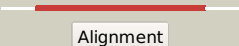



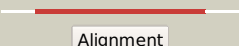





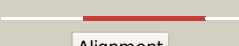




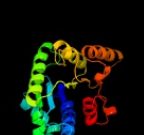





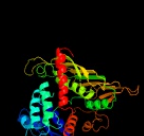


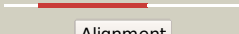

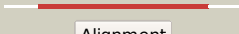




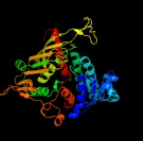






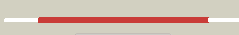


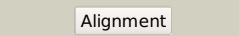
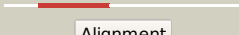
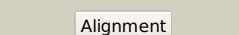

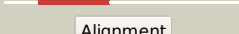




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1447c_zwf2_1625424_1626968
Date	Fri Aug 2 13:30:02 BST 2019
Unique Job ID	d2eb36099e692098

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2bhlB_</a>	 Alignment		100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> x-ray structure of human glucose-6-phosphate dehydrogenase (deletion2 variant) complexed with glucose-6-phosphate
2	<a href="#">c1h9aA_</a>	 Alignment		100.0	34	<b>PDB header:</b> oxidoreductase (choh(d) - nad(p)) <b>Chain:</b> A: <b>PDB Molecule:</b> glucose 6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> complex of active mutant (q365->c) of glucose 6-phosphate2 dehydrogenase from I. mesenteroides with coenzyme nadp
3	<a href="#">c1qkiE_</a>	 Alignment		100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> x-ray structure of human glucose 6-phosphate dehydrogenase (variant2 canton r459I) complexed with structural nadp+
4	<a href="#">c4e9iB_</a>	 Alignment		100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> glucose-6-p dehydrogenase (apo form) from trypanosoma cruzi
5	<a href="#">c4lqvA_</a>	 Alignment		100.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate 1-dehydrogenase; <b>PDBTitle:</b> x-ray crystal structure of glucose-6-phosphate 1-dehydrogenase from2 mycobacterium avium
6	<a href="#">d1qkia2</a>	 Alignment		100.0	40	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Glucose 6-phosphate dehydrogenase-like
7	<a href="#">d1h9aa2</a>	 Alignment		100.0	34	<b>Fold:</b> FwdE/GAPDH domain-like <b>Superfamily:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain <b>Family:</b> Glucose 6-phosphate dehydrogenase-like
8	<a href="#">d1h9aa1</a>	 Alignment		100.0	30	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
9	<a href="#">d1qkia1</a>	 Alignment		100.0	31	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
10	<a href="#">c5uibA_</a>	 Alignment		97.7	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase protein; <b>PDBTitle:</b> crystal structure of an oxidoreductase from agrobacterium radiobacter2 in complex with nad+, l-tartaric acid and magnesium
11	<a href="#">c4gqaC_</a>	 Alignment		97.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nad binding oxidoreductase; <b>PDBTitle:</b> crystal structure of nad binding oxidoreductase from klebsiella2 pneumoniae

12	<a href="#">c3kuxA_</a>	 Alignment		97.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> structure of the ypo2259 putative oxidoreductase from yersinia pestis
13	<a href="#">c3btuD_</a>	 Alignment		97.6	18	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> galactose/lactose metabolism regulatory protein <b>PDBTitle:</b> crystal structure of the super-repressor mutant of gal80p2 from saccharomyces cerevisiae; gal80(s2) [e351k]
14	<a href="#">c5yabD_</a>	 Alignment		97.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> scyllo-inositol dehydrogenase with l-glucose dehydrogenase <b>PDBTitle:</b> crystal structure of scyllo-inositol dehydrogenase with l-glucose2 dehydrogenase activity
15	<a href="#">c3rbvA_</a>	 Alignment		97.5	25	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> sugar 3-ketoreductase; <b>PDBTitle:</b> crystal structure of kijd10, a 3-ketoreductase from actinomadura2 kijaniata incomplex with nadp
16	<a href="#">c4h3vA_</a>	 Alignment		97.4	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase domain protein; <b>PDBTitle:</b> crystal structure of oxidoreductase domain protein from kribbella2 flavida
17	<a href="#">c1evjC_</a>	 Alignment		97.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> crystal structure of glucose-fructose oxidoreductase (gfor)2 delta1-22 s64d
18	<a href="#">c3nt5B_</a>	 Alignment		97.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol dehydrogenase from bacillus subtilis2 with bound cofactor and product inosose
19	<a href="#">c4mkzA_</a>	 Alignment		97.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol dehydrogenase; <b>PDBTitle:</b> crystal structure of apo scyllo-inositol dehydrogenase from2 lactobacillus casei at 77k
20	<a href="#">c5a06E_</a>	 Alignment		97.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> aldose-aldose oxidoreductase; <b>PDBTitle:</b> crystal structure of aldose-aldose oxidoreductase from2 caulobacter crescentus complexed with sorbitol
21	<a href="#">c3db2C_</a>	 Alignment	not modelled	97.3	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative nadph-dependent oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
22	<a href="#">c3gfgB_</a>	 Alignment	not modelled	97.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized oxidoreductase yvaa; <b>PDBTitle:</b> structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
23	<a href="#">c1zh8B_</a>	 Alignment	not modelled	97.3	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of oxidoreductase (tm0312) from thermotoga maritima2 at 2.50 a resolution
24	<a href="#">d1h6da1</a>	 Alignment	not modelled	97.3	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
25	<a href="#">c3u3xJ_</a>	 Alignment	not modelled	97.3	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> J: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021
26	<a href="#">c4hadD_</a>	 Alignment	not modelled	97.3	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> probable oxidoreductase protein; <b>PDBTitle:</b> crystal structure of probable oxidoreductase protein from rhizobium2 etli cfn 42
27	<a href="#">c5b3uB_</a>	 Alignment	not modelled	97.3	22	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> biliverdin reductase; <b>PDBTitle:</b> crystal structure of biliverdin reductase in complex with nadp+ from2 synechocystis sp. pcc 6803
28	<a href="#">c3ozvB_</a>	 Alignment	not modelled	97.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> dehydrogenase;

28	<a href="#">c3ezyB</a>	Alignment	not modelled	97.2	14	<b>PDBTitle:</b> crystal structure of probable dehydrogenase tm_0414 from thermotoga2 maritima <b>PDB header:</b> oxidoreductase
29	<a href="#">c3m2tA</a>	Alignment	not modelled	97.2	14	<b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> the crystal structure of dehydrogenase from chromobacterium2 violaceum
30	<a href="#">c3e18A</a>	Alignment	not modelled	97.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of nad-binding protein from listeria innocua
31	<a href="#">c3e9mC</a>	Alignment	not modelled	97.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
32	<a href="#">c4hktA</a>	Alignment	not modelled	97.1	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol 2-dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative myo-inositol dehydrogenase from2 sinorhizobium meliloti 1021 (target psi-012312)
33	<a href="#">c3uuwB</a>	Alignment	not modelled	97.1	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase with nad(p)-binding rossmann-fold <b>PDBTitle:</b> 1.63 angstrom resolution crystal structure of dehydrogenase (mvim)2 from clostridium difficile.
34	<a href="#">c1h6dL</a>	Alignment	not modelled	97.0	22	<b>PDB header:</b> protein translocation <b>Chain:</b> L: <b>PDB Molecule:</b> precursor form of glucose-fructose <b>PDBTitle:</b> oxidized precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
35	<a href="#">c1ofgF</a>	Alignment	not modelled	97.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> glucose-fructose oxidoreductase
36	<a href="#">c3euwB</a>	Alignment	not modelled	96.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> myo-inositol dehydrogenase; <b>PDBTitle:</b> crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
37	<a href="#">c3fd8A</a>	Alignment	not modelled	96.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from enterococcus2 faecalis
38	<a href="#">c3e82A</a>	Alignment	not modelled	96.8	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from2 klebsiella pneumoniae
39	<a href="#">d2nvwa1</a>	Alignment	not modelled	96.8	14	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
40	<a href="#">d1zh8a1</a>	Alignment	not modelled	96.8	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
41	<a href="#">c4ew6A</a>	Alignment	not modelled	96.6	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> d-galactose-1-dehydrogenase protein; <b>PDBTitle:</b> crystal structure of d-galactose-1-dehydrogenase protein from2 rhizobium etli
42	<a href="#">c2ho3D</a>	Alignment	not modelled	96.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of oxidoreductase, gfo/idh/moca family from2 streptococcus pneumoniae
43	<a href="#">c3c1aB</a>	Alignment	not modelled	96.5	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (zp_00056571.1) from2 magnetospirillum magnetotacticum ms-1 at 1.85 a resolution
44	<a href="#">c6a3fB</a>	Alignment	not modelled	96.5	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dehydrogenase; <b>PDBTitle:</b> levoglucosan dehydrogenase, apo form
45	<a href="#">c3dtyA</a>	Alignment	not modelled	96.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of an oxidoreductase from pseudomonas2 syringae
46	<a href="#">c3ec7C</a>	Alignment	not modelled	96.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative dehydrogenase; <b>PDBTitle:</b> crystal structure of putative dehydrogenase from salmonella2 typhimurium lt2
47	<a href="#">d1ryda1</a>	Alignment	not modelled	96.3	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
48	<a href="#">c4fb5A</a>	Alignment	not modelled	96.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable oxidoreductase protein; <b>PDBTitle:</b> crystal structure of a probable oxidoreductase protein
49	<a href="#">c2nvwB</a>	Alignment	not modelled	96.0	13	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> galactose/lactose metabolism regulatory protein <b>PDBTitle:</b> crystal structure of transcriptional regulator gal80p from2 kluveromyces lactis
50	<a href="#">c3ceaA</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> myo-inositol 2-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol 2-dehydrogenase (np_786804.1) from2 lactobacillus plantarum at 2.40 a resolution
51	<a href="#">c6norB</a>	Alignment	not modelled	96.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative nad dependent dehydrogenase; <b>PDBTitle:</b> crystal structure of gend2 from gentamicin a biosynthesis in complex2 with nad
52	<a href="#">c3f4fF</a>	Alignment	not modelled	95.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> putative oxidoreductase yhhx; <b>PDBTitle:</b> crystal structure of a probable oxidoreductase yhhx in2 triclinic form. northeast structural genomics target er647
53	<a href="#">d1vdwa1</a>	Alignment	not modelled	95.7	26	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains

53	<a href="#">u1yuwA</a>	Alignment	not modelled	93.7	20	<b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> lipopolysaccharide biosynthesis protein wbbp; <b>PDBTitle:</b> crystal structure of the wlbA (wbbp) dehydrogenase from thermus2 thermophilus in complex with nad and udp-glcnaC
54	<a href="#">c3oa0B</a>	Alignment	not modelled	95.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of a gfo/idh/moca family oxidoreductase2 from vibrio cholerae
55	<a href="#">c1xeaD</a>	Alignment	not modelled	95.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of the putative oxidoreductase from streptococcus2 agalactiae 2603v/r
56	<a href="#">c3evnA</a>	Alignment	not modelled	95.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of myo-inositol dehydrogenase from lactobacillus2 casei in complex with nad and myo-inositol
57	<a href="#">c4mlyB</a>	Alignment	not modelled	95.1	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
58	<a href="#">d1xeaa1</a>	Alignment	not modelled	94.8	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from bacteroides2 fragilis nctc 9343
59	<a href="#">c3fhlC</a>	Alignment	not modelled	94.8	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> wbbp; <b>PDBTitle:</b> crystal structure of the wlbA (wbbp) dehydrogenase from pseudomonas2 aeruginosa in complex with nad at 1.5 angstrom resolution
60	<a href="#">c3oa2B</a>	Alignment	not modelled	94.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> the crystal structure of the putative dehydrogenase from bordetella2 bronchiseptica rb50
61	<a href="#">c3moiA</a>	Alignment	not modelled	94.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 1,5-anhydro-d-fructose reductase; <b>PDBTitle:</b> crystal structure analysis of bacterial 1,5-af reductase
62	<a href="#">c2qlxD</a>	Alignment	not modelled	94.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable oxidoreductase at4g09670; <b>PDBTitle:</b> ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at4g09670
63	<a href="#">c2q4eB</a>	Alignment	not modelled	94.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> biliverdin reductase a; <b>PDBTitle:</b> crystal structure of a biliverdin reductase enzyme-cofactor2 complex
64	<a href="#">c1lc3A</a>	Alignment	not modelled	94.6	23	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
65	<a href="#">d1tita1</a>	Alignment	not modelled	94.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase (virulence factor mvim homolog); <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (virulence factor mvim2 homolog)
66	<a href="#">c1titB</a>	Alignment	not modelled	94.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of the wlbA dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaC
67	<a href="#">c3q2kB</a>	Alignment	not modelled	94.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-arabinose 1-dehydrogenase (nad(p)(+)); <b>PDBTitle:</b> crystal structure of azospirillum brasilense l-arabinose 1-2 dehydrogenase (nadp-bound form)
68	<a href="#">c6jnkA</a>	Alignment	not modelled	94.2	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase (yp_050235.1) from2 erwinia carotovora atroseptica scri1043 at 1.25 a resolution
69	<a href="#">c2p2sA</a>	Alignment	not modelled	94.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
70	<a href="#">c3oqbF</a>	Alignment	not modelled	93.7	27	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
71	<a href="#">d1lc0a1</a>	Alignment	not modelled	93.5	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> dimeric dihydrodiol dehydrogenase; <b>PDBTitle:</b> crystal structure of mammalian dimeric dihydrodiol dehydrogenase
72	<a href="#">c2o48X</a>	Alignment	not modelled	92.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iridoid synthase; <b>PDBTitle:</b> iridoid synthase from catharanthus roseus - ternary complex with nadp+2 and geranic acid
73	<a href="#">c5df1A</a>	Alignment	not modelled	92.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative oxidoreductase (parmer_00841) from2 parabacteroides merdae atcc 43184 at 2.23 a resolution
74	<a href="#">c4oo3A</a>	Alignment	not modelled	92.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, putative; <b>PDBTitle:</b> structure of putative oxidoreductase (tm_0425) from thermotoga2 maritima
75	<a href="#">c3ip3D</a>	Alignment	not modelled	92.0	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-n-acetylgalactosaminidase; <b>PDBTitle:</b> a-zyme, n-acetylgalactosaminidase
76	<a href="#">c2ixaA</a>	Alignment	not modelled	91.9	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
77	<a href="#">d1oi7a1</a>	Alignment	not modelled	90.2	10	

78	<a href="#">c2zcuA</a>	Alignment	not modelled	89.2	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized oxidoreductase ytfq; <b>PDBTitle:</b> crystal structure of a new type of nadph-dependent quinone2 oxidoreductase (qor2) from escherichia coli
79	<a href="#">c2c20D</a>	Alignment	not modelled	83.9	29	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of udp-glucose 4-epimerase
80	<a href="#">d1xgka</a>	Alignment	not modelled	83.6	10	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
81	<a href="#">c3wj7B</a>	Alignment	not modelled	82.6	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of gox2253
82	<a href="#">c2v6gA</a>	Alignment	not modelled	82.4	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> progesterone 5-beta-reductase; <b>PDBTitle:</b> structure of progesterone 5beta-reductase from digitalis2 lanata in complex with nadp
83	<a href="#">c2vrcD</a>	Alignment	not modelled	81.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> triphenylmethane reductase; <b>PDBTitle:</b> crystal structure of the citrobacter sp. triphenylmethane2 reductase complexed with nadp(h)
84	<a href="#">d1wvga1</a>	Alignment	not modelled	77.0	18	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
85	<a href="#">c1t2aC</a>	Alignment	not modelled	76.9	20	<b>PDB header:</b> structural genomics,lyase <b>Chain:</b> C: <b>PDB Molecule:</b> gdp-mannose 4,6 dehydratase; <b>PDBTitle:</b> crystal structure of human gdp-d-mannose 4,6-dehydratase
86	<a href="#">d1t2aa</a>	Alignment	not modelled	76.9	20	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
87	<a href="#">c2z1mC</a>	Alignment	not modelled	73.8	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> gdp-d-mannose dehydratase; <b>PDBTitle:</b> crystal structure of gdp-d-mannose dehydratase from aquifex aeolicus2 vf5
88	<a href="#">c3v5nA</a>	Alignment	not modelled	73.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> the crystal structure of oxidoreductase from sinorhizobium meliloti
89	<a href="#">c5l3zA</a>	Alignment	not modelled	72.4	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> polyketide ketoreductase simc7; <b>PDBTitle:</b> polyketide ketoreductase simc7 - binary complex with nadp+
90	<a href="#">c4idgB</a>	Alignment	not modelled	70.9	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> short-chain dehydrogenase/reductase; <b>PDBTitle:</b> crystal structure of a short-chain dehydrogenase/reductase superfamily2 protein from agrobacterium tumefaciens (target efi-506441) with bound3 nad, monoclinic form 2
91	<a href="#">c2qx7A</a>	Alignment	not modelled	70.9	25	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> eugenol synthase 1; <b>PDBTitle:</b> structure of eugenol synthase from ocimum basilicum
92	<a href="#">c4pivB</a>	Alignment	not modelled	70.4	21	<b>PDB header:</b> transferase/transferase inhibitor <b>Chain:</b> B: <b>PDB Molecule:</b> fatty acid synthase; <b>PDBTitle:</b> human fatty acid synthase psi/kr tri-domain with nadph and gsk2194069
93	<a href="#">c2gn9B</a>	Alignment	not modelled	70.0	18	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-glcnac c6 dehydratase; <b>PDBTitle:</b> crystal structure of udp-glcnac inverting 4,6-dehydratase in complex2 with nadp and udp-glc
94	<a href="#">c4gmfD</a>	Alignment	not modelled	68.9	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> yersiniabactin biosynthetic protein ybtu; <b>PDBTitle:</b> apo structure of a thiazoliny1 imine reductase from yersinia2 enterocolitica (irp3)
95	<a href="#">d1db3a</a>	Alignment	not modelled	68.8	27	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
96	<a href="#">c6el3A</a>	Alignment	not modelled	68.4	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-oxo-delta(4,5)-steroid 5-beta-reductase; <b>PDBTitle:</b> structure of progesterone 5beta-reductase from arabidopsis thaliana in2 complex with nadp
97	<a href="#">c3wycB</a>	Alignment	not modelled	68.3	4	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> meso-diaminopimelate d-dehydrogenase; <b>PDBTitle:</b> structure of a meso-diaminopimelate dehydrogenase in complex with nadp
98	<a href="#">d2nu7a1</a>	Alignment	not modelled	68.1	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
99	<a href="#">c2iodD</a>	Alignment	not modelled	68.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydroflavonol 4-reductase; <b>PDBTitle:</b> binding of two substrate analogue molecules to2 dihydroflavonol-4-reductase alters the functional geometry3 of the catalytic site
100	<a href="#">c2p5uC</a>	Alignment	not modelled	67.8	25	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of thermus thermophilus hb8 udp-glucose 4-epimerase2 complex with nad
101	<a href="#">c5ffqA</a>	Alignment	not modelled	67.5	11	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> shuy-like protein; <b>PDBTitle:</b> chuy: an anaerobillin reductase from escherichia coli o157:h7
102	<a href="#">d1n7ha</a>	Alignment	not modelled	67.2	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
103	<a href="#">d1z45a2</a>	Alignment	not modelled	65.6	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases

104	<a href="#">c5msuC_</a>	Alignment	not modelled	64.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> carboxylic acid reductase; <b>PDBTitle:</b> structure of the r domain of carboxylic acid reductase (car) from <i>Mycobacterium marinum</i> in complex with nadp, p21 form
105	<a href="#">c5uzhA_</a>	Alignment	not modelled	64.5	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nafoa.00085.b; <b>PDBTitle:</b> crystal structure of a gdp-mannose dehydratase from <i>Naegleria fowleri</i>
106	<a href="#">d1x1na1</a>	Alignment	not modelled	61.5	30	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
107	<a href="#">c3s9fA_</a>	Alignment	not modelled	60.6	9	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> tryparedoxin; <b>PDBTitle:</b> the structure of tryparedoxin i from <i>Leishmania major</i>
108	<a href="#">d1udca_</a>	Alignment	not modelled	60.5	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
109	<a href="#">c4qukA_</a>	Alignment	not modelled	60.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroflavonol-4-reductase; <b>PDBTitle:</b> crystal structure of cinnamyl-alcohol dehydrogenase 2 mutant k169a
110	<a href="#">d1tz7a1</a>	Alignment	not modelled	60.1	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
111	<a href="#">c4s3rA_</a>	Alignment	not modelled	59.6	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-alpha-glucanotransferase; <b>PDBTitle:</b> amylomaltase malq from <i>Escherichia coli</i> in complex with the pseudo-2 heptasaccharide acarviosine-glucose-acarbose
112	<a href="#">c4lisA_</a>	Alignment	not modelled	58.9	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-glucose 4-epimerase; <b>PDBTitle:</b> crystal structure of udp-galactose-4-epimerase from <i>Aspergillus nidulans</i>
113	<a href="#">d2blla1</a>	Alignment	not modelled	58.5	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
114	<a href="#">c2pk3B_</a>	Alignment	not modelled	57.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gdp-6-deoxy-d-lyxo-4-hexulose reductase; <b>PDBTitle:</b> crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
115	<a href="#">d2q46a1</a>	Alignment	not modelled	57.6	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases
116	<a href="#">d1eswa_</a>	Alignment	not modelled	57.5	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> (Trans)glycosidases <b>Family:</b> Amylase, catalytic domain
117	<a href="#">c5f5nA_</a>	Alignment	not modelled	57.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> the structure of monooxygenase ksta11 in complex with nad and its2 substrate
118	<a href="#">d1f06a1</a>	Alignment	not modelled	56.8	11	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
119	<a href="#">c3slgB_</a>	Alignment	not modelled	56.2	14	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pbgp3 protein; <b>PDBTitle:</b> crystal structure of pbgp3 protein from <i>Burkholderia pseudomallei</i>
120	<a href="#">d1rkxa_</a>	Alignment	not modelled	56.0	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Tyrosine-dependent oxidoreductases