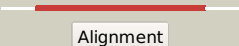



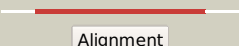





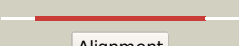













Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0751c_(mmsB)_842350_843234
Date	Fri Jul 26 01:50:33 BST 2019
Unique Job ID	d84090b97115fbd0

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cumA_	 Alignment		100.0	44	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
2	c5y8mA_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthibadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba)
3	c1vpdA_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
4	c4dlIB_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-hydroxy-3-oxopropionate reductase; PDBTitle: crystal structure of a 2-hydroxy-3-oxopropionate reductase from2 polaromonas sp. js666
5	c1yb4A_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronic semialdehyde reductase; PDBTitle: crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
6	c2cvzD_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8
7	c3ckyA_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-hydroxymethyl glutarate dehydrogenase; PDBTitle: structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
8	c4gjbB_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase nad-binding; PDBTitle: crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans
9	c2gf2B_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase
10	c3w6uA_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, nad-binding protein; PDBTitle: crystal structure of nadp bound l-serine 3-dehydrogenase from2 hyperthermophilic archaeon pyrobaculum calidifontis
11	c3dojA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis (atglyr1)

12	c5u5gC_	Alignment		100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: psf3 in complex with nadp+ and 2-opp
13	c5je8A_	Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: the crystal structure of bacillus cereus 3-hydroxyisobutyrate2 dehydrogenase in complex with nad
14	c3g0aA_	Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
15	c3pduF_	Alignment		100.0	31	PDB header: oxidoreductase Chain: F: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase family protein; PDBTitle: crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+
16	c4e21B_	Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase (decarboxylating); PDBTitle: the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens
17	c3pefA_	Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, nad-binding; PDBTitle: crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+
18	c3l6dB_	Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
19	c2uyyD_	Alignment		100.0	26	PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac
20	c5g6sD_	Alignment		100.0	14	PDB header: oxidoreductase Chain: D: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus oryzae in complex with nadp(h) and2 (r)-rasagiline
21	c4d3fB_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: imine reductase; PDBTitle: bcslred from bacillus cereus in complex with nadph
22	c5ocmA_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nad_gly3p_dh, nad-dependent glycerol-3-phosphate PDBTitle: imine reductase from streptosporangium roseum in complex with nadp+2 and 2,2,2-trifluoroacetophenone hydrate
23	c4d3sA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: imine reductase; PDBTitle: imine reductase from nocardioptis halophila
24	c5a9tA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dehydrogenase; PDBTitle: imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisoquinoline
25	c6grlA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: beta-hydroxyacid dehydrogenase, 3-hydroxyisobutyrate PDBTitle: structure of imine reductase (apo form) at 1.6 a resolution from2 saccharomonospora xinjiangensis
26	c3qhaB_	Alignment	not modelled	100.0	30	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
27	c5ojlA_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: imine reductase; PDBTitle: imine reductase from aspergillus terreus in complex with nadph4 and2 dibenz[c,e]azepine
28	c4oqzA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase yfjr; PDBTitle: streptomyces aurantiacus imine reductase

29	c4ezbA	Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of the conserved hypothetical protein from <i>Sinorhizobium meliloti</i> 1021
30	c2p4qA	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of <i>gnd1</i> in <i>Saccharomyces cerevisiae</i>
31	c4oqyA	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: (s)-imine reductase; PDBTitle: streptomyces sp. gf3546 imine reductase
32	c3zbcC	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: r-imine reductase; PDBTitle: r-imine reductase from streptomyces kanamyceticus in 2 complex with nadp.
33	c6fqzB	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: plasmodium falciparum 6-phosphogluconate dehydrogenase in its apo2 form, in complex with its cofactor nadp+ and in complex with its3 substrate 6-phosphogluconate
34	c3fwnB	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
35	c2iz1C	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
36	c1pgqA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase (choh(d)-nadp+(a)) Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
37	c1pgiA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
38	c4wb1B	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: cals8; PDBTitle: crystal structure of <i>cals8</i> from <i>Micromonospora echinospora</i> (p294s2 mutant)
39	c3vtfA	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaeon <i>Pyrobaculum islandicum</i>
40	c3qsgA	Alignment	not modelled	100.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-binding phosphogluconate dehydrogenase-like protein; PDBTitle: crystal structure of nad-binding phosphogluconate dehydrogenase-like2 protein from <i>Alicyclobacillus acidocaldarius</i>
41	c1mv8A	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: gdp-mannose 6-dehydrogenase; PDBTitle: 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from <i>Pseudomonas aeruginosa</i>
42	c2y0dB	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
43	c3gg2B	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: sugar dehydrogenase, udp-glucose/gdp-mannose dehydrogenase PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from <i>Porphyromonas2 gingivalis</i> bound to product udp-glucuronate
44	c2q3eH	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
45	c4a7pA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: se-met derivatized udgd, udp-glucose dehydrogenase from <i>Sphingomonas2 elodea</i>
46	c4r16A	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: 418aa long hypothetical udp-n-acetyl-d-mannosaminuronic PDBTitle: structure of udp-d-mannac dehydrogenase from <i>Pyrococcus horikoshii</i>
47	c3prjB	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
48	c3plnA	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: crystal structure of <i>Klebsiella pneumoniae</i> udp-glucose 6-dehydrogenase2 complexed with udp-glucose
49	c2o3jC	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of <i>Caenorhabditis elegans</i> udp-glucose dehydrogenase
50	c3g79A	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; PDBTitle: crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from <i>Methanosarcina mazei</i> go1
51	c3ojlA	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: cap5o; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from <i>Staphylococcus aureus</i>
						PDB header: oxidoreductase

52	c1dliA_	Alignment	not modelled	100.0	18	Chain: A: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation
53	c3k96B_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
54	c4edfC_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: dimeric hugdh, k94e
55	c1bg6A_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; PDBTitle: crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c
56	c1i36A_	Alignment	not modelled	100.0	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein mth1747; PDBTitle: structure of conserved protein mth1747 of unknown function reveals2 structural similarity with 3-hydroxyacid dehydrogenases
57	c1m67A_	Alignment	not modelled	100.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of leishmania mexicana gpdh complexed with inhibitor2 2-bromo-6-hydroxy-purine
58	c1txgA_	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
59	c3hn2A_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
60	c6c4jA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: ligand bound full length hugdh with a104l substitution
61	d1vpda2	Alignment	not modelled	99.9	34	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
62	c3hwrA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of pane/apba family ketopantoate reductase2 (yp_299159.1) from ralstonia eutropha jmp134 at 2.15 a resolution
63	d3cuma2	Alignment	not modelled	99.9	49	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
64	c2ep9A_	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: l-gulonate 3-dehydrogenase; PDBTitle: crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
65	c2ew2B_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase, putative; PDBTitle: crystal structure of the putative 2-dehydropantoate 2-reductase from2 enterococcus faecalis
66	c1z82A_	Alignment	not modelled	99.9	11	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of glycerol-3-phosphate dehydrogenase (tm0378) from2 thermotoga maritima at 2.00 a resolution
67	c3wfd_	Alignment	not modelled	99.9	11	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: the complex structure of d-mandelate dehydrogenase with nadh
68	c5zikC_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: C: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of ketopantoate reductase from pseudomonas2 aeruginosa
69	c4ol9A_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of putative 2-dehydropantoate 2-reductase pane from2 mycobacterium tuberculosis complexed with nadp and oxamate
70	c2ofpB_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ketopantoate reductase; PDBTitle: crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
71	c1vj8C_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase
72	c5t57A_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: semialdehyde dehydrogenase nad-binding protein; PDBTitle: crystal structure of a semialdehyde dehydrogenase nad-binding protein2 from cupriavidus necator in complex with calcium and nad
73	c1wpgB_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad+], PDBTitle: ternary complex of glycerol 3-phosphate dehydrogenase 12 with nad and dihydroxyactone
74	c3d1lB_	Alignment	not modelled	99.9	10	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
75	c3ghyA_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase

						from ralstonia2 solanacearum molk2
76	c3triB_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
77	c5ayvB_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of archaeal ketopantoate reductase complexed with2 coenzyme a and 2-oxopantoate
78	d2cvza2	Alignment	not modelled	99.9	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
79	c2izzE_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: E: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase
80	c4wjiA_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative cyclohexadienyl dehydrogenase and adh prephenate PDBTitle: crystal structure of cyclohexadienyl dehydrogenase from sinorhizobium2 meliloti in complex with nadp and tyrosine
81	c1ks9A_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli
82	c2graA_	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp
83	c2ahrB_	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative pyrroline carboxylate reductase; PDBTitle: crystal structures of 1-pyrroline-5-carboxylate reductase from human2 pathogen streptococcus pyogenes
84	d2pgda2	Alignment	not modelled	99.9	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
85	c3g17H_	Alignment	not modelled	99.9	13	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: similar to 2-dehydropantoate 2-reductase; PDBTitle: structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus
86	c5bseF_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: F: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: crystal structure of medicago truncatula (delta)1-pyrroline-5-2 carboxylate reductase (mtp5cr)
87	c2pv7B_	Alignment	not modelled	99.9	14	PDB header: isomerase, oxidoreductase Chain: B: PDB Molecule: t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) PDBTitle: crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
88	c4j0eB_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: probable 3-hydroxyacyl-coa dehydrogenase f5c8.1; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase from2 caenorhadbitis elegans in p1 space group
89	d1pgja2	Alignment	not modelled	99.9	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
90	c4e12A_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: diketoreductase; PDBTitle: substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase
91	c3dzbA_	Alignment	not modelled	99.9	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
92	c4ypoB_	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
93	c3b1fA_	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
94	c4om8B_	Alignment	not modelled	99.8	21	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 5-formly-3-hydroxy-2-methylpyridine 4-carboxylic2 acid (fhmpc) 5-dehydrogenase, an nad+ dependent dismutase.
95	c4xdzB_	Alignment	not modelled	99.8	10	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
96	c2f1kD_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis aroenate dehydrogenase
97	c2g5cD_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
98	c3gt0A_	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
99	c4fgwA_	Alignment	not modelled	99.8	11	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(+)] 1; PDBTitle: structure of glycerol-3-phosphate dehydrogenase, gpd1, from2 sacharomyces cerevisiae

100	c2ag8A	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
101	c4kqxB	Alignment	not modelled	99.8	11	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: mutant slackia exigua kari ddv in complex with nad and an inhibitor
102	c3ggpA	Alignment	not modelled	99.8	14	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+
103	c3egoB	Alignment	not modelled	99.8	9	PDB header: oxidoreductase Chain: B: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of probable 2-dehydropantoate 2-reductase pane from2 bacillus subtilis
104	c4xdyB	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archean
105	d1i36a2	Alignment	not modelled	99.8	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
106	c3rqsB	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: hydroxyacyl-coenzyme a dehydrogenase, mitochondrial; PDBTitle: crystal structure of human l-3- hydroxyacyl-coa dehydrogenase2 (ec1.1.1.35) from mitochondria at the resolution 2.0 a, northeast3 structural genomics consortium target hr487, mitochondrial protein4 partnership
107	c2rcyB	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline carboxylate reductase; PDBTitle: crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (ma113p1.284) with nadp bound
108	c1m75B	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of the n208s mutant of l-3-hydroxyacyl-coa2 dehydrogenase in complex with nad and acetoacetyl-coa
109	c6hrdD	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of m. tuberculosis fadB2 (rv0468)
110	c1np3B	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomereductase from2 pseudomonas aeruginosa
111	c5t8xA	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: prephenate dehydrogenase 1; PDBTitle: prephenate dehydrogenase from soybean
112	c3i83B	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from methylococcus2 capsulatus
113	c5n2iC	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: C: PDB Molecule: reduced coenzyme f420:nadp oxidoreductase; PDBTitle: f420:nadph oxidoreductase from thermobifida fusca with nadp+ bound
114	c4pzdB	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of (s)-3-hydroxybutyryl-coa dehydrogenase paah1 in2 complex with nad+
115	c4kueA	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 clostridium butyricum
116	c5uscB	Alignment	not modelled	99.8	13	PDB header: hydrolase Chain: B: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
117	c3mogA	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
118	c2yzC	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: C: PDB Molecule: metalloreductase steap4; PDBTitle: rat steap4 oxidoreductase domain complexed with nadp
119	d3cuma1	Alignment	not modelled	99.8	39	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
120	c2qytA	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83