Phyre^2

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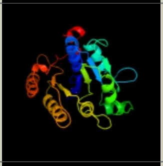
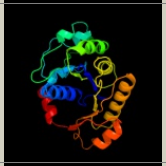
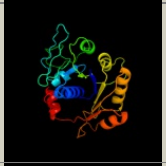
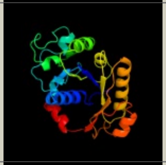
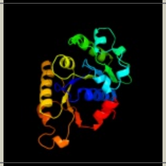
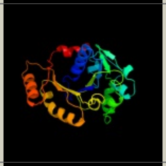
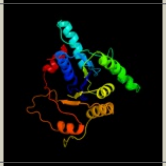
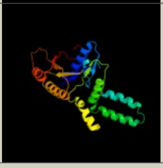
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1byia_	Alignment		100.0	100	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
2	c3of5A_	Alignment		100.0	31	**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	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dethiobiotin synthetase; **PDBTitle:** crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
4	c3fmfA_	Alignment		100.0	26	**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		100.0	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
6	d1g3qa_	Alignment		100.0	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
7	c2ph1A_	Alignment		100.0	12	**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
8	d1cp2a_	Alignment		100.0	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
9	d1iona_	Alignment		100.0	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
10	c1hyqA_	Alignment		99.9	18	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division inhibitor (mind-1); **PDBTitle:** mind bacterial cell division regulator from a. fulgidus
11	d1hyqa_	Alignment		99.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like

12	c3kjgB_	Alignment		99.9	18	**PDB header:**hydrolase, metal binding protein **Chain:** B: **PDB Molecule:**co dehydrogenase/acetyl-coa synthase complex, accessory **PDBTitle:** adp-bound state of cooc1
13	c3endA_	Alignment		99.9	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
14	c3ea0B_	Alignment		99.9	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atpase, para family; **PDBTitle:** crystal structure of para family atpase from chlorobium tepidum tls
15	c2ozeA_	Alignment		99.9	10	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**orf delta'; **PDBTitle:** the crystal structure of delta protein of psm19035 from2 streptoccocus pyogenes
16	c3q9lB_	Alignment		99.9	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
17	c3ez6B_	Alignment		99.9	13	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**plasmid partition protein a; **PDBTitle:** structure of para-adp complex:tetragonal form
18	c2bekB_	Alignment		99.9	15	**PDB header:**chromosome segregation **Chain:** B: **PDB Molecule:**segregation protein; **PDBTitle:** structure of the bacterial chromosome segregation protein2 soj
19	c2xj9B_	Alignment		99.9	12	**PDB header:**replication **Chain:** B: **PDB Molecule:**mipz; **PDBTitle:** dimer structure of the bacterial cell division regulator mipz
20	c3ug7D_	Alignment		99.9	15	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**arsenical pump-driving atpase; **PDBTitle:** crystal structure of get3 from methanocaldococcus jannaschii
21	c3fkqA_	Alignment	not modelled	99.9	10	**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
22	c2wojD_	Alignment	not modelled	99.9	10	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atpase get3; **PDBTitle:** adp-alf4 complex of s. cerevisiae get3
23	c3zq6D_	Alignment	not modelled	99.9	18	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative arsenical pump-driving atpase; **PDBTitle:** adp-alf4 complex of m. therm. trc40
24	c3k9gA_	Alignment	not modelled	99.9	11	**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
25	c1ii0A_	Alignment	not modelled	99.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**arsenical pump-driving atpase; **PDBTitle:** crystal structure of the escherichia coli arsenite-translocating2 atpase
26	d1ihua2	Alignment	not modelled	99.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
27	c3la6P_	Alignment	not modelled	99.9	12	**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
28	c3cioA_	Alignment	not modelled	99.9	14	**PDB header:**signaling protein, transferase **Chain:** A: **PDB Molecule:**tyrosine-protein kinase etk; **PDBTitle:** the kinase domain of escherichia coli tyrosine kinase etk
						Fold:P-loop containing nucleoside triphosphate hydrolases

29	d1ihua1	Alignment	not modelled	99.9	18	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
30	c3ibgF_	Alignment	not modelled	99.9	14	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**atpase, subunit of the get complex; **PDBTitle:** crystal structure of aspergillus fumigatus get3 with bound2 adp
31	c2wooC_	Alignment	not modelled	99.9	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**atpase get3; **PDBTitle:** nucleotide-free form of s. pombe get3
32	c3cwqB_	Alignment	not modelled	99.9	13	**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
33	c3pg5A_	Alignment	not modelled	99.9	11	**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
34	c3io3A_	Alignment	not modelled	99.9	15	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**deha2d07832p; **PDBTitle:** get3 with adp from d. hansenii in closed form
35	c2vedA_	Alignment	not modelled	99.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**membrane protein capa1, protein tyrosine kinase; **PDBTitle:** crystal structure of the chimerical mutant capabk55m2 protein
36	c3ezfA_	Alignment	not modelled	99.9	11	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**para; **PDBTitle:** partition protein
37	c3igfB_	Alignment	not modelled	99.7	13	**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	c1zu4A_	Alignment	not modelled	99.4	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**ftsy; **PDBTitle:** crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
39	c3dm5A_	Alignment	not modelled	99.4	15	**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.
40	c2qy9A_	Alignment	not modelled	99.4	16	**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	c2v3cC_	Alignment	not modelled	99.4	13	**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
42	c1vmaA_	Alignment	not modelled	99.3	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
43	c2og2A_	Alignment	not modelled	99.3	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**putative signal recognition particle receptor; **PDBTitle:** crystal structure of chloroplast ftsy from arabidopsis2 thaliana
44	c3b9qA_	Alignment	not modelled	99.3	15	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**chloroplast srp receptor homolog, alpha subunit **PDBTitle:** the crystal structure of cpftsy from arabidopsis thaliana
45	c2j37W_	Alignment	not modelled	99.3	12	**PDB header:**ribosome **Chain:** W: **PDB Molecule:**signal recognition particle 54 kda protein **PDBTitle:** model of mammalian srp bound to 80s rncs
46	c2iy3A_	Alignment	not modelled	99.3	15	**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
47	c1qzwC_	Alignment	not modelled	99.3	14	**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
48	c2cnwF_	Alignment	not modelled	99.2	18	**PDB header:**signal recognition **Chain:** F: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** gdpalf4 complex of the srp gtpases ffh and ftsy
49	c2yhsA_	Alignment	not modelled	99.2	15	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**cell division protein ftsy; **PDBTitle:** structure of the e. coli srp receptor ftsy
50	c2j7pA_	Alignment	not modelled	99.2	16	**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
51	c3dmdA_	Alignment	not modelled	99.2	17	**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
52	c2j289_	Alignment	not modelled	99.0	15	**PDB header:**ribosome **Chain:** 9: **PDB Molecule:**signal recognition particle 54; **PDBTitle:** model of e. coli srp bound to 70s rncs
53	c2obnA_	Alignment	not modelled	98.8	23	**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
54	c2px0D_	Alignment	not modelled	98.7	12	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**flagellar biosynthesis protein flhf; **PDBTitle:** crystal structure of flhf complexed with gmppnp/mg(2+)
55	d1qzxa3	Alignment	not modelled	98.7	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
56	d1vmaa2	Alignment	not modelled	98.6	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
57	d1ls1a2	Alignment	not modelled	98.3	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
58	c2f1rA_	Alignment	not modelled	98.3	18	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin-guanine dinucleotide biosynthesis **PDBTitle:** crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
59	c2npiB_	Alignment	not modelled	98.2	9	**PDB header:**transcription **Chain:** B: **PDB Molecule:**protein clp1; **PDBTitle:** clp1-atp-pcf11 complex
60	d2qy9a2	Alignment	not modelled	98.1	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
61	d1xjca_	Alignment	not modelled	98.1	25	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
62	d1j8yf2	Alignment	not modelled	98.0	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
63	d1s1ma2	Alignment	not modelled	98.0	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
64	c2ad5B_	Alignment	not modelled	97.9	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.
65	d1vcoa2	Alignment	not modelled	97.8	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
66	c2w0mA_	Alignment	not modelled	97.8	10	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso2452; **PDBTitle:** crystal structure of sso2452 from sulfolobus solfataricus2 p2
67	c2q6tB_	Alignment	not modelled	97.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dnab replication fork helicase; **PDBTitle:** crystal structure of the thermus aquaticus dnab monomer
68	c3cm0A_	Alignment	not modelled	97.7	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenylate kinase; **PDBTitle:** crystal structure of adenylate kinase from thermus2 thermophilus hb8
69	d1okkd2	Alignment	not modelled	97.7	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
70	c2h5eB_	Alignment	not modelled	97.7	16	**PDB header:**translation **Chain:** B: **PDB Molecule:**peptide chain release factor rf-3; **PDBTitle:** crystal structure of e.coli polypeptide release factor rf3
71	c1j8yF_	Alignment	not modelled	97.7	13	**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
72	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"
73	d2vo1a1	Alignment	not modelled	97.7	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
74	c3tr5C_	Alignment	not modelled	97.7	14	**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
75	d1nija1	Alignment	not modelled	97.6	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
76	c1vcnA_	Alignment	not modelled	97.6	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
77	c3nvaB_	Alignment	not modelled	97.6	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
78	d1yrba1	Alignment	not modelled	97.6	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
						Fold:P-loop containing nucleoside triphosphate hydrolases

79	d1nlfa_	Alignment	not modelled	97.5	8	**Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
80	c1xnjB_	Alignment	not modelled	97.5	23	**PDB header:**transferase **Chain:** B: **PDB Molecule:**bifunctional 3'-phosphoadenosine 5'-phosphosulfate **PDBTitle:** aps complex of human paps synthetase 1
81	c3bgwD_	Alignment	not modelled	97.5	8	**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
82	c2recB_	Alignment	not modelled	97.5	22	**PDB header:**helicase **PDB COMPND:**
83	d1cr2a_	Alignment	not modelled	97.5	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
84	d1x6va3	Alignment	not modelled	97.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Adenosine-5'phosphosulfate kinase (APS kinase)
85	c2gksB_	Alignment	not modelled	97.4	18	**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
86	d1e6ca_	Alignment	not modelled	97.4	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Shikimate kinase (AroK)
87	d1ubea1	Alignment	not modelled	97.4	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
88	d1jjva_	Alignment	not modelled	97.4	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
89	d2g0ta1	Alignment	not modelled	97.4	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
90	c2zroA_	Alignment	not modelled	97.4	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** msreca adp form iv
91	d1mo6a1	Alignment	not modelled	97.4	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
92	d1u94a1	Alignment	not modelled	97.4	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
93	c3akcA_	Alignment	not modelled	97.3	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cytidylate kinase; **PDBTitle:** crystal structure of cmp kinase in complex with cdp and adp from2 thermus thermophilus hb8
94	c1u9iA_	Alignment	not modelled	97.3	14	**PDB header:**circadian clock protein **Chain:** A: **PDB Molecule:**kaic; **PDBTitle:** crystal structure of circadian clock protein kaic with phosphorylation2 sites
95	c2ztsB_	Alignment	not modelled	97.3	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
96	d2i3ba1	Alignment	not modelled	97.3	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
97	c3hr8A_	Alignment	not modelled	97.3	19	**PDB header:**recombination **Chain:** A: **PDB Molecule:**protein reca; **PDBTitle:** crystal structure of thermotoga maritima reca
98	d1np6a_	Alignment	not modelled	97.3	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
99	c3lv8A_	Alignment	not modelled	97.3	17	**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
100	c1znyA_	Alignment	not modelled	97.3	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**guanylate kinase; **PDBTitle:** crystal structure of mycobacterium tuberculosis guanylate kinase in2 complex with gdp
101	d1vhta_	Alignment	not modelled	97.3	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
102	d1o5za2	Alignment	not modelled	97.3	28	**Fold:**Ribokinase-like **Superfamily:**MurD-like peptide ligases, catalytic domain **Family:**Folylpolyglutamate synthetase
103	d1nksa_	Alignment	not modelled	97.3	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
104	c3cr8C_	Alignment	not modelled	97.2	24	**PDB header:**transferase **Chain:** C: **PDB Molecule:**sulfate adenylyltranferase, adenylylsulfate **PDBTitle:** hexameric aps kinase from thiobacillus denitrificans

105	c2qgzA_	Alignment	not modelled	97.2	23	**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
106	c2ywfA_	Alignment	not modelled	97.2	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** crystal structure of gmppnp-bound lepa from aquifex aeolicus
107	d1ki9a_	Alignment	not modelled	97.2	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
108	c2yvuA_	Alignment	not modelled	97.2	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable adenylyl-sulfate kinase; **PDBTitle:** crystal structure of ape1195
109	d1xp8a1	Alignment	not modelled	97.2	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RecA protein-like (ATPase-domain)
110	d1khta_	Alignment	not modelled	97.2	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
111	d1nn5a_	Alignment	not modelled	97.2	28	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
112	d2qm8a1	Alignment	not modelled	97.2	33	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like
113	d1rz3a_	Alignment	not modelled	97.2	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Phosphoribulokinase/pantothenate kinase
114	c2w58B_	Alignment	not modelled	97.2	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**primosome component (helicase loader); **PDBTitle:** crystal structure of the dnai
115	c1o5zA_	Alignment	not modelled	97.2	28	**PDB header:**ligase **Chain:** A: **PDB Molecule:**folylpolyglutamate synthase/dihydrofolate synthase; **PDBTitle:** crystal structure of folylpolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
116	c3degC_	Alignment	not modelled	97.1	13	**PDB header:**ribosome **Chain:** C: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** complex of elongating escherichia coli 70s ribosome and ef4(lepa)-2 gmppnp
117	c2wwiC_	Alignment	not modelled	97.1	22	**PDB header:**transferase **Chain:** C: **PDB Molecule:**thymidilate kinase, putative; **PDBTitle:** plasmodium falciparum thymidylate kinase in complex with2 aztmp and adp
118	c3cmvG_	Alignment	not modelled	97.1	22	**PDB header:**recombination **Chain:** G: **PDB Molecule:**protein reca; **PDBTitle:** mechanism of homologous recombination from the reca-2 ssdna/dsdna structures
119	d1ly1a_	Alignment	not modelled	97.1	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
120	c1ly1A_	Alignment	not modelled	97.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide kinase; **PDBTitle:** structure and mechanism of t4 polynucleotide kinase