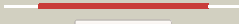



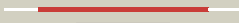

















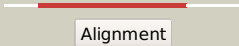

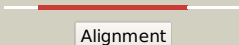

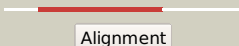



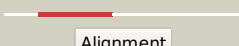



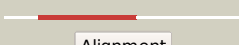







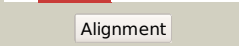
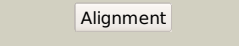
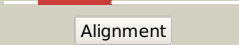





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1294_(thrA)_1449381_1450706
Date	Wed Jul 31 22:05:39 BST 2019
Unique Job ID	1147241e5ff51fbc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6dzsD_	 Alignment		100.0	86	PDB header: oxidoreductase Chain: D: PDB Molecule: homoserine dehydrogenase; PDBTitle: mycobacterial homoserine dehydrogenase thra in complex with nadp
2	c3mtjA_	 Alignment		100.0	38	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
3	c4pg8B_	 Alignment		100.0	38	PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of s. aureus homoserine dehydrogenase at ph8.5
4	c2ejwB_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: B: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase from thermus thermophilus hb8
5	c3do5A_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
6	c3c8mA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
7	c3ingA_	 Alignment		100.0	26	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution
8	c4xb1B_	 Alignment		100.0	31	PDB header: oxidoreductase Chain: B: PDB Molecule: 319aa long hypothetical homoserine dehydrogenase; PDBTitle: hyperthermophilic archaeal homoserine dehydrogenase in complex with2 nadph
9	c1ebuA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: homoserine dehydrogenase complex with nad analogue and l-2 homoserine
10	c5avoA_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: crystal structure of the reduced form of homoserine dehydrogenase from2 sulfolobus tokodaii.
11	d1ebfa2	 Alignment		100.0	26	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: Homoserine dehydrogenase-like

12	c6iauB_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: amine dehydrogenase; PDBTitle: amine dehydrogenase from cystobacter fuscus in complex with nadp+ and2 cyclohexylamine
13	c6iaqA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase n-terminus domain-containing PDBTitle: structure of amine dehydrogenase from mycobacterium smegmatis
14	c3upyB_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the brucella abortus enzyme catalyzing the first2 committed step of the methylerythritol 4-phosphate pathway.
15	c6g1mA_	 Alignment		99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: amine dehydrogenase from petrotoga mobilis; open and closed form
16	d1ebfa1	 Alignment		99.9	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
17	c2jcyA_	 Alignment		99.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: x-ray structure of mutant 1-deoxy-d-xylulose 5-phosphate2 reductoisomerase, dxr, rv2870c, from mycobacterium tuberculosis
18	c2eghA_	 Alignment		99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase2 complexed with a magnesium ion, nadph and fosmidomycin
19	c1r0ID_	 Alignment		99.8	22	PDB header: oxidoreductase Chain: D: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from zymomonas mobilis2 in complex with nadph
20	c3a14B_	 Alignment		99.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of dxr from thermotoga maritima, in complex with2 nadph
21	c5yabD_	 Alignment	not modelled	99.7	24	PDB header: oxidoreductase Chain: D: PDB Molecule: scyllo-inositol dehydrogenase with l-glucose dehydrogenase PDBTitle: crystal structure of scyllo-inositol dehydrogenase with l-glucose2 dehydrogenase activity
22	c6a3fB_	 Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative dehydrogenase; PDBTitle: levoglucosan dehydrogenase, apo form
23	c2ixaA_	 Alignment	not modelled	99.7	13	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylgalactosaminidase; PDBTitle: a-zyme, n-acetylgalactosaminidase
24	c3e18A_	 Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
25	c4gqaC_	 Alignment	not modelled	99.7	21	PDB header: oxidoreductase Chain: C: PDB Molecule: nad binding oxidoreductase; PDBTitle: crystal structure of nad binding oxidoreductase from klebsiella2 pneumoniae
26	c1lc3A_	 Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: biliverdin reductase a; PDBTitle: crystal structure of a biliverdin reductase enzyme-cofactor2 complex
27	c3fd8A_	 Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
28	c3evnA_	 Alignment	not modelled	99.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r

29	c2dc1A	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
30	c3fh1C	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: C: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
31	c3ceaA	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: myo-inositol 2-dehydrogenase; PDBTitle: crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
32	c4fb5A	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of a probable oxidoreductase protein
33	c1zh8B	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
34	c3e9mC	Alignment	not modelled	99.7	24	PDB header: oxidoreductase Chain: C: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from enterococcus2 faecalis
35	c2q4eB	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: probable oxidoreductase at4g09670; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
36	c3kuxA	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the ypo2259 putative oxidoreductase from yersinia pestis
37	c1ofgF	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: F: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: glucose-fructose oxidoreductase
38	c3ec7C	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
39	c1h6dL	Alignment	not modelled	99.7	14	PDB header: protein translocation Chain: L: PDB Molecule: precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
40	c3e82A	Alignment	not modelled	99.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
41	c3gfgB	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
42	c5uibA	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase protein; PDBTitle: crystal structure of an oxidoreductase from agrobacterium radiobacter2 in complex with nad+, l-tartaric acid and magnesium
43	c3dtyA	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of an oxidoreductase from pseudomonas2 syringae
44	d1q0qa2	Alignment	not modelled	99.7	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
45	d1r0ka2	Alignment	not modelled	99.7	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
46	c3m2tA	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of dehydrogenase from chromobacterium2 violaceum
47	c4h3vA	Alignment	not modelled	99.7	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: oxidoreductase domain protein; PDBTitle: crystal structure of oxidoreductase domain protein from kribbella2 flavida
48	c2o48X	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: X: PDB Molecule: dimeric dihydrodiol dehydrogenase; PDBTitle: crystal structure of mammalian dimeric dihydrodiol dehydrogenase
49	c3euwB	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
50	c4mkzA	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol dehydrogenase; PDBTitle: crystal structure of apo scyllo-inositol dehydrogenase from2 lactobacillus casei at 77k
51	c3db2C	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
52	c5b3uB	Alignment	not modelled	99.7	18	PDB header: transferase Chain: B: PDB Molecule: biliverdin reductase; PDBTitle: crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
53	c3c1aB	Alignment	not modelled	99.7	23	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution

54	c3moiA	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
55	c2ho3D	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
56	d1j5pa4	Alignment	not modelled	99.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
57	c4hktA	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: A: PDB Molecule: inositol 2-dehydrogenase; PDBTitle: crystal structure of a putative myo-inositol dehydrogenase from2 sinorhizobium meliloti 1021 (target psi-012312)
58	c4hadD	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: D: PDB Molecule: probable oxidoreductase protein; PDBTitle: crystal structure of probable oxidoreductase protein from rhizobium2 etli cfn 42
59	c3ezyB	Alignment	not modelled	99.6	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: dehydrogenase; PDBTitle: crystal structure of probable dehydrogenase tm_0414 from thermotoga2 maritima
60	c6norB	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nad dependent dehydrogenase; PDBTitle: crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
61	c3v5nA	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of oxidoreductase from sinorhizobium meliloti
62	c3nt5B	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; PDBTitle: crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
63	c6jnkA	Alignment	not modelled	99.6	19	PDB header: oxidoreductase Chain: A: PDB Molecule: l-arabinose 1-dehydrogenase (nad(p)(+)); PDBTitle: crystal structure of azospirillum brasilense l-arabinose 1-2 dehydrogenase (nadp-bound form)
64	c3q2kB	Alignment	not modelled	99.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcna
65	c5a06E	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: E: PDB Molecule: aldose-aldose oxidoreductase; PDBTitle: crystal structure of aldose-aldose oxidoreductase from2 caulobacter crescentus complexed with sorbitol
66	c2nvwB	Alignment	not modelled	99.6	14	PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal scture of transcriptional regulator gal80p from2 kluveromyces lactis
67	c3f4IF	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: F: PDB Molecule: putative oxidoreductase yhhx; PDBTitle: crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
68	c3rbvA	Alignment	not modelled	99.6	22	PDB header: sugar binding protein Chain: A: PDB Molecule: sugar 3-ketoreductase; PDBTitle: crystal structure of kjid10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
69	c2qlxD	Alignment	not modelled	99.6	21	PDB header: oxidoreductase Chain: D: PDB Molecule: 1,5-anhydro-d-fructose reductase; PDBTitle: crystal structure analysis of bacterial 1,5-af reductase
70	c4ew6A	Alignment	not modelled	99.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: d-galactose-1-dehydrogenase protein; PDBTitle: crystal structure of d-galactose-1-dehydrogenase protein from2 rhizobium etli
71	d2nvwa1	Alignment	not modelled	99.6	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
72	c1j5pA	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: aspartate dehydrogenase; PDBTitle: crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
73	c3oqbF	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: F: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
74	d1h6da1	Alignment	not modelled	99.6	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
75	c4gmfD	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: D: PDB Molecule: yersiniabactin biosynthetic protein ybtu; PDBTitle: apo structure of a thiazoliny imine reductase from yersinia2 enterocolitica (irp3)
76	c3btuD	Alignment	not modelled	99.6	16	PDB header: transcription Chain: D: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
77	c1evjC	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose-fructose oxidoreductase; PDBTitle: crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
78	c3u3xl	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: J: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from

						sinorhizobium2 melloti 1021 PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
79	c2p2sA	Alignment	not modelled	99.6	15	
80	d1ydw1	Alignment	not modelled	99.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
81	c3wycB	Alignment	not modelled	99.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: meso-diaminopimelate d-dehydrogenase; PDBTitle: structure of a meso-diaminopimelate dehydrogenase in complex with nadp
82	d1zh8a1	Alignment	not modelled	99.5	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
83	c4miyB	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; PDBTitle: crystal structure of myo-inositol dehydrogenase from lactobacillus2 casei in complex with nad and myo-inositol
84	c1xeaD	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
85	c3ip3D	Alignment	not modelled	99.5	13	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, putative; PDBTitle: structure of putative oxidoreductase (tm_0425) from thermotoga2 maritima
86	c3uuwB	Alignment	not modelled	99.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase with nad(p)-binding rossmann-fold PDBTitle: 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
87	d1ryda1	Alignment	not modelled	99.5	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
88	d1f06a1	Alignment	not modelled	99.4	23	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
89	c3dapB	Alignment	not modelled	99.4	19	PDB header: oxidoreductase Chain: B: PDB Molecule: diaminopimelic acid dehydrogenase; PDBTitle: c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
90	d1lc0a1	Alignment	not modelled	99.4	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
91	c3wb9A	Alignment	not modelled	99.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: diaminopimelate dehydrogenase; PDBTitle: crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum
92	d1tita1	Alignment	not modelled	99.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
93	c3wgzB	Alignment	not modelled	99.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: meso-diaminopimelate dehydrogenase; PDBTitle: crystal structure of meso-dapdh q154l/t173l/r199m/p248s/h249n/n276s2 mutant with d-leucine of from clostridium tetani e88
94	c5ugjC	Alignment	not modelled	99.3	21	PDB header: oxidoreductase Chain: C: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of htpa reductase from neisseria meningitidis
95	c3bioB	Alignment	not modelled	99.3	18	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase, gfo/idh/moca family; PDBTitle: crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
96	c5kt0A	Alignment	not modelled	99.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anaabaena variabilis.
97	c1titB	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase (virulence factor mvim homolog); PDBTitle: crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
98	c3oa0B	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: lipopolysaccharide biosynthesis protein wbbp; PDBTitle: crystal structure of the wlba (wbbp) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glcna
99	c3oa2B	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: wbbp; PDBTitle: crystal structure of the wlba (wbbp) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
100	c5z2fA	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: nadph/pda bound dihydrodipicolinate reductase from paenisporsarcina2 sp. tg-14
101	d1xeea1	Alignment	not modelled	99.3	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
						PDB header: oxidoreductase

102	c1drwA_	Alignment	not modelled	99.2	16	Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: escherichia coli dhpr/nhdh complex
103	c4f3yA_	Alignment	not modelled	99.1	22	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis
104	d2nu7a1	Alignment	not modelled	99.1	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
105	d1oi7a1	Alignment	not modelled	99.1	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
106	c5tenH_	Alignment	not modelled	99.1	17	PDB header: oxidoreductase Chain: H: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag
107	c2axqA_	Alignment	not modelled	99.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
108	c3au9A_	Alignment	not modelled	99.0	19	PDB header: isomerase/isomerase inhibitor Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: crystal structure of the quaternary complex-1 of an isomerase
109	c5kqoA_	Alignment	not modelled	99.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose 5-phosphate reductoisomerase from vibrio vulnificus
110	c4zn6B_	Alignment	not modelled	99.0	28	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose 5-phosphate reductoisomerase; PDBTitle: x-ray crystal structure of 1-deoxy-d-xylulose 5-phosphate reductoisomerase (ispc) from acinetobacter baumannii
111	c1k5hB_	Alignment	not modelled	99.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: 1-deoxy-d-xylulose-5-phosphate reductoisomerase; PDBTitle: 1-deoxy-d-xylulose-5-phosphate reductoisomerase
112	c5I78A_	Alignment	not modelled	99.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-aminoadipic semialdehyde synthase, mitochondrial; PDBTitle: crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)
113	c4oo3A_	Alignment	not modelled	98.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a putative oxidoreductase (parmer_00841) from2 parabacteroides merdae atcc 43184 at 2.23 a resolution
114	d2dt5a2	Alignment	not modelled	98.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Transcriptional repressor Rex, C-terminal domain
115	c1e5IA_	Alignment	not modelled	98.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
116	c2z2vA_	Alignment	not modelled	98.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1688; PDBTitle: crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
117	c4ywjB_	Alignment	not modelled	98.8	22	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa
118	c5wolA_	Alignment	not modelled	98.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-tetrahydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase dapb from coxiella2 burnetii
119	d1euca1	Alignment	not modelled	98.7	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
120	c3ijpA_	Alignment	not modelled	98.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrodipicolinate reductase; PDBTitle: crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution