









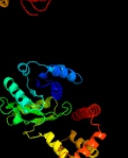

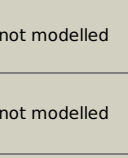


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1715_(fadB3)_1942666_1943580
Date	Fri Aug 2 13:30:31 BST 2019
Unique Job ID	82cd82ebf73c9bcc

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3mogA_</a>	 Alignment		100.0	36	<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
2	<a href="#">c2d3tB_</a>	 Alignment		100.0	29	<b>PDB header:</b> lyase, oxidoreductase/transferase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty oxidation complex alpha subunit; <b>PDBTitle:</b> fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
3	<a href="#">c2x58B_</a>	 Alignment		100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme; <b>PDBTitle:</b> the crystal structure of mfe1 liganded with coa
4	<a href="#">c6iunB_</a>	 Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> enoyl-coa hydratase/delta(3)-cis-delta(2)-trans-enoyl-coa <b>PDBTitle:</b> crystal structure of enoyl-coa hydratase (ech) from ralstonia eutropha2 h16 in complex with nad
5	<a href="#">c4b3hA_</a>	 Alignment		100.0	30	<b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fatty acid beta-oxidation complex alpha-chain fadB; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis fatty acid2 beta-oxidation complex
6	<a href="#">c4om8B_</a>	 Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxybutyryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of 5-formly-3-hydroxy-2-methylpyridine 4-carboxylic2 acid (fhmpc) 5-dehydrogenase, an nad+ dependent dismutase.
7	<a href="#">c1zciA_</a>	 Alignment		100.0	29	<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
8	<a href="#">c3k6jA_</a>	 Alignment		100.0	24	<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
9	<a href="#">c3rqsB_</a>	 Alignment		100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> hydroxyacyl-coenzyme a dehydrogenase, mitochondrial; <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
10	<a href="#">c5zqzC_</a>	 Alignment		100.0	27	<b>PDB header:</b> lyase,hydrolase/transferase <b>Chain:</b> C: <b>PDB Molecule:</b> trifunctional enzyme subunit alpha, mitochondrial; <b>PDBTitle:</b> structure of human mitochondrial trifunctional protein, tetramer
11	<a href="#">c4kueA_</a>	 Alignment		100.0	35	<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

12	<a href="#">c6hrdD_</a>	Alignment		100.0	37	<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)
13	<a href="#">c1m75B_</a>	Alignment		100.0	36	<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
14	<a href="#">c1zejA_</a>	Alignment		100.0	32	<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
15	<a href="#">c2wtbA_</a>	Alignment		100.0	25	<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
16	<a href="#">c4pzdB_</a>	Alignment		100.0	31	<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+
17	<a href="#">c4e12A_</a>	Alignment		100.0	31	<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
18	<a href="#">c4j0eB_</a>	Alignment		100.0	34	<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
19	<a href="#">c2ep9A_</a>	Alignment		100.0	29	<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)
20	<a href="#">d1wdka3</a>	Alignment		100.0	33	<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
21	<a href="#">d1f0ya2</a>	Alignment	not modelled	100.0	36	<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
22	<a href="#">c1vpdA_</a>	Alignment	not modelled	100.0	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]
23	<a href="#">d1f0ya1</a>	Alignment	not modelled	99.9	37	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> HCDH C-domain-like
24	<a href="#">d1wdka1</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> HCDH C-domain-like
25	<a href="#">d3hdha1</a>	Alignment	not modelled	99.9	35	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> HCDH C-domain-like
26	<a href="#">c3pduF_</a>	Alignment	not modelled	99.9	14	<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+
27	<a href="#">c4gbjB_</a>	Alignment	not modelled	99.9	16	<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
						<b>PDB header:</b> oxidoreductase

28	<a href="#">c3d1lB_</a>	Alignment	not modelled	99.9	16	<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
29	<a href="#">c4wjiA_</a>	Alignment	not modelled	99.9	19	<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
30	<a href="#">c6grlA_</a>	Alignment	not modelled	99.9	21	<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
31	<a href="#">c5je8A_</a>	Alignment	not modelled	99.9	14	<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
32	<a href="#">d1dlja2</a>	Alignment	not modelled	99.9	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
33	<a href="#">c4xdyB_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ketol-acid reductoisomerase; <b>PDBTitle:</b> structure of nadh-preferring ketol-acid reductoisomerase from an2 uncultured archaean
34	<a href="#">c2uyyD_</a>	Alignment	not modelled	99.9	15	<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
35	<a href="#">c5ocmA_</a>	Alignment	not modelled	99.9	18	<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
36	<a href="#">c3ckyA_</a>	Alignment	not modelled	99.9	16	<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
37	<a href="#">c4xdzB_</a>	Alignment	not modelled	99.9	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
38	<a href="#">c4d3fB_</a>	Alignment	not modelled	99.9	14	<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
39	<a href="#">c3pefA_</a>	Alignment	not modelled	99.9	16	<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+
40	<a href="#">c4oqyA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> (s)-imine reductase; <b>PDBTitle:</b> streptomyces sp. gf3546 imine reductase
41	<a href="#">c4d3sA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> imine reductase; <b>PDBTitle:</b> imine reductase from nocardioopsis halophila
42	<a href="#">c3dojA_</a>	Alignment	not modelled	99.8	12	<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="#">c3zbcC_</a>	Alignment	not modelled	99.8	24	<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.
44	<a href="#">c5ojlA_</a>	Alignment	not modelled	99.8	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
45	<a href="#">c3g0oA_</a>	Alignment	not modelled	99.8	19	<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
46	<a href="#">c2g5cD_</a>	Alignment	not modelled	99.8	18	<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
47	<a href="#">c3l6dB_</a>	Alignment	not modelled	99.8	18	<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
48	<a href="#">d1wdka2</a>	Alignment	not modelled	99.8	30	<b>Fold:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Superfamily:</b> 6-phosphogluconate dehydrogenase C-terminal domain-like <b>Family:</b> HCDH C-domain-like
49	<a href="#">c2pv7B_</a>	Alignment	not modelled	99.8	20	<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
50	<a href="#">c3dzbA_</a>	Alignment	not modelled	99.8	17	<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
51	<a href="#">c3cumA_</a>	Alignment	not modelled	99.8	19	<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 <b>PDB header:</b> oxidoreductase

52	<a href="#">c5y8mA</a>	Alignment	not modelled	99.8	19	<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)
53	<a href="#">c3ggpA</a>	Alignment	not modelled	99.8	20	<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+
54	<a href="#">c1yb4A</a>	Alignment	not modelled	99.8	17	<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
55	<a href="#">c5u5gC</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> pzf3 in complex with nadp+ and 2-opp
56	<a href="#">c3w6uA</a>	Alignment	not modelled	99.8	18	<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
57	<a href="#">c3b1fA</a>	Alignment	not modelled	99.8	17	<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
58	<a href="#">c6fqzB</a>	Alignment	not modelled	99.8	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
59	<a href="#">c5uscB</a>	Alignment	not modelled	99.8	18	<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
60	<a href="#">c5g6sD</a>	Alignment	not modelled	99.8	19	<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
61	<a href="#">c2gf2B</a>	Alignment	not modelled	99.8	17	<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
62	<a href="#">c1np3B</a>	Alignment	not modelled	99.8	20	<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 isomeroreductase from2 pseudomonas aeruginosa
63	<a href="#">c2f1kD</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> prephenate dehydrogenase; <b>PDBTitle:</b> crystal structure of synechocystis arogenate dehydrogenase
64	<a href="#">c2ahrB</a>	Alignment	not modelled	99.8	14	<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
65	<a href="#">c4dlIB</a>	Alignment	not modelled	99.8	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
66	<a href="#">c2i76B</a>	Alignment	not modelled	99.7	14	<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
67	<a href="#">d1ez4a1</a>	Alignment	not modelled	99.7	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
68	<a href="#">c4ypoB</a>	Alignment	not modelled	99.7	12	<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+
69	<a href="#">c3fwnB</a>	Alignment	not modelled	99.7	17	<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
70	<a href="#">c2iz1C</a>	Alignment	not modelled	99.7	18	<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
71	<a href="#">c2cvzD</a>	Alignment	not modelled	99.7	19	<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
72	<a href="#">c1pgjA</a>	Alignment	not modelled	99.7	16	<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
73	<a href="#">c5t57A</a>	Alignment	not modelled	99.7	17	<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
74	<a href="#">c6aqjB</a>	Alignment	not modelled	99.7	17	<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. <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase,



75	<a href="#">c2p4qA_</a>	Alignment	not modelled	99.7	14	decarboxylating 1; <b>PDBTitle:</b> crystal structure analysis of gnd1 in saccharomyces cerevisiae
76	<a href="#">d2g5ca2</a>	Alignment	not modelled	99.7	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
77	<a href="#">c3triB_</a>	Alignment	not modelled	99.7	17	<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
78	<a href="#">d2ahra2</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
79	<a href="#">c2ag8A_</a>	Alignment	not modelled	99.7	19	<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
80	<a href="#">c3gt0A_</a>	Alignment	not modelled	99.7	14	<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
81	<a href="#">c4hujB_</a>	Alignment	not modelled	99.7	21	<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
82	<a href="#">c4oqzA_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase yfjr; <b>PDBTitle:</b> streptomyces aurantiacus imine reductase
83	<a href="#">c3ktdC_</a>	Alignment	not modelled	99.7	21	<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
84	<a href="#">c4r16A_</a>	Alignment	not modelled	99.7	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 dehydrogenase from pyrococcus horikoshii
85	<a href="#">c1pgqA_</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> oxidoreductase (choh(d)-nadp+(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphogluconate dehydrogenase; <b>PDBTitle:</b> crystallographic study of coenzyme, coenzyme analogue and substrate2 binding in 6-phosphogluconate dehydrogenase: implications for nadp3 specificity and the enzyme mechanism
86	<a href="#">c3plnA_</a>	Alignment	not modelled	99.7	16	<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
87	<a href="#">d1yqga2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> 6-phosphogluconate dehydrogenase-like, N-terminal domain
88	<a href="#">d1ldna1</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
89	<a href="#">c3ojlA_</a>	Alignment	not modelled	99.7	16	<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
90	<a href="#">c5a9tA_</a>	Alignment	not modelled	99.7	16	<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
91	<a href="#">c3vtfA_</a>	Alignment	not modelled	99.7	15	<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
92	<a href="#">c1mv8A_</a>	Alignment	not modelled	99.7	19	<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
93	<a href="#">d2f1ka2</a>	Alignment	not modelled	99.7	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
94	<a href="#">c3dttA_</a>	Alignment	not modelled	99.7	22	<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
95	<a href="#">c5bseF_</a>	Alignment	not modelled	99.7	13	<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)
96	<a href="#">d3cuma2</a>	Alignment	not modelled	99.7	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
97	<a href="#">c3qhaB_</a>	Alignment	not modelled	99.7	21	<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
98	<a href="#">c4wb1B_</a>	Alignment	not modelled	99.7	20	<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)
99	<a href="#">c2y0dB_</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glucose dehydrogenase; <b>PDBTitle:</b> bcec mutation y10k
						<b>Fold:</b> NAD(P)-binding Rossmann-fold domains

100	<a href="#">d1ldma1</a>	Alignment	not modelled	99.7	17	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
101	<a href="#">c4ezbA</a>	Alignment	not modelled	99.7	18	<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
102	<a href="#">d1luxja1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
103	<a href="#">d9ldta1</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
104	<a href="#">c1m67A</a>	Alignment	not modelled	99.6	13	<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
105	<a href="#">d1mv8a2</a>	Alignment	not modelled	99.6	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
106	<a href="#">c3ctvA</a>	Alignment	not modelled	99.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-hydroxyacyl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of central domain of 3-hydroxyacyl-coa dehydrogenase2 from archaeoglobus fulgidus
107	<a href="#">c2vq3B</a>	Alignment	not modelled	99.6	15	<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
108	<a href="#">c3k96B</a>	Alignment	not modelled	99.6	14	<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
109	<a href="#">c5t8xA</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prephenate dehydrogenase 1; <b>PDBTitle:</b> prephenate dehydrogenase from soybean
110	<a href="#">c4e21B</a>	Alignment	not modelled	99.6	16	<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
111	<a href="#">c2izzE</a>	Alignment	not modelled	99.6	11	<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
112	<a href="#">d1vpda2</a>	Alignment	not modelled	99.6	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
113	<a href="#">c1i36A</a>	Alignment	not modelled	99.6	13	<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
114	<a href="#">d1n1ea2</a>	Alignment	not modelled	99.6	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
115	<a href="#">d1pgja2</a>	Alignment	not modelled	99.6	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="#">c3gg2B</a>	Alignment	not modelled	99.6	17	<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
117	<a href="#">d1ojua1</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
118	<a href="#">d1llca1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
119	<a href="#">c4a7pA</a>	Alignment	not modelled	99.6	21	<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
120	<a href="#">c3hn2A</a>	Alignment	not modelled	99.6	16	<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