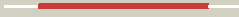























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0115_(hddA)_138511_139671
Date	Tue Jul 23 14:50:15 BST 2019
Unique Job ID	27fcc975065da71c

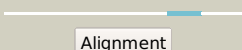
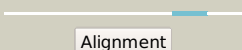
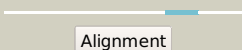
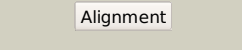
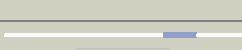
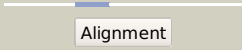
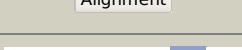
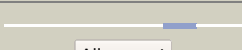

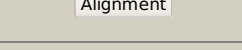
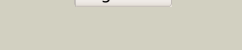

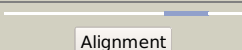
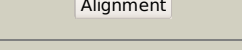
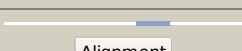
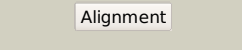
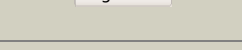

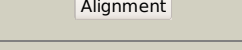

Detailed template information


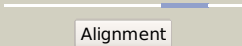

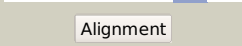
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1	c4ut4B_	 Alignment		100.0	48	PDB header: transferase Chain: B: PDB Molecule: putative sugar kinase; PDBTitle: burkholderia pseudomallei heptokinase wcbl, d-mannose complex.
2	c5yysC_	 Alignment		100.0	24	PDB header: transferase Chain: C: PDB Molecule: l-fucokinase, l-fucose-1-p guanylyltransferase; PDBTitle: cryo-em structure of l-fucokinase, gdp-fucose pyrophosphorylase (fkp)2 in bacteroides fragilis
3	c4n3oB_	 Alignment		100.0	39	PDB header: transferase Chain: B: PDB Molecule: putative d-glycero-d-manno-heptose 7-phosphate kinase; PDBTitle: 2.4 angstrom resolution crystal structure of putative sugar kinase2 from campylobacter jejuni.
4	c3k85B_	 Alignment		100.0	44	PDB header: transferase Chain: B: PDB Molecule: d-glycero-d-manno-heptose 1-phosphate kinase; PDBTitle: crystal structure of a d-glycero-d-manno-heptose 1-phosphate2 kinase from bacteriodes thetaiotaomicron
5	c1wuua_	 Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: galactokinase; PDBTitle: crystal structure of human galactokinase complexed with2 mgampnp and galactose
6	c1pieA_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: galactokinase; PDBTitle: crystal structure of lactococcus lactis galactokinase2 complexed with galactose
7	c2a2cA_	 Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: n-acetylgalactosamine kinase; PDBTitle: x-ray structure of human n-acetyl galactosamine kinase2 complexed with mg- adp and n-acetyl galactosamine 1-3 phosphate
8	c2cz9A_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: probable galactokinase; PDBTitle: crystal structure of galactokinase from pyrococcus horikoshi
9	c2aj4B_	 Alignment		100.0	24	PDB header: transferase Chain: B: PDB Molecule: galactokinase; PDBTitle: crystal structure of saccharomyces cerevisiae galactokinase2 in complex with galactose and mg:ampnp
10	c2r42A_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: the biochemical and structural basis for feedback2 inhibition of mevalonate kinase and isoprenoid metabolism
11	c3v2uC_	 Alignment		100.0	21	PDB header: transcription Chain: C: PDB Molecule: protein gal3; PDBTitle: crystal structure of the yeast gal regulon complex of the repressor,2 gal80p, and the transducer, gal3p, with galactose and atp

12	c3k17A_	Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: lin0012 protein; PDBTitle: crystal structure of a lin0012 protein from listeria innocua
13	c4hacA_	Alignment		100.0	24	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: crystal structure of the mevalonate kinase from an archaeon2 methanosarcina maezi
14	c2hfuB_	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: mevalonate kinase, putative; PDBTitle: crystal structure of l. major mevalonate kinase in complex2 with r-mevalonate
15	c1kkhA_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: crystal structure of the methanococcus jannaschii2 mevalonate kinase
16	c1k47F_	Alignment		100.0	18	PDB header: transferase Chain: F: PDB Molecule: phosphomevalonate kinase; PDBTitle: crystal structure of the streptococcus pneumoniae2 phosphomevalonate kinase (pmk)
17	c2oi2A_	Alignment		100.0	17	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: streptococcus pneumoniae mevalonate kinase in complex with2 diphosphomevalonate
18	c2x7iA_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: mevalonate kinase; PDBTitle: crystal structure of mevalonate kinase from methicillin-2 resistant staphylococcus aureus mrsa252
19	c4rpfA_	Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: crystal structure of homoserine kinase from yersinia pestis nepal516,2 nysgrc target 032715
20	c3pygA_	Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: 4-diphosphocytidyl-2-c-methyl-d-erythritol kinase; PDBTitle: mycobacterium tuberculosis 4-diphosphocytidyl-2-c-methyl-d-erythritol2 kinase (ispe) in complex with adp
21	c4p52A_	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: crystal structure of homoserine kinase from cytophaga hutchinsonii2 atcc 33406, nysgrc target 032717.
22	c1fwID_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: D: PDB Molecule: homoserine kinase; PDBTitle: crystal structure of homoserine kinase
23	c4z7cA_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: diphosphomevalonate decarboxylase from the sulfobolus solfataricus,2 space group h32
24	c2hk3A_	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: crystal structure of mevalonate diphosphate decarboxylase2 from staphylococcus aureus (orthorhombic form)
25	d1piea1	Alignment	not modelled	100.0	18	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
26	c5v2IA_	Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: mevalonate diphosphate decarboxylase; PDBTitle: mevalonate diphosphate mediated atp binding mechanism of the2 mevalonate diphosphate decarboxylase from enterococcus faecalis
27	c3hulA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: structure of putative homoserine kinase thrb from listeria2 monocytogenes
28	c6n0yB_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: crystal structure of anaerolinea thermophila mevalonate 5-phosphate2 decarboxylase complexed with (r)-mvapp

29	c2gs8A	Alignment	not modelled	100.0	13	PDB header: lyase Chain: A: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: structure of mevalonate pyrophosphate decarboxylase from streptococcus2 pyogenes
30	d1wuua1	Alignment	not modelled	100.0	19	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
31	c6cyzA	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: homoserine kinase; PDBTitle: mycobacterial homoserine kinase thrb in complex with amppnp
32	c5watB	Alignment	not modelled	100.0	17	PDB header: transferase Chain: B: PDB Molecule: homoserine kinase; PDBTitle: corynebacterium glutamicum full length homoserine kinase
33	d1kkha1	Alignment	not modelled	100.0	18	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
34	c2v34B	Alignment	not modelled	100.0	19	PDB header: transferase Chain: B: PDB Molecule: 4-diphosphocytidyl-2c-methyl-d-erythritol kinase; PDBTitle: ispe in complex with cytidine and ligand
35	d1kvka1	Alignment	not modelled	100.0	24	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
36	d1s4ea1	Alignment	not modelled	100.0	24	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
37	c1uekA	Alignment	not modelled	100.0	19	PDB header: transferase Chain: A: PDB Molecule: 4-(cytidine 5'-diphospho)-2c-methyl-d-erythritol PDBTitle: crystal structure of 4-(cytidine 5'-diphospho)-2c-methyl-d-2 erythritol kinase
38	c1oj4B	Alignment	not modelled	100.0	21	PDB header: transferase Chain: B: PDB Molecule: 4-diphosphocytidyl-2-c-methyl-d-erythritol PDBTitle: ternary complex of 2 4-diphosphocytidyl-2-c-methyl-d-erythritol kinase
39	d1k47a1	Alignment	not modelled	100.0	18	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
40	d1h72c1	Alignment	not modelled	100.0	24	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
41	c3ltoB	Alignment	not modelled	100.0	12	PDB header: lyase Chain: B: PDB Molecule: mevalonate diphosphate decarboxylase; PDBTitle: crystal structure of a mevalonate diphosphate decarboxylase2 from legionella pneumophila
42	d1kvka2	Alignment	not modelled	99.9	19	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate kinase
43	d1k47a2	Alignment	not modelled	99.9	18	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Phosphomevalonate kinase (PMK)
44	d1kkha2	Alignment	not modelled	99.9	17	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate kinase
45	d1wuua2	Alignment	not modelled	99.9	18	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase
46	d1s4ea2	Alignment	not modelled	99.9	27	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase
47	d1piea2	Alignment	not modelled	99.9	17	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Galactokinase
48	d1oj4a1	Alignment	not modelled	99.8	20	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
49	c2hkeB	Alignment	not modelled	99.8	15	PDB header: lyase Chain: B: PDB Molecule: diphosphomevalonate decarboxylase, putative; PDBTitle: mevalonate diphosphate decarboxylase from trypanosoma brucei
50	c1fi4A	Alignment	not modelled	99.7	15	PDB header: lyase Chain: A: PDB Molecule: mevalonate 5-diphosphate decarboxylase; PDBTitle: the x-ray crystal structure of mevalonate 5-diphosphate decarboxylase2 at 2.3 angstrom resolution.
51	c6n10A	Alignment	not modelled	99.7	17	PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase mvd1, peroxisomal; PDBTitle: crystal structure of arabidopsis thaliana mevalonate 5-diphosphate2 decarboxylase 1 complexed with (r)-mvapp
52	d1ueka1	Alignment	not modelled	99.6	21	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
53	d1fi4a1	Alignment	not modelled	99.6	19	Fold: Ribosomal protein S5 domain 2-like Superfamily: Ribosomal protein S5 domain 2-like Family: GHMP Kinase, N-terminal domain
54	c4rksB	Alignment	not modelled	99.4	12	PDB header: transferase Chain: B: PDB Molecule: putative uncharacterized protein ta1305; PDBTitle: crystal structure of mevalonate-3-kinase from thermoplasma acidophilum2 (mevalonate bound)

55	c3f0nB	Alignment	not modelled	99.3	15	PDB header: lyase Chain: B: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: mus musculus mevalonate pyrophosphate decarboxylase
56	d1h72c2	Alignment	not modelled	98.8	14	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Homoserine kinase
57	d1ueka2	Alignment	not modelled	97.4	20	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: 4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
58	d1oj4a2	Alignment	not modelled	94.5	11	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: 4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
59	d1fi4a2	Alignment	not modelled	86.3	10	Fold: Ferredoxin-like Superfamily: GHMP Kinase, C-terminal domain Family: Mevalonate 5-diphosphate decarboxylase
60	d1kona	Alignment	not modelled	81.5	17	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
61	c3m05A	Alignment	not modelled	80.4	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pepe_1480; PDBTitle: the crystal structure of a functionally unknown protein pepe_1480 from2 pediococcus pentosaceus atcc 25745
62	d3c7bb2	Alignment	not modelled	79.9	14	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
63	c4rwwB	Alignment	not modelled	77.8	18	PDB header: protein binding Chain: B: PDB Molecule: lmo2692 protein; PDBTitle: crystal structure of l. monocytogenes psta in complex with cyclic-di-2 amp
64	c4f3qA	Alignment	not modelled	71.2	10	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulatory protein cbu_1566; PDBTitle: structure of a yebc family protein (cbu_1566) from coxiella burnetii
65	d1zj8a1	Alignment	not modelled	70.6	8	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
66	d1lfpa	Alignment	not modelled	65.8	25	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
67	d2g5ca1	Alignment	not modelled	61.6	13	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
68	c4wk1A	Alignment	not modelled	60.7	22	PDB header: signaling protein Chain: A: PDB Molecule: psta; PDBTitle: crystal structure of staphylococcus aureus psta in complex with c-di-2 amp
69	d2v4jb2	Alignment	not modelled	55.0	14	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
70	c2v36A	Alignment	not modelled	48.0	28	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase large chain; PDBTitle: crystal structure of gamma-glutamyl transferase from bacillus subtilis
71	c4gdxA	Alignment	not modelled	45.0	25	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase 1 heavy chain; PDBTitle: crystal structure of human gamma-glutamyl transpeptidase--glutamate2 complex
72	c2y9jt	Alignment	not modelled	44.8	11	PDB header: protein transport Chain: T: PDB Molecule: protein prgh; PDBTitle: three-dimensional model of salmonella's needle complex at subnanometer2 resolution
73	d2f1ka1	Alignment	not modelled	41.1	8	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: TyrA dimerization domain-like
74	c2qm6C	Alignment	not modelled	40.8	23	PDB header: transferase Chain: C: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of helicobacter pylori gamma-glutamyltranspeptidase2 in complex with glutamate
75	c2v4jE	Alignment	not modelled	40.0	13	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrC provides3 novel insights into the mechanism of sulfate respiration
76	d1nc7a	Alignment	not modelled	39.8	33	Fold: Hypothetical protein TM1070 Superfamily: Hypothetical protein TM1070 Family: Hypothetical protein TM1070
77	c3c7bE	Alignment	not modelled	39.5	7	PDB header: oxidoreductase Chain: E: PDB Molecule: sulfite reductase, dissimilatory-type subunit beta; PDBTitle: structure of the dissimilatory sulfite reductase from archaeoglobus2 fulgidus
78	c4rleA	Alignment	not modelled	38.4	14	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein yaaq; PDBTitle: crystal structure of the c-di-amp binding pii-like protein dara
79	c2ii8F	Alignment	not modelled	38.3	38	PDB header: signaling protein Chain: F: PDB Molecule: anabaena sensory rhodopsin transducer protein; PDBTitle: anabaena sensory rhodopsin transducer

80	c4y23A_		Alignment	not modelled	34.7	28	PDB header: transferase Chain: A: PDB Molecule: gamma glutamyl transpeptidase,gamma-glutamyltranspeptidase; PDBTitle: crystal structure of t399a precursor mutant protein of gamma-glutamyl2 transpeptidase from bacillus licheniformis
81	c6bwqB_		Alignment	not modelled	32.2	7	PDB header: metal binding protein Chain: B: PDB Molecule: pyridinium-3,5-bisthiocarboxylic acid mononucleotide nickel PDBTitle: larc2, the c-terminal domain of a cyclometallase involved in the2 synthesis of the npn cofactor of lactate racemase, in complex with3 mnctp
82	c2z8jA_		Alignment	not modelled	31.2	20	PDB header: transferase Chain: A: PDB Molecule: gamma-glutamyltranspeptidase; PDBTitle: crystal structure of escherichia coli gamma-glutamyltranspeptidase in2 complex with azaserine prepared in the dark
83	d2cz4a1		Alignment	not modelled	30.4	17	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
84	c3mnfA_		Alignment	not modelled	29.1	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pac2 family protein; PDBTitle: crystal structure of pac2 family protein from streptomyces avermitilis2 ma
85	d2nlza1		Alignment	not modelled	28.4	20	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Gamma-glutamyltranspeptidase-like
86	c3vr0D_		Alignment	not modelled	27.9	22	PDB header: protein binding Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of pyrococcus furiosus pbab, an archaeal proteasome2 activator
87	d1ztpa1		Alignment	not modelled	26.2	18	Fold: eIF4e-like Superfamily: eIF4e-like Family: BLES03-like
88	c1yj7A_		Alignment	not modelled	25.8	14	PDB header: protein transport Chain: A: PDB Molecule: escj; PDBTitle: crystal structure of enteropathogenic e.coli (epec) type iii secretion2 system protein escj
89	c5zjgC_		Alignment	not modelled	24.8	23	PDB header: transferase Chain: C: PDB Molecule: gamma-glutamyltransferase 1 threonine peptidase. merops PDBTitle: gamma-glutamyltranspeptidase from pseudomonas nitroreducens complexed2 with gly-gly
90	c2yxzA_		Alignment	not modelled	24.8	13	PDB header: transferase Chain: A: PDB Molecule: thiamin-monophosphate kinase; PDBTitle: crystal structure of tt0281 from thermus thermophilus hb8
91	c3g9kD_		Alignment	not modelled	24.6	31	PDB header: hydrolase Chain: D: PDB Molecule: capsule biosynthesis protein capd; PDBTitle: crystal structure of bacillus anthracis transpeptidase enzyme capd
92	c2v4jA_		Alignment	not modelled	24.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfite reductase, dissimilatory-type subunit PDBTitle: the crystal structure of desulfovibrio vulgaris2 dissimilatory sulfite reductase bound to dsrc provides3 novel insights into the mechanism of sulfate respiration
93	d1qy7a_		Alignment	not modelled	23.9	20	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
94	c5h92A_		Alignment	not modelled	23.6	9	PDB header: oxidoreductase/electron transport Chain: A: PDB Molecule: sulfite reductase [ferredoxin], chloroplastic; PDBTitle: crystal structure of the complex between maize sulfite reductase and2 ferredoxin in the form-3 crystal
95	d1vfja_		Alignment	not modelled	23.5	13	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
96	d1zhva2		Alignment	not modelled	23.5	21	Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like
97	c2p90B_		Alignment	not modelled	23.3	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein cg1923; PDBTitle: the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
98	c3ggpA_		Alignment	not modelled	23.0	11	PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
99	d1txna_		Alignment	not modelled	22.8	33	Fold: Coproporphyrinogen III oxidase Superfamily: Coproporphyrinogen III oxidase Family: Coproporphyrinogen III oxidase
100	c2wamB_		Alignment	not modelled	22.3	19	PDB header: unknown function Chain: B: PDB Molecule: conserved hypothetical alanine and leucine rich PDBTitle: crystal structure of mycobacterium tuberculosis unknown2 function protein rv2714
101	d1mw7a_		Alignment	not modelled	22.3	10	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
102	d1aopa2		Alignment	not modelled	22.1	7	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
103	d1tkla_		Alignment	not modelled	21.1	33	Fold: Coproporphyrinogen III oxidase Superfamily: Coproporphyrinogen III oxidase Family: Coproporphyrinogen III oxidase PDB header: apoptosis

104	c5un02_	 Alignment	not modelled	21.0	15	Chain: 2; PDB Molecule: proteasome assembly chaperone 2 (pac2) homologue rv2125; PDB Fragment: unp residues 17-260; PDB Title: crystal structure of mycobacterium tuberculosis proteasome-assembly2 chaperone homologue rv2125
105	c3bzqA_	 Alignment	not modelled	20.6	22	PDB header: signaling protein/transcription Chain: A; PDB Molecule: nitrogen regulatory protein p-ii; PDB Title: high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis
106	d1x4aa1	 Alignment	not modelled	20.4	16	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
107	d1ul3a_	 Alignment	not modelled	20.1	21	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein