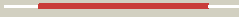























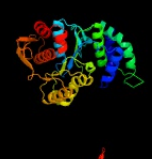
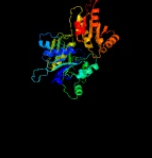



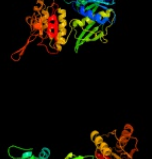
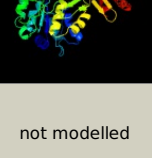


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2447c_(fo)C_2746145_2747608
Date	Wed Aug 7 12:50:07 BST 2019
Unique Job ID	4214d841b5690c63

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2vosA_	 Alignment		100.0	98	PDB header: ligase Chain: A: PDB Molecule: folypolyglutamate synthase protein folc; PDBTitle: mycobacterium tuberculosis folypolyglutamate synthase2 complexed with adp
2	c1o5zA_	 Alignment		100.0	34	PDB header: ligase Chain: A: PDB Molecule: folypolyglutamate synthase/dihydrofolate synthase; PDBTitle: crystal structure of folypolyglutamate synthase (tm0166) from2 thermotoga maritima at 2.10 a resolution
3	c1w78A_	 Alignment		100.0	31	PDB header: synthase Chain: A: PDB Molecule: folc bifunctional protein; PDBTitle: e.coli folc in complex with dhpp and adp
4	c2gc6A_	 Alignment		100.0	31	PDB header: ligase Chain: A: PDB Molecule: folypolyglutamate synthase; PDBTitle: s73a mutant of l. casei fpgs
5	c3n2aA_	 Alignment		100.0	30	PDB header: ligase Chain: A: PDB Molecule: bifunctional folypolyglutamate synthase/dihydrofolate PDBTitle: crystal structure of bifunctional folypolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92
6	c4c13A_	 Alignment		100.0	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--l-lysine ligase; PDBTitle: x-ray crystal structure of staphylococcus aureus mure with udp-murnac-2 ala-glu-lys
7	c1e8cB_	 Alignment		100.0	21	PDB header: ligase Chain: B: PDB Molecule: udp-n-acetylmuramoylalanyl-d-glutamate--2,6-diaminopimelate PDBTitle: structure of mure the udp-n-acetylmuramyl tripeptide synthetase from2 e. coli
8	c2xjaD_	 Alignment		100.0	24	PDB header: ligase Chain: D: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2,6- PDBTitle: structure of mure from m.tuberculosis with dipeptide and adp
9	c4bubA_	 Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--ld-lysine PDBTitle: crystal structure of mure ligase from thermotoga maritima2 in complex with adp
10	d2gc6a2	 Alignment		100.0	32	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: Folypolyglutamate synthetase
11	c2wtzC_	 Alignment		100.0	25	PDB header: ligase Chain: C: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate- PDBTitle: mure ligase of mycobacterium tuberculosis

12	c4qdiA	Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine ligase; PDBTitle: crystal structure ii of murf from acinetobacter baumannii
13	c2f00A	Alignment		100.0	17	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
14	d1o5za2	Alignment		100.0	36	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: Folylpolyglutamate synthetase
15	c3hn7A	Alignment		100.0	16	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
16	c2am1A	Alignment		100.0	16	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine-d-glutamyl-lysine-d-alanyl-d- PDBTitle: sp protein ligand 1
17	c1gqgA	Alignment		100.0	14	PDB header: cell wall biosynthesis Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: murc - crystal structure of the apo-enzyme from haemophilus influenzae
18	c4cvkA	Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine PDBTitle: pamurf in complex with udp-murnac-tripeptide (mdap)
19	c3zl8A	Alignment		100.0	15	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoyl-tripeptide--d-alanyl-d-alanine PDBTitle: crystal structure of murf ligase from thermotoga maritima2 in complex with adp
20	c6gs2B	Alignment		100.0	20	PDB header: biosynthetic protein Chain: B: PDB Molecule: sa1708 protein; PDBTitle: crystal structure of the gatd/murt enzyme complex from staphylococcus2 aureus
21	c1j6uA	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetylmuramate-alanine ligase murc (tm0231)2 from thermotoga maritima at 2.3 a resolution
22	c3lk7A	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine--d-glutamate ligase; PDBTitle: the crystal structure of udp-n-acetylmuramoylalanine-d-glutamate2 (murd) ligase from streptococcus agalactiae to 1.5a
23	c1gg4A	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanyl-d-glutamyl-2,6-diaminopimelate- PDBTitle: crystal structure of escherichia coli udpmurnac-tripeptide d-alanyl-d-2 alanine-adding enzyme (murf) at 2.3 angstrom resolution
24	c3uagA	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: protein (udp-n-acetylmuramoyl-l-alanine:d- PDBTitle: udp-n-acetylmuramoyl-l-alanine:d-glutamate ligase
25	c6fqbd	Alignment	not modelled	100.0	18	PDB header: ligase Chain: D: PDB Molecule: mur ligase family protein; PDBTitle: murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
26	c4bucA	Alignment	not modelled	100.0	15	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramoylalanine--d-glutamate ligase; PDBTitle: crystal structure of murd ligase from thermotoga maritima in apo form
27	c5vwwA	Alignment	not modelled	100.0	23	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: structure of murc from pseudomonas aeruginosa

28	d1e8ca3	Alignment	not modelled	100.0	18	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
29	d1p3da3	Alignment	not modelled	100.0	22	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
30	c3eagA	Alignment	not modelled	100.0	15	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
31	c6cauA	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: udp-n-acetylmuramate--alanine ligase from acinetobacter baumannii2 ab5075-uw with ampnpn
32	d1j6ua3	Alignment	not modelled	100.0	19	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
33	d2jfga3	Alignment	not modelled	100.0	23	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
34	d1gg4a4	Alignment	not modelled	100.0	25	Fold: Ribokinase-like Superfamily: MurD-like peptide ligases, catalytic domain Family: MurCDEF
35	d1o5za1	Alignment	not modelled	99.9	32	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folypolyglutamate synthetase, C-terminal domain
36	d2gc6a1	Alignment	not modelled	99.9	33	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: Folypolyglutamate synthetase, C-terminal domain
37	d1p3da2	Alignment	not modelled	99.8	11	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
38	d1e8ca2	Alignment	not modelled	99.8	28	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
39	c3mvaA	Alignment	not modelled	99.7	24	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- PDBTitle: crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-meso-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
40	d1j6ua2	Alignment	not modelled	99.6	21	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
41	d2jfga2	Alignment	not modelled	99.3	18	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
42	d1gg4a1	Alignment	not modelled	99.3	21	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
43	c3fmaA	Alignment	not modelled	97.2	19	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
44	c3of5A	Alignment	not modelled	96.6	17	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
45	c2j37W	Alignment	not modelled	96.4	10	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
46	c3cioA	Alignment	not modelled	96.4	14	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
47	d1byia	Alignment	not modelled	96.1	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
48	c6cy1B	Alignment	not modelled	96.1	10	PDB header: signaling protein Chain: B: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: crystal structure of signal recognition particle receptor ftsy from2 elizabethkingia anophelis
49	c4dzzB	Alignment	not modelled	96.0	12	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
50	c2og2A	Alignment	not modelled	95.9	14	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
51	c5j3qB	Alignment	not modelled	95.9	11	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle receptor subunit alpha; PDBTitle: structure of the gtpase heterodimer of human srp54 and sralpha
52	c1zu4A	Alignment	not modelled	95.8	9	PDB header: protein transport Chain: A: PDB Molecule: ftsyl; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212

53	d1a7ja_	Alignment	not modelled	95.8	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
54	d2afhe1	Alignment	not modelled	95.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
55	c2iy3A_	Alignment	not modelled	95.5	15	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
56	c2ozeA_	Alignment	not modelled	95.3	18	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
57	d1hyqa_	Alignment	not modelled	95.2	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
58	c1hyqA_	Alignment	not modelled	95.2	19	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
59	c3b9qA_	Alignment	not modelled	95.1	13	PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
60	c3ea0B_	Alignment	not modelled	95.1	11	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
61	c2qmoA_	Alignment	not modelled	95.1	31	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biot) from helicobacter2 pylori
62	c2cnwF_	Alignment	not modelled	95.0	16	PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
63	c3ez6B_	Alignment	not modelled	95.0	18	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para- adp complex:tetragonal form
64	c4rz3B_	Alignment	not modelled	95.0	10	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase flhg
65	c2yhsA_	Alignment	not modelled	95.0	15	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
66	c5l3sF_	Alignment	not modelled	94.9	19	PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
67	c3tqcB_	Alignment	not modelled	94.9	33	PDB header: transferase Chain: B: PDB Molecule: pantothenate kinase; PDBTitle: structure of the pantothenate kinase (coaa) from coxiella burnetii
68	c5gafi_	Alignment	not modelled	94.9	19	PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein I10; PDBTitle: rnc in complex with srp
69	c5j1jA_	Alignment	not modelled	94.8	16	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
70	c2f1rA_	Alignment	not modelled	94.8	23	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
71	c4pfsA_	Alignment	not modelled	94.6	28	PDB header: ligase Chain: A: PDB Molecule: cobyrinic acid a,c-diamide synthase; PDBTitle: crystal structure of cobyrinic acid a,c-diamide synthase from2 mycobacterium smegmatis
72	c2vedA_	Alignment	not modelled	94.6	17	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
73	c2bekB_	Alignment	not modelled	94.6	27	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
74	c3endA_	Alignment	not modelled	94.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: light-independent protochlorophyllide reductase PDBTitle: crystal structure of the I protein of rhodobacter2 sphaeroides light-independent protochlorophyllide3 reductase (bchl) with mgadp bound: a homologue of the4 nitrogenase fe protein
75	c3la6P_	Alignment	not modelled	94.4	21	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
76	d1cp2a_	Alignment	not modelled	94.2	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
77	d1g3qa_	Alignment	not modelled	94.2	29	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
78	c4v02B_	Alignment	not modelled	94.2	19	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: minc:mind cell division protein complex, aquifex aeolicus

79	d1vmaa2	Alignment	not modelled	94.1	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
80	c4a0gC	Alignment	not modelled	94.1	26	PDB header: transferase Chain: C: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana in its apo form.
81	c4ak9A	Alignment	not modelled	94.1	18	PDB header: protein transport Chain: A: PDB Molecule: cpftsyt; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
82	c4ru8C	Alignment	not modelled	94.1	26	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: structure of pnob8 para with amppnp
83	c3c8uA	Alignment	not modelled	94.0	12	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
84	c1vmaA	Alignment	not modelled	94.0	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
85	c4nkrB	Alignment	not modelled	93.9	16	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
86	d1iona	Alignment	not modelled	93.7	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
87	c2qy9A	Alignment	not modelled	93.6	13	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
88	d1rz3a	Alignment	not modelled	93.6	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
89	c3dm5A	Alignment	not modelled	93.4	19	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 assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
90	d1np6a	Alignment	not modelled	93.4	25	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
91	c2v3cC	Alignment	not modelled	93.2	19	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
92	c2xj9B	Alignment	not modelled	93.2	19	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
93	c2q9cA	Alignment	not modelled	92.9	18	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmppnp with mgcl complex
94	d2qy9a2	Alignment	not modelled	92.8	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
95	c1qzwC	Alignment	not modelled	92.7	26	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
96	c6g2gA	Alignment	not modelled	92.7	23	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
97	c3dmdA	Alignment	not modelled	92.5	18	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
98	c3q9lB	Alignment	not modelled	92.4	23	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
99	c2px0D	Alignment	not modelled	91.4	19	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
100	d1sq5a	Alignment	not modelled	91.4	37	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Phosphoribulokinase/pantothenate kinase
101	c2j7pA	Alignment	not modelled	91.4	21	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
102	c5zmfA	Alignment	not modelled	91.3	14	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: atpase arsa1; PDBTitle: amppnp complex of c. reinhardtii arsa1
103	c3vx3A	Alignment	not modelled	91.2	23	PDB header: adp binding protein Chain: A: PDB Molecule: atpase involved in chromosome partitioning, para/mind PDBTitle: crystal structure of [nife] hydrogenase maturation protein hypb from2 thermococcus kodakarensis kod1 PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein.

104	c5l3rC_	Alignment	not modelled	91.2	21	chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
105	c2ph1A_	Alignment	not modelled	91.1	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
106	d1okkd2	Alignment	not modelled	90.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
107	c2gesA_	Alignment	not modelled	90.1	35	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)
108	d1xjca_	Alignment	not modelled	90.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
109	d2vo1a1	Alignment	not modelled	90.0	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
110	d1ihua2	Alignment	not modelled	89.6	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
111	d1j8yf2	Alignment	not modelled	89.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
112	c6bs5B_	Alignment	not modelled	89.4	20	PDB header: unknown function Chain: B: PDB Molecule: anion transporter; PDBTitle: crystal structure of amp-pnp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
113	c3igfB_	Alignment	not modelled	88.6	14	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
114	c3k9gA_	Alignment	not modelled	88.4	27	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
115	c2j289_	Alignment	not modelled	88.4	19	PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
116	c6iucC_	Alignment	not modelled	88.3	26	PDB header: dna binding protein/dna Chain: C: PDB Molecule: spooj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna
117	d1qzxa3	Alignment	not modelled	88.3	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
118	d1nk5a_	Alignment	not modelled	88.3	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
119	c5u03C_	Alignment	not modelled	88.2	33	PDB header: ligase, protein fibril Chain: C: PDB Molecule: ctp synthase 1; PDBTitle: cryo-em structure of the human ctp synthase filament
120	c3zq6D_	Alignment	not modelled	87.6	20	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40