Phyre^2

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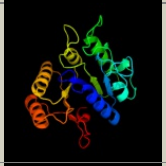
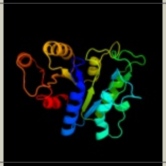
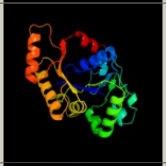
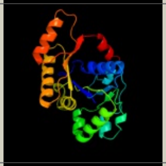
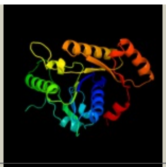
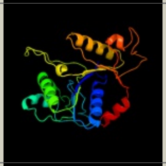
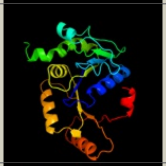
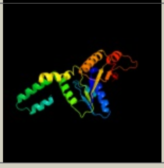
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1byia_	Alignment		100.0	52	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
2	c3of5A_	Alignment		100.0	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
3	c2qmoA_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
4	c3fmfA_	Alignment		100.0	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
5	d2afhe1	Alignment		99.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
6	d1cp2a_	Alignment		99.9	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
7	d1g3qa_	Alignment		99.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
8	d1hyqa_	Alignment		99.9	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
9	c1hyqA_	Alignment		99.9	20	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division inhibitor (mind-1); **PDBTitle:** mind bacterial cell division regulator from a. fulgidus
10	d1iona_	Alignment		99.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
11	c2ph1A_	Alignment		99.9	16	**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

12	c3kjgB_	Alignment		99.9	17	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**co dehydrogenase/acetyl-coa synthase complex, accessory **PDBTitle:** adp-bound state of cooc1
13	c3ea0B_	Alignment		99.9	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atpase, para family; **PDBTitle:** crystal structure of para family atpase from chlorobium tepidum tls
14	c2ozeA_	Alignment		99.9	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf delta'; **PDBTitle:** the crystal structure of delta protein of psm19035 from2 streptoccocus pyogenes
15	c3endA_	Alignment		99.9	20	**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
16	c2bekB_	Alignment		99.9	17	**PDB header:**chromosome segregation **Chain:** B: **PDB Molecule:**segregation protein; **PDBTitle:** structure of the bacterial chromosome segregation protein2 soj
17	c3fkqA_	Alignment		99.9	13	**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
18	c3ez6B_	Alignment		99.9	14	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**plasmid partition protein a; **PDBTitle:** structure of para-adp complex:tetragonal form
19	c3q9lB_	Alignment		99.9	12	**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
20	c3ug7D_	Alignment		99.9	20	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**arsenical pump-driving atpase; **PDBTitle:** crystal structure of get3 from methanocaldococcus jannaschii
21	c2xj9B_	Alignment	not modelled	99.9	12	**PDB header:**replication **Chain:** B: **PDB Molecule:**mipz; **PDBTitle:** dimer structure of the bacterial cell division regulator mipz
22	c3zq6D_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative arsenical pump-driving atpase; **PDBTitle:** adp-alf4 complex of m. therm. trc40
23	c2wojD_	Alignment	not modelled	99.8	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atpase get3; **PDBTitle:** adp-alf4 complex of s. cerevisiae get3
24	c2wooC_	Alignment	not modelled	99.8	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atpase get3; **PDBTitle:** nucleotide-free form of s. pombe get3
25	c3cioA_	Alignment	not modelled	99.8	14	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase etk; **PDBTitle:** the kinase domain of escherichia coli tyrosine kinase etk
26	c3la6P_	Alignment	not modelled	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
27	c1ii0A_	Alignment	not modelled	99.8	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**arsenical pump-driving atpase; **PDBTitle:** crystal structure of the escherichia coli arsenite-translocating2 atpase
28	c3k9gA_	Alignment	not modelled	99.8	13	**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
						PDB header:hydrolase

29	c3ibgF_	Alignment	not modelled	99.8	15	**Chain:** F: **PDB Molecule:**atpase, subunit of the get complex; **PDBTitle:** crystal structure of aspergillus fumigatus get3 with bound2 adp
30	d1ihua1	Alignment	not modelled	99.8	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
31	d1ihua2	Alignment	not modelled	99.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
32	c2vedA_	Alignment	not modelled	99.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane protein capa1, protein tyrosine kinase; **PDBTitle:** crystal structure of the chimerical mutant capabk55m2 protein
33	c3io3A_	Alignment	not modelled	99.8	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**deha2d07832p; **PDBTitle:** get3 with adp from d. hansenii in closed form
34	c3ezfA_	Alignment	not modelled	99.8	9	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**para; **PDBTitle:** partition protein
35	c3pg5A_	Alignment	not modelled	99.8	10	**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
36	c3cwqB_	Alignment	not modelled	99.8	18	**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
37	c3igfB_	Alignment	not modelled	99.7	16	**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
38	c3dm5A_	Alignment	not modelled	99.4	12	**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.
39	c1zu4A_	Alignment	not modelled	99.4	14	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides- space2 group p21212
40	c2qy9A_	Alignment	not modelled	99.3	15	**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
41	c2iy3A_	Alignment	not modelled	99.3	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
42	c2v3cC_	Alignment	not modelled	99.3	14	**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
43	c1vmaA_	Alignment	not modelled	99.3	13	**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
44	c2j37W_	Alignment	not modelled	99.2	11	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
45	c3b9qA_	Alignment	not modelled	99.2	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
46	c3dmdA_	Alignment	not modelled	99.2	13	**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
47	c2j7pA_	Alignment	not modelled	99.2	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
48	c2og2A_	Alignment	not modelled	99.2	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
49	c1qzwC_	Alignment	not modelled	99.1	13	**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
50	c2yhsA_	Alignment	not modelled	99.1	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
51	c2cnwF_	Alignment	not modelled	99.1	17	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
52	c2j289_	Alignment	not modelled	99.0	14	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
53	c2ohnA	Alignment	not modelled	98.8	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein;

[illegible]	[illegible]	Alignment	not modelled	[illegible]	[illegible]	**PDBTitle:** crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution
54	c2px0D_	Alignment	not modelled	98.7	13	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
55	d1vmaa2	Alignment	not modelled	98.5	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
56	d1qzxa3	Alignment	not modelled	98.5	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
57	d1j8yf2	Alignment	not modelled	98.1	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
58	d1ls1a2	Alignment	not modelled	98.1	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
59	c2f1rA_	Alignment	not modelled	98.1	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin-guanine dinucleotide biosynthesis **PDBTitle:** crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
60	c2npiB_	Alignment	not modelled	98.1	14	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protein clp1; **PDBTitle:** clp1-atp-pcf11 complex
61	d1xjca_	Alignment	not modelled	98.0	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
62	d2vo1a1	Alignment	not modelled	98.0	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
63	d1s1ma2	Alignment	not modelled	97.8	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
64	c2h5eB_	Alignment	not modelled	97.8	18	**PDB header:**translation **Chain:** B: **PDB Molecule:**peptide chain release factor rf-3; **PDBTitle:** crystal structure of e.coli polypeptide release factor rf3
65	c2ad5B_	Alignment	not modelled	97.8	17	**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.
66	d1yrba1	Alignment	not modelled	97.8	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
67	d2qy9a2	Alignment	not modelled	97.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
68	d2g0ta1	Alignment	not modelled	97.8	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
69	c1j8yF_	Alignment	not modelled	97.7	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
70	c1xnjB_	Alignment	not modelled	97.7	11	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'-phosphosulfate **PDBTitle:** aps complex of human paps synthetase 1
71	c1xp8A_	Alignment	not modelled	97.7	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**reca protein; **PDBTitle:** "deinococcus radiodurans reca in complex with atp-gamma-s"
72	c2recB_	Alignment	not modelled	97.6	23	**PDB header:**helicase **PDB COMPND:**
73	d1nija1	Alignment	not modelled	97.5	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
74	d1x6va3	Alignment	not modelled	97.5	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Adenosine-5'phosphosulfate kinase (APS kinase)
75	c3nvaB_	Alignment	not modelled	97.4	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
76	d1okkd2	Alignment	not modelled	97.4	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
77	d1vcoa2	Alignment	not modelled	97.4	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
78	c2q6tB_	Alignment	not modelled	97.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
						PDB header:ligase

79	c1vcnA_	Alignment	not modelled	97.4	18	**Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
80	d1cr2a_	Alignment	not modelled	97.4	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
81	c3tr5C_	Alignment	not modelled	97.4	15	**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
82	d1nksa_	Alignment	not modelled	97.4	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
83	c3hr8A_	Alignment	not modelled	97.3	24	**PDB header:**recombination **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** crystal structure of thermotoga maritima reca
84	c2w0mA_	Alignment	not modelled	97.3	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso2452; **PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus2 p2
85	d1xp8a1	Alignment	not modelled	97.3	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
86	d1nlfa_	Alignment	not modelled	97.2	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
87	c3cm0A_	Alignment	not modelled	97.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase; **PDBTitle:** crystal structure of adenylate kinase from thermus2 thermophilus hb8
88	c2ywfA_	Alignment	not modelled	97.1	18	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus
89	c3cr8C_	Alignment	not modelled	97.1	29	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sulfate adenylyltranferase, adenylylsulfate **PDBTitle:** hexameric aps kinase from thiobacillus denitrificans
90	d2dy1a2	Alignment	not modelled	97.1	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**G proteins
91	c2gksB_	Alignment	not modelled	97.1	21	**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
92	d1tf7a2	Alignment	not modelled	97.1	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
93	c2dy1A_	Alignment	not modelled	97.1	17	**PDB header:**signaling protein, translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of ef-g-2 from thermus thermophilus
94	c3bgwD_	Alignment	not modelled	97.0	16	**PDB header:**replication **Chain:** D: **PDB Molecule:**dnab-like replicative helicase; **PDBTitle:** the structure of a dnab-like replicative helicase and its interactions2 with primase
95	c3degC_	Alignment	not modelled	97.0	14	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
96	d1rz3a_	Alignment	not modelled	97.0	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
97	d2qm8a1	Alignment	not modelled	97.0	34	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
98	c2ar7A_	Alignment	not modelled	96.9	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase 4; **PDBTitle:** crystal structure of human adenylate kinase 4, ak4
99	d1ubea1	Alignment	not modelled	96.9	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
100	d1mo6a1	Alignment	not modelled	96.9	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
101	c2qgzA_	Alignment	not modelled	96.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative primosome component; **PDBTitle:** crystal structure of a putative primosome component from2 streptococcus pyogenes serotype m3. northeast structural3 genomics target dr58
102	d1e6ca_	Alignment	not modelled	96.8	38	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
103	d1u94a1	Alignment	not modelled	96.8	31	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
104	c2zroA_	Alignment	not modelled	96.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** msreca adp form iv

105	c3c8uA_	Alignment	not modelled	96.8	26	**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
106	c2w58B_	Alignment	not modelled	96.7	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**primosome component (helicase loader); **PDBTitle:** crystal structure of the dnai
107	c2yvuA_	Alignment	not modelled	96.7	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable adenylyl-sulfate kinase; **PDBTitle:** crystal structure of ape1195
108	c3i4fD_	Alignment	not modelled	96.7	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-oxoacyl-[acyl-carrier protein] reductase; **PDBTitle:** structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
109	d1khta_	Alignment	not modelled	96.7	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
110	d1np6a_	Alignment	not modelled	96.7	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
111	c3bosA_	Alignment	not modelled	96.6	13	**PDB header:**hydrolase regulator,dna binding protein **Chain:** A: **PDB Molecule:**putative dna replication factor; **PDBTitle:** crystal structure of a putative dna replication regulator hda2 (sama_1916) from shewanella amazonensis sb2b at 1.75 a resolution
112	d1ki9a_	Alignment	not modelled	96.6	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
113	d2i3ba1	Alignment	not modelled	96.6	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
114	d1odfa_	Alignment	not modelled	96.6	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
115	c3cmvG_	Alignment	not modelled	96.6	30	**PDB header:**recombination **Chain:** G: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
116	d1eg7a_	Alignment	not modelled	96.6	42	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
117	c3tqcB_	Alignment	not modelled	96.6	29	**PDB header:**transferase **Chain:** B: **PDB Molecule:**pantothenate kinase; **PDBTitle:** structure of the pantothenate kinase (coaa) from coxiella burnetii
118	d1g5ta_	Alignment	not modelled	96.6	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
119	c2bm0A_	Alignment	not modelled	96.6	15	**PDB header:**elongation factor **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
120	c3lv8A_	Alignment	not modelled	96.6	21	**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