


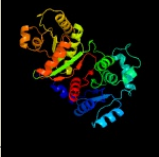
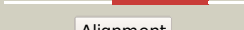



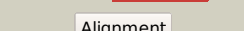

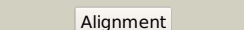

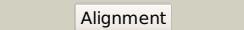

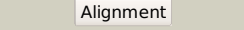

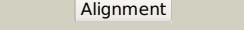
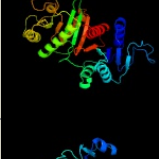
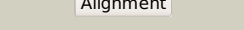

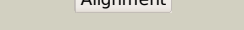



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0408_(pta)_491789_493861
Date	Tue Jul 23 14:50:48 BST 2019
Unique Job ID	37d3ea110d554d44

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6ioxB_	 Alignment		100.0	44	PDB header: transferase Chain: B: PDB Molecule: phosphotransacetylase; PDBTitle: crystal structure of porphyromonas gingivalis phosphotransacetylase in2 complex with acetyl-coa
2	c1vmiA_	 Alignment		100.0	39	PDB header: transferase Chain: A: PDB Molecule: putative phosphate acetyltransferase; PDBTitle: crystal structure of putative phosphate acetyltransferase2 (np_416953.1) from escherichia coli k12 at 2.32 a resolution
3	d1vmia_	 Alignment		100.0	39	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
4	c4e4rA_	 Alignment		100.0	45	PDB header: transferase Chain: A: PDB Molecule: phosphate acetyltransferase; PDBTitle: eutd phosphotransacetylase from staphylococcus aureus
5	d1xcoa_	 Alignment		100.0	43	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
6	d2af4c1	 Alignment		100.0	43	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
7	d1r5ja_	 Alignment		100.0	45	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: Phosphotransacetylase
8	c3tngA_	 Alignment		100.0	26	PDB header: transferase Chain: A: PDB Molecule: lmo1369 protein; PDBTitle: the crystal structure of a possible phosphate acetyl/butaryl2 transferase from listeria monocytogenes egd-e.
9	c1ycoA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: branched-chain phosphotransacylase; PDBTitle: crystal structure of a branched-chain phosphotransacylase from2 enterococcus faecalis v583
10	d1viiA_	 Alignment		100.0	16	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PlsX-like
11	d1u7na_	 Alignment		100.0	24	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PlsX-like

12	c3fmfA_	Alignment		99.9	16	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
13	d1byia_	Alignment		99.9	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
14	d2ioja1	Alignment		99.9	26	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: DRTGG domain
15	c3of5A_	Alignment		99.9	14	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of a dethiobiotin synthetase from francisella2 tularensis subsp. tularensis schu s4
16	c2qmoA_	Alignment		99.9	16	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of dethiobiotin synthetase (biod) from helicobacter2 pylori
17	d1ptma_	Alignment		99.8	18	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like
18	c4a0gC_	Alignment		99.8	15	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.
19	c4a0rB_	Alignment		99.8	14	PDB header: transferase Chain: B: PDB Molecule: adenosylmethionine-8-amino-7-oxononanoate PDBTitle: structure of bifunctional dapa aminotransferase-dtb synthetase from2 arabidopsis thaliana bound to dethiobiotin (dtb).
20	c4rz3B_	Alignment		99.7	12	PDB header: structural protein Chain: B: PDB Molecule: site-determining protein; PDBTitle: crystal structure of the mind-like atpase flhg
21	c3la6P_	Alignment	not modelled	99.7	13	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
22	c3cioA_	Alignment	not modelled	99.7	14	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
23	d1iona_	Alignment	not modelled	99.7	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
24	d2afhe1	Alignment	not modelled	99.7	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
25	c5lj1A_	Alignment	not modelled	99.6	14	PDB header: transcription Chain: A: PDB Molecule: site-determining protein; PDBTitle: structure of flen-ampnp complex
26	c1hyqA_	Alignment	not modelled	99.6	16	PDB header: cell cycle Chain: A: PDB Molecule: cell division inhibitor (mind-1); PDBTitle: mind bacterial cell division regulator from a. fulgidus
27	d1hyqa_	Alignment	not modelled	99.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
28	c2ph1A_	Alignment	not modelled	99.6	15	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
						PDB header: transferase Chain: A: PDB Molecule: membrane protein capa1, protein tyrosine

29	c2vedA	Alignment	not modelled	99.6	16	kinase; PDBTitle: crystal structure of the chimerical mutant capabk55m2 protein
30	d1g3qa	Alignment	not modelled	99.6	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
31	d1cp2a	Alignment	not modelled	99.6	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
32	c3vx3A	Alignment	not modelled	99.6	16	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
33	c1yx0B	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase 1; PDBTitle: crystal structure of pyridoxal phosphate biosynthetic protein pdxa2 pa0593
34	c6g2gA	Alignment	not modelled	99.6	16	PDB header: cytosolic protein Chain: A: PDB Molecule: cytosolic fe-s cluster assembly factor cfd1; PDBTitle: fe-s assembly cfd1
35	c3kjgB	Alignment	not modelled	99.6	13	PDB header: hydrolase, metal binding protein Chain: B: PDB Molecule: co dehydrogenase/acetyl-coa synthase complex, accessory PDBTitle: adp-bound state of cooc1
36	c3endA	Alignment	not modelled	99.6	11	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
37	d1ko7a1	Alignment	not modelled	99.5	11	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: HPr kinase/phosphatase HprK N-terminal domain
38	c4v02B	Alignment	not modelled	99.5	16	PDB header: cell cycle Chain: B: PDB Molecule: site-determining protein; PDBTitle: minc:mind cell division protein complex, aquifex aeolicus
39	c3ea0B	Alignment	not modelled	99.5	14	PDB header: hydrolase Chain: B: PDB Molecule: atpase, para family; PDBTitle: crystal structure of para family atpase from chlorobium tepidum t1s
40	c3q9lB	Alignment	not modelled	99.5	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
41	c2xj9B	Alignment	not modelled	99.5	19	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
42	c6iucC	Alignment	not modelled	99.5	13	PDB header: dna binding protein/dna Chain: C: PDB Molecule: spooj regulator (soj); PDBTitle: structure of helicobacter pylori soj-atp complex bound to dna
43	d1r8ka	Alignment	not modelled	99.5	22	Fold: Isocitrate/Isopropylmalate dehydrogenase-like Superfamily: Isocitrate/Isopropylmalate dehydrogenase-like Family: PdxA-like
44	c3ug7D	Alignment	not modelled	99.4	16	PDB header: hydrolase Chain: D: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of get3 from methanocaldococcus jannaschii
45	c6nonB	Alignment	not modelled	99.4	14	PDB header: dna binding protein Chain: B: PDB Molecule: cobyrinic acid ac-diamide synthase; PDBTitle: structure of cyanthece apo mcda
46	c3zq6D	Alignment	not modelled	99.4	19	PDB header: hydrolase Chain: D: PDB Molecule: putative arsenical pump-driving atpase; PDBTitle: adp-alf4 complex of m. therm. trc40
47	c3fkqA	Alignment	not modelled	99.4	14	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
48	c2ozeA	Alignment	not modelled	99.4	10	PDB header: dna binding protein Chain: A: PDB Molecule: orf delta'; PDBTitle: the crystal structure of delta protein of psm19035 from2 streptococcus pyogenes
49	c2wojD	Alignment	not modelled	99.4	10	PDB header: hydrolase Chain: D: PDB Molecule: atpase get3; PDBTitle: adp-alf4 complex of s. cerevisiae get3
50	c4pfsA	Alignment	not modelled	99.4	12	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
51	c1ii0A	Alignment	not modelled	99.4	15	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
52	c2wooC	Alignment	not modelled	99.4	14	PDB header: hydrolase Chain: C: PDB Molecule: atpase get3; PDBTitle: nucleotide-free form of s. pombe get3
53	c6bs5B	Alignment	not modelled	99.4	28	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
54	c3k9gA	Alignment	not modelled	99.4	16	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
55	c5zmfA	Alignment	not modelled	99.4	11	PDB header: hydrolase/transport protein Chain: A: PDB Molecule: atpase arsa1; PDBTitle: amppnp complex of c. reinhardtii arsa1
56	d1ihua2	Alignment	not modelled	99.4	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
57	c6bs3A	Alignment	not modelled	99.3	21	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
58	c4ru8C	Alignment	not modelled	99.3	15	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: structure of pnob8 para with amppnp
59	c2bekB	Alignment	not modelled	99.3	17	PDB header: chromosome segregation Chain: B: PDB Molecule: segregation protein; PDBTitle: structure of the bacterial chromosome segregation protein soj
60	c1ko7B	Alignment	not modelled	99.2	12	PDB header: transferase,hydrolase Chain: B: PDB Molecule: hpr kinase/phosphatase; PDBTitle: x-ray structure of the hpr kinase/phosphatase from staphylococcus2 xylosus at 1.95 a resolution
61	d1ihua1	Alignment	not modelled	99.2	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
62	c5l3qB	Alignment	not modelled	99.2	14	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
63	c3ibgF	Alignment	not modelled	99.2	13	PDB header: hydrolase Chain: F: PDB Molecule: atpase, subunit of the get complex; PDBTitle: crystal structure of aspergillus fumigatus get3 with bound2 adp
64	c4dzzB	Alignment	not modelled	99.2	15	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
65	c3ez6B	Alignment	not modelled	99.1	9	PDB header: dna binding protein Chain: B: PDB Molecule: plasmid partition protein a; PDBTitle: structure of para-adp complex:tetragonal form
66	c5bwkA	Alignment	not modelled	99.1	11	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
67	c3io3A	Alignment	not modelled	99.1	14	PDB header: chaperone Chain: A: PDB Molecule: deha2d07832p; PDBTitle: get3 with adp from d. hansenii in closed form
68	c2qy9A	Alignment	not modelled	99.1	15	PDB header: protein transport Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the ng+1 construct of the e. coli srp receptor2 ftsy
69	c3dm5A	Alignment	not modelled	99.1	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 assembling the2 ribonucleic core of the signal recognition particle from the archaeon3 pyrococcus furiosus.
70	c1zu4A	Alignment	not modelled	99.0	12	PDB header: protein transport Chain: A: PDB Molecule: ftsy; PDBTitle: crystal structure of ftsy from mycoplasma mycoides-space2 group p21212
71	c3igfB	Alignment	not modelled	99.0	16	PDB header: atp binding protein Chain: B: PDB Molecule: all4481 protein; PDBTitle: crystal structure of the all4481 protein from nostoc sp. pcc 7120,2 northeast structural genomics consortium target nsr300
72	c3pg5A	Alignment	not modelled	99.0	17	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
73	c2q9cA	Alignment	not modelled	99.0	14	PDB header: signaling protein Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of ftsy:gmpnp with mgcl complex
74	c5l3rC	Alignment	not modelled	99.0	13	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
75	c2j37W	Alignment	not modelled	99.0	12	PDB header: ribosome Chain: W: PDB Molecule: signal recognition particle 54 kda protein (srp54); PDBTitle: model of mammalian srp bound to 80s rncs
76	c1vmaA	Alignment	not modelled	99.0	14	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
77	c2og2A	Alignment	not modelled	99.0	15	PDB header: protein transport Chain: A: PDB Molecule: putative signal recognition particle receptor; PDBTitle: crystal structure of chloroplast ftsy from arabidopsis2 thaliana
78	c3cwqB	Alignment	not modelled	98.9	12	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
						PDB header: protein transport

79	c5l3sF_	Alignment	not modelled	98.9	12	Chain: F; PDB Molecule: signal recognition particle receptor ftsy; PDBTitle: structure of the gtpase heterodimer of crenarchaeal srp54 and ftsy
80	c2iy3A_	Alignment	not modelled	98.9	15	PDB header: rna-binding Chain: A; PDB Molecule: signal recognition particle protein,signal recognition PDBTitle: structure of the e. coli signal recognition particle
81	c2cnwF_	Alignment	not modelled	98.9	17	PDB header: signal recognition Chain: F; PDB Molecule: cell division protein ftsy; PDBTitle: gdpalf4 complex of the srp gtpases ffh and ftsy
82	c2j7pA_	Alignment	not modelled	98.9	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
83	c2yhsA_	Alignment	not modelled	98.9	15	PDB header: cell cycle Chain: A; PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
84	c6cy1B_	Alignment	not modelled	98.8	16	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
85	c3dmdA_	Alignment	not modelled	98.8	14	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
86	c5gafi_	Alignment	not modelled	98.8	18	PDB header: ribosome Chain: I; PDB Molecule: 50s ribosomal protein l10; PDBTitle: rnc in complex with srp
87	c3b9gA_	Alignment	not modelled	98.8	16	PDB header: protein transport Chain: A; PDB Molecule: chloroplast srp receptor homolog, alpha subunit PDBTitle: the crystal structure of cpftsyl from arabidopsis thaliana
88	c2v3cC_	Alignment	not modelled	98.8	11	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
89	c3ezfA_	Alignment	not modelled	98.8	10	PDB header: biosynthetic protein Chain: A; PDB Molecule: para; PDBTitle: partition protein
90	c1qzwC_	Alignment	not modelled	98.8	17	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
91	c4ak9A_	Alignment	not modelled	98.7	15	PDB header: protein transport Chain: A; PDB Molecule: cpftsyl; PDBTitle: structure of chloroplast ftsy from physcomitrella patens
92	c4jqpA_	Alignment	not modelled	98.6	19	PDB header: oxidoreductase Chain: A; PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase; PDBTitle: x-ray crystal structure of a 4-hydroxythreonine-4-phosphate2 dehydrogenase from burkholderia phymatum
93	c2j289_	Alignment	not modelled	98.6	15	PDB header: ribosome Chain: 9; PDB Molecule: signal recognition particle 54; PDBTitle: model of e. coli srp bound to 70s rncs
94	c4atyA_	Alignment	not modelled	98.6	16	PDB header: oxidoreductase Chain: A; PDB Molecule: terephthalate 1,2-cis-dihydrodiol dehydrogenase; PDBTitle: crystal structure of a terephthalate 1,2-cis-2 dihydrodioldehydrogenase from burkholderia xenovorans3 lb400
95	c2obnA_	Alignment	not modelled	98.3	13	PDB header: unknown function Chain: A; PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1611 family protein (ava_3511) from anaerobaculum variabilis atcc 29413 at 2.30 a resolution
96	c2hi1A_	Alignment	not modelled	98.1	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase 2; PDBTitle: the structure of a putative 4-hydroxythreonine-4-phosphate2 dehydrogenase from salmonella typhimurium.
97	c4nkrB_	Alignment	not modelled	98.1	12	PDB header: unknown function Chain: B; PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis protein b; PDBTitle: the crystal structure of bacillus subtilis mobb
98	c2px0D_	Alignment	not modelled	98.1	12	PDB header: biosynthetic protein Chain: D; PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
99	d1j8yf2	Alignment	not modelled	97.9	12	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
100	d1xjca_	Alignment	not modelled	97.8	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
101	c2f1rA_	Alignment	not modelled	97.7	13	PDB header: biosynthetic protein Chain: A; PDB Molecule: molybdopterin-guanine dinucleotide biosynthesis PDBTitle: crystal structure of molybdopterin-guanine biosynthesis2 protein b (mobb)
102	c4xc8B_	Alignment	not modelled	97.7	13	PDB header: isomerase Chain: B; PDB Molecule: isobutyryl-coa mutase fused; PDBTitle: isobutyryl-coa mutase fused with bound butyryl-coa, gdp, and mg and2 without cobalamin (apo-icmf/gdp)
103	d2g0ta1	Alignment	not modelled	97.7	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
104	c3hwwD_	Alignment	not modelled	97.7	16	PDB header: replication Chain: D; PDB Molecule: dnab-like replicative helicase;

104	c3ugwD_	Alignment	not modelled	97.7	10	PDBTitle: the structure of a dnab-like replicative helicase and its interactions2 with primase
105	d1mo6a1	Alignment	not modelled	97.6	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
106	c1nijA_	Alignment	not modelled	97.6	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yjia; PDBTitle: yjia protein
107	d1ubea1	Alignment	not modelled	97.6	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
108	c3tsnD_	Alignment	not modelled	97.6	14	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxythreonine-4-phosphate dehydrogenase; PDBTitle: 4-hydroxythreonine-4-phosphate dehydrogenase from campylobacter jejuni
109	c2recB_	Alignment	not modelled	97.6	14	PDB header: helicase PDB COMPND:
110	c1j8yF_	Alignment	not modelled	97.6	14	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
111	d1nija1	Alignment	not modelled	97.5	11	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
112	c5hcnA_	Alignment	not modelled	97.5	13	PDB header: hydrolase Chain: A: PDB Molecule: gpn-loop gtpase 1; PDBTitle: gpn-loop gtpase npa3 in complex with gmppcp
113	c2q6tB_	Alignment	not modelled	97.5	16	PDB header: hydrolase Chain: B: PDB Molecule: dnab replication fork helicase; PDBTitle: crystal structure of the thermus aquaticus dnab monomer
114	c1xp8A_	Alignment	not modelled	97.4	18	PDB header: dna binding protein Chain: A: PDB Molecule: reca protein; PDBTitle: deinococcus radiodurans reca in complex with atp-gamma-s
115	d1u94a1	Alignment	not modelled	97.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
116	c3bh0A_	Alignment	not modelled	97.4	15	PDB header: replication Chain: A: PDB Molecule: dnab-like replicative helicase; PDBTitle: atpase domain of g40p
117	d1xp8a1	Alignment	not modelled	97.3	20	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
118	c2i1vB_	Alignment	not modelled	97.3	15	PDB header: transferase, hydrolase Chain: B: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6- PDBTitle: crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
119	c6qe1B_	Alignment	not modelled	97.3	13	PDB header: replication Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: e. coli dnabc apo complex
120	c4a1fB_	Alignment	not modelled	97.3	11	PDB header: hydrolase Chain: B: PDB Molecule: replicative dna helicase; PDBTitle: crystal structure of c-terminal domain of helicobacter2 pylori dnab helicase