

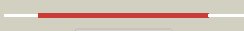





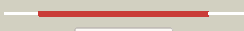















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1m67A_</a>	 Alignment		100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of leishmania mexicana gpdh complexed with inhibitor 2-bromo-6-hydroxy-purine
2	<a href="#">c3k96B_</a>	 Alignment		100.0	50	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad(p)+]; <b>PDBTitle:</b> 2.1 angstrom resolution crystal structure of glycerol-3-phosphate2 dehydrogenase (gpsa) from coxiella burnetii
3	<a href="#">c1wpqB_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad+]; <b>PDBTitle:</b> ternary complex of glycerol 3-phosphate dehydrogenase 12 with nad and dihydroxyactone
4	<a href="#">c1yj8C_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase
5	<a href="#">c1z82A_</a>	 Alignment		100.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of glycerol-3-phosphate dehydrogenase (tm0378) from thermotoga maritima at 2.00 a resolution
6	<a href="#">c1txgA_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad(p)+]; <b>PDBTitle:</b> structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
7	<a href="#">c1bg6A_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n-(1-d-carboxylethyl)-l-norvaline dehydrogenase; <b>PDBTitle:</b> crystal structure of the n-(1-d-carboxylethyl)-l-norvaline2 dehydrogenase from arthrobacter sp. strain 1c
8	<a href="#">c2ew2B_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase, putative; <b>PDBTitle:</b> crystal structure of the putative 2-dehydropantoate 2-reductase from enterococcus faecalis
9	<a href="#">c3hn2A_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of 2-dehydropantoate 2-reductase from geobacter2 metallireducens gs-15
10	<a href="#">c3hwrA_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of pane/apba family ketopantoate reductase2 (yp_299159.1) from ralstonia eutropha jmp134 at 2.15 a resolution
11	<a href="#">c2qytA_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83

12	<a href="#">c2y0dB_</a>	Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> bcec mutation y10k
13	<a href="#">c3ghyA_</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ketopantoate reductase protein; <b>PDBTitle:</b> crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
14	<a href="#">c1mv8A_</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gdp-mannose 6-dehydrogenase; <b>PDBTitle:</b> 1.55 a crystal structure of a ternary complex of gdp-mannose2 dehydrogenase from psuedomonas aeruginosa
15	<a href="#">c2ofpB_</a>	Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketopantoate reductase; <b>PDBTitle:</b> crystal structure of escherichia coli ketopantoate2 reductase in a ternary complex with nadp+ and pantoate
16	<a href="#">c3gg2B_</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar dehydrogenase, udp-glucose/gdp-mannose <b>PDBTitle:</b> crystal structure of udp-glucose 6-dehydrogenase from2 porphyromonas gingivalis bound to product udp-glucuronate
17	<a href="#">c1ks9A_</a>	Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> ketopantoate reductase from escherichia coli
18	<a href="#">c3g17H_</a>	Alignment		100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> H: <b>PDB Molecule:</b> similar to 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> structure of putative 2-dehydropantoate 2-reductase from2 staphylococcus aureus
19	<a href="#">c1pgiA_</a>	Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
20	<a href="#">c1pggA_</a>	Alignment		100.0	14	<b>PDB header:</b> oxidoreductase (choh(d)-nadp+ (a)) <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
21	<a href="#">c3egoB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of probable 2-dehydropantoate 2-reductase2 pane from bacillus subtilis
22	<a href="#">c2iz1C_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> 6pdh complexed with pex inhibitor synchrotron data
23	<a href="#">c2q3eH_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
24	<a href="#">c3i83B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of 2-dehydropantoate 2-reductase from methylococcus2 capsulatus
25	<a href="#">c2p4qA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating 1; <b>PDBTitle:</b> crystal structure analysis of gnd1 in saccharomyces cerevisiae
26	<a href="#">c3cumA_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
27	<a href="#">c3prjB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> role of packing defects in the evolution of allostery and induced fit2 in human udp-glucose dehydrogenase.
28	<a href="#">c3ghsB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase;

28	<a href="#">c3qndB</a>	Alignment	not modelled	100.0	13	<b>PDBTitle:</b> crystal structure of a putative oxidoreductase from mycobacterium2 avium 104 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> structure of caenorhabditis elegans udp-glucose dehydrogenase
29	<a href="#">c2o3jC</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphoglucanate dehydrogenase, decarboxylating; <b>PDBTitle:</b> dimeric 6-phosphoglucanate dehydrogenase complexed with 6-2 phosphoglucanate and 2'-monophosphoadenosine-5'-diphosphate
30	<a href="#">c3fwnB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hdb8
31	<a href="#">c2cvzD</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tartronate semialdehyde reductase; <b>PDBTitle:</b> x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
32	<a href="#">c1vpdA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
33	<a href="#">c3g0oA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tartronic semialdehyde reductase; <b>PDBTitle:</b> crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
34	<a href="#">c1yb4A</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-hydroxymethyl glutarate dehydrogenase; <b>PDBTitle:</b> structural and kinetic properties of a beta-hydroxyacid dehydrogenase2 involved in nicotinate fermentation
35	<a href="#">c3ckyA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cap5o; <b>PDBTitle:</b> native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus
36	<a href="#">c3ojlA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> crystal structure of klebsiella pneumoniae udp-glucose 6-dehydrogenase2 complexed with udp-glucose
37	<a href="#">c3plnA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
38	<a href="#">c3l6dB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ndp-n-acetyl-d-galactosaminuronic acid dehydrogenase; <b>PDBTitle:</b> crystal structure of ndp-n-acetyl-d-galactosaminuronic acid2 dehydrogenase from methanosarcina mazei go1
39	<a href="#">c3g79A</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphoglucanate dehydrogenase-like, N-terminal domain
40	<a href="#">d1n1ea2</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> crystal structure of human hydroxyisobutyrate dehydrogenase
41	<a href="#">c2gf2B</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> cytokine <b>Chain:</b> D: <b>PDB Molecule:</b> n-pac protein; <b>PDBTitle:</b> structure of the cytokine-like nuclear factor n-pac
42	<a href="#">c2uyvD</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> the first structure of udp-glucose dehydrogenase (udpgdh) reveals the2 catalytic residues necessary for the two-fold oxidation
43	<a href="#">c1ldiA</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> 6-phosphoglucanate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphoglucanate dehydrogenase C-terminal domain-like <b>Family:</b> Glycerol-3-phosphate dehydrogenase
44	<a href="#">d1n1ea1</a>	Alignment	not modelled	99.9	44	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dehydrogenase-like protein; <b>PDBTitle:</b> structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
45	<a href="#">c3dojA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> 3-hydroxyisobutyrate dehydrogenase family protein; <b>PDBTitle:</b> crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter sulfurreducens in complex with nadp+
46	<a href="#">c3pduF</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> octopine dehydrogenase; <b>PDBTitle:</b> a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
47	<a href="#">c3c7cB</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nad-binding phosphoglucanate dehydrogenase-like protein; <b>PDBTitle:</b> crystal structure of nad-binding phosphoglucanate dehydrogenase-like2 protein from alicyclobacillus acidocaldarius
48	<a href="#">c3qsgA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphoglucanate dehydrogenase, nad-binding; <b>PDBTitle:</b> crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+
49	<a href="#">c3pefA</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphoglucanate dehydrogenase-like, N-terminal domain
50	<a href="#">d1txga2</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> 6-phosphoglucanate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphoglucanate dehydrogenase C-terminal domain-like
51	<a href="#">d1txga1</a>	Alignment	not modelled	99.9	34	

					<b>Family:</b> Glycerol-3-phosphate dehydrogenase <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadp oxidoreductase bf3122; <b>PDBTitle:</b> crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
52	<a href="#">c3d1lB_</a>	Alignment	not modelled	99.9	15
53	<a href="#">d1bg6a2</a>	Alignment	not modelled	99.9	19
54	<a href="#">c1i36A_</a>	Alignment	not modelled	99.9	15
55	<a href="#">c2izzE_</a>	Alignment	not modelled	99.9	15
56	<a href="#">c2graA_</a>	Alignment	not modelled	99.9	15
57	<a href="#">d1mv8a2</a>	Alignment	not modelled	99.9	18
58	<a href="#">c3triB_</a>	Alignment	not modelled	99.9	15
59	<a href="#">c1np3B_</a>	Alignment	not modelled	99.9	14
60	<a href="#">c2ep9A_</a>	Alignment	not modelled	99.9	16
61	<a href="#">d2pgda2</a>	Alignment	not modelled	99.8	13
62	<a href="#">c2ahrB_</a>	Alignment	not modelled	99.8	16
63	<a href="#">c3gt0A_</a>	Alignment	not modelled	99.8	12
64	<a href="#">c3dttA_</a>	Alignment	not modelled	99.8	15
65	<a href="#">d1vpda2</a>	Alignment	not modelled	99.8	18
66	<a href="#">d1ks9a2</a>	Alignment	not modelled	99.8	19
67	<a href="#">d1java_</a>	Alignment	not modelled	99.8	15
68	<a href="#">c3dzba_</a>	Alignment	not modelled	99.8	16
69	<a href="#">d3cuma2</a>	Alignment	not modelled	99.8	15
70	<a href="#">c2pv7B_</a>	Alignment	not modelled	99.8	16
71	<a href="#">c2f1kD_</a>	Alignment	not modelled	99.8	15
72	<a href="#">c3c24A_</a>	Alignment	not modelled	99.8	13
73	<a href="#">c3b1fA_</a>	Alignment	not modelled	99.8	14
74	<a href="#">d1pgia2</a>	Alignment	not modelled	99.8	14
75	<a href="#">c3k6jA_</a>	Alignment	not modelled	99.8	17

76	<a href="#">d2cvza2</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
77	<a href="#">c2g5cD</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from aquifex aeolicus
78	<a href="#">c2ag8A</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase; <b>PDBTitle:</b> nadp complex of pyrroline-5-carboxylate reductase from neisseria meningitidis
79	<a href="#">c3mogA</a>	Alignment	not modelled	99.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 3-hydroxybutyryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of 3-hydroxybutyryl-coa dehydrogenase from escherichia coli k12 substr. mg1655
80	<a href="#">c1m75B</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of the n208s mutant of l-3-hydroxyacyl-coa dehydrogenase in complex with nad and acetoacetyl-coa
81	<a href="#">c2rcyB</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyrroline carboxylate reductase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
82	<a href="#">d2ahra2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
83	<a href="#">d2f1ka2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
84	<a href="#">d1f0ya2</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
85	<a href="#">c1zczA</a>	Alignment	not modelled	99.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme; <b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-coa dehydrogenase
86	<a href="#">d1dlja2</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
87	<a href="#">c3ggpA</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from a. aeolicus in2 complex with hydroxyphenyl propionate and nad+
88	<a href="#">d1yqga2</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
89	<a href="#">d1i36a2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
90	<a href="#">d1wdka3</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
91	<a href="#">c2x58B</a>	Alignment	not modelled	99.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme; <b>PDBTitle:</b> the crystal structure of mfe1 liganded with coa
92	<a href="#">d2pv7a2</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
93	<a href="#">c2wtbA</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid multifunctional protein (atnfp2); <b>PDBTitle:</b> arabidopsis thaliana multifunctional protein, mfp2
94	<a href="#">c2vq3B</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> metalloredutase steep3; <b>PDBTitle:</b> crystal structure of the membrane proximal oxidoreductase2 domain of human steep3, the dominant ferric reductase of3 the erythroid transferrin cycle
95	<a href="#">c2d3tB</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> lyase, oxidoreductase/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty oxidation complex alpha subunit; <b>PDBTitle:</b> fatty acid beta-oxidation multienzyme complex from pseudomonas fragi, form v
96	<a href="#">d2g5ca2</a>	Alignment	not modelled	99.6	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
97	<a href="#">c1zejA</a>	Alignment	not modelled	99.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of the 3-hydroxyacyl-coa dehydrogenase (hbd-9,2 af2017) from archaeoglobus fulgidus dsm 4304 at 2.00 a resolution
98	<a href="#">c2i76B</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of protein tm1727 from thermotoga maritima
99	<a href="#">c3ktdC</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
100	<a href="#">d2i76a2</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain

101	<a href="#">d1np3a2</a>	Alignment	not modelled	99.5	24	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
102	<a href="#">d1luxa1</a>	Alignment	not modelled	99.4	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
103	<a href="#">d1pzga1</a>	Alignment	not modelled	99.3	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
104	<a href="#">d1ez4a1</a>	Alignment	not modelled	99.3	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
105	<a href="#">d1ks9a1</a>	Alignment	not modelled	99.3	9	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Ketopantoate reductase PanE
106	<a href="#">d9lta1</a>	Alignment	not modelled	99.3	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
107	<a href="#">c2rafC_</a>	Alignment	not modelled	99.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative dinucleotide-binding oxidoreductase; <b>PDBTitle:</b> crystal structure of putative dinucleotide-binding2 oxidoreductase (np_786167.1) from lactobacillus plantarum3 at 1.60 a resolution
108	<a href="#">d1i10a1</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
109	<a href="#">d1i0za1</a>	Alignment	not modelled	99.2	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
110	<a href="#">d1ldma1</a>	Alignment	not modelled	99.2	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
111	<a href="#">d1ldna1</a>	Alignment	not modelled	99.2	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
112	<a href="#">c2rirA_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase, a chain; <b>PDBTitle:</b> crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
113	<a href="#">d1hya1</a>	Alignment	not modelled	99.2	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
114	<a href="#">d5ldha1</a>	Alignment	not modelled	99.2	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
115	<a href="#">d1obba1</a>	Alignment	not modelled	99.2	22	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
116	<a href="#">c3d4oA_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dipicolinate synthase subunit a; <b>PDBTitle:</b> crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
117	<a href="#">c8ldha_</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> oxidoreductase(choh(d)-nad(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> m4 apo-lactate dehydrogenase; <b>PDBTitle:</b> refined crystal structure of dogfish m4 apo-lactate2 dehydrogenase
118	<a href="#">d1ojua1</a>	Alignment	not modelled	99.1	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
119	<a href="#">c3d0oA_</a>	Alignment	not modelled	99.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lactate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of lactate dehydrogenase from2 staphylococcus aureus
120	<a href="#">c1e5lA_</a>	Alignment	not modelled	99.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea