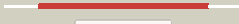



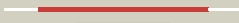



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1175c_(fadH)_1306207_1308231
Date	Wed Jul 31 22:05:26 BST 2019
Unique Job ID	edda6183e7fbf344

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1ps9A_</a>	 Alignment		100.0	52	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
2	<a href="#">c6qkgB_</a>	 Alignment		100.0	29	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> ncr a; <b>PDBTitle:</b> 2-naphthoyl-coa reductase(ncr)
3	<a href="#">c3k30B_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> histamine dehydrogenase from nocardiodes simplex
4	<a href="#">c1djnB_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trimethylamine dehydrogenase; <b>PDBTitle:</b> structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
5	<a href="#">c6de6B_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> 2.1 a resolution structure of histamine dehydrogenase from rhizobium2 sp. 4-9
6	<a href="#">c5ocsB_</a>	 Alignment		100.0	29	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> putative nadh-dependent flavin oxidoreductase; <b>PDBTitle:</b> ene-reductase (er/oye) from ralstonia (cupriavidus) metallidurans
7	<a href="#">d1z41a1</a>	 Alignment		100.0	28	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
8	<a href="#">d1gwja_</a>	 Alignment		100.0	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
9	<a href="#">d1ps9a1</a>	 Alignment		100.0	56	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
10	<a href="#">d1loyaa_</a>	 Alignment		100.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
11	<a href="#">c4jicB_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gtn reductase; <b>PDBTitle:</b> glycerol trinitrate reductase nera from agrobacterium radiobacter

12	<a href="#">c3kruC_</a>	Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh:flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> crystal structure of the thermostable old yellow enzyme from <i>Thermoanaerobacter pseudethanolicus</i> e39
13	<a href="#">c3l5aA_</a>	Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh/flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> crystal structure of a probable nadh-dependent flavin oxidoreductase2 from <i>Staphylococcus aureus</i>
14	<a href="#">c3gkaB_</a>	Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> n-ethylmaleimide reductase; <b>PDBTitle:</b> crystal structure of n-ethylmaleimidine reductase from <i>Burkholderia pseudomallei</i>
15	<a href="#">c3atyA_</a>	Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> prostaglandin f2a synthase; <b>PDBTitle:</b> crystal structure of tcoye
16	<a href="#">c2h90A_</a>	Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> xenobiotic reductase a; <b>PDBTitle:</b> xenobiotic reductase a in complex with coumarin
17	<a href="#">c3hf3A_</a>	Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chromate reductase; <b>PDBTitle:</b> old yellow enzyme from <i>Thermus scotoductus</i> sa-01
18	<a href="#">c5dxxA_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> artemisinin aldehyde delta(11(13)) reductase; <b>PDBTitle:</b> crystal structure of dbr2
19	<a href="#">d1vjia_</a>	Alignment		100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
20	<a href="#">c2gq8A_</a>	Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, fmn-binding; <b>PDBTitle:</b> structure of sye1, an oye homologue from <i>S. ondesidensis</i> , in complex2 with p-hydroxyacetophenone
21	<a href="#">d1q45a_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
22	<a href="#">c4tmcB_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> old yellow enzyme; <b>PDBTitle:</b> crystal structure of old yellow enzyme from <i>Candida macedoniensis</i> 2 aku4588 complexed with p-hydroxybenzaldehyde
23	<a href="#">c5epdA_</a>	Alignment	not modelled	100.0	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol trinitrate reductase; <b>PDBTitle:</b> crystal structure of glycerol trinitrate reductase xdpb from <i>Agrobacterium</i> sp. r89-1 (apo form)
24	<a href="#">c3gr7A_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh dehydrogenase; <b>PDBTitle:</b> structure of oye from <i>Geobacillus kaustophilus</i> , hexagonal crystal form
25	<a href="#">c6agzA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> old yellow enzyme; <b>PDBTitle:</b> crystal structure of old yellow enzyme from <i>Pichia</i> sp. aku4542
26	<a href="#">d1vyra_</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
27	<a href="#">c4b5nA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, fmn-binding; <b>PDBTitle:</b> crystal structure of oxidized shewanella yellow enzyme 4 (sye4)
28	<a href="#">c4a3uB_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh\flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> x-structure of the old yellow enzyme homologue from <i>Zymomonas mobilis</i> 2 (ncr)
						<b>Fold:</b> TIM beta/alpha-barrel

29	<a href="#">d1djqa1</a>	Alignment	not modelled	100.0	23	<b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
30	<a href="#">c4qnwA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> chanoclavine-i aldehyde reductase; <b>PDBTitle:</b> crystal structure of easa, an old yellow enzyme from aspergillus2 fumigatus
31	<a href="#">c6mywA_</a>	Alignment	not modelled	100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> n-ethylmaleimide reductase; <b>PDBTitle:</b> gluconobacter ene-reductase (gluer) mutant - t36a
32	<a href="#">d1icpa_</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
33	<a href="#">c4df2A_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh dehydrogenase; <b>PDBTitle:</b> p. stiptitis oye2.6 complexed with p-chlorophenol
34	<a href="#">c4rvnD_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase/inhibitor <b>Chain:</b> D: <b>PDB Molecule:</b> nadh dehydrogenase 1; <b>PDBTitle:</b> g303 circular permutation of old yellow enzyme with the inhibitor p-2 hydroxybenzaldehyde
35	<a href="#">c4ot7A_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh:flavin oxidoreductase/nadh oxidase; <b>PDBTitle:</b> x-structure of a variant of ncr from zymomonas mobilis
36	<a href="#">c4rnxA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh dehydrogenase 1; <b>PDBTitle:</b> k154 circular permutation of old yellow enzyme
37	<a href="#">c6ei9A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase b; <b>PDBTitle:</b> crystal structure of e. coli trna-dihydrouridine synthase b (dusb)
38	<a href="#">c3w9zA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine synthase c; <b>PDBTitle:</b> crystal structure of dusc
39	<a href="#">d1gtea2</a>	Alignment	not modelled	100.0	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
40	<a href="#">d1ep3a_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
41	<a href="#">c1gthD_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase; <b>PDBTitle:</b> dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
42	<a href="#">c4ylfD_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase subunit a; <b>PDBTitle:</b> insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadh oxidoreductase structure
43	<a href="#">c5w1jA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase; <b>PDBTitle:</b> echinococcus granulosus thioredoxin glutathione reductase (egtgr)
44	<a href="#">c5jcaL_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> nadh-dependent ferredoxin:nadh oxidoreductase (nfni) <b>PDBTitle:</b> nadp(h) bound nadh-dependent ferredoxin:nadh oxidoreductase (nfni)2 from pyrococcus furiosus
45	<a href="#">c2vdcl_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> glutamate synthase [nadph] small chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
46	<a href="#">c4xp7A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna-dihydrouridine(20) synthase [nad(p+)]-like; <b>PDBTitle:</b> crystal structure of human trna dihydrouridine synthase 2
47	<a href="#">c2v6oA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase; <b>PDBTitle:</b> structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
48	<a href="#">d1djqa3</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
49	<a href="#">c1hyuA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> crystal structure of intact ahpf
50	<a href="#">c3ntaA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide <b>PDBTitle:</b> structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
51	<a href="#">d1vhna_</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
52	<a href="#">c3icrA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme a-disulfide reductase; <b>PDBTitle:</b> crystal structure of oxidized bacillus anthracis coad-rhd
53	<a href="#">c2c3dB_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxopropyl-com reductase; <b>PDBTitle:</b> 2.15 angstrom crystal structure of 2-ketopropyl coenzyme m2 oxidoreductase carboxylase with a coenzyme m disulfide3 bound at the active site
54	<a href="#">c4g6gB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> rotenone-insensitive nadh-ubiquinone oxidoreductase,

						<b>PDBTitle:</b> crystal structure of ndh with trt <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e3 component; <b>PDBTitle:</b> crystal structure of lipamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
55	<a href="#">c2eq7B_</a>	Alignment	not modelled	99.9	26	
56	<a href="#">d1ps9a3</a>	Alignment	not modelled	99.9	50	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
57	<a href="#">c3oc4A_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, pyridine nucleotide-disulfide family; <b>PDBTitle:</b> crystal structure of a pyridine nucleotide-disulfide family2 oxidoreductase from the enterococcus faecalis v583
58	<a href="#">c4gapB_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> rotenone-insensitive nadh-ubiquinone oxidoreductase; <b>PDBTitle:</b> structure of the nd1 protein from saccharomyces cerevisiae in complex2 with nad+
59	<a href="#">c3b0vD_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase/rna <b>Chain:</b> D: <b>PDB Molecule:</b> trna-dihydrouridine synthase; <b>PDBTitle:</b> trna-dihydrouridine synthase from thermus thermophilus in complex with2 trna
60	<a href="#">c5jwcA_</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> nadh dehydrogenase, putative; <b>PDBTitle:</b> structure of ndh2 from plasmodium falciparum in complex with ryl-552
61	<a href="#">c2v3aA_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin reductase; <b>PDBTitle:</b> crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa.
62	<a href="#">c2cduB_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph oxidase; <b>PDBTitle:</b> the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
63	<a href="#">c2qaeA_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure analysis of trypanosoma cruzi lipamide2 dehydrogenase
64	<a href="#">c4nzwA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulfide oxidoreductase; <b>PDBTitle:</b> structure of bacterial type ii nadh dehydrogenase from2 caldalkalibacillus thermarum at 2.5a resolution
65	<a href="#">c2bcpA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidase; <b>PDBTitle:</b> structural analysis of streptococcus pyogenes nadh oxidase: c44s nox2 with azide
66	<a href="#">c1zx9A_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> crystal structure of tn501 mera
67	<a href="#">c3iwaA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide <b>PDBTitle:</b> crystal structure of a fad-dependent pyridine nucleotide-disulphide2 oxidoreductase from desulfovibrio vulgaris
68	<a href="#">c1ojtA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> surface protein; <b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase
69	<a href="#">c4xdbC_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase, membrane protein, flavop <b>Chain:</b> C: <b>PDB Molecule:</b> nadh dehydrogenase-like protein saouhsc_00878; <b>PDBTitle:</b> nadh:quinone oxidoreductase (ndh-ii) from staphylococcus aureus -2 holoprotein structure
70	<a href="#">c6du7C_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> glutathione reductase from streptococcus pneumoniae
71	<a href="#">c3dggA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2; <b>PDBTitle:</b> crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
72	<a href="#">c1zmcG_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
73	<a href="#">c1zkgA_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2, mitochondrial; <b>PDBTitle:</b> crystal structure of mouse thioredoxin reductase type 2
74	<a href="#">c1gv4A_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 8; <b>PDBTitle:</b> murine apoptosis-inducing factor (aif)
75	<a href="#">c1nhqA_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> oxidoreductase (h2o2(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> nadh peroxidase; <b>PDBTitle:</b> crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303
76	<a href="#">c3urhB_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
77	<a href="#">c3kd9B_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> coenzyme a disulfide reductase; <b>PDBTitle:</b> crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
78	<a href="#">c3lxdA_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide <b>PDBTitle:</b> crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans

79	<a href="#">c4jdrB_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase of pyruvate dehydrogenase from2 escherichia coli
80	<a href="#">c1xdia_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> rv3303c-lpda; <b>PDBTitle:</b> crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
81	<a href="#">c1dxlc_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
82	<a href="#">c1q1wA_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putidaredoxin reductase; <b>PDBTitle:</b> crystal structure of putidaredoxin reductase from2 pseudomonas putida
83	<a href="#">c4j56A_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2; <b>PDBTitle:</b> structure of plasmodium falciparum thioredoxin reductase-thioredoxin2 complex
84	<a href="#">c3kpgA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfide-quinone reductase, putative; <b>PDBTitle:</b> crystal structure of sulfide:quinone oxidoreductase from2 acidithiobacillus ferrooxidans in complex with decylubiquinone
85	<a href="#">c6bz0C_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> 1.83 angstrom resolution crystal structure of dihydrolipoamide dehydrogenase from acinetobacter baumannii in complex with fad.
86	<a href="#">c1v59B_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
87	<a href="#">c3ic9D_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
88	<a href="#">c5jciA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> os09g0567300 protein; <b>PDBTitle:</b> structure and catalytic mechanism of monodehydroascorbate reductase,2 mdhar, from oryza sativa l. japonica
89	<a href="#">c2eq8E_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
90	<a href="#">c4ywoA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> mercuric reductase from metallosphaera sedula
91	<a href="#">c3fg2P_</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> putative rubredoxin reductase; <b>PDBTitle:</b> crystal structure of ferredoxin reductase for the cyp199a2 system from2 rhodospseudomonas palustris
92	<a href="#">c1yqzA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme a disulfide reductase; <b>PDBTitle:</b> structure of coenzyme a-disulfide reductase from2 staphylococcus aureus refined at 1.54 angstrom resolution
93	<a href="#">c1lvIA_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution
94	<a href="#">c2gr2A_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin reductase; <b>PDBTitle:</b> crystal structure of ferredoxin reductase, bpha4 (oxidized form)
95	<a href="#">c6aonB_</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> 1.72 angstrom resolution crystal structure of 2-oxoglutarate2 dehydrogenase complex subunit dihydrolipoamide dehydrogenase from3 bordetella pertussis in complex with fad
96	<a href="#">c1lqtB_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fpra; <b>PDBTitle:</b> a covalent modification of nadp+ revealed by the atomic resolution2 structure of fpra, a mycobacterium tuberculosis oxidoreductase
97	<a href="#">c4b1bB_</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum oxidised2 thioredoxin reductase at 2.9 angstrom
98	<a href="#">c3ef6A_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> toluene 1,2-dioxygenase system ferredoxin--nad(+) <b>PDBTitle:</b> crystal structure of toluene 2,3-dioxygenase reductase
99	<a href="#">c2a8xA_</a>	Alignment	not modelled	99.9	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
100	<a href="#">c3hyxC_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfide-quinone reductase; <b>PDBTitle:</b> 3-d x-ray structure of the sulfide:quinone oxidoreductase from aquifex2 aeolicus in complex with aurachin c
101	<a href="#">c3l8kB_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoamide dehydrogenase from sulfolobus2 solfataricus
102	<a href="#">c1bwcA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glutathione reductase); <b>PDBTitle:</b> structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
103	<a href="#">c1cicA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (adrenodoxin reductase);

103	<a href="#">c1qjA</a>	Alignment	not modelled	99.9	17	<b>PDBTitle:</b> structure of adrenodoxin reductase of mitochondrial p450 systems <b>PDB header:</b> oxidoreductase
104	<a href="#">c2nvkX</a>	Alignment	not modelled	99.9	20	<b>Chain:</b> X: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase from drosophila2 melanogaster
105	<a href="#">c1ebdB</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> complex (oxidoreductase/transferase) <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
106	<a href="#">c5w4cA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase from cryptococcus2 neoformans in complex with fad (fo conformation)
107	<a href="#">c1tytA</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trypanothione reductase, oxidized form; <b>PDBTitle:</b> crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution
108	<a href="#">c5x1yC</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> structure of mercuric reductase from lysinibacillus sphaericus
109	<a href="#">c2hqmB</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
110	<a href="#">c4dnaA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable glutathione reductase; <b>PDBTitle:</b> crystal structure of putative glutathione reductase from sinorhizobium2 meliloti 1021
111	<a href="#">c1ndaD</a>	Alignment	not modelled	99.9	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> trypanothione oxidoreductase; <b>PDBTitle:</b> the structure of trypanosoma cruzi trypanothione reductase in the2 oxidized and nadph reduced state
112	<a href="#">c6b4oB</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> 1.73 angstrom resolution crystal structure of glutathione reductase2 from enterococcus faecalis in complex with fad
113	<a href="#">c2r9zB</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione amide reductase; <b>PDBTitle:</b> glutathione amide reductase from chromatium gracile
114	<a href="#">c1m6iA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 8; <b>PDBTitle:</b> crystal structure of apoptosis inducing factor (aif)
115	<a href="#">c1lpfB</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> three-dimensional structure of lipoamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties
116	<a href="#">c2cfyB</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1; <b>PDBTitle:</b> crystal structure of human thioredoxin reductase 1
117	<a href="#">c1geuA</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> oxidoreductase(flavoenzyme) <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> anatomy of an engineered nad-binding site
118	<a href="#">c1x31A</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sarcosine oxidase alpha subunit; <b>PDBTitle:</b> crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
119	<a href="#">c3o0hA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of glutathione reductase from bartonella henselae
120	<a href="#">c5er0D</a>	Alignment	not modelled	99.9	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nadh oxidase; <b>PDBTitle:</b> water-forming nadh oxidase from lactobacillus brevis (lbnx)