.7	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
26	c3endA_	Alignment	not modelled	99.7	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**light-independent protochlorophyllide reductase **PDBTitle:** crystal structure of the l protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
27	c2xj9B_	Alignment	not modelled	99.7	13	**PDB header:**replication **Chain:** B: **PDB Molecule:**mipz; **PDBTitle:** dimer structure of the bacterial cell division regulator mipz
						PDB header:hydrolase

28	c3ea0B_	Alignment	not modelled	99.7	10	**Chain:** B: **PDB Molecule:**atpase, para family; **PDBTitle:** crystal structure of para family atpase from chlorobium tepidum tls
29	c3kjgB_	Alignment	not modelled	99.7	13	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**co dehydrogenase/acetyl-coa synthase complex, accessory **PDBTitle:** adp-bound state of cooc1
30	c3q9lB_	Alignment	not modelled	99.7	13	**PDB header:**cell cycle, hydrolase **Chain:** B: **PDB Molecule:**septum site-determining protein mind; **PDBTitle:** the structure of the dimeric e.coli mind-atp complex
31	c2ozeA_	Alignment	not modelled	99.6	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf delta'; **PDBTitle:** the crystal structure of delta protein of psm19035 from2 streptoccocus pyogenes
32	c3fkqA_	Alignment	not modelled	99.6	11	**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
33	c1yxoB_	Alignment	not modelled	99.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 1; **PDBTitle:** crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593
34	d1ko7a1	Alignment	not modelled	99.6	14	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
35	c3k9gA_	Alignment	not modelled	99.6	10	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**pf-32 protein; **PDBTitle:** crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak
36	c3ug7D_	Alignment	not modelled	99.6	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**arsenical pump-driving atpase; **PDBTitle:** crystal structure of get3 from methanocaldococcus jannaschii
37	c1ii0A_	Alignment	not modelled	99.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**arsenical pump-driving atpase; **PDBTitle:** crystal structure of the escherichia coli arsenite-translocating2 atpase
38	c3zq6D_	Alignment	not modelled	99.5	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative arsenical pump-driving atpase; **PDBTitle:** adp-alf4 complex of m. therm. trc40
39	c2bekB_	Alignment	not modelled	99.5	14	**PDB header:**chromosome segregation **Chain:** B: **PDB Molecule:**segregation protein; **PDBTitle:** structure of the bacterial chromosome segregation protein2 soj
40	c2wooC_	Alignment	not modelled	99.5	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atpase get3; **PDBTitle:** nucleotide-free form of s. pombe get3
41	c2wojD_	Alignment	not modelled	99.5	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atpase get3; **PDBTitle:** adp-alf4 complex of s. cerevisiae get3
42	d1r8ka_	Alignment	not modelled	99.5	18	**Fold:**Isocitrate/Isopropylmalate dehydrogenase-like **Superfamily:**Isocitrate/Isopropylmalate dehydrogenase-like **Family:**PdxA-like
43	c3ibgF_	Alignment	not modelled	99.5	13	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**atpase, subunit of the get complex; **PDBTitle:** crystal structure of aspergillus fumigatus get3 with bound2 adp
44	d1ihua2	Alignment	not modelled	99.5	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
45	c1ko7B_	Alignment	not modelled	99.4	16	**PDB header:**transferase,hydrolase **Chain:** B: **PDB Molecule:**hpr kinase/phosphatase; **PDBTitle:** x-ray structure of the hpr kinase/phosphatase from2 staphylococcus xylosus at 1.95 a resolution
46	c3ez6B_	Alignment	not modelled	99.3	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**plasmid partition protein a; **PDBTitle:** structure of para-adp complex:tetragonal form
47	d1ihua1	Alignment	not modelled	99.3	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
48	c3io3A_	Alignment	not modelled	99.3	12	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**deha2d07832p; **PDBTitle:** get3 with adp from d. hansenii in closed form
49	c3pg5A_	Alignment	not modelled	99.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of protein dip2308 from corynebacterium diphtheriae,2 northeast structural genomics consortium target cdr78
50	c3cwqB_	Alignment	not modelled	99.2	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**para family chromosome partitioning protein; **PDBTitle:** crystal structure of chromosome partitioning protein (para) in complex2 with adp from synechocystis sp. northeast structural genomics3 consortium target sgr89
51	c3igfB_	Alignment	not modelled	99.2	11	**PDB header:**atp binding protein **Chain:** B: **PDB Molecule:**all4481 protein; **PDBTitle:** crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
52	c1zu4A_	Alignment	not modelled	99.2	17	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
53	c2qy9A_	Alignment	not modelled	99.1	19	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**cell division protein ftsy;

53	c2qy9A_	Alignment	not modelled	99.1	19	**PDBTitle:** structure of the ng+1 construct of the e. coli srp receptor2 ftsy
54	c3dm5A_	Alignment	not modelled	99.1	13	**PDB header:**rna binding protein, transport protein **Chain:** A: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** structures of srp54 and srp19, the two proteins assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
55	c2og2A_	Alignment	not modelled	99.1	18	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
56	c1vmaA_	Alignment	not modelled	99.1	16	**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
57	c3ezfA_	Alignment	not modelled	99.1	9	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**para; **PDBTitle:** partition protein
58	c2j37W_	Alignment	not modelled	99.1	15	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
59	c2iy3A_	Alignment	not modelled	99.0	14	**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
60	c3b9qA_	Alignment	not modelled	99.0	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
61	c2cnwF_	Alignment	not modelled	99.0	19	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
62	c2yhsA_	Alignment	not modelled	99.0	17	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
63	c2v3cC_	Alignment	not modelled	99.0	17	**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
64	c2j7pA_	Alignment	not modelled	99.0	13	**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
65	c3dmdA_	Alignment	not modelled	98.9	14	**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
66	c1qzwC_	Alignment	not modelled	98.9	10	**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
67	c2obnA_	Alignment	not modelled	98.7	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution
68	c2j289_	Alignment	not modelled	98.6	17	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
69	c2px0D_	Alignment	not modelled	98.2	16	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
70	d1xjca_	Alignment	not modelled	98.1	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
71	d2g0ta1	Alignment	not modelled	98.0	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
72	c2hi1A_	Alignment	not modelled	98.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**4-hydroxythreonine-4-phosphate dehydrogenase 2; **PDBTitle:** the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
73	d1j8yf2	Alignment	not modelled	97.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
74	c2f1rA_	Alignment	not modelled	97.8	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin-guanine dinucleotide biosynthesis **PDBTitle:** crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
75	c1j8yF_	Alignment	not modelled	97.8	10	**PDB header:**signaling protein **Chain:** F: **PDB Molecule:**signal recognition 54 kda protein; **PDBTitle:** signal recognition particle conserved gtpase domain from a.2 ambivalens t112a mutant
76	d1qzxa3	Alignment	not modelled	97.7	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
77	c1knxF_	Alignment	not modelled	97.6	8	**PDB header:**transferase/hydrolase **Chain:** F: **PDB Molecule:**probable hpr(ser) kinase/phosphatase; **PDBTitle:** hpr kinase/phosphatase from mycoplasma pneumoniae
78	c3bgwD_	Alignment	not modelled	97.5	12	**PDB header:**replication **Chain:** D: **PDB Molecule:**dnab-like replicative helicase;

78	c3bgwD_	Alignment	not modelled	97.5	12	**PDBTitle:** the structure of a dnab-like replicative helicase and its interactions2 with primase
79	c2q6tB_	Alignment	not modelled	97.4	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
80	d1vmaa2	Alignment	not modelled	97.3	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
81	d1knxa1	Alignment	not modelled	97.3	7	**Fold:**MurF and HprK N-domain-like **Superfamily:**HprK N-terminal domain-like **Family:**HPr kinase/phoshatase HprK N-terminal domain
82	d1yrba1	Alignment	not modelled	97.3	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
83	c2recB_	Alignment	not modelled	97.2	22	**PDB header:**helicase **PDB COMPND:**
84	d1ubea1	Alignment	not modelled	97.1	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
85	d1mo6a1	Alignment	not modelled	97.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
86	c3bh0A_	Alignment	not modelled	97.0	12	**PDB header:**replication **Chain:** A: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** atpase domain of g40p
87	d1nija1	Alignment	not modelled	96.9	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
88	c1xp8A_	Alignment	not modelled	96.8	18	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"
89	c2ad5B_	Alignment	not modelled	96.8	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
90	c2npiB_	Alignment	not modelled	96.8	15	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protein clp1; **PDBTitle:** clp1-atp-pcf11 complex
91	c1nijA_	Alignment	not modelled	96.7	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein yjia; **PDBTitle:** yjia protein
92	d1u94a1	Alignment	not modelled	96.7	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
93	d1s1ma2	Alignment	not modelled	96.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
94	c2w0mA_	Alignment	not modelled	96.7	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso2452; **PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus2 p2
95	d2qm8a1	Alignment	not modelled	96.6	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
96	c2vyeA_	Alignment	not modelled	96.6	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**replicative dna helicase; **PDBTitle:** crystal structure of the dnac-ssdna complex
97	d1tf7a2	Alignment	not modelled	96.6	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
98	d1nlfa_	Alignment	not modelled	96.5	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
99	d1k6ma1	Alignment	not modelled	96.5	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, kinase domain
100	d1xp8a1	Alignment	not modelled	96.5	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
101	c2yvuA_	Alignment	not modelled	96.5	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable adenylyl-sulfate kinase; **PDBTitle:** crystal structure of ape1195
102	c2i1vB_	Alignment	not modelled	96.4	15	**PDB header:**transferase, hydrolase **Chain:** B: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
103	c1k6mA_	Alignment	not modelled	96.4	16	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of human liver 6-phosphofructo-2-2 kinase/fructose-2,6-bisphosphatase
						PDB header:dna binding protein

104	c3io5B_	Alignment	not modelled	96.4	14	**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
105	d2vo1a1	Alignment	not modelled	96.4	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
106	c2h5eB_	Alignment	not modelled	96.2	20	**PDB header:**translation **Chain:** B: **PDB Molecule:**peptide chain release factor rf-3; **PDBTitle:** crystal structure of e.coli polypeptide release factor rf3
107	c3hr8A_	Alignment	not modelled	96.2	19	**PDB header:**recombination **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** crystal structure of thermotoga maritima reca
108	c3tr5C_	Alignment	not modelled	96.1	17	**PDB header:**translation **Chain:** C: **PDB Molecule:**peptide chain release factor 3; **PDBTitle:** structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
109	c1q57G_	Alignment	not modelled	96.0	6	**PDB header:**transferase **Chain:** G: **PDB Molecule:**dna primase/helicase; **PDBTitle:** the crystal structure of the bifunctional primase-helicase of2 bacteriophage t7
110	c3cm0A_	Alignment	not modelled	95.9	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase; **PDBTitle:** crystal structure of adenylate kinase from thermus2 thermophilus hb8
111	d1eg7a_	Alignment	not modelled	95.9	37	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
112	d1ls1a2	Alignment	not modelled	95.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
113	c3do6B_	Alignment	not modelled	95.8	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**formate--tetrahydrofolate ligase; **PDBTitle:** crystal structure of putative formyltetrahydrofolate2 synthetase (tm1766) from thermotoga maritima at 1.85 a3 resolution
114	d1x6va3	Alignment	not modelled	95.7	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Adenosine-5'phosphosulfate kinase (APS kinase)
115	d1cr2a_	Alignment	not modelled	95.7	7	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
116	c2ztsB_	Alignment	not modelled	95.7	15	**PDB header:**atp-binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein ph0186; **PDBTitle:** crystal structure of kaic-like protein ph0186 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
117	c2gksB_	Alignment	not modelled	95.6	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional sat/aps kinase; **PDBTitle:** crystal structure of the bi-functional atp sulfurylase-aps kinase from2 aquifex aeolicus, a chemolithotrophic thermophile
118	c2ywfA_	Alignment	not modelled	95.5	15	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus
119	d1w36d1	Alignment	not modelled	95.5	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
120	c2bm0A_	Alignment	not modelled	95.4	13	**PDB header:**elongation factor **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a