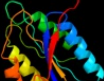
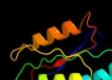
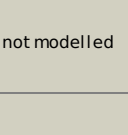
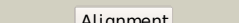
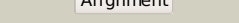
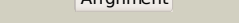
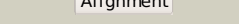
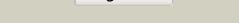
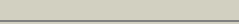
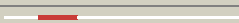
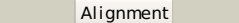
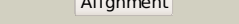
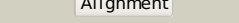
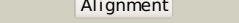
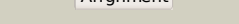
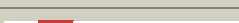


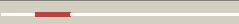
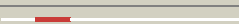
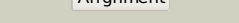
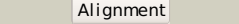
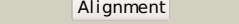
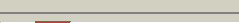
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qm8a1	 Alignment		99.0	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
2	c2j37W_	 Alignment		98.7	17	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein PDBTitle: model of mammalian srp bound to 80s rncs
3	c3dm5A_	 Alignment		98.7	21	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.
4	c2iy3A_	 Alignment		98.7	19	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
5	c2yhsA_	 Alignment		98.7	20	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
6	c3dm4A_	 Alignment		98.7	26	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
7	c3b9qA_	 Alignment		98.7	23	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpfts from arabidopsis thaliana
8	c2j7pA_	 Alignment		98.6	19	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
9	c1zu4A_	 Alignment		98.6	20	PDB header: protein transport Chain: A: PDB Molecule: ftsy; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
10	c1vmaA_	 Alignment		98.6	22	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
11	c2og2A_	 Alignment		98.6	24	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana

12	c2v3cC_	Alignment		98.6	21	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
13	c2qy9A_	Alignment		98.6	21	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
14	c3nxsA_	Alignment		98.6	15	PDB header: transport protein Chain: A: PDB Molecule: lao/ao transport system atpase; PDBTitle: crystal structure of lao/ao transport system from mycobacterium2 smegmatis bound to gdp
15	c2cnwF_	Alignment		98.5	16	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
16	c1qzwC_	Alignment		98.5	23	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
17	d2p67a1	Alignment		98.3	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
18	c2j289_	Alignment		98.3	21	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
19	c2px0D_	Alignment		98.2	19	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
20	c2wwwB_	Alignment		98.2	15	PDB header: transport protein Chain: B: PDB Molecule: methylmalonic aciduria type a protein, PDBTitle: crystal structure of methylmalonic acidemia type a protein
21	c2f1rA_	Alignment	not modelled	98.0	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobbb)
22	c3md0A_	Alignment	not modelled	98.0	21	PDB header: transport protein Chain: A: PDB Molecule: arginine/ornithine transport system atpase; PDBTitle: crystal structure of arginine/ornithine transport system2 atpase from mycobacterium tuberculosis bound to gdp (a ras-3 like gtpase superfamily protein)
23	d1j8yf2	Alignment	not modelled	97.9	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
24	d1nija1	Alignment	not modelled	97.9	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
25	d1xjca_	Alignment	not modelled	97.9	28	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
26	d2afhe1	Alignment	not modelled	97.7	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
27	c2xj9B_	Alignment	not modelled	97.7	18	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
						Fold: P-loop containing nucleoside triphosphate hydrolases

28	dlqza3	Alignment	not modelled	97.7	29	Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
29	dliona	Alignment	not modelled	97.7	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
30	dlvmaa2	Alignment	not modelled	97.7	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
31	c3endA	Alignment	not modelled	97.7	17	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
32	c3la6P	Alignment	not modelled	97.6	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
33	c3cioA	Alignment	not modelled	97.6	11	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
34	dlcp2a	Alignment	not modelled	97.5	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
35	c3fkqA	Alignment	not modelled	97.5	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: intrc-like two-domain protein; PDBTitle: crystal structure of ntrc-like two-domain protein (rer070207001320)2 from eubacterium rectale at 2.10 a resolution
36	c3q9lB	Alignment	not modelled	97.5	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
37	clj8yF	Alignment	not modelled	97.5	19	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
38	dlrz3a	Alignment	not modelled	97.4	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
39	c3kjgB	Alignment	not modelled	97.4	13	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
40	dlokkd2	Alignment	not modelled	97.4	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
41	c2wsmB	Alignment	not modelled	97.4	13	PDB header: metal binding protein Chain: B: PDB Molecule: hydrogenase expression/formation protein (hybp); PDBTitle: crystal structure of hydrogenase maturation factor hybp from2 archaeoglobus fulgidus
42	c3k9gA	Alignment	not modelled	97.3	19	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
43	c3ea0B	Alignment	not modelled	97.3	17	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
44	dl1s1a2	Alignment	not modelled	97.3	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
45	dlg3qa	Alignment	not modelled	97.3	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
46	d2qy9a2	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
47	c3ibgF	Alignment	not modelled	97.2	20	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
48	dl1hua2	Alignment	not modelled	97.2	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
49	clii0A	Alignment	not modelled	97.1	29	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
50	clnija	Alignment	not modelled	97.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein
51	dlnp6a	Alignment	not modelled	97.1	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
52	clw78A	Alignment	not modelled	97.1	27	PDB header: synthase Chain: A: PDB Molecule: folc bifunctional protein; PDBTitle: e.coli folc in complex with dhpp and adp
						PDB header: hydrolase

53	c3zq6D_	Alignment	not modelled	97.0	28	Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
54	c2vosA_	Alignment	not modelled	97.0	32	PDB header: ligase Chain: A: PDB Molecule: folylpolyglutamate synthase protein folc; PDBTitle: mycobacterium tuberculosis folylpolyglutamate synthase2 complexed with adp
55	c2hf9A_	Alignment	not modelled	97.0	13	PDB header: hydrolase, metal binding protein Chain: A: PDB Molecule: probable hydrogenase nickel incorporation PDBTitle: crystal structure of hypb from methanocaldococcus2 jannaschii in the triphosphate form
56	c2qmoA_	Alignment	not modelled	96.9	12	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biob) from helicobacter2 pylori
57	c3n2aA_	Alignment	not modelled	96.9	27	PDB header: ligase Chain: A: PDB Molecule: bifunctional folylpolyglutamate synthase/dihydrofolate PDBTitle: crystal structure of bifunctional folylpolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
58	c2gc6A_	Alignment	not modelled	96.9	32	PDB header: ligase Chain: A: PDB Molecule: folylpolyglutamate synthase; PDBTitle: s73a mutant of l. casei fpgs
59	c3fmfA_	Alignment	not modelled	96.9	17	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
60	c3of5A_	Alignment	not modelled	96.9	15	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
61	c2wwiC_	Alignment	not modelled	96.9	23	PDB header: transferase Chain: C: PDB Molecule: thymidilate kinase, putative; PDBTitle: plasmodium falciparum thymidylate kinase in complex with2 aztmp and adp
62	c2ozeA_	Alignment	not modelled	96.8	29	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
63	d1s96a_	Alignment	not modelled	96.8	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
64	c1o5zA_	Alignment	not modelled	96.8	21	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
65	d2gc6a2	Alignment	not modelled	96.7	32	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: Folylpolyglutamate synthetase
66	d1nn5a_	Alignment	not modelled	96.7	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
67	c3c8uA_	Alignment	not modelled	96.6	21	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
68	c3jvvA_	Alignment	not modelled	96.6	13	PDB header: atp binding protein Chain: A: PDB Molecule: twitching mobility protein; PDBTitle: crystal structure of p. aeruginosa pilt with bound amp-pcp
69	c2vedA_	Alignment	not modelled	96.6	16	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
70	d1odfa_	Alignment	not modelled	96.6	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
71	c3asyB_	Alignment	not modelled	96.6	43	PDB header: transferase Chain: B: PDB Molecule: uridine kinase; PDBTitle: ligand-free structure of uridine kinase from thermophilus hb8
72	c2wooC_	Alignment	not modelled	96.5	33	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
73	d1ihua1	Alignment	not modelled	96.5	38	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
74	c3neyC_	Alignment	not modelled	96.5	12	PDB header: membrane protein Chain: C: PDB Molecule: 55 kda erythrocyte membrane protein; PDBTitle: crystal structure of the kinase domain of mpp1/p55
75	c3ug7D_	Alignment	not modelled	96.4	31	PDB header: hydrolase Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
76	d1o5za2	Alignment	not modelled	96.4	21	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: Folylpolyglutamate synthetase
77	c3tqcB_	Alignment	not modelled	96.3	21	PDB header: transferase Chain: B: PDB Molecule: pantothenate kinase; PDBTitle: structure of the pantothenate kinase (coaa) from coxiella burnetii

78	c2ph1A	 Alignment	not modelled	96.3	35	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
79	d1p3da3	 Alignment	not modelled	96.2	15	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
80	d1ki9a	 Alignment	not modelled	96.2	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
81	d1sq5a	 Alignment	not modelled	96.1	35	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
82	c2wojD	 Alignment	not modelled	96.1	22	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
83	c1e8cB	 Alignment	not modelled	96.1	21	PDB header: ligase Chain: B: PDB Molecule: udp-n-acetylmuramoyl-alanyl-d-glutamate--2,6- PDBTitle: structure of mure the udp-n-acetylmuramyl tripeptide2 synthetase from e. coli
84	c2bekB	 Alignment	not modelled	96.1	36	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein2 soj
85	c2gesA	 Alignment	not modelled	96.1	31	PDB header: transferase Chain: A: PDB Molecule: pantothenate kinase; PDBTitle: pantothenate kinase from mycobacterium tuberculosis (mtpank) in2 complex with a coenzyme a derivative, form-i (rt)
86	d1hyqa	 Alignment	not modelled	96.1	40	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
87	c1hyqA	 Alignment	not modelled	96.1	40	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
88	c3io3A	 Alignment	not modelled	96.1	24	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
89	d1kgda	 Alignment	not modelled	96.0	10	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
90	c3tauB	 Alignment	not modelled	96.0	15	PDB header: transferase Chain: B: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of a putative guanylate monophosphate kinase from2 listeria monocytogenes egd-e
91	d1e8ca3	 Alignment	not modelled	95.9	21	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
92	c2plrB	 Alignment	not modelled	95.7	20	PDB header: transferase Chain: B: PDB Molecule: probable thymidylate kinase; PDBTitle: crystal structure of dtmp kinase (st1543) from sulfolobus tokodaii2 strain7
93	c3pg5A	 Alignment	not modelled	95.7	38	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
94	c2eyuA	 Alignment	not modelled	95.7	16	PDB header: protein transport Chain: A: PDB Molecule: twitching motility protein pilt; PDBTitle: the crystal structure of the c-terminal domain of aquifex2 aeolicus pilt
95	c3e1sA	 Alignment	not modelled	95.6	24	PDB header: hydrolase Chain: A: PDB Molecule: exodeoxyribonuclease v, subunit recd; PDBTitle: structure of an n-terminal truncation of deinococcus radiodurans recd2
96	c2j41A	 Alignment	not modelled	95.6	15	PDB header: transferase Chain: A: PDB Molecule: guanylate kinase; PDBTitle: crystal structure of staphylococcus aureus guanylate2 monophosphate kinase
97	c2pbrB	 Alignment	not modelled	95.6	32	PDB header: transferase Chain: B: PDB Molecule: thymidylate kinase; PDBTitle: crystal structure of thymidylate kinase (aq_969) from aquifex aeolicus2 vf5
98	d1yrba1	 Alignment	not modelled	95.6	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
99	d4tmka	 Alignment	not modelled	95.6	31	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
100	d1khta	 Alignment	not modelled	95.6	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
101	c2wtzC	 Alignment	not modelled	95.5	33	PDB header: ligase Chain: C: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate- PDBTitle: mure ligase of mycobacterium tuberculosis
102	c3lv8A	 Alignment	not modelled	95.5	26	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

103	c2ja1A_	 Alignment	not modelled	95.4	12	PDB header: transferase Chain: A: PDB Molecule: thymidine kinase; PDBTitle: thymidine kinase from b. cereus with ttp bound as phosphate2 donor.
104	c3igfB_	 Alignment	not modelled	95.4	26	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
105	d1uj2a_	 Alignment	not modelled	95.3	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
106	d1uf9a_	 Alignment	not modelled	95.3	39	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
107	c1ueiB_	 Alignment	not modelled	95.3	27	PDB header: transferase Chain: B: PDB Molecule: uridine-cytidine kinase 2; PDBTitle: crystal structure of human uridine-cytidine kinase 22 complexed with a feedback-inhibitor, utp
108	c1j6uA_	 Alignment	not modelled	95.3	15	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
109	c3ld9D_	 Alignment	not modelled	95.3	27	PDB header: transferase Chain: D: PDB Molecule: thymidylate kinase; PDBTitle: crystal structure of thymidylate kinase from ehrlichia chaffeensis at2 2.15a resolution
110	c3lk7A_	 Alignment	not modelled	95.3	27	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine--d-glutamate ligase; PDBTitle: the crystal structure of udp-n-acetylmuramoylalanine-d-2 glutamate (murd) ligase from streptococcus agalactiae to3 1.5a
111	c3eagA_	 Alignment	not modelled	95.2	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- PDBTitle: the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitides
112	c3cwqB_	 Alignment	not modelled	95.2	33	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
113	c2kjqA_	 Alignment	not modelled	95.2	15	PDB header: replication Chain: A: PDB Molecule: dnaa-related protein; PDBTitle: solution structure of protein nmb1076 from neisseria meningitidis.2 northeast structural genomics consortium target mr101b.
114	c2gszE_	 Alignment	not modelled	95.2	17	PDB header: protein transport Chain: E: PDB Molecule: twitching motility protein pilt; PDBTitle: structure of a. aeolicus pilt with 6 monomers per2 asymmetric unit
115	c2w0sB_	 Alignment	not modelled	95.1	28	PDB header: transferase Chain: B: PDB Molecule: thymidylate kinase; PDBTitle: crystal structure of vaccinia virus thymidylate kinase2 bound to brivudin-5'-monophosphate
116	d1byia_	 Alignment	not modelled	95.1	27	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
117	d2jfga3	 Alignment	not modelled	95.0	19	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
118	c3ez6B_	 Alignment	not modelled	95.0	26	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
119	d1gsia_	 Alignment	not modelled	95.0	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
120	d1j6ua3	 Alignment	not modelled	95.0	18	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF