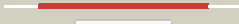



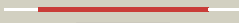




























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3213c_(-)_3590689_3591489
Date	Thu Aug 8 16:20:41 BST 2019
Unique Job ID	9bbd5e64f3796f81

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6iucC_	 Alignment		100.0	39	PDB header: dna binding protein/dna Chain: C: PDB Molecule: spooj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna
2	c4pfsA_	 Alignment		100.0	87	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
3	c2ozeA_	 Alignment		100.0	22	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
4	d2afhe1	 Alignment		100.0	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
5	c2bekB_	 Alignment		100.0	42	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
6	c6nonB_	 Alignment		100.0	24	PDB header: dna binding protein Chain: B: PDB Molecule: cobyrinic acid ac-diamide synthase; PDBTitle: structure of cyanthece apo mcda
7	c3ez6B_	 Alignment		100.0	21	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
8	c5i1jA_	 Alignment		100.0	22	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-amppnp complex
9	d1cp2a_	 Alignment		100.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
10	c3endA_	 Alignment		100.0	23	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
11	c3q9lB_	 Alignment		100.0	22	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

12	d1iona_	Alignment		100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
13	d1g3qa_	Alignment		100.0	22	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
14	c4rz3B_	Alignment		100.0	18	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase flhg
15	c3kjqB_	Alignment		100.0	20	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
16	d1hyqa_	Alignment		100.0	23	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
17	c1hyqA_	Alignment		100.0	23	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
18	c6g2gA_	Alignment		100.0	18	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
19	c4dzzB_	Alignment		100.0	21	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
20	c2xj9B_	Alignment		100.0	20	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
21	c3ea0B_	Alignment	not modelled	100.0	16	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
22	c4ru8C_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: structure of pnob8 para with amppnp
23	c4v02B_	Alignment	not modelled	100.0	19	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: mind:mind cell division protein complex, aquifex aeolicus
24	c3ezfA_	Alignment	not modelled	100.0	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: para; PDBTitle: partition protein
25	c3cwqB_	Alignment	not modelled	100.0	25	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
26	c2ph1A_	Alignment	not modelled	100.0	18	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
27	c3k9gA_	Alignment	not modelled	100.0	21	PDB header: biosynthetic protein Chain: A: PDB Molecule: pf-32 protein; PDBTitle: crystal structure of a plasmid partition protein from borrelia burgdorferi at 2.25a resolution, iodide soak
						PDB header: adp binding protein Chain: A: PDB Molecule: atpase involved in chromosome

28	c3vx3A_	Alignment	not modelled	100.0	23	partitioning, para/mind PDBTitle: crystal structure of [nife] hydrogenase maturation protein hyb from2 thermococcus kodakarensis kod1
29	c3fkqA_	Alignment	not modelled	100.0	17	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
30	c3pg5A_	Alignment	not modelled	100.0	25	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
31	d1byia_	Alignment	not modelled	100.0	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
32	c2wooc_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
33	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
34	c2wojd_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
35	d1ihua1	Alignment	not modelled	99.9	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
36	c3ug7D_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
37	c3cioA_	Alignment	not modelled	99.9	16	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
38	c5bwkA_	Alignment	not modelled	99.9	22	PDB header: hydrolase/transport Chain: A: PDB Molecule: atpase get3; PDBTitle: 6.0 a crystal structure of a get3-get4-get5 intermediate complex from2 s.cerevisiae
39	c3of5A_	Alignment	not modelled	99.9	11	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
40	c6bs3A_	Alignment	not modelled	99.9	16	PDB header: unknown function Chain: A: PDB Molecule: putative atpase rv3679; PDBTitle: crystal structure of adp-bound bacterial get3-like a and b in2 mycobacterium tuberculosis
41	c3la6P_	Alignment	not modelled	99.9	19	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
42	c3io3A_	Alignment	not modelled	99.9	20	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
43	c5zmfA_	Alignment	not modelled	99.9	20	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: atpase arsa1; PDBTitle: amppnp complex of c. reinhardtii arsa1
44	c6bs5B_	Alignment	not modelled	99.9	27	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
45	c2vedA_	Alignment	not modelled	99.9	15	PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
46	c3ibgf_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
47	c1ii0A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
48	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
49	c2qmoA_	Alignment	not modelled	99.9	12	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
50	c3igfB_	Alignment	not modelled	99.9	20	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
51	c3fmfA_	Alignment	not modelled	99.9	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
52	c5l3qB_	Alignment	not modelled	99.5	19	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
53	c1zu4A_	Alignment	not modelled	99.3	21	PDB header: protein transport Chain: A: PDB Molecule: ftsyt; PDBTitle: crystal structure of ftsyt from mycoplasma mycoides-

					space2 group p21212
54	c2qy9A_	Alignment	not modelled	99.3	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
55	c1vmaA_	Alignment	not modelled	99.3	20 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
56	c2og2A_	Alignment	not modelled	99.3	16 PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
57	c2cnwF_	Alignment	not modelled	99.2	25 PDB header: signal recognition Chain: F: PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
58	c3dm5A_	Alignment	not modelled	99.2	20 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.
59	c2iy3A_	Alignment	not modelled	99.2	28 PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
60	c3b9qA_	Alignment	not modelled	99.2	16 PDB header: protein transport Chain: A: PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyt from arabidopsis thaliana
61	c2j37W_	Alignment	not modelled	99.2	19 PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
62	c5l3rC_	Alignment	not modelled	99.2	19 PDB header: protein transport Chain: C: PDB Molecule: signal recognition particle 54 kda protein, chloroplastic; PDBTitle: structure of the gtpase heterodimer of chloroplast srp54 and ftsy from2 arabidopsis thaliana
63	c2yhsA_	Alignment	not modelled	99.2	22 PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
64	c6cy1B_	Alignment	not modelled	99.2	23 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
65	c2q9cA_	Alignment	not modelled	99.2	22 PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmpnp with mgcl complex
66	c2j7pA_	Alignment	not modelled	99.1	21 PDB header: signal recognition Chain: A: PDB Molecule: signal recognition particle protein; PDBTitle: gmpnp-stabilized ng domain complex of the srp gtpases ffh2 and ftsy
67	c5l3sF_	Alignment	not modelled	99.1	25 PDB header: protein transport Chain: F: PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
68	c4ak9A_	Alignment	not modelled	99.1	24 PDB header: protein transport Chain: A: PDB Molecule: cpftsyt; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
69	c1qzwC_	Alignment	not modelled	99.0	22 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
70	c2v3cC_	Alignment	not modelled	99.0	20 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
71	c5gafi_	Alignment	not modelled	99.0	16 PDB header: ribosome Chain: I: PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
72	c3dmdA_	Alignment	not modelled	98.9	23 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
73	c2j289_	Alignment	not modelled	98.8	21 PDB header: ribosome Chain: 9: PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
74	d1qzxa3	Alignment	not modelled	98.5	22 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
75	d1vmaa2	Alignment	not modelled	98.3	21 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
76	c4ohvA_	Alignment	not modelled	98.3	20 PDB header: rna binding protein Chain: A: PDB Molecule: protein clpf-1; PDBTitle: c. elegans clp1 bound to amp-pnp, and mg2+
77	c2obnA_	Alignment	not modelled	98.2	13 PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1611 family protein (ava_3511) from anaebaena2 variabilis atcc 29413 at 2.30 a resolution
78	c5hcnA_	Alignment	not modelled	98.2	14 PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp PDB header: translation

79	c3tr5C_	Alignment	not modelled	98.2	17	Chain: C: PDB Molecule: peptide chain release factor 3; PDBTitle: structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
80	c2h5eB_	Alignment	not modelled	98.2	19	PDB header: translation Chain: B: PDB Molecule: peptide chain release factor rf-3; PDBTitle: crystal structure of e.coli polypeptide release factor rf3
81	d1j8yf2	Alignment	not modelled	98.1	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
82	d2qy9a2	Alignment	not modelled	98.1	26	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
83	d1okkd2	Alignment	not modelled	97.9	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
84	d1ls1a2	Alignment	not modelled	97.8	40	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
85	c4nkrB_	Alignment	not modelled	97.8	16	PDB header: unknown function Chain: B: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
86	c1j8yF_	Alignment	not modelled	97.8	18	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
87	c4zciA_	Alignment	not modelled	97.8	17	PDB header: gtp-binding protein Chain: A: PDB Molecule: gtp-binding protein typha/bipa; PDBTitle: crystal structure of escherichia coli gtpase bipa/typha
88	c4fn5A_	Alignment	not modelled	97.8	18	PDB header: translation/antibiotic Chain: A: PDB Molecule: elongation factor g 1; PDBTitle: elongation factor g 1 (pseudomonas aeruginosa) in complex with argyri2 b
89	c2npiB_	Alignment	not modelled	97.7	20	PDB header: transcription Chain: B: PDB Molecule: protein clp1; PDBTitle: clp1-atp-pcf11 complex
90	c1xnjB_	Alignment	not modelled	97.7	28	PDB header: transferase Chain: B: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate PDBTitle: aps complex of human paps synthetase 1
91	d2qm8a1	Alignment	not modelled	97.7	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
92	c3degC_	Alignment	not modelled	97.6	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
93	c2xexA_	Alignment	not modelled	97.6	18	PDB header: translation Chain: A: PDB Molecule: elongation factor g; PDBTitle: crystal structure of staphylococcus aureus elongation factor2 g
94	c2px0D_	Alignment	not modelled	97.6	26	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
95	c2f1rA_	Alignment	not modelled	97.6	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
96	c2ywfA_	Alignment	not modelled	97.6	15	PDB header: translation Chain: A: PDB Molecule: gtp-binding protein lepa; PDBTitle: crystal structure of gmppnp-bound lepa from aquifex aeolicus
97	c1zn0B_	Alignment	not modelled	97.6	19	PDB header: translation/biosynthetic protein/rna Chain: B: PDB Molecule: elongation factor g; PDBTitle: coordinates of rrf and ef-g fitted into cryo-em map of the2 50s subunit bound with both ef-g (gdnp) and rrf
98	c2bm0A_	Alignment	not modelled	97.5	18	PDB header: elongation factor Chain: A: PDB Molecule: elongation factor g; PDBTitle: ribosomal elongation factor g (ef-g) fusidic acid resistant mutant2 t84a
99	d2bv3a2	Alignment	not modelled	97.5	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
100	d1xjca_	Alignment	not modelled	97.5	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
101	c1xp8A_	Alignment	not modelled	97.4	12	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
102	d1xp8a1	Alignment	not modelled	97.4	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
103	c2yvua_	Alignment	not modelled	97.3	27	PDB header: transferase Chain: A: PDB Molecule: probable adenyllyl-sulfate kinase; PDBTitle: crystal structure of ape1195
104	c2rdo7_	Alignment	not modelled	97.3	16	PDB header: ribosome Chain: 7: PDB Molecule: elongation factor g; PDBTitle: 50s subunit with ef-g(gdnp) and rrf bound
105	c1xjqA_	Alignment	not modelled	97.2	24	PDB header: transferase Chain: A: PDB Molecule: bifunctional 3'-phosphoadenosine 5'-phosphosulfate

				PDBTitle: adp complex of human paps synthetase 1	
106	c2recB_	Alignment	not modelled	97.2	19 PDB header: helicase PDB COMPND:
107	d1np6a_	Alignment	not modelled	97.2	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
108	c3bgwD_	Alignment	not modelled	97.2	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
109	c4zc0A_	Alignment	not modelled	97.2	PDB header: hydrolase Chain: A: PDB Molecule: replicative dna helicase; PDBTitle: structure of a dodecameric bacterial helicase
110	d1ki9a_	Alignment	not modelled	97.2	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
111	d1nksa_	Alignment	not modelled	97.2	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nucleotide and nucleoside kinases
112	d1u94a1	Alignment	not modelled	97.1	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
113	d1yrba1	Alignment	not modelled	97.1	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
114	d1mo6a1	Alignment	not modelled	97.1	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
115	c4wiaA_	Alignment	not modelled	97.1	PDB header: atp-binding protein Chain: A: PDB Molecule: putative flagella-related protein h; PDBTitle: crystal structure of flagellar accessory protein flah from2 methanocaldococcus jannaschii
116	d1x6va3	Alignment	not modelled	97.1	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Adenosine-5'-phosphosulfate kinase (APS kinase)
117	c3hr8A_	Alignment	not modelled	97.0	PDB header: recombination Chain: A: PDB Molecule: protein reca; PDBTitle: crystal structure of thermotoga maritima reca
118	c2gksB_	Alignment	not modelled	97.0	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
119	c3uieB_	Alignment	not modelled	97.0	PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: adenylyl-sulfate kinase 1, chloroplastic; PDBTitle: crystal structure of adenosine 5'-phosphosulfate kinase from2 arabidopsis thaliana in complex with amppnp and aps
120	c4a1fB_	Alignment	not modelled	97.0	PDB header: hydrolase Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase