
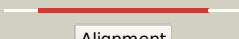











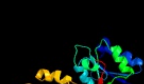



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2252_(-)_2526999_2527928
Date	Mon Aug 5 13:25:39 BST 2019
Unique Job ID	cc0d9d8587e60a30

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2qv7A_	 Alignment		100.0	23	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	24	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
3	c3s40C_	 Alignment		100.0	23	PDB header: transferase Chain: C; PDB Molecule: diacylglycerol kinase; PDBTitle: the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
4	c3vzdB_	 Alignment		100.0	23	PDB header: transferase/inhibitor Chain: B; PDB Molecule: sphingosine kinase 1; PDBTitle: crystal structure of sphingosine kinase 1 with inhibitor and adp
5	c4werA_	 Alignment		100.0	28	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
6	d2bona1	 Alignment		100.0	26	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
7	d2p1ra1	 Alignment		100.0	24	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
8	c2bonB_	 Alignment		100.0	28	PDB header: transferase Chain: B; PDB Molecule: lipid kinase; PDBTitle: structure of an escherichia coli lipid kinase (yegs)
9	d2jgra1	 Alignment		100.0	29	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: Diacylglycerol kinase-like
10	d1u0ta_	 Alignment		99.6	18	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
11	c1yt5A_	 Alignment		99.4	17	PDB header: transferase Chain: A; PDB Molecule: inorganic polyphosphate/atp-nad kinase; PDBTitle: crystal structure of nad kinase from thermotoga maritima

12	c2an1D_	Alignment		99.2	19	PDB header: transferase Chain: D: PDB Molecule: putative kinase; PDBTitle: structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
13	dlz0sa1	Alignment		98.7	16	Fold: NAD kinase/diacylglycerol kinase-like Superfamily: NAD kinase/diacylglycerol kinase-like Family: NAD kinase-like
14	c1z0zC_	Alignment		98.7	17	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
15	c2i2aA_	Alignment		98.6	13	PDB header: transferase Chain: A: PDB Molecule: probable inorganic polyphosphate/atp-nad kinase 1; PDBTitle: crystal structure of lmnadk1 from listeria monocytogenes
16	c3pfnB_	Alignment		98.5	17	PDB header: transferase Chain: B: PDB Molecule: nad kinase; PDBTitle: crystal structure of human nad kinase
17	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
18	c3ox4D_	Alignment		97.4	18	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
19	d1vlja_	Alignment		97.4	26	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Iron-containing alcohol dehydrogenase
20	c3okfA_	Alignment		97.3	18	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
21	c4p53A_	Alignment	not modelled	97.2	19	PDB header: lyase Chain: A: PDB Molecule: cyclase; PDBTitle: vala (2-epi-5-epi-valiolone synthase) from streptomyces hygrosopicus2 subsp. jinggangensis 5008 with nad+ and zn2+ bound
22	c5zxlD_	Alignment	not modelled	97.2	18	PDB header: oxidoreductase Chain: D: PDB Molecule: glycerol dehydrogenase; PDBTitle: structure of glda from e.coli
23	c3qbeA_	Alignment	not modelled	97.2	22	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: crystal structure of the 3-dehydroquinase synthase (arob) from2 mycobacterium tuberculosis
24	c3zokB_	Alignment	not modelled	97.2	18	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: structure of 3-dehydroquinase synthase from actinidia chinensis in2 complex with nad
25	c3bfjK_	Alignment	not modelled	97.1	20	PDB header: oxidoreductase Chain: K: PDB Molecule: 1,3-propanediol oxidoreductase; PDBTitle: crystal structure analysis of 1,3-propanediol oxidoreductase
26	c3ce9A_	Alignment	not modelled	97.0	14	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
27	c1ta9A_	Alignment	not modelled	97.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
28	c1zxxA_	Alignment	not modelled	96.9	24	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase; PDBTitle: the crystal structure of phosphofructokinase from lactobacillus2 delbrueckii

29	d1jq5a_	Alignment	not modelled	96.9	19	Fold: Dehydroquininate synthase-like Superfamily: Dehydroquininate synthase-like Family: Iron-containing alcohol dehydrogenase
30	d1rrma_	Alignment	not modelled	96.8	16	Fold: Dehydroquininate synthase-like Superfamily: Dehydroquininate synthase-like Family: Iron-containing alcohol dehydrogenase
31	c5tpRB_	Alignment	not modelled	96.7	13	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquininate synthase; PDBTitle: desmethyl-4-deoxygadusol synthase from anabaena variabilis (ava_3858)2 with nad+ and zn2+ bound
32	c5eksB_	Alignment	not modelled	96.6	18	PDB header: lyase Chain: B: PDB Molecule: 3-dehydroquininate synthase; PDBTitle: structure of 3-dehydroquininate synthase from acinetobacter baumannii n2 complex with nad
33	c6c76A_	Alignment	not modelled	96.6	26	PDB header: oxidoreductase Chain: A: PDB Molecule: alcohol dehydrogenase; PDBTitle: structure of iron containing alcohol dehydrogenase from thermococcus2 thioreducens in an orthorhombic crystal form
34	c5yvmA_	Alignment	not modelled	96.5	20	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
35	c4fr2A_	Alignment	not modelled	96.4	20	PDB header: oxidoreductase, metal binding protein Chain: A: PDB Molecule: 1,3-propanediol dehydrogenase; PDBTitle: alcohol dehydrogenase from oenococcus oeni
36	c5z6vA_	Alignment	not modelled	96.3	7	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
37	d1o2da_	Alignment	not modelled	96.3	14	Fold: Dehydroquininate synthase-like Superfamily: Dehydroquininate synthase-like Family: Iron-containing alcohol dehydrogenase
38	c4mcaB_	Alignment	not modelled	96.2	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol dehydrogenase; PDBTitle: crystal structure of glycerol dehydrogenase from serratia to 1.9a
39	c3zdrA_	Alignment	not modelled	96.0	19	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
40	c4irxA_	Alignment	not modelled	95.8	17	PDB header: transport protein Chain: A: PDB Molecule: sugar abc transporter, periplasmic sugar-binding protein; PDBTitle: crystal structure of caulobacter myo-inositol binding protein bound to2 myo-inositol
41	d4pfka_	Alignment	not modelled	95.6	26	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
42	c3clhA_	Alignment	not modelled	95.6	23	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquininate synthase; PDBTitle: crystal structure of 3-dehydroquininate synthase (dhqs)from2 helicobacter pylori
43	c2gruB_	Alignment	not modelled	95.3	17	PDB header: lyase Chain: B: PDB Molecule: 2-deoxy-scylo-inosose synthase; PDBTitle: crystal structure of 2-deoxy-scylo-inosose synthase2 complexed with carbaglucoase-6-phosphate, nad+ and co2+
44	c5xoeA_	Alignment	not modelled	95.3	21	PDB header: transferase Chain: A: PDB Molecule: atp-dependent 6-phosphofructokinase; PDBTitle: crystal structure of the apo staphylococcus aureus phosphofructokinase
45	d1pfka_	Alignment	not modelled	95.3	28	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
46	d1oj7a_	Alignment	not modelled	95.2	20	Fold: Dehydroquininate synthase-like Superfamily: Dehydroquininate synthase-like Family: Iron-containing alcohol dehydrogenase
47	c6c5cA_	Alignment	not modelled	95.1	10	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquininate synthase; PDBTitle: crystal structure of aro1p from candida albicans sc5314 in complex2 with nadh
48	c6jkpD_	Alignment	not modelled	95.1	16	PDB header: oxidoreductase Chain: D: PDB Molecule: methanol dehydrogenase; PDBTitle: crystal structure of sulfoacetaldehyde reductase from bifidobacterium2 kashiwanohense in complex with nad+
49	c3rf7A_	Alignment	not modelled	94.9	19	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
50	c3uhjE_	Alignment	not modelled	94.9	17	PDB header: oxidoreductase Chain: E: PDB Molecule: probable glycerol dehydrogenase; PDBTitle: crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
51	d1kq3a_	Alignment	not modelled	94.8	17	Fold: Dehydroquininate synthase-like Superfamily: Dehydroquininate synthase-like Family: Iron-containing alcohol dehydrogenase
52	c6csjD_	Alignment	not modelled	94.8	13	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
53	c3orsD_	Alignment	not modelled	94.7	13	PDB header: isomerase,biosynthetic protein Chain: D: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole

						ribonucleotide mutase2 from staphylococcus aureus PDB header: oxidoreductase
54	c3jzdA_	Alignment	not modelled	94.4	20	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
55	c3o1hB_	Alignment	not modelled	94.4	17	PDB header: signaling protein Chain: B: PDB Molecule: periplasmic protein tort; PDBTitle: crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
56	d1sg6a_	Alignment	not modelled	94.3	14	Fold: Dehydroquinase synthase-like Superfamily: Dehydroquinase synthase-like Family: Dehydroquinase synthase, DHQS
57	c4lruA_	Alignment	not modelled	94.3	17	PDB header: lyase Chain: A: PDB Molecule: glyoxalase iii (glutathione-independent); PDBTitle: crystal structure of glyoxalase iii (orf 19.251) from candida albicans
58	c5hvnA_	Alignment	not modelled	94.2	20	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinase synthase; PDBTitle: 3.0 angstrom crystal structure of 3-dehydroquinase synthase (arob)2 from francisella tularensis in complex with nad.
59	c6cv6L_	Alignment	not modelled	94.1	20	PDB header: lyase Chain: L: PDB Molecule: 3-dehydroquinase dehydratase; PDBTitle: crystal structure of 3-dehydroquinase dehydratase, type ii, from2 burkholderia phymatum stm815
60	c6c2uA_	Alignment	not modelled	94.0	18	PDB header: de novo protein Chain: A: PDB Molecule: phosphate-loop protein; PDBTitle: solution structure of a phosphate-loop protein
61	c3hl0B_	Alignment	not modelled	93.7	21	PDB header: oxidoreductase Chain: B: PDB Molecule: maleylacetate reductase; PDBTitle: crystal structure of maleylacetate reductase from agrobacterium2 tumefaciens
62	d1o4va_	Alignment	not modelled	93.6	13	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
63	d1u11a_	Alignment	not modelled	93.4	10	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
64	d1vhqa_	Alignment	not modelled	93.4	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
65	c2ejbA_	Alignment	not modelled	93.4	10	PDB header: lyase Chain: A: PDB Molecule: probable aromatic acid decarboxylase; PDBTitle: crystal structure of phenylacrylic acid decarboxylase from2 aquifex aeolicus
66	c2fw9A_	Alignment	not modelled	93.4	10	PDB header: lyase Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
67	c6o55B_	Alignment	not modelled	93.4	11	PDB header: isomerase Chain: B: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 (pure) from legionella pneumophila
68	c3lp6D_	Alignment	not modelled	93.1	15	PDB header: lyase Chain: D: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
69	c4yccC_	Alignment	not modelled	93.1	11	PDB header: hydrolase Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of putative lipoprotein from peptoclostridium2 difficile 630 (fragment)
70	c3iv7B_	Alignment	not modelled	92.9	18	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
71	c4p5pA_	Alignment	not modelled	92.7	16	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
72	d1qcza_	Alignment	not modelled	92.5	15	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
73	d1xmpa_	Alignment	not modelled	92.5	11	Fold: Flavodoxin-like Superfamily: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) Family: N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
74	c4kzkA_	Alignment	not modelled	92.4	11	PDB header: sugar binding protein Chain: A: PDB Molecule: l-arabinose abc transporter, periplasmic l-arabinose- PDBTitle: the structure of the periplasmic l-arabinose binding protein from2 burkholderia thailandensis
75	c4grdA_	Alignment	not modelled	92.3	16	PDB header: lyase,isomerase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase catalytic subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from burkholderia cenocepacia j2315
76	d1p80a1	Alignment	not modelled	92.1	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain

77	c3opyH	Alignment	not modelled	91.8	23	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
78	c3opyB	Alignment	not modelled	91.8	23	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
79	c4yhsA	Alignment	not modelled	91.4	19	PDB header: solute-binding protein Chain: A: PDB Molecule: monosaccharide abc transporter substrate-binding protein, PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from bradyrhizobium sp. btai1 (bbta_2440, target efi-3 511490) with bound bis-tris
80	c4b4kK	Alignment	not modelled	91.2	11	PDB header: isomerase Chain: K: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide mutase; PDBTitle: crystal structure of bacillus anthracis pure
81	c4kqcA	Alignment	not modelled	91.1	21	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: abc transporter, laci family transcriptional regulator from2 brachyspira murdochii
82	c3opyE	Alignment	not modelled	91.0	18	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
83	c3opyG	Alignment	not modelled	91.0	18	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
84	c3trhl	Alignment	not modelled	90.9	16	PDB header: lyase Chain: I: PDB Molecule: phosphoribosylaminoimidazole carboxylase PDBTitle: structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
85	c1sy7B	Alignment	not modelled	90.8	17	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.
86	d2f48a1	Alignment	not modelled	90.8	19	Fold: Phosphofructokinase Superfamily: Phosphofructokinase Family: Phosphofructokinase
87	c4rxuA	Alignment	not modelled	90.6	15	PDB header: transport protein Chain: A: PDB Molecule: periplasmic sugar-binding protein; PDBTitle: crystal structure of carbohydrate transporter solute binding protein2 caur_1924 from chloroflexus aurantiacus, target efi-511158, in3 complex with d-glucose
88	c5dkvD	Alignment	not modelled	90.6	19	PDB header: sugar binding protein Chain: D: PDB Molecule: abc transporter substrate binding protein (ribose); PDBTitle: crystal structure of an abc transporter solute binding protein from2 agrobacterium vitis(avis_5339, target efi-511225) bound with alpha-d-3 tagatopyranose
89	d1vmea1	Alignment	not modelled	90.6	25	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
90	c1xahA	Alignment	not modelled	90.3	12	PDB header: lyase Chain: A: PDB Molecule: 3-dehydroquinate synthase; PDBTitle: crystal structure of staphylococcus aureus 3-dehydroquinate2 synthase (dhqs) in complex with zn2+ and nad+
91	c3k2qA	Alignment	not modelled	90.0	20	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
92	c2higA	Alignment	not modelled	89.8	25	PDB header: transferase Chain: A: PDB Molecule: 6-phospho-1-fructokinase; PDBTitle: crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
93	d1ycga1	Alignment	not modelled	89.8	17	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
94	c2fqxA	Alignment	not modelled	89.8	11	PDB header: transport protein Chain: A: PDB Molecule: membrane lipoprotein tmpc; PDBTitle: pnra from treponema pallidum complexed with guanosine
95	c3h5oB	Alignment	not modelled	89.8	20	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator gntr; PDBTitle: the crystal structure of transcription regulator gntr from2 chromobacterium violaceum
96	c3o8nA	Alignment	not modelled	89.1	16	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
97	c6ndiB	Alignment	not modelled	88.6	8	PDB header: sugar binding protein Chain: B: PDB Molecule: transcriptional regulator; PDBTitle: 2.60 angstrom resolution crystal structure of periplasmic binding and2 sugar binding domain of laci family protein from klebsiella3 pneumoniae.
98	d1uqra	Alignment	not modelled	88.4	14	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinate dehydratase Family: Type II 3-dehydroquinate dehydratase
99	c5fb3C	Alignment	not modelled	88.3	24	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-1-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerophosphate dehydrogenase in complex with nadph PDB header: unknown function Chain: A: PDB Molecule: 3-dehydroquinate dehydratase, type ii;

100	c3u80A_	Alignment	not modelled	88.3	17	PDBTitle: 1.60 angstrom resolution crystal structure of a 3-dehydroquinase 2 dehydratase-like protein from bifidobacterium longum
101	c3o8oC_	Alignment	not modelled	88.3	21	PDB header: transferase Chain: C: PDB Molecule: 6-phosphofructokinase subunit alpha; PDBTitle: structure of phosphofructokinase from saccharomyces cerevisiae
102	c3ej6D_	Alignment	not modelled	88.2	26	PDB header: oxidoreductase Chain: D: PDB Molecule: catalase-3; PDBTitle: neurospora crassa catalase-3 crystal structure
103	c3uugB_	Alignment	not modelled	88.2	18	PDB header: sugar binding protein Chain: B: PDB Molecule: multiple sugar-binding periplasmic receptor chve; PDBTitle: crystal structure of the periplasmic sugar binding protein chve
104	d2a5la1	Alignment	not modelled	88.2	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
105	c3fniA_	Alignment	not modelled	88.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: putative diflavin flavoprotein a 3; PDBTitle: crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
106	c5f4bB_	Alignment	not modelled	87.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: nad(p)h dehydrogenase (quinone); PDBTitle: structure of b. abortus wrba-related protein a (wrpa)
107	d1qvwa_	Alignment	not modelled	87.7	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
108	c3k9cA_	Alignment	not modelled	87.6	11	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator, lacI family protein; PDBTitle: crystal structure of lacI transcriptional regulator from rhodococcus2 species.
109	c5dteD_	Alignment	not modelled	87.4	22	PDB header: transport protein Chain: D: PDB Molecule: monosaccharide-transporting atpase; PDBTitle: crystal structure of an abc transporter periplasmic solute binding2 protein (ipr025997) from actinobacillus succinogenes 130z(asuc_0081,3 target efi-511065) with bound d-allose
110	d1jx6a_	Alignment	not modelled	87.3	11	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
111	d1mkza_	Alignment	not modelled	87.1	24	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
112	c4ry8D_	Alignment	not modelled	87.1	11	PDB header: transport protein Chain: D: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of 5-methylthioribose transporter solute binding2 protein tlet_1677 from thermotoga lettingae tmo target efi-511109 in3 complex with 5-methylthioribose
113	c6dspB_	Alignment	not modelled	86.9	22	PDB header: signaling protein Chain: B: PDB Molecule: autoinducer 2-binding protein lsrb; PDBTitle: lsrb from clostridium saccharobutylicum in complex with ai-2
114	d1ydga_	Alignment	not modelled	86.9	20	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like
115	c3c5yD_	Alignment	not modelled	86.8	17	PDB header: isomerase Chain: D: PDB Molecule: ribose/galactose isomerase; PDBTitle: crystal structure of a putative ribose 5-phosphate isomerase2 (saro_3514) from novosphingobium aromaticivorans dsm at 1.81 a3 resolution
116	c3qjgD_	Alignment	not modelled	86.8	16	PDB header: oxidoreductase Chain: D: PDB Molecule: epidermin biosynthesis protein epid; PDBTitle: epidermin biosynthesis protein epid from staphylococcus aureus
117	d1b1ca_	Alignment	not modelled	86.8	16	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Cytochrome p450 reductase N-terminal domain-like
118	c5ulbA_	Alignment	not modelled	86.1	12	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar abc transporter; PDBTitle: crystal structure of sugar abc transporter from yersinia2 enterocolitica subsp. enterocolitica 8081
119	d1ydha_	Alignment	not modelled	85.9	28	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
120	d1e5da1	Alignment	not modelled	85.8	18	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related