






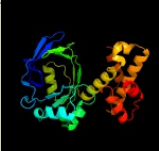

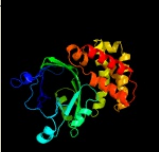





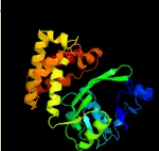


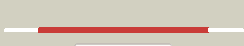


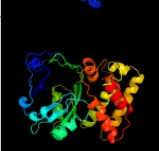


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2573 (-) _2897966_2898793
Date	Wed Aug 7 12:50:21 BST 2019
Unique Job ID	1224ff19b75099a6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ol9A_</a>	 Alignment		100.0	100	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of putative 2-dehydropantoate 2-reductase pane from2 mycobacterium tuberculosis complexed with nadp and oxamate
2	<a href="#">c2ew2B_</a>	 Alignment		100.0	23	<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 from2 enterococcus faecalis
3	<a href="#">c3g17H_</a>	 Alignment		100.0	28	<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
4	<a href="#">c2qytA_</a>	 Alignment		100.0	20	<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
5	<a href="#">c3i83B_</a>	 Alignment		100.0	22	<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
6	<a href="#">c3egoB_</a>	 Alignment		100.0	17	<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-reductase pane from2 bacillus subtilis
7	<a href="#">c5zikC_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> probable 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of ketopantoate reductase from pseudomonas2 aeruginosa
8	<a href="#">c3hwrA_</a>	 Alignment		100.0	27	<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
9	<a href="#">c2ofpB_</a>	 Alignment		100.0	20	<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
10	<a href="#">c3wfiD_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> the complex structure of d-mandelate dehydrogenase with nadh
11	<a href="#">c3hn2A_</a>	 Alignment		100.0	22	<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

12	<a href="#">c1ks9A_</a>	Alignment		100.0	20	<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
13	<a href="#">c3ghyA_</a>	Alignment		100.0	24	<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="#">c5ayvB_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-dehydropantoate 2-reductase; <b>PDBTitle:</b> crystal structure of archaeal ketopantoate reductase complexed with2 coenzyme a and 2-oxopantoate
15	<a href="#">c4fgwA_</a>	Alignment		100.0	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol-3-phosphate dehydrogenase [nad(+)] 1; <b>PDBTitle:</b> structure of glycerol-3-phosphate dehydrogenase, gpd1, from2 sacharomyces cerevisiae
16	<a href="#">c3k96B_</a>	Alignment		100.0	16	<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
17	<a href="#">c1bg6A_</a>	Alignment		100.0	14	<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
18	<a href="#">c1z82A_</a>	Alignment		100.0	16	<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) from2 thermotoga maritima at 2.00 a resolution
19	<a href="#">c1yj8C_</a>	Alignment		100.0	11	<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
20	<a href="#">c1wpgB_</a>	Alignment		100.0	13	<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
21	<a href="#">c1m67A_</a>	Alignment	not modelled	100.0	11	<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 inhibitor2 2-bromo-6-hydroxy-purine
22	<a href="#">c1txgA_</a>	Alignment	not modelled	100.0	10	<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
23	<a href="#">d1ks9a1</a>	Alignment	not modelled	99.9	27	<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
24	<a href="#">c3c7cB_</a>	Alignment	not modelled	99.9	15	<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)
25	<a href="#">c6c4lC_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> yersinopine dehydrogenase; <b>PDBTitle:</b> yersinopine dehydrogenase (ypodh) - apo
26	<a href="#">c6c4nB_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pseudopaline dehydrogenase; <b>PDBTitle:</b> pseudopaline dehydrogenase (paodh) - nadp+ bound
27	<a href="#">c3qhaB_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
28	<a href="#">c6c4rA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> staphylopine dehydrogenase; <b>PDBTitle:</b> staphylopine dehydrogenase (saodh) - apo

29	<a href="#">c4oqzA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase yfjr; <b>PDBTitle:</b> streptomyces aurantiacus imine reductase
30	<a href="#">c5ojIA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> imine reductase; <b>PDBTitle:</b> imine reductase from aspergillus terreus in complex with nadph4 and2 dibenz[c,e]azepine
31	<a href="#">c5a9tA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dehydrogenase; <b>PDBTitle:</b> imine reductase from amycolatopsis orientalis in complex2 with (r)-methyltetrahydroisoquinoline
32	<a href="#">c5y8mA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> mycobacterium tuberculosis 3-hydroxyisobutyrate dehydrogenase2 (mthibadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba)
33	<a href="#">d1ks9a2</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
34	<a href="#">c5g6sD_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> imine reductase; <b>PDBTitle:</b> imine reductase from aspergillus oryzae in complex with nadp(h) and2 (r)-rasagiline
35	<a href="#">c4d3fB_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> imine reductase; <b>PDBTitle:</b> bcsired from bacillus cereus in complex with nadph
36	<a href="#">c3w6uA_</a>	Alignment	not modelled	99.7	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, nad-binding protein; <b>PDBTitle:</b> crystal structure of nadp bound l-serine 3-dehydrogenase from2 hyperthermophilic archaeon pyrobaculum calidifontis
37	<a href="#">c2gf2B_</a>	Alignment	not modelled	99.7	15	<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
38	<a href="#">c6grIA_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> beta-hydroxyacid dehydrogenase, 3-hydroxyisobutyrate <b>PDBTitle:</b> structure of imine reductase (apo form) at 1.6 a resolution from2 saccharomonospora xinjiangensis
39	<a href="#">c4oqyA_</a>	Alignment	not modelled	99.7	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (s)-imine reductase; <b>PDBTitle:</b> streptomyces sp. gf3546 imine reductase
40	<a href="#">c5ocmA_</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad_gly3p_dh, nad-dependent glycerol-3-phosphate <b>PDBTitle:</b> imine reductase from streptosporangium roseum in complex with nadp+2 and 2,2,2-trifluoroacetophenone hydrate
41	<a href="#">c4d3sA_</a>	Alignment	not modelled	99.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> imine reductase; <b>PDBTitle:</b> imine reductase from nocardiosis halophila
42	<a href="#">c3dojA_</a>	Alignment	not modelled	99.6	16	<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 arabidopsis (atglyr1)
43	<a href="#">c2uyyD_</a>	Alignment	not modelled	99.6	17	<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
44	<a href="#">c3zhhC_</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> r-imine reductase; <b>PDBTitle:</b> r-imine reductase from streptomyces kanamyceticus in2 complex with nadp.
45	<a href="#">c3cumA_</a>	Alignment	not modelled	99.6	17	<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
46	<a href="#">d1bg6a2</a>	Alignment	not modelled	99.5	11	<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
47	<a href="#">c3pduF_</a>	Alignment	not modelled	99.5	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+
48	<a href="#">c3g0oA_</a>	Alignment	not modelled	99.5	21	<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
49	<a href="#">c1yb4A_</a>	Alignment	not modelled	99.5	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
50	<a href="#">c3ckyA_</a>	Alignment	not modelled	99.5	12	<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
51	<a href="#">c4dlIB_</a>	Alignment	not modelled	99.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-hydroxy-3-oxopropionate reductase; <b>PDBTitle:</b> crystal structure of a 2-hydroxy-3-oxopropionate reductase from2 polaromonas sp. js666
52	<a href="#">c3l6dB_</a>	Alignment	not modelled	99.4	13	<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

53	<a href="#">c4qbjB_</a>	Alignment	not modelled	99.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase nad-binding; <b>PDBTitle:</b> crystal structure of nad-binding 6-phosphogluconate dehydrogenase from2 dyadobacter fermentans
54	<a href="#">c5je8A_</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyisobutyrate dehydrogenase; <b>PDBTitle:</b> the crystal structure of bacillus cereus 3-hydroxyisobutyrate2 dehydrogenase in complex with nad
55	<a href="#">c1vpdA_</a>	Alignment	not modelled	99.4	17	<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]
56	<a href="#">c4wb1B_</a>	Alignment	not modelled	99.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cals8; <b>PDBTitle:</b> crystal structure of cal8 from micromonospora echinospora (p294s2 mutant)
57	<a href="#">c3pefA_</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, nad-binding; <b>PDBTitle:</b> crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+
58	<a href="#">c2y0dB_</a>	Alignment	not modelled	99.3	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> bcec mutation y10k
59	<a href="#">c3gg2B_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sugar dehydrogenase, udp-glucose/gdp-mannose dehydrogenase <b>PDBTitle:</b> crystal structure of udp-glucose 6-dehydrogenase from porphyromonas2 gingivalis bound to product udp-glucuronate
60	<a href="#">c5t57A_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> semialdehyde dehydrogenase nad-binding protein; <b>PDBTitle:</b> crystal structure of a semialdehyde dehydrogenase nad-binding protein2 from cupriavidus necator in complex with calcium and nad
61	<a href="#">c4ezbA_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> crystal structure of the conserved hypothetical protein from2 sinorhizobium meliloti 1021
62	<a href="#">c4j0eB_</a>	Alignment	not modelled	99.2	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable 3-hydroxyacyl-coa dehydrogenase f54c8.1; <b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-coa dehydrogenase from2 caenorhabditis elegans in p1 space group
63	<a href="#">c4a7pA_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> se-met derivatized udg, udp-glucose dehydrogenase from sphingomonas2 elodea
64	<a href="#">c4e21B_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase (decarboxylating); <b>PDBTitle:</b> the crystal structure of 6-phosphogluconate dehydrogenase from2 geobacter metallireducens
65	<a href="#">c1mv8A_</a>	Alignment	not modelled	99.2	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
66	<a href="#">c5bseF_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase; <b>PDBTitle:</b> crystal structure of medicago truncatula (delta)1-pyrroline-5-2 carboxylate reductase (mtp5cr)
67	<a href="#">c3qsgA_</a>	Alignment	not modelled	99.2	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> nad-binding phosphogluconate dehydrogenase-like protein; <b>PDBTitle:</b> crystal structure of nad-binding phosphogluconate dehydrogenase-like2 protein from alicyclobacillus acidocaldarius
68	<a href="#">c4kqxB_</a>	Alignment	not modelled	99.2	10	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> mutant slackia exigua kari ddv in complex with nad and an inhibitor
69	<a href="#">c2izzE_</a>	Alignment	not modelled	99.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase 1; <b>PDBTitle:</b> crystal structure of human pyrroline-5-carboxylate reductase
70	<a href="#">c2cvzD_</a>	Alignment	not modelled	99.2	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 hb8
71	<a href="#">d1txga2</a>	Alignment	not modelled	99.1	9	<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
72	<a href="#">c3vtfA_</a>	Alignment	not modelled	99.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose 6-dehydrogenase; <b>PDBTitle:</b> structure of a udp-glucose dehydrogenase from the hyperthermophilic2 archaeon pyrobaculum islandicum
73	<a href="#">c3fwnB_</a>	Alignment	not modelled	99.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> dimeric 6-phosphogluconate dehydrogenase complexed with 6-2 phosphogluconate and 2'-monophosphoadenosine-5'-diphosphate
74	<a href="#">c1pgiA_</a>	Alignment	not modelled	99.1	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
75	<a href="#">c5u5gC_</a>	Alignment	not modelled	99.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> psf3 in complex with nadp+ and 2-opp
						<b>PDB header:</b> oxidoreductase



76	<a href="#">c2iz1C_</a>	Alignment	not modelled	99.1	16	<b>Chain:</b> C: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> 6pdh complexed with pex inhibitor synchrotron data
77	<a href="#">c2graA_</a>	Alignment	not modelled	99.1	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase 1; <b>PDBTitle:</b> crystal structure of human pyrroline-5-carboxylate reductase complexed2 with nadp
78	<a href="#">d1jaya_</a>	Alignment	not modelled	99.0	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
79	<a href="#">c2p4qA_</a>	Alignment	not modelled	99.0	12	<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
80	<a href="#">c6aqjB_</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase (nadp(+)); <b>PDBTitle:</b> crystal structures of staphylococcus aureus ketol-acid2 reductoisomerase in complex with two transition state analogs that3 have biocidal activity.
81	<a href="#">d1n1ea2</a>	Alignment	not modelled	99.0	10	<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
82	<a href="#">c3triB_</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase; <b>PDBTitle:</b> structure of a pyrroline-5-carboxylate reductase (proc) from coxiella2 burnetii
83	<a href="#">c3d1lB_</a>	Alignment	not modelled	99.0	12	<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
84	<a href="#">c3dttA_</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative f420 dependent nadp-reductase2 (arth_0613) from arthrobacter sp. fb24 at 1.70 a resolution
85	<a href="#">c1pgqA_</a>	Alignment	not modelled	98.9	13	<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
86	<a href="#">c4e12A_</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> diketoreductase; <b>PDBTitle:</b> substrate-directed dual catalysis of dicarbonyl compounds by2 diketoreductase
87	<a href="#">c5n2iC_</a>	Alignment	not modelled	98.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> reduced coenzyme f420:nadp oxidoreductase; <b>PDBTitle:</b> f420:nadph oxidoreductase from thermobifida fusca with nadp+ bound
88	<a href="#">c2ahrB_</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative pyrroline carboxylate reductase; <b>PDBTitle:</b> crystal structures of 1-pyrroline-5-carboxylate reductase from human2 pathogen streptococcus pyogenes
89	<a href="#">c4xdzB_</a>	Alignment	not modelled	98.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> holo structure of ketol-acid reductoisomerase from ignisphaera2 aggregans
90	<a href="#">c3plnA_</a>	Alignment	not modelled	98.9	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
91	<a href="#">c4r16A_</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 418aa long hypothetical udp-n-acetyl-d-mannosaminuronic <b>PDBTitle:</b> structure of udp-d-mannac dehydrogeanse from pyrococcus horikoshii
92	<a href="#">c1i36A_</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> conserved hypothetical protein mth1747; <b>PDBTitle:</b> structure of conserved protein mth1747 of unknown function reveals2 structural similarity with 3-hydroxyacid dehydrogenases
93	<a href="#">c2f1kD_</a>	Alignment	not modelled	98.9	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of synechocystis arogenate dehydrogenase
94	<a href="#">c2o3jC_</a>	Alignment	not modelled	98.8	13	<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
95	<a href="#">c5yeqB_</a>	Alignment	not modelled	98.8	10	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase (nadp(+)); <b>PDBTitle:</b> the structure of sac-kari protein
96	<a href="#">c6fqzB_</a>	Alignment	not modelled	98.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase, decarboxylating; <b>PDBTitle:</b> plasmodium falciparum 6-phosphogluconate dehydrogenase in its apo2 form, in complex with its cofactor nadp+ and in complex with its3 substrate 6-phosphogluconate
97	<a href="#">c2q3eH_</a>	Alignment	not modelled	98.8	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
98	<a href="#">c3prjB_</a>	Alignment	not modelled	98.8	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.
99	<a href="#">c2ep9A_</a>	Alignment	not modelled	98.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-gulonate 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of the rabbit l-gulonate 3-dehydrogenase2 (nadh form)

100	<a href="#">c2pv7B</a>	Alignment	not modelled	98.7	12	<b>PDB header:</b> isomerase, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) <b>PDBTitle:</b> crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
101	<a href="#">c4ypoB</a>	Alignment	not modelled	98.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis ketol-acid2 reductoisomerase in complex with mg2+
102	<a href="#">c1dliA</a>	Alignment	not modelled	98.6	11	<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
103	<a href="#">c4pzdB</a>	Alignment	not modelled	98.6	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of (s)-3-hydroxybutyryl-coa dehydrogenase paah1 in2 complex with nad+
104	<a href="#">c3c24A</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (yp_511008.1) from2 jannaschia sp. ccs1 at 1.62 a resolution
105	<a href="#">c2ag8A</a>	Alignment	not modelled	98.6	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 neisseria2 meningitidis
106	<a href="#">c5t8xA</a>	Alignment	not modelled	98.6	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prephenate dehydrogenase 1; <b>PDBTitle:</b> prephenate dehydrogenase from soybean
107	<a href="#">c2rcyB</a>	Alignment	not modelled	98.5	9	<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
108	<a href="#">d2ahra2</a>	Alignment	not modelled	98.5	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
109	<a href="#">c3ojjA</a>	Alignment	not modelled	98.5	12	<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
110	<a href="#">d1f0ya2</a>	Alignment	not modelled	98.5	12	<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
111	<a href="#">d1n1ea1</a>	Alignment	not modelled	98.5	14	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> Glycerol-3-phosphate dehydrogenase
112	<a href="#">c1m75B</a>	Alignment	not modelled	98.5	13	<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-coa2 dehydrogenase in complex with nad and acetoacetyl-coa
113	<a href="#">c4wjiA</a>	Alignment	not modelled	98.5	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cyclohexadienyl dehydrogenase and adh prephenate <b>PDBTitle:</b> crystal structure of cyclohexadienyl dehydrogenase from sinorhizobium2 melloti in complex with nadp and tyrosine
114	<a href="#">c2g5cD</a>	Alignment	not modelled	98.5	9	<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
115	<a href="#">d2f1ka2</a>	Alignment	not modelled	98.5	10	<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
116	<a href="#">c3qt0A</a>	Alignment	not modelled	98.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrroline-5-carboxylate reductase; <b>PDBTitle:</b> crystal structure of pyrroline 5-carboxylate reductase from bacillus2 cereus. northeast structural genomics consortium target bcr38b
117	<a href="#">d1yqga2</a>	Alignment	not modelled	98.4	20	<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
118	<a href="#">c6hcyA</a>	Alignment	not modelled	98.4	19	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> metalloreductase steap4; <b>PDBTitle:</b> human steap4 bound to nadp, fad, heme and fe(iii)-nta.
119	<a href="#">c1np3B</a>	Alignment	not modelled	98.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> crystal structure of class i acetohydroxy acid isomeroeductase from2 pseudomonas aeruginosa
120	<a href="#">c4kueA</a>	Alignment	not modelled	98.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxybutyryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 clostridium butyricum