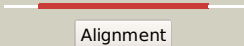

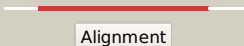

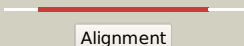







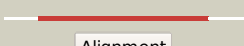











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3218 (-)_3594465_3595430
Date	Thu Aug 8 16:20:41 BST 2019
Unique Job ID	36fc378c0d45f9d3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qv7A_	 Alignment		100.0	19	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase dgkb; PDBTitle: crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
2	d2qv7a1	 Alignment		100.0	19	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
3	c3s40C_	 Alignment		100.0	21	PDB header: transferase Chain: C: PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
4	d2bona1	 Alignment		100.0	22	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
5	c3vzdB_	 Alignment		100.0	20	PDB header: transferase/inhibitor Chain: B: PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
6	c4werA_	 Alignment		100.0	21	PDB header: transferase Chain: A: PDB Molecule: diacylglycerol kinase catalytic domain protein; PDBTitle: crystal structure of diacylglycerol kinase catalytic domain protein2 from enterococcus faecalis v583
7	c2bonB_	 Alignment		100.0	22	PDB header: transferase Chain: B: PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
8	d2p1ra1	 Alignment		100.0	20	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
9	d2jgra1	 Alignment		100.0	22	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
10	d1u0ta_	 Alignment		99.5	16	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
11	c1yt5A_	 Alignment		99.4	15	PDB header: transferase Chain: A: PDB Molecule: inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of nad kinase from thermotoga maritima

12	c2an1D_	Alignment		98.6	15	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim It2
13	c1z0zC_	Alignment		98.6	13	PDB header: transferase Chain: C: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of a nad kinase from archaeoglobus2 fulgidus in complex with nad
14	d1z0sa1	Alignment		98.5	13	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
15	c2i2aA_	Alignment		98.3	11	PDB header: transferase Chain: A: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase 1; PDBTitle: crystal structure of lmnadk1 from listeria monocytogenes
16	c3afoB_	Alignment		98.3	18	PDB header: transferase Chain: B: PDB Molecule: nadh kinase pos5; PDBTitle: crystal structure of yeast nadh kinase complexed with nadh
17	c3pfnB_	Alignment		97.7	17	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
18	c6c2uA_	Alignment		96.6	21	PDB header: de novo protein Chain: A: PDB Molecule: phosphate-loop protein; PDBTitle: solution structure of a phosphate-loop protein
19	d1vlja_	Alignment		95.3	13	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
20	c5eksB_	Alignment		94.8	13	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: structure of 3-dehydroquinase synthase from acinetobacter baumannii in2 complex with nad
21	c4p53A_	Alignment	not modelled	94.8	19	PDB header: lyase Chain: A: PDB Molecule: cyclase; PDBTitle: vala (2-epi-5-epi-valiolone synthase) from streptomyces hygrosopicus2 subsp. jinggansensis 5008 with nad+ and zn2+ bound
22	c5zxlD_	Alignment	not modelled	94.7	15	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of glda from e.coli
23	d1jq5a_	Alignment	not modelled	94.0	13	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
24	d1o2da_	Alignment	not modelled	93.8	19	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
25	c3zokB_	Alignment	not modelled	93.7	14	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: structure of 3-dehydroquinase synthase from actinidia chinensis in2 complex with nad
26	c3qbeA_	Alignment	not modelled	93.5	11	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of the 3-dehydroquinase synthase (arob) from2 mycobacterium tuberculosis
27	c3okfA_	Alignment	not modelled	93.5	12	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: 2.5 angstrom resolution crystal structure of 3-dehydroquinase synthase2 (arob) from vibrio cholerae
28	c4mcaB_	Alignment	not modelled	93.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from serratia to 1.9a

29	c3ce9A	Alignment	not modelled	92.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
30	c4fr2A	Alignment	not modelled	92.9	16	PDB header: oxidoreductase, metal binding protein Chain: A: PDB Molecule: 1,3-propanediol dehydrogenase; PDBTitle: alcohol dehydrogenase from oenococcus oeni
31	c3ox4D	Alignment	not modelled	92.7	11	PDB header: oxidoreductase Chain: D: PDB Molecule: alcohol dehydrogenase 2; PDBTitle: structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
32	c3uhjE	Alignment	not modelled	92.7	17	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
33	c5tprB	Alignment	not modelled	92.5	18	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: desmethyl-4-deoxygadusol synthase from anabaena variabilis (ava_3858)2 with nad+ and zn2+ bound
34	d1rrma	Alignment	not modelled	92.1	12	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
35	c3trhl	Alignment	not modelled	91.8	13	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
36	c6csjD	Alignment	not modelled	91.5	19	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of a bacillus coagulans polyol dehydrogenase double mutant2 with an acquired d-lactate dehydrogenase activity
37	c3opyG	Alignment	not modelled	91.5	12	PDB header: transferase Chain: G: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
38	c1ta9A	Alignment	not modelled	91.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
39	c5yvmA	Alignment	not modelled	91.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: crystal structure of the archaeal halo-thermophilic red sea brine pool2 alcohol dehydrogenase adh/d1 bound to nzq
40	c3opyE	Alignment	not modelled	90.9	9	PDB header: transferase Chain: E: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
41	c3bfjK	Alignment	not modelled	90.7	16	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
42	c4yccC	Alignment	not modelled	89.8	13	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)
43	c6c5cA	Alignment	not modelled	89.8	15	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of aro1p from candida albicans sc5314 in complex2 with nadh
44	c3orsD	Alignment	not modelled	89.8	12	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
45	d1oj7a	Alignment	not modelled	89.6	11	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
46	c3qvjB	Alignment	not modelled	88.6	20	PDB header: isomerase Chain: B: PDB Molecule: putative hydantoin racemase; PDBTitle: allantoin racemase from klebsiella pneumoniae
47	c3zdrA	Alignment	not modelled	87.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase domain of the bifunctional PDBTitle: structure of the alcohol dehydrogenase (adh) domain of a2 bifunctional adhe dehydrogenase from geobacillus3 thermoglucosidasius ncimb 11955
48	c3iv7B	Alignment	not modelled	87.4	16	PDB header: oxidoreductase Chain: B: PDB Molecule: alcohol dehydrogenase iv; PDBTitle: crystal structure of iron-containing alcohol dehydrogenase2 (np_602249.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.07 a resolution
49	c6c76A	Alignment	not modelled	87.4	17	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: structure of iron containing alcohol dehydrogenase from thermococcus2 thioreducens in an orthorhombic crystal form
50	c3opyH	Alignment	not modelled	87.2	13	PDB header: transferase Chain: H: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
51	c3opyB	Alignment	not modelled	87.2	13	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructo-1-kinase beta-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
52	d1kq3a	Alignment	not modelled	87.0	18	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
53	c3clhA	Alignment	not modelled	86.9	15	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of 3-dehydroquinase synthase (dhqs)from2 helicobacter pylori

54	c1zxxA	Alignment	not modelled	86.9	24	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii
55	c3o8oC	Alignment	not modelled	86.8	11	PDB header: transferase Chain: C: PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
56	c3lcmB	Alignment	not modelled	86.5	10	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of smu.1420 from streptococcus mutans ua159
57	d1xmpa	Alignment	not modelled	85.6	19	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
58	d2a9va1	Alignment	not modelled	85.5	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
59	c4b4kK	Alignment	not modelled	85.4	19	PDB header: isomerase Chain: K: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of bacillus anthracis pure
60	c3rf7A	Alignment	not modelled	85.2	18	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of an iron-containing alcohol dehydrogenase2 (sden_2133) from shewanella denitrificans os-217 at 2.12 a resolution
61	c2higA	Alignment	not modelled	84.5	21	PDB header: transferase Chain: A: PDB Molecule: 6-phospho-1-fructokinase; PDBTitle: crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
62	c2fqxA	Alignment	not modelled	84.0	8	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
63	d1mkza	Alignment	not modelled	83.5	18	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
64	d2f48a1	Alignment	not modelled	83.4	22	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
65	c5xoeA	Alignment	not modelled	83.4	21	PDB header: transferase Chain: A: PDB Molecule: atp-dependent 6-phosphofructokinase; PDBTitle: crystal structure of the apo staphylococcus aureus phosphofructokinase
66	d1pfka	Alignment	not modelled	83.2	21	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
67	c4dzzB	Alignment	not modelled	83.0	19	PDB header: unknown function Chain: B: PDB Molecule: plasmid partitioning protein parf; PDBTitle: structure of parf-adp, crystal form 1
68	d4pfka	Alignment	not modelled	83.0	22	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
69	c3o8oB	Alignment	not modelled	82.2	12	PDB header: transferase Chain: B: PDB Molecule: 6-phosphofructokinase subunit beta; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
70	c5hvnA	Alignment	not modelled	81.5	13	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinate synthase; PDBTitle: 3.0 angstrom crystal structure of 3-dehydroquinate synthase (arob)2 from francisella tularensis in complex with nad.
71	d1o1ya	Alignment	not modelled	81.4	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
72	d2nqra3	Alignment	not modelled	81.4	21	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
73	c3o8nA	Alignment	not modelled	81.4	16	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
74	c4e5sC	Alignment	not modelled	81.1	16	PDB header: hydrolase Chain: C: PDB Molecule: mccflike protein (ba_5613); PDBTitle: crystal structure of mccflike protein (ba_5613) from bacillus2 anthracis str. ames
75	d1zl0a2	Alignment	not modelled	80.8	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
76	c3hl0B	Alignment	not modelled	80.7	24	PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
77	d2c4va1	Alignment	not modelled	80.7	20	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinate dehydratase Family: Type II 3-dehydroquinate dehydratase
78	c3jzdA	Alignment	not modelled	79.6	22	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-containing alcohol dehydrogenase; PDBTitle: crystal structure of putative alcohol dehydrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
79	c6jkdD	Alignment	not modelled	79.3	16	PDB header: oxidoreductase Chain: D: PDB Molecule: methanol dehydrogenase; PDBTitle: crystal structure of sulfoacetaldehyde reductase from bifidobacterium2 kashiwanohense in complex with nad+

80	c2iv3B_	Alignment	not modelled	79.2	20	PDB header: transferase Chain: B: PDB Molecule: glycosyltransferase; PDBTitle: crystal structure of avigt4, a glycosyltransferase involved2 in avilamycin a biosynthesis
81	c6d9tA_	Alignment	not modelled	78.6	12	PDB header: transferase Chain: A: PDB Molecule: glycosyl transferase; PDBTitle: bsha from staphylococcus aureus complexed with udp
82	d1ydga_	Alignment	not modelled	78.1	2	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
83	c4p5pA_	Alignment	not modelled	78.0	12	PDB header: hydrolase Chain: A: PDB Molecule: thij/pfpi family protein; PDBTitle: x-ray structure of francisella tularensis rapid encystment protein 242 kda (rep24), gene product of ftn_0841
84	c5z6vA_	Alignment	not modelled	77.7	14	PDB header: protein transport Chain: A: PDB Molecule: abc-type uncharacterized transport system periplasmic PDBTitle: crystal structure of a substrate-binding protein from rhodothermus2 marinus
85	c4grdA_	Alignment	not modelled	76.9	15	PDB header: lyase, isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
86	c3k2qA_	Alignment	not modelled	76.6	17	PDB header: transferase Chain: A: PDB Molecule: pyrophosphate-dependent phosphofructokinase; PDBTitle: crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
87	c1zrsB_	Alignment	not modelled	76.0	14	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein; PDBTitle: wild-type ld-carboxypeptidase
88	c1sy7B_	Alignment	not modelled	75.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase 1; PDBTitle: crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
89	c3tlgB_	Alignment	not modelled	73.9	15	PDB header: hydrolase Chain: B: PDB Molecule: mccf; PDBTitle: microcin c7 self immunity protein mccf in the inactive mutant apo2 state
90	d2g2ca1	Alignment	not modelled	73.9	20	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
91	d2auna2	Alignment	not modelled	73.5	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
92	c2ywjA_	Alignment	not modelled	73.1	11	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
93	c2ejbA_	Alignment	not modelled	72.8	21	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
94	c3l7nA_	Alignment	not modelled	72.6	23	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
95	c2gejA_	Alignment	not modelled	72.0	10	PDB header: transferase Chain: A: PDB Molecule: phosphatidylinositol mannosyltransferase (pima); PDBTitle: crystal structure of phosphatidylinositol mannosyltransferase (pima)2 from mycobacterium smegmatis in complex with gdp-man
96	d1gpma2	Alignment	not modelled	71.6	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
97	c5vegC_	Alignment	not modelled	71.2	11	PDB header: electron transport Chain: C: PDB Molecule: flavodoxin; PDBTitle: structure of a short-chain flavodoxin associated with a non-canonical2 pdu bacterial microcompartment
98	c5widB_	Alignment	not modelled	70.6	11	PDB header: flavoprotein Chain: B: PDB Molecule: flavodoxin; PDBTitle: structure of a flavodoxin from the domain archaea
99	c2yyaB_	Alignment	not modelled	70.3	18	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
100	d1vhqa_	Alignment	not modelled	69.7	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
101	c1rcuB_	Alignment	not modelled	69.2	31	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein vt76; PDBTitle: x-ray structure of tm1055 northeast structural genomics2 consortium target vt76
102	d1rcua_	Alignment	not modelled	69.2	31	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
103	c3lp6D_	Alignment	not modelled	68.9	25	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
104	c3kkIA_	Alignment	not modelled	68.7	10	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2

						saccharomyces cerevisiae
105	c4h1hB_	Alignment	not modelled	68.2	12	PDB header: hydrolase Chain: B: PDB Molecule: lmo1638 protein; PDBTitle: crystal structure of mccf homolog from listeria monocytogenes egd-e
106	d1qcza_	Alignment	not modelled	67.5	18	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
107	c3u7rB_	Alignment	not modelled	67.5	14	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh-dependent fmn reductase; PDBTitle: ferb - flavoenzyme nad(p)h:(acceptor) oxidoreductase (ferb) from2 paracoccus denitrificans
108	d1jija_	Alignment	not modelled	67.4	12	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
109	d1p80a1	Alignment	not modelled	67.1	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
110	c5f4bB_	Alignment	not modelled	67.0	6	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: structure of b. abortus wrba-related protein a (wrpa)
111	c6cv6L_	Alignment	not modelled	66.9	27	PDB header: lyase Chain: L: PDB Molecule: 3-dehydroquininate dehydratase; PDBTitle: crystal structure of 3-dehydroquininate dehydratase, type ii, from2 burkholderia phymatum stm815
112	c5fb3C_	Alignment	not modelled	66.8	21	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerophosphate dehydrogenase in complex with nadph
113	c2xd4A_	Alignment	not modelled	66.4	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycylamide2 ribonucleotide synthetase
114	c3l3bA_	Alignment	not modelled	66.0	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: es1 family protein; PDBTitle: crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
115	d1s3ia2	Alignment	not modelled	65.6	16	Fold: Formyltransferase Superfamily: Formyltransferase Family: Formyltransferase
116	c4e94A_	Alignment	not modelled	65.5	21	PDB header: hydrolase Chain: A: PDB Molecule: mccc family protein; PDBTitle: crystal structure of mccf-like protein from streptococcus pneumoniae
117	c2jimH_	Alignment	not modelled	65.1	13	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from bacillus2 anthracis orf ba1558.
118	c3gjzB_	Alignment	not modelled	64.9	15	PDB header: immune system Chain: B: PDB Molecule: microcin immunity protein mccf; PDBTitle: crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
119	d1rtta_	Alignment	not modelled	64.1	7	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: NADPH-dependent FMN reductase
120	d1wl8a1	Alignment	not modelled	63.8	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)