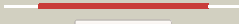



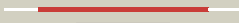



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0926c_(-)_1032714_1033790
Date	Fri Jul 26 01:50:52 BST 2019
Unique Job ID	0e2b3e7182becd53

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6g1mA_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> amine dehydrogenase from petrotoga mobilis; open and closed form
2	<a href="#">c6iaqA_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase n-terminus domain-containing <b>PDBTitle:</b> structure of amine dehydrogenase from mycobacterium smegmatis
3	<a href="#">c6iauB_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> amine dehydrogenase; <b>PDBTitle:</b> amine dehydrogenase from cystobacter fuscus in complex with nadp+ and2 cyclohexylamine
4	<a href="#">c2ixaA_</a>	 Alignment		100.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-n-acetylgalactosaminidase; <b>PDBTitle:</b> a-zyme, n-acetylgalactosaminidase
5	<a href="#">c3moiA_</a>	 Alignment		100.0	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
6	<a href="#">c3e18A_</a>	 Alignment		100.0	19	<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
7	<a href="#">c2q4eB_</a>	 Alignment		100.0	13	<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
8	<a href="#">c3euwB_</a>	 Alignment		100.0	15	<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
9	<a href="#">c4gqaC_</a>	 Alignment		100.0	15	<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
10	<a href="#">c5yabD_</a>	 Alignment		100.0	19	<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
11	<a href="#">c3dtyA_</a>	 Alignment		100.0	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 an oxidoreductase from pseudomonas2 syringae

12	<a href="#">c3db2C_</a>	Alignment		100.0	10	<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
13	<a href="#">c5uibA_</a>	Alignment		100.0	11	<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
14	<a href="#">c3e9mC_</a>	Alignment		100.0	13	<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
15	<a href="#">c1h6dL_</a>	Alignment		100.0	13	<b>PDB header:</b> protein translocation <b>Chain:</b> L: <b>PDB Molecule:</b> precursor form of glucose-fructose oxidoreductase2 from zymomonas mobilis complexed with glycerol
16	<a href="#">c1ofgF_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> glucose-fructose oxidoreductase; <b>PDBTitle:</b> glucose-fructose oxidoreductase
17	<a href="#">c2glxD_</a>	Alignment		100.0	11	<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
18	<a href="#">c3m2tA_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable dehydrogenase; <b>PDBTitle:</b> the crystal structure of dehydrogenase from chromobacterium2 violaceum
19	<a href="#">c2o48X_</a>	Alignment		100.0	14	<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
20	<a href="#">c3oqbF_</a>	Alignment		100.0	16	<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
21	<a href="#">c6a3fB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dehydrogenase; <b>PDBTitle:</b> levoglucosan dehydrogenase, apo form
22	<a href="#">c3fd8A_</a>	Alignment	not modelled	100.0	12	<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
23	<a href="#">c3ezyB_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> dehydrogenase; <b>PDBTitle:</b> crystal structure of probable dehydrogenase tm_0414 from thermotoga2 maritima
24	<a href="#">c4h3vA_</a>	Alignment	not modelled	100.0	16	<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
25	<a href="#">c2p2sA_</a>	Alignment	not modelled	100.0	14	<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
26	<a href="#">c6norB_</a>	Alignment	not modelled	100.0	16	<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
27	<a href="#">c3nt5B_</a>	Alignment	not modelled	100.0	13	<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 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inositol 2-dehydrogenase;

28	<a href="#">c4hktA_</a>	Alignment	not modelled	100.0	18	<b>PDBTitle:</b> crystal structure of a putative myo-inositol dehydrogenase from2 sinorhizobium meliloti 1021 (target psi-012312)
29	<a href="#">c3evnA_</a>	Alignment	not modelled	100.0	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 putative oxidoreductase from streptococcus2 agalactiae 2603v/r
30	<a href="#">c4mkzA_</a>	Alignment	not modelled	100.0	16	<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
31	<a href="#">c3gfgB_</a>	Alignment	not modelled	100.0	14	<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
32	<a href="#">c3kuxA_</a>	Alignment	not modelled	100.0	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
33	<a href="#">c5b3uB_</a>	Alignment	not modelled	100.0	16	<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
34	<a href="#">c3ceaA_</a>	Alignment	not modelled	100.0	13	<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
35	<a href="#">c3f4f_</a>	Alignment	not modelled	100.0	12	<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
36	<a href="#">c3q2kB_</a>	Alignment	not modelled	100.0	16	<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-glcna
37	<a href="#">c5a06E_</a>	Alignment	not modelled	100.0	12	<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
38	<a href="#">c3e82A_</a>	Alignment	not modelled	100.0	14	<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="#">c3ec7C_</a>	Alignment	not modelled	100.0	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
40	<a href="#">c4ew6A_</a>	Alignment	not modelled	100.0	15	<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
41	<a href="#">c4miyB_</a>	Alignment	not modelled	100.0	14	<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
42	<a href="#">c3btuD_</a>	Alignment	not modelled	100.0	9	<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]
43	<a href="#">c3u3xj_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase <b>PDBTitle:</b> crystal structure of a putative oxidoreductase from sinorhizobium2 meliloti 1021
44	<a href="#">c1evjC_</a>	Alignment	not modelled	100.0	17	<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
45	<a href="#">c1zh8B_</a>	Alignment	not modelled	100.0	14	<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
46	<a href="#">c3ip3D_</a>	Alignment	not modelled	100.0	12	<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
47	<a href="#">c4fb5A_</a>	Alignment	not modelled	100.0	17	<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
48	<a href="#">c3wycB_</a>	Alignment	not modelled	100.0	14	<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
49	<a href="#">c6jnkA_</a>	Alignment	not modelled	100.0	16	<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)
50	<a href="#">c2nvwB_</a>	Alignment	not modelled	100.0	11	<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
51	<a href="#">c3rbvA_</a>	Alignment	not modelled	100.0	18	<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
52	<a href="#">c3c1aB_</a>	Alignment	not modelled	100.0	14	<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

53	<a href="#">c3v5nA</a>	Alignment	not modelled	100.0	16	<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
54	<a href="#">c3fhIC</a>	Alignment	not modelled	100.0	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
55	<a href="#">c4hadD</a>	Alignment	not modelled	100.0	9	<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
56	<a href="#">c1xeaD</a>	Alignment	not modelled	100.0	15	<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
57	<a href="#">c2ho3D</a>	Alignment	not modelled	100.0	12	<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
58	<a href="#">c4gmfD</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> yersiniabactin biosynthetic protein ybtu; <b>PDBTitle:</b> apo structure of a thiazoliny imine reductase from yersinia2 enterocolitica (irp3)
59	<a href="#">c3oa0B</a>	Alignment	not modelled	100.0	13	<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-glcna
60	<a href="#">c3uuwB</a>	Alignment	not modelled	100.0	11	<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.
61	<a href="#">c1lc3A</a>	Alignment	not modelled	100.0	16	<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
62	<a href="#">c1titB</a>	Alignment	not modelled	100.0	15	<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)
63	<a href="#">c3oa2B</a>	Alignment	not modelled	100.0	14	<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
64	<a href="#">c3wb9A</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate dehydrogenase; <b>PDBTitle:</b> crystal structures of meso-diaminopimelate dehydrogenase from2 symbiobacterium thermophilum
65	<a href="#">c3dapB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelic acid dehydrogenase; <b>PDBTitle:</b> c. glutamicum dap dehydrogenase in complex with nadp+ and2 the inhibitor 5s-isoxazoline
66	<a href="#">c3wgzB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> meso-diaminopimelate dehydrogenase; <b>PDBTitle:</b> crystal structure of meso-dapdh q154i/t173i/r199m/p248s/h249n/n276s2 mutant with d-leucine of from clostridium tetani e88
67	<a href="#">d1h6da1</a>	Alignment	not modelled	100.0	16	<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
68	<a href="#">c4oo3A</a>	Alignment	not modelled	100.0	14	<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
69	<a href="#">d1ryda1</a>	Alignment	not modelled	99.9	16	<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
70	<a href="#">d1zh8a1</a>	Alignment	not modelled	99.9	13	<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="#">d1f06a1</a>	Alignment	not modelled	99.9	18	<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
72	<a href="#">c3bioB</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase, gfo/idh/moca family; <b>PDBTitle:</b> crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
73	<a href="#">d1ydwa1</a>	Alignment	not modelled	99.9	16	<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
74	<a href="#">d2nvwa1</a>	Alignment	not modelled	99.9	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
75	<a href="#">c3mtjA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
76	<a href="#">c6dzsD</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> mycobacterial homoserine dehydrogenase thra in complex with nadp <b>Fold:</b> NAD(P)-binding Rossmann-fold domains

77	<a href="#">d1tita1</a>	Alignment	not modelled	99.9	18	<b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
78	<a href="#">d1xeaa1</a>	Alignment	not modelled	99.9	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
79	<a href="#">c1j5pA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate dehydrogenase; <b>PDBTitle:</b> crystal structure of aspartate dehydrogenase (tm1643) from thermotoga2 maritima at 1.9 a resolution
80	<a href="#">d1lc0a1</a>	Alignment	not modelled	99.9	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
81	<a href="#">c4pg8B_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of s. aureus homoserine dehydrogenase at ph8.5
82	<a href="#">c4xb1B_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 319aa long hypothetical homoserine dehydrogenase; <b>PDBTitle:</b> hyperthermophilic archaeal homoserine dehydrogenase in complex with2 nadph
83	<a href="#">c3do5A_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of putative homoserine dehydrogenase (np_069768.1)2 from archaeoglobus fulgidus at 2.20 a resolution
84	<a href="#">c2dc1A_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-aspartate dehydrogenase; <b>PDBTitle:</b> crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
85	<a href="#">c3upyB_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> crystal structure of the brucella abortus enzyme catalyzing the first2 committed step of the methylerythritol 4-phosphate pathway.
86	<a href="#">c1ebuA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> homoserine dehydrogenase complex with nad analogue and l-2 homoserine
87	<a href="#">c5kt0A_</a>	Alignment	not modelled	99.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> dihydrodipicolinate reductase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
88	<a href="#">c5avoA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of the reduced form of homoserine dehydrogenase from2 sulfobolus tokodaii.
89	<a href="#">c2ejwB_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> homoserine dehydrogenase from thermus thermophilus hb8
90	<a href="#">c5z2fA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> nadph/pda bound dihydrodipicolinate reductase from paenisporosarcina2 sp. tg-14
91	<a href="#">d2nu7a1</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
92	<a href="#">d1oi7a1</a>	Alignment	not modelled	99.8	19	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
93	<a href="#">c3c8mA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of homoserine dehydrogenase from thermoplasma2 volcanium
94	<a href="#">d1j5pa4</a>	Alignment	not modelled	99.7	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
95	<a href="#">c5ugjC_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of htpa reductase from neisseria meningitidis
96	<a href="#">d2dt5a2</a>	Alignment	not modelled	99.7	21	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Transcriptional repressor Rex, C-terminal domain
97	<a href="#">c2axqA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
98	<a href="#">c5tenH_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> structure of 4-hydroxy-tetrahydrodipicolinate reductase from vibrio2 vulnificus with 2,5 furan dicarboxylic and nadh with intact3 polyhistidine tag
99	<a href="#">c2ph5A_</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homospermidine synthase; <b>PDBTitle:</b> crystal structure of the homospermidine synthase hss from legionella2 pneumophila in complex with nad, northeast structural genomics target3 lgr54
100	<a href="#">d1euca1</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> CoA-binding domain
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-aminoadipic semialdehyde



101	<a href="#">c5i78A_</a>	Alignment	not modelled	99.6	16	synthase, mitochondrial; <b>PDBTitle:</b> crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)
102	<a href="#">c1drwA_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> escherichia coli dhpr/nhdh complex
103	<a href="#">c4f3yA_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> x-ray crystal structure of dihydrodipicolinate reductase from2 burkholderia thailandensis
104	<a href="#">d1ebfa1</a>	Alignment	not modelled	99.6	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
105	<a href="#">c3ijpA_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate reductase from bartonella2 henselae at 2.0a resolution
106	<a href="#">c3ingA_</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine dehydrogenase; <b>PDBTitle:</b> crystal structure of homoserine dehydrogenase (np_394635.1) from2 thermoplasma acidophilum at 1.95 a resolution
107	<a href="#">d1e5qa1</a>	Alignment	not modelled	99.5	16	<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
108	<a href="#">c3ketA_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
109	<a href="#">c1e5lA_</a>	Alignment	not modelled	99.5	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine reductase; <b>PDBTitle:</b> apo saccharopine reductase from magnaporthe grisea
110	<a href="#">c3wg9D_</a>	Alignment	not modelled	99.5	18	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> crystal structure of rsp, a rex-family repressor
111	<a href="#">c2dt5A_</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> at-rich dna-binding protein; <b>PDBTitle:</b> crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
112	<a href="#">c5zz5D_</a>	Alignment	not modelled	99.5	24	<b>PDB header:</b> gene regulation <b>Chain:</b> D: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> redox-sensing transcriptional repressor rex
113	<a href="#">c4rl6A_</a>	Alignment	not modelled	99.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> crystal structure of the q04i03_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105
114	<a href="#">c4inaA_</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> saccharopine dehydrogenase; <b>PDBTitle:</b> crystal structure of the q7mss8_wolsu protein from wolfinella2 succinogenes. northeast structural genomics consortium target wsr35
115	<a href="#">c4ywjB_</a>	Alignment	not modelled	99.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate reductase; <b>PDBTitle:</b> crystal structure of 4-hydroxy-tetrahydrodipicolinate reductase (htpa2 reductase) from pseudomonas aeruginosa
116	<a href="#">c3ic5A_</a>	Alignment	not modelled	99.3	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase; <b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
117	<a href="#">d1diha1</a>	Alignment	not modelled	99.3	22	<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
118	<a href="#">d1omoa_</a>	Alignment	not modelled	99.3	13	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Ornithine cyclodeaminase-like
119	<a href="#">c1r0lD_</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase; <b>PDBTitle:</b> 1-deoxy-d-xylulose 5-phosphate reductoisomerase from zymomonas mobilis2 in complex with nadph
120	<a href="#">c2z2vA_</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1688; <b>PDBTitle:</b> crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii