Phyre2

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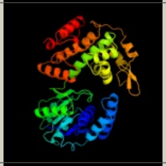
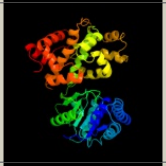
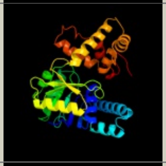
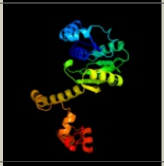
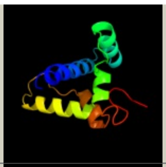
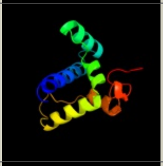
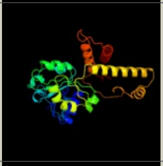
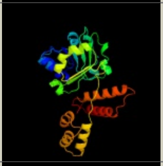
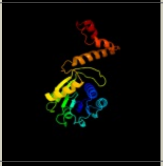
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mogA_	Alignment		100.0	100	**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
2	c2d3tB_	Alignment		100.0	29	**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
3	c2x58B_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** the crystal structure of mfe1 liganded with coa
4	c1zcjA_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**peroxisomal bifunctional enzyme; **PDBTitle:** crystal structure of 3-hydroxyacyl-coa dehydrogenase
5	c3k6jA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein f01g10.3, confirmed by transcript evidence; **PDBTitle:** crystal structure of the dehydrogenase part of multifuctional enzyme 12 from c.elegans
6	c2wtbA_	Alignment		100.0	33	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fatty acid multifunctional protein (atmfp2); **PDBTitle:** arabidopsis thaliana multifuctional protein, mfp2
7	c1m75B_	Alignment		100.0	42	**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
8	c1zejA_	Alignment		100.0	33	**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
9	c2ep9A_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-gulonate 3-dehydrogenase; **PDBTitle:** crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)
10	d1wdka3	Alignment		100.0	33	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
11	d1f0ya2	Alignment		100.0	43	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain

12	d3hdha1	Alignment		100.0	41	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
13	d1f0ya1	Alignment		100.0	39	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
14	d1wdka1	Alignment		100.0	26	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
15	c1vpdA_	Alignment		99.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase; **PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
16	d1dlja2	Alignment		99.9	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
17	c3pduF_	Alignment		99.9	13	**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+
18	c3d1lB_	Alignment		99.9	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative nadp oxidoreductase bf3122; **PDBTitle:** crystal structure of putative nadp oxidoreductase bf3122 from2 bacteroides fragilis
19	d1wdka2	Alignment		99.8	20	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**HCDH C-domain-like
20	c3ctvA_	Alignment		99.8	37	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyacyl-coa dehydrogenase; **PDBTitle:** crystal structure of central domain of 3-hydroxyacyl-coa2 dehydrogenase from archaeoglobus fulgidus
21	c3pefA_	Alignment	not modelled	99.8	15	**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+
22	c3ckyA_	Alignment	not modelled	99.8	16	**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
23	d1ez4a1	Alignment	not modelled	99.8	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
24	c3ggpA_	Alignment	not modelled	99.8	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+
25	c3dzbA_	Alignment	not modelled	99.8	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
26	c2g5cD_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from aquifex aeolicus
27	c2pv7B_	Alignment	not modelled	99.8	20	**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

28	c2uyyD_	Alignment	not modelled	99.8	12	**PDB header:**cytokine **Chain:** D: **PDB Molecule:**n-pac protein; **PDBTitle:** structure of the cytokine-like nuclear factor n-pac
29	c3l6dB_	Alignment	not modelled	99.8	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of putative oxidoreductase from pseudomonas putida2 kt2440
30	c3dojA_	Alignment	not modelled	99.7	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dehydrogenase-like protein; **PDBTitle:** structure of glyoxylate reductase 1 from arabidopsis2 (atglyr1)
31	c3b1fA_	Alignment	not modelled	99.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative prephenate dehydrogenase; **PDBTitle:** crystal structure of prephenate dehydrogenase from streptococcus2 mutans
32	c3cumA_	Alignment	not modelled	99.7	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
33	d2g5ca2	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
34	d1uxja1	Alignment	not modelled	99.7	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
35	c1np3B_	Alignment	not modelled	99.7	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ketol-acid reductoisomerase; **PDBTitle:** crystal structure of class i acetohydroxy acid isomeroreductase from2 pseudomonas aeruginosa
36	c3g0oA_	Alignment	not modelled	99.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of 3-hydroxyisobutyrate dehydrogenase2 (ygbj) from salmonella typhimurium
37	c2gf2B_	Alignment	not modelled	99.7	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of human hydroxyisobutyrate dehydrogenase
38	d2f1ka2	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
39	c2y0dB_	Alignment	not modelled	99.7	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**udp-glucose dehydrogenase; **PDBTitle:** bcec mutation y10k
40	c2f1kD_	Alignment	not modelled	99.7	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of synechocystis arogenate dehydrogenase
41	c1yb4A_	Alignment	not modelled	99.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronic semialdehyde reductase; **PDBTitle:** crystal structure of the tartronic semialdehyde reductase from2 salmonella typhimurium lt2
42	c2ahrB_	Alignment	not modelled	99.7	15	**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
43	c2i76B_	Alignment	not modelled	99.7	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of protein tm1727 from thermotoga maritima
44	d2ahra2	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
45	c1mv8A_	Alignment	not modelled	99.7	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 psuedomonas aeruginosa
46	d1yqga2	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
47	c3qhaB_	Alignment	not modelled	99.6	20	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
48	c3ojlA_	Alignment	not modelled	99.6	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cap5o; **PDBTitle:** native structure of the udp-n-acetyl-mannosamine dehydrogenase cap5o2 from staphylococcus aureus
49	d1ojua1	Alignment	not modelled	99.6	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
50	c3gg2B_	Alignment	not modelled	99.6	19	**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
51	c3k96B_	Alignment	not modelled	99.6	12	**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
52	c3triB_	Alignment	not modelled	99.6	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyrroline-5-carboxylate reductase; **PDBTitle:** structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
						PDB header:oxidoreductase

53	c2ag8A_	Alignment	not modelled	99.6	16	**Chain:** A: **PDB Molecule:**pyrroline-5-carboxylate reductase; **PDBTitle:** nadp complex of pyrroline-5-carboxylate reductase from neisseria2 meningitidis
54	d2b0ja2	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
55	c3gt0A_	Alignment	not modelled	99.6	13	**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
56	d1guza1	Alignment	not modelled	99.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
57	d1mv8a2	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
58	c3dttA_	Alignment	not modelled	99.6	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
59	c3prjB_	Alignment	not modelled	99.6	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.
60	c3hn2A_	Alignment	not modelled	99.6	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
61	c1m67A_	Alignment	not modelled	99.6	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
62	d1ldma1	Alignment	not modelled	99.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
63	c3ktdC_	Alignment	not modelled	99.6	19	**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
64	d1llca1	Alignment	not modelled	99.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
65	d1ldna1	Alignment	not modelled	99.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
66	d9ldta1	Alignment	not modelled	99.6	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
67	d1gv0a1	Alignment	not modelled	99.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
68	d1t2da1	Alignment	not modelled	99.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
69	c3c24A_	Alignment	not modelled	99.5	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
70	c3g79A_	Alignment	not modelled	99.5	16	**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
71	d1pzga1	Alignment	not modelled	99.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
72	c2izzE_	Alignment	not modelled	99.5	12	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyrroline-5-carboxylate reductase 1; **PDBTitle:** crystal structure of human pyrroline-5-carboxylate2 reductase
73	c2q3eH_	Alignment	not modelled	99.5	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
74	c2vq3B_	Alignment	not modelled	99.5	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
75	d1i10a1	Alignment	not modelled	99.5	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
76	d3cuma2	Alignment	not modelled	99.5	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
77	d1llda1	Alignment	not modelled	99.5	25	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
78	c2cvzD_	Alignment	not modelled	99.5	19	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase;

78	c2cvzD_	Alignment	not modelled	99.5	19	**PDBTitle:** structure of hydroxyisobutyrate dehydrogenase from thermus2 thermophilus hb8
79	d1n1ea2	Alignment	not modelled	99.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
80	c3plnA_	Alignment	not modelled	99.5	20	**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
81	d1y6ja1	Alignment	not modelled	99.5	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
82	c2rcyB_	Alignment	not modelled	99.5	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
83	c2o3jC_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**udp-glucose 6-dehydrogenase; **PDBTitle:** structure of caenorhabditis elegans udp-glucose dehydrogenase
84	c1pgjA_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase; **PDBTitle:** x-ray structure of 6-phosphogluconate dehydrogenase from the protozoan2 parasite t. brucei
85	d1i0za1	Alignment	not modelled	99.4	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
86	c1wpqB_	Alignment	not modelled	99.4	15	**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
87	d2ldxa1	Alignment	not modelled	99.4	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
88	c2graA_	Alignment	not modelled	99.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyrroline-5-carboxylate reductase 1; **PDBTitle:** crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp
89	c1i36A_	Alignment	not modelled	99.4	13	**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
90	d2pv7a2	Alignment	not modelled	99.4	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
91	d1vpda2	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
92	c2iz1C_	Alignment	not modelled	99.4	14	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating; **PDBTitle:** 6pdh complexed with pex inhibitor synchrotron data
93	c1ks9A_	Alignment	not modelled	99.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-dehydropantoate 2-reductase; **PDBTitle:** ketopantoate reductase from escherichia coli
94	c2p4qA_	Alignment	not modelled	99.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase, decarboxylating 1; **PDBTitle:** crystal structure analysis of gnd1 in saccharomyces cerevisiae
95	d1pgja2	Alignment	not modelled	99.3	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
96	c3fwnB_	Alignment	not modelled	99.3	17	**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
97	c1dliA_	Alignment	not modelled	99.3	19	**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
98	c2vhyB_	Alignment	not modelled	99.3	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
99	d2pgda2	Alignment	not modelled	99.3	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
100	c1bg6A_	Alignment	not modelled	99.3	18	**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
101	c2ofpB_	Alignment	not modelled	99.3	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
102	d1bg6a2	Alignment	not modelled	99.3	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal

						domain
103	c3hwrA_	Alignment	not modelled	99.3	15	**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
104	c1txgA_	Alignment	not modelled	99.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glycerol-3-phosphate dehydrogenase [nad(p)+]; **PDBTitle:** structure of glycerol-3-phosphate dehydrogenase from archaeoglobus2 fulgidus
105	d1jaya_	Alignment	not modelled	99.3	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
106	d5ldha1	Alignment	not modelled	99.3	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
107	c1pgqA_	Alignment	not modelled	99.3	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
108	d1np3a2	Alignment	not modelled	99.3	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
109	d1txga2	Alignment	not modelled	99.2	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
110	d1hyha1	Alignment	not modelled	99.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**LDH N-terminal domain-like
111	c3qsgA_	Alignment	not modelled	99.2	15	**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
112	c3ghyA_	Alignment	not modelled	99.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ketopantoate reductase protein; **PDBTitle:** crystal structure of a putative ketopantoate reductase from ralstonia2 solanacearum molk2
113	c2ew2B_	Alignment	not modelled	99.2	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
114	d1i36a2	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
115	c1z82A_	Alignment	not modelled	99.1	14	**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
116	d2cvza2	Alignment	not modelled	99.1	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
117	c3c7cB_	Alignment	not modelled	99.1	19	**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)
118	c1gv1D_	Alignment	not modelled	99.1	20	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** structural basis for thermophilic protein stability:2 structures of thermophilic and mesophilic malate3 dehydrogenases
119	c1yj8C_	Alignment	not modelled	99.1	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glycerol-3-phosphate dehydrogenase; **PDBTitle:** initial structural analysis of plasmodium falciparum glycerol-3-2 phosphate dehydrogenase
120	c1ur5C_	Alignment	not modelled	99.1	23	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**malate dehydrogenase; **PDBTitle:** stabilization of a tetrameric malate dehydrogenase by2 introduction of a disulfide bridge at the dimer/dimer3 interface