

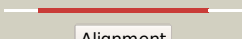













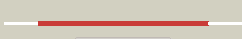













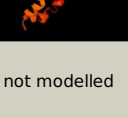


# Phyre2

Email [mdejesus@rockefeller.edu](mailto:mdejesus@rockefeller.edu)  
 Description RVBD3754\_(tyrA)\_4200599\_4201504  
 Date Fri Aug 9 18:20:45 BST 2019  
 Unique Job ID 0e91b96616be1515

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3ktdC_</a>	 Alignment		100.0	48	<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
2	<a href="#">c5uscB_</a>	 Alignment		100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase tyra from bacillus2 anthracis in complex with nad and l-tyrosine
3	<a href="#">c2g5cD_</a>	 Alignment		100.0	21	<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
4	<a href="#">c3ggpA_</a>	 Alignment		100.0	21	<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+
5	<a href="#">c5t8xA_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prephenate dehydrogenase 1; <b>PDBTitle:</b> prephenate dehydrogenase from soybean
6	<a href="#">c2f1kD_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of synechocystis arogenate dehydrogenase
7	<a href="#">c4wjiA_</a>	 Alignment		100.0	27	<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 meliloti in complex with nadp and tyrosine
8	<a href="#">c3b1fA_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from streptococcus2 mutans
9	<a href="#">c3dzbA_</a>	 Alignment		100.0	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of prephenate dehydrogenase from streptococcus2 thermophilus
10	<a href="#">c2pv7B_</a>	 Alignment		100.0	18	<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
11	<a href="#">d2f1ka1</a>	 Alignment		100.0	27	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> TyrA dimerization domain-like

12	<a href="#">d2g5ca1</a>	Alignment		99.9	23	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> TyrA dimerization domain-like
13	<a href="#">d2pv7a1</a>	Alignment		99.9	17	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> TyrA dimerization domain-like
14	<a href="#">c3triB_</a>	Alignment		99.9	15	<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
15	<a href="#">d2f1ka2</a>	Alignment		99.9	23	<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
16	<a href="#">d2g5ca2</a>	Alignment		99.8	19	<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
17	<a href="#">c2ag8A_</a>	Alignment		99.8	15	<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
18	<a href="#">d2pv7a2</a>	Alignment		99.8	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
19	<a href="#">c2graA_</a>	Alignment		99.8	15	<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
20	<a href="#">c2ahrB_</a>	Alignment		99.8	11	<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
21	<a href="#">c2izzE_</a>	Alignment	not modelled	99.8	15	<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
22	<a href="#">c3d1lB_</a>	Alignment	not modelled	99.7	13	<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
23	<a href="#">d2b0ja2</a>	Alignment	not modelled	99.7	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
24	<a href="#">c3c24A_</a>	Alignment	not modelled	99.7	12	<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
25	<a href="#">c5bseF_</a>	Alignment	not modelled	99.7	16	<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)
26	<a href="#">c1i36A_</a>	Alignment	not modelled	99.7	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
27	<a href="#">c4tskA_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> oxidoreductase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> ketol-acid reductoisomerase from alicyclobacillus acidocaldarius
28	<a href="#">c6jczL_</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> isomerase <b>Chain:</b> L: <b>PDB Molecule:</b> putative ketol-acid reductoisomerase 2; <b>PDBTitle:</b> cryo-em structure of sulfolobus solfataricus ketol-acid2 reductoisomerase (sso-kari) in complex with mg2+, nadph, and cpd

						at3 ph7.5
29	<a href="#">c5t57A_</a>	Alignment	not modelled	99.6	14	<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
30	<a href="#">c2rcyB_</a>	Alignment	not modelled	99.6	15	<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
31	<a href="#">c2ep9A_</a>	Alignment	not modelled	99.5	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)
32	<a href="#">c4d3fB_</a>	Alignment	not modelled	99.5	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
33	<a href="#">c6huxA_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> h(2)-forming methylenetetrahydromethanopterin <b>PDBTitle:</b> hmdii from methanocaldococcus jannaschii reconstituted with fe-2 guanylylpyridinol (fegp) cofactor and co-crystallized with methenyl-3 tetrahydromethanopterin at 2.5 a resolution
34	<a href="#">c5g6sD_</a>	Alignment	not modelled	99.5	13	<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="#">c5u5gC_</a>	Alignment	not modelled	99.5	15	<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
36	<a href="#">c4yt2A_</a>	Alignment	not modelled	99.5	14	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> h(2)-forming methylenetetrahydromethanopterin <b>PDBTitle:</b> hmd ii from methanocaldococcus jannaschii
37	<a href="#">c5ocmA_</a>	Alignment	not modelled	99.5	17	<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
38	<a href="#">c4oqyA_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (s)-imine reductase; <b>PDBTitle:</b> streptomyces sp. gf3546 imine reductase
39	<a href="#">c3pduF_</a>	Alignment	not modelled	99.4	12	<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+
40	<a href="#">c3zhbC_</a>	Alignment	not modelled	99.4	20	<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.
41	<a href="#">c3gt0A_</a>	Alignment	not modelled	99.4	11	<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
42	<a href="#">c3l6dB_</a>	Alignment	not modelled	99.4	16	<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
43	<a href="#">c2iz1C_</a>	Alignment	not modelled	99.4	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
44	<a href="#">c4oqzA_</a>	Alignment	not modelled	99.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase yfjr; <b>PDBTitle:</b> streptomyces aurantiacus imine reductase
45	<a href="#">c4gbjB_</a>	Alignment	not modelled	99.3	12	<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
46	<a href="#">c3g0oA_</a>	Alignment	not modelled	99.3	13	<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
47	<a href="#">c3ckyA_</a>	Alignment	not modelled	99.3	14	<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
48	<a href="#">c5je8A_</a>	Alignment	not modelled	99.3	11	<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
49	<a href="#">c5a9tA_</a>	Alignment	not modelled	99.3	17	<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
50	<a href="#">c4d3sA_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> imine reductase; <b>PDBTitle:</b> imine reductase from nocardiosis halophila
51	<a href="#">c6grlA_</a>	Alignment	not modelled	99.2	16	<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

52	<a href="#">c4om8B_</a>	Alignment	not modelled	99.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxybutyryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of 5-formyl-3-hydroxy-2-methylpyridine 4-carboxylic acid (fhmpc) 5-dehydrogenase, an nad+ dependent dismutase.
53	<a href="#">c3cumA_</a>	Alignment	not modelled	99.2	16	<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
54	<a href="#">d1wdka3</a>	Alignment	not modelled	99.2	14	<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
55	<a href="#">c4ypoB_</a>	Alignment	not modelled	99.2	10	<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+
56	<a href="#">c6fqzB_</a>	Alignment	not modelled	99.2	14	<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
57	<a href="#">c2uyyD_</a>	Alignment	not modelled	99.2	13	<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
58	<a href="#">d1vpda2</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> 6-phosphogluconate dehydrogenase-like, N-terminal domain
59	<a href="#">c5y8mA_</a>	Alignment	not modelled	99.2	15	<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 (mthbadh) + nad + (r)-3-hydroxyisobutyrate (r-hiba)
60	<a href="#">c3pefA_</a>	Alignment	not modelled	99.2	14	<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+
61	<a href="#">d1f0ya2</a>	Alignment	not modelled	99.2	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
62	<a href="#">d3cuma2</a>	Alignment	not modelled	99.1	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
63	<a href="#">d2ahra2</a>	Alignment	not modelled	99.1	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
64	<a href="#">c4dlIB_</a>	Alignment	not modelled	99.1	15	<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
65	<a href="#">c3qsgA_</a>	Alignment	not modelled	99.1	20	<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
66	<a href="#">c1vpdA_</a>	Alignment	not modelled	99.1	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]
67	<a href="#">d2pgda2</a>	Alignment	not modelled	99.1	14	<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
68	<a href="#">c1np3B_</a>	Alignment	not modelled	99.1	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
69	<a href="#">c4e12A_</a>	Alignment	not modelled	99.1	16	<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
70	<a href="#">c5n2iC_</a>	Alignment	not modelled	99.1	18	<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
71	<a href="#">c5ojlA_</a>	Alignment	not modelled	99.1	18	<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
72	<a href="#">c3w6uA_</a>	Alignment	not modelled	99.1	12	<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 caldifontis
73	<a href="#">c1m75B_</a>	Alignment	not modelled	99.1	11	<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
74	<a href="#">c3dojA_</a>	Alignment	not modelled	99.1	10	<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)
75	<a href="#">c3phaB_</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase;

75	<a href="#">c3qndB</a>	Alignment	not modelled	99.0	14	<b>PDBTitle:</b> crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
76	<a href="#">c6c4lC</a>	Alignment	not modelled	99.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> yersinopine dehydrogenase; <b>PDBTitle:</b> yersinopine dehydrogenase (ypodh) - apo
77	<a href="#">c4r16A</a>	Alignment	not modelled	99.0	12	<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 dehydrogenase from pyrococcus horikoshii
78	<a href="#">c4kueA</a>	Alignment	not modelled	99.0	17	<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
79	<a href="#">c4xdzB</a>	Alignment	not modelled	99.0	13	<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
80	<a href="#">d1yqga2</a>	Alignment	not modelled	99.0	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
81	<a href="#">c4j0eB</a>	Alignment	not modelled	99.0	16	<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
82	<a href="#">c3hn2A</a>	Alignment	not modelled	98.9	13	<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
83	<a href="#">c6hrdD</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 3-hydroxybutyryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of m. tuberculosis fabb2 (rv0468)
84	<a href="#">c2vq3B</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> metalloreductase steap3; <b>PDBTitle:</b> crystal structure of the membrane proximal oxidoreductase2 domain of human steap3, the dominant ferric reductase of3 the erythroid transferrin cycle
85	<a href="#">c3vtfA</a>	Alignment	not modelled	98.9	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
86	<a href="#">c4a7pA</a>	Alignment	not modelled	98.9	12	<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
87	<a href="#">c4pzdB</a>	Alignment	not modelled	98.9	15	<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+
88	<a href="#">c2i76B</a>	Alignment	not modelled	98.9	12	<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
89	<a href="#">c2y0dB</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> bcec mutation y10k
90	<a href="#">c2rafC</a>	Alignment	not modelled	98.9	22	<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-binding oxidoreductase2 (np_786167.1) from lactobacillus plantarum at 1.60 a resolution
91	<a href="#">c3mogA</a>	Alignment	not modelled	98.9	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 from2 escherichia coli k12 substr. mg1655
92	<a href="#">c2yzjC</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> metalloreductase steap4; <b>PDBTitle:</b> rat steap4 oxidoreductase domain complexed with nadp
93	<a href="#">c4ezbA</a>	Alignment	not modelled	98.8	11	<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
94	<a href="#">c3k6jA</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein f01g10.3, confirmed by transcript evidence; <b>PDBTitle:</b> crystal structure of the dehydrogenase part of multifunctional enzyme 12 from c.elegans
95	<a href="#">c1mv8A</a>	Alignment	not modelled	98.8	13	<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
96	<a href="#">c4hujB</a>	Alignment	not modelled	98.8	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a hypothetical protein sma0349 from sinorhizobium2 meliloti
97	<a href="#">c1yb4A</a>	Alignment	not modelled	98.8	14	<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
98	<a href="#">c4wb1B</a>	Alignment	not modelled	98.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cals8; <b>PDBTitle:</b> crystal structure of cals8 from micromonospora echinospora (p294s2 mutant)
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxyacyl-coenzyme a dehydrogenase, mitochondrial;



99	<a href="#">c3rqsB</a>	Alignment	not modelled	98.8	14	<b>PDBTitle:</b> crystal structure of human l-3- hydroxyacyl-coa dehydrogenase2 (ec1.1.1.35) from mitochondria at the resolution 2.0 a, northeast3 structural genomics consortium target hr487, mitochondrial protein4 partnership <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
100	<a href="#">c2gf2B</a>	Alignment	not modelled	98.8	13	<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
101	<a href="#">c3k96B</a>	Alignment	not modelled	98.8	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
102	<a href="#">c3oj1A</a>	Alignment	not modelled	98.8	14	<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
103	<a href="#">d1mv8a2</a>	Alignment	not modelled	98.8	15	<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.
104	<a href="#">c6aqjB</a>	Alignment	not modelled	98.8	13	<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
105	<a href="#">c2p4qA</a>	Alignment	not modelled	98.7	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
106	<a href="#">d1pgja2</a>	Alignment	not modelled	98.7	13	<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
107	<a href="#">c3fwnB</a>	Alignment	not modelled	98.7	15	<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
108	<a href="#">c2o3jC</a>	Alignment	not modelled	98.7	8	<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
109	<a href="#">c1zciA</a>	Alignment	not modelled	98.6	23	<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
110	<a href="#">c3gg2B</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> coenzyme f420-dependent n(5),n(10)- <b>PDBTitle:</b> hmdii from desulfurobacterium thermolithotrophum reconstituted with fe-2 guanylylpyridinol (fegp) cofactor and co-crystallized with methenyl-3 tetrahydrofolate form a
111	<a href="#">c6huyB</a>	Alignment	not modelled	98.6	12	<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
112	<a href="#">c1pgjA</a>	Alignment	not modelled	98.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid multifunctional protein (atmfp2); <b>PDBTitle:</b> arabidopsis thaliana multifunctional protein, mfp2
113	<a href="#">c2wtbA</a>	Alignment	not modelled	98.6	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
114	<a href="#">d1bg6a2</a>	Alignment	not modelled	98.6	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
115	<a href="#">d1jaya</a>	Alignment	not modelled	98.6	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
116	<a href="#">d1i36a2</a>	Alignment	not modelled	98.6	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
117	<a href="#">c5zikC</a>	Alignment	not modelled	98.6	10	<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
118	<a href="#">c1zejA</a>	Alignment	not modelled	98.5	18	<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
119	<a href="#">c5yeqB</a>	Alignment	not modelled	98.5	11	<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
120	<a href="#">d2i76a2</a>	Alignment	not modelled	98.5	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