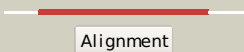

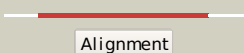
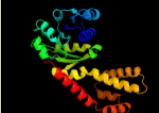
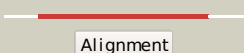

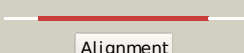



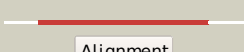

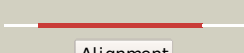

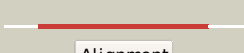


















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2izzE_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: E: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate2 reductase
2	c3triB_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
3	c2ahrB_	 Alignment		100.0	34	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
4	c2rcyB_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: B: PDB Molecule: pyrroline carboxylate reductase; PDBTitle: crystal structure of plasmodium falciparum pyrroline carboxylate2 reductase (mal13p1.284) with nadp bound
5	c2ag8A_	 Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase; PDBTitle: nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
6	c2graA_	 Alignment		100.0	37	PDB header: oxidoreductase Chain: A: PDB Molecule: pyrroline-5-carboxylate reductase 1; PDBTitle: crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp
7	c3gt0A_	 Alignment		100.0	47	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
8	c3d1lB_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative nadp oxidoreductase bf3122; PDBTitle: crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
9	c3c24A_	 Alignment		100.0	16	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
10	c3b1fA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 mutans
11	c3ggpA_	 Alignment		100.0	16	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+

12	c3dzbA_	Alignment		100.0	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
13	c3l6dB_	Alignment		100.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
14	c2g5cD_	Alignment		100.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of prephenate dehydrogenase from aquifex aeolicus
15	c3g0oA_	Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
16	c2pv7B_	Alignment		100.0	16	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
17	c3qsgA_	Alignment		100.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-binding phosphoglucanate dehydrogenase-like protein; PDBTitle: crystal structure of nad-binding phosphoglucanate dehydrogenase-like2 protein from alicyclobacillus acidocaldarius
18	c2f1kD_	Alignment		99.9	15	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase
19	d2ahra2	Alignment		99.9	31	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphoglucanate dehydrogenase-like, N-terminal domain
20	c3ktdC_	Alignment		99.9	16	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
21	c2uyyD_	Alignment	not modelled	99.9	18	PDB header: cytokine Chain: D: PDB Molecule: n-pac protein; PDBTitle: structure of the cytokine-like nuclear factor n-pac
22	d1yqga2	Alignment	not modelled	99.9	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphoglucanate dehydrogenase-like, N-terminal domain
23	c3pduF_	Alignment	not modelled	99.9	14	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+
24	c3cumA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
25	c1vpdA_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: tartronate semialdehyde reductase; PDBTitle: x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
26	c3pefA_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphoglucanate dehydrogenase, nad-binding; PDBTitle: crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+
27	c2p4gA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphoglucanate dehydrogenase, decarboxylating 1; PDBTitle: crystal structure analysis of gnd1 in saccharomyces

					cerevisiae
28	c2cvzD_	Alignment	not modelled	99.9	15 PDB header: oxidoreductase Chain: D: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8
29	c3ckyA_	Alignment	not modelled	99.9	17 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
30	c3dojA_	Alignment	not modelled	99.9	14 PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase-like protein; PDBTitle: structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
31	c2iz1C_	Alignment	not modelled	99.9	13 PDB header: oxidoreductase Chain: C: PDB Molecule: 6-phosphogluconate dehydrogenase, decarboxylating; PDBTitle: 6pdh complexed with pex inhibitor synchrotron data
32	c1pgqA_	Alignment	not modelled	99.9	14 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
33	cli36A_	Alignment	not modelled	99.9	11 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
34	c1pgjA_	Alignment	not modelled	99.9	14 PDB header: oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconate dehydrogenase; PDBTitle: x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
35	c3fwnB_	Alignment	not modelled	99.9	14 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
36	dlyqga1	Alignment	not modelled	99.9	32 Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
37	c1yb4A_	Alignment	not modelled	99.9	16 PDB header: oxidoreductase Chain: A: PDB Molecule: tartronic semialdehyde reductase; PDBTitle: crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
38	c3k96B_	Alignment	not modelled	99.9	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
39	c2ep9A_	Alignment	not modelled	99.9	17 PDB header: oxidoreductase Chain: A: PDB Molecule: l-gulonate 3-dehydrogenase; PDBTitle: crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
40	c2gf2B_	Alignment	not modelled	99.9	18 PDB header: oxidoreductase Chain: B: PDB Molecule: 3-hydroxyisobutyrate dehydrogenase; PDBTitle: crystal structure of human hydroxyisobutyrate dehydrogenase
41	c3qhaB_	Alignment	not modelled	99.9	15 PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
42	d2ahra1	Alignment	not modelled	99.9	38 Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: ProC C-terminal domain-like
43	c2i76B_	Alignment	not modelled	99.8	13 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of protein tm1727 from thermotoga maritima
44	c1m67A_	Alignment	not modelled	99.8	15 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
45	c1np3B_	Alignment	not modelled	99.8	18 PDB header: oxidoreductase Chain: B: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: crystal structure of class i acetoacetyl acid isomeroeductase from2 pseudomonas aeruginosa
46	d1f0ya2	Alignment	not modelled	99.8	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
47	c3dttA_	Alignment	not modelled	99.8	20 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
48	c1m75B_	Alignment	not modelled	99.8	13 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
49	c3hn2A_	Alignment	not modelled	99.8	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
50	c2ew2B_	Alignment	not modelled	99.8	15 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
51	d1wdka3	Alignment	not modelled	99.8	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal

						domain
52	c3k6jA_	Alignment	not modelled	99.8	13	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
53	c3mogA_	Alignment	not modelled	99.7	14	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
54	c3gg2B_	Alignment	not modelled	99.7	14	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
55	d3cuma2	Alignment	not modelled	99.7	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
56	d1n1ea2	Alignment	not modelled	99.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
57	d1jaya_	Alignment	not modelled	99.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
58	d1vpda2	Alignment	not modelled	99.7	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
59	c1wpgB_	Alignment	not modelled	99.7	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
60	d2f1ka2	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
61	c1zcyjA_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase
62	d2cvza2	Alignment	not modelled	99.7	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
63	d2g5ca2	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
64	c1mv8A_	Alignment	not modelled	99.7	17	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
65	c1bg6A_	Alignment	not modelled	99.7	13	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
66	c2ofpB_	Alignment	not modelled	99.7	13	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
67	c1yj8C_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: C: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase
68	c3hwrA_	Alignment	not modelled	99.7	16	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
69	c2y0dB_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: udp-glucose dehydrogenase; PDBTitle: bcec mutation y10k
70	c2x58B_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: peroxisomal bifunctional enzyme; PDBTitle: the crystal structure of nfe1 liganded with coa
71	d2pgda2	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
72	c1txgA_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase [nad(p)+]; PDBTitle: structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
73	c1ks9A_	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: ketopantoate reductase from escherichia coli
74	c2wtbA_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: fatty acid multifunctional protein (atmfp2); PDBTitle: arabidopsis thaliana multifunctional protein, mfp2
75	c1z82A_	Alignment	not modelled	99.7	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

76	d2pv7a2	Alignment	not modelled	99.7	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
77	d2i76a2	Alignment	not modelled	99.7	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
78	d1i36a2	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
79	c2d3tB_	Alignment	not modelled	99.7	16	PDB header: lyase, oxidoreductase/transferase Chain: B: PDB Molecule: fatty oxidation complex alpha subunit; PDBTitle: fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragil, form v
80	c3ghyA_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: ketopantoate reductase protein; PDBTitle: crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
81	d1np3a2	Alignment	not modelled	99.7	20	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
82	d1txga2	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
83	c2q3eH_	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: H: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of human udp-glucose dehydrogenase complexed with nadh and2 udp-glucose
84	c2o3jC_	Alignment	not modelled	99.6	18	PDB header: oxidoreductase Chain: C: PDB Molecule: udp-glucose 6-dehydrogenase; PDBTitle: structure of caenorhabditis elegans udp-glucose dehydrogenase
85	d1pgja2	Alignment	not modelled	99.6	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
86	c3ojlA_	Alignment	not modelled	99.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: cap5o; PDBTitle: native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus
87	c2vq3B_	Alignment	not modelled	99.6	17	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	c1zejA_	Alignment	not modelled	99.6	17	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
89	c3prjB_	Alignment	not modelled	99.6	13	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.
90	c3plnA_	Alignment	not modelled	99.6	12	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
91	c3g79A_	Alignment	not modelled	99.6	15	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
92	c3g17H_	Alignment	not modelled	99.6	12	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
93	c3egoB_	Alignment	not modelled	99.6	15	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
94	c1dliA_	Alignment	not modelled	99.5	13	PDB header: oxidoreductase 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
95	c3dfuB_	Alignment	not modelled	99.5	12	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
96	d1bg6a2	Alignment	not modelled	99.5	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
97	c2qytA_	Alignment	not modelled	99.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from porphyromonas2 gingivalis w83
98	d1mv8a2	Alignment	not modelled	99.4	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
99	d1ks9a2	Alignment	not modelled	99.4	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain

100	c3c7cB	Alignment	not modelled	99.4	15	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)
101	c2rafC	Alignment	not modelled	99.4	17	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
102	d1dlja2	Alignment	not modelled	99.4	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
103	c1yveK	Alignment	not modelled	99.3	17	PDB header: oxidoreductase Chain: K: PDB Molecule: acetohydroxy acid isomeroreductase; PDBTitle: acetohydroxy acid isomeroreductase complexed with nadph,2 magnesium and inhibitor ipoha (n-hydroxy-n-3 isopropylxamate)
104	c3i83B	Alignment	not modelled	99.1	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-dehydropantoate 2-reductase; PDBTitle: crystal structure of 2-dehydropantoate 2-reductase from methylococcus2 capsulatus
105	d1luxa1	Alignment	not modelled	99.1	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
106	d1ez4a1	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
107	c1yrlD	Alignment	not modelled	99.0	15	PDB header: oxidoreductase Chain: D: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: escherichia coli ketol-acid reductoisomerase
108	c3euwB	Alignment	not modelled	98.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: myo-inositol dehydrogenase; PDBTitle: crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
109	c1e5IA	Alignment	not modelled	98.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
110	c1gpjA	Alignment	not modelled	98.9	22	PDB header: reductase Chain: A: PDB Molecule: glutamyl-trna reductase; PDBTitle: glutamyl-trna reductase from methanopyrus kandleri
111	c2axqA	Alignment	not modelled	98.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
112	d1gdha1	Alignment	not modelled	98.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain
113	d1e5qa1	Alignment	not modelled	98.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
114	d9ldta1	Alignment	not modelled	98.8	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: LDH N-terminal domain-like
115	d1gpja2	Alignment	not modelled	98.8	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
116	c3moiA	Alignment	not modelled	98.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: probable dehydrogenase; PDBTitle: the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
117	c2rirA	Alignment	not modelled	98.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: dipicolinate synthase, a chain; PDBTitle: crystal structure of dipicolinate synthase, a chain, from bacillus2 subtilis
118	c3db2C	Alignment	not modelled	98.8	14	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
119	d1qmgA2	Alignment	not modelled	98.8	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
120	d2naca1	Alignment	not modelled	98.8	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Formate/glycerate dehydrogenases, NAD-domain