












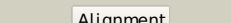

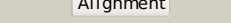
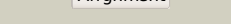
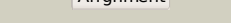
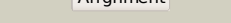



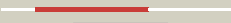

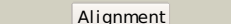




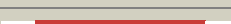



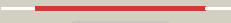




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1vpdA_	Alignment		100.0	92	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
2	c1yb4A_	Alignment		100.0	40	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronic semialdehyde reductase; PDBTitle: crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
3	c3ckyA_	Alignment		100.0	37	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
4	c3cumA_	Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
5	c2cvzD_	Alignment		100.0	31	PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8
6	c3g0oA_	Alignment		100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
7	c3dojA_	Alignment		100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
8	c2uyyD_	Alignment		100.0	29	PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac
9	c3pefA_	Alignment		100.0	37	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+
10	c2gf2B_	Alignment		100.0	35	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase
11	c3l6dB_	Alignment		100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440

12	c3qhaB_	Alignment		100.0	32	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
13	c1pgjA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan parasite t. brucei
14	c2p4qA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces cerevisiae
15	c3fwnB_	Alignment		100.0	21	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
16	c1pgqA_	Alignment		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
17	c2iz1C_	Alignment		100.0	21	PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
18	c3qsgA_	Alignment		100.0	17	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 alicyclobacillus acidocaldarius
19	c2y0dB_	Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
20	c1mv8A_	Alignment		100.0	16	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 psuedomonas aeruginosa
21	c3gg2B_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: sugar dehydrogenase, udp-glucose/gdp-mannose PDBTitle: crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
22	c3prjB_	Alignment	not modelled	100.0	18	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.
23	c2q3eH_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
24	cli36A_	Alignment	not modelled	100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein mth1747; PDBTitle: structure of conserved protein mth1747 of unknown function2 reveals structural similarity with 3-hydroxyacid3 dehydrogenases
25	c3plnA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
26	c2o3jC_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of caenorhabditis elegans udp-glucose dehydrogenase
27	c3ojlA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cap50; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap502 from staphylococcus aureus
						PDB header: oxidoreductase Chain: A: PDB Molecule: udp-glucose dehydrogenase;

28	c1dliA	Alignment	not modelled	100.0	17	PDBTitle: the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation
29	c2ep9A	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: l-gulonate 3-dehydrogenase; PDBTitle: crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
30	c3g79A	Alignment	not modelled	100.0	18	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 methanosarcina mazei go1
31	d1vpda2	Alignment	not modelled	99.9	92	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
32	c1bg6A	Alignment	not modelled	99.9	17	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
33	d3cuma2	Alignment	not modelled	99.9	41	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
34	c3k96B	Alignment	not modelled	99.9	13	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
35	c1m67A	Alignment	not modelled	99.9	18	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
36	c2izzE	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: E: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate2 reductase
37	c3d1lB	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
38	c1txgA	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
39	c2graA	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp
40	c3mogA	Alignment	not modelled	99.9	15	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
41	c1m75B	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of the n208s mutant of l-3-hydroxyacyl-2 coa dehydrogenase in complex with nad and acetoacetyl-coa
42	c3hn2A	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
43	c3triB	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
44	c2ahrB	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: putative pyrroline carboxylate reductase; PDBTitle: crystal structures of l-pyrroline-5-carboxylate reductase from human2 pathogen streptococcus pyogenes
45	c3k6jA	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: protein f01g10.3, confirmed by transcript evidence; PDBTitle: crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans
46	c2ofpB	Alignment	not modelled	99.9	14	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
47	d1vpda1	Alignment	not modelled	99.9	92	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
48	d1pgia2	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
49	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
50	c1ks9A	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli
51	c3hwrA	Alignment	not modelled	99.9	12	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

52	c1zejA	 Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase; PDBTitle: crystal structure of the 3-hydroxyacyl-coa dehydrogenase (hbd-9,2 af2017) from archaeoglobus fulgidus dsm 4304 at 2.00 a resolution
53	d2cvza2	 Alignment	not modelled	99.9	35	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
54	c1z82A	 Alignment	not modelled	99.9	13	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
55	d2pgda2	 Alignment	not modelled	99.9	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
56	c3ghyA	 Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
57	c2f1kD	 Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
58	c3g17H	 Alignment	not modelled	99.9	14	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
59	c2d3tB	 Alignment	not modelled	99.9	14	PDB header: lyase, oxidoreductase/transferase Chain: B: PDB Molecule: fatty oxidation complex alpha subunit; PDBTitle: fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
60	c1zcjA	 Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase
61	c3dzba	 Alignment	not modelled	99.9	15	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
62	c2ag8A	 Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
63	c1vj8C	 Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase
64	d1i36a2	 Alignment	not modelled	99.9	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
65	c3b1fA	 Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
66	c2x58B	 Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: the crystal structure of mfe1 liganded with coa
67	c2pv7B	 Alignment	not modelled	99.9	17	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
68	c3gt0A	 Alignment	not modelled	99.9	14	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
69	c2rcyB	 Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline carboxylate reductase; PDBTitle: crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
70	d2cvza1	 Alignment	not modelled	99.8	27	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
71	c2g5cD	 Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
72	c3egoB	 Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: B: PDB Molecule: probable 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of probable 2-dehydropantoate 2-reductase2 pane from bacillus subtilis
73	c1wpqB	 Alignment	not modelled	99.8	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	c2wtbA	 Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fatty acid multifunctional protein (atmfp2); PDBTitle: arabidopsis thaliana multifunctional protein, mfp2
75	c2i76B	 Alignment	not modelled	99.8	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein tm1727 from thermotoga maritima
		 Alignment				PDB header: oxidoreductase

76	c3ggpA	Alignment	not modelled	99.8	17	Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+ Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain
77	d3cuma1	Alignment	not modelled	99.8	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
78	d1mv8a2	Alignment	not modelled	99.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
79	d1f0ya2	Alignment	not modelled	99.8	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
80	c1np3B	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
81	c2rafC	Alignment	not modelled	99.8	12	PDB header: oxidoreductase Chain: C: PDB Molecule: putative dinucleotide-binding oxidoreductase; PDBTitle: crystal structure of putative dinucleotide-binding2 oxidoreductase (np_786167.1) from lactobacillus plantarum3 at 1.60 a resolution
82	c3ktdC	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: C: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
83	c3i83B	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from methylococcus2 capsulatus
84	d1jaya	Alignment	not modelled	99.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
85	c3dttA	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadp oxidoreductase; PDBTitle: crystal structure of a putative f420 dependent nadp-reductase2 (arth_0613) from arthrobacter sp. fb24 at 1.70 a resolution
86	d2f1ka2	Alignment	not modelled	99.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
87	c2vq3B	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: metalloreductase steap3; PDBTitle: crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle
88	d1wdka3	Alignment	not modelled	99.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
89	c2qytA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83
90	d2ahra2	Alignment	not modelled	99.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
91	d1dlja2	Alignment	not modelled	99.7	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
92	d1n1ea2	Alignment	not modelled	99.7	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
93	d1txga2	Alignment	not modelled	99.7	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
94	c3c24A	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (yp_511008.1) from2 jannaschia sp. ccs1 at 1.62 a resolution
95	c3c7cB	Alignment	not modelled	99.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: octopine dehydrogenase; PDBTitle: a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
96	d2g5ca2	Alignment	not modelled	99.6	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
97	d2pv7a2	Alignment	not modelled	99.6	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
98	d1yqga2	Alignment	not modelled	99.6	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
99	d2i76a2	Alignment	not modelled	99.5	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
100	d1ha6a2	Alignment	not modelled	99.5	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains

100	d1b9da2	Alignment	not modelled	99.3	17	Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
101	d1np3a2	Alignment	not modelled	99.4	17	Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
102	c3dfuB	Alignment	not modelled	99.3	15	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized protein from 6-phosphogluconate PDBTitle: crystal structure of a putative rossmann-like dehydrogenase (cgl2689)2 from corynebacterium glutamicum at 2.07 a resolution
103	d1ks9a2	Alignment	not modelled	99.2	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
104	d1gdha1	Alignment	not modelled	99.1	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
105	d2naca1	Alignment	not modelled	99.1	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
106	c3n7uD	Alignment	not modelled	99.1	22	PDB header: oxidoreductase Chain: D: PDB Molecule: formate dehydrogenase; PDBTitle: nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
107	d1uxja1	Alignment	not modelled	99.1	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
108	c2nacA	Alignment	not modelled	99.1	17	PDB header: oxidoreductase(aldehyde(d),nad+(a)) Chain: A: PDB Molecule: nad-dependent formate dehydrogenase; PDBTitle: high resolution structures of holo and apo formate dehydrogenase
109	d1ojua1	Alignment	not modelled	99.0	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
110	c1gdhA	Alignment	not modelled	99.0	15	PDB header: oxidoreductase(choh (d)-nad(p)+ (a)) Chain: A: PDB Molecule: d-glycerate dehydrogenase; PDBTitle: crystal structure of a nad-dependent d-glycerate2 dehydrogenase at 2.4 angstroms resolution
111	d1qp8a1	Alignment	not modelled	99.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
112	d1ez4a1	Alignment	not modelled	99.0	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
113	c3gg9C	Alignment	not modelled	99.0	18	PDB header: oxidoreductase Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase oxidoreductase protein; PDBTitle: crystal structure of putative d-3-phosphoglycerate dehydrogenase2 oxidoreductase from ralstonia solanacearum
114	d1guza1	Alignment	not modelled	99.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
115	d1mx3a1	Alignment	not modelled	99.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
116	c2rirA	Alignment	not modelled	99.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
117	c2omeA	Alignment	not modelled	98.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: c-terminal-binding protein 2; PDBTitle: crystal structure of human ctbp2 dehydrogenase complexed with nad(h)
118	d1qv0a1	Alignment	not modelled	98.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
119	d1a5za1	Alignment	not modelled	98.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
120	d1t2da1	Alignment	not modelled	98.9	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like