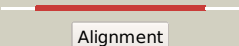
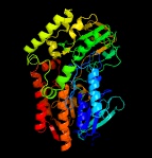


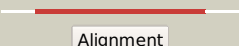





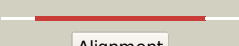













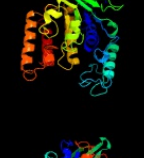





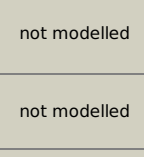


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3083 (-)_3448501_3449988
Date	Thu Aug 8 16:20:26 BST 2019
Unique Job ID	c5c8735caf480cd1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5m0zA_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexanone monooxygenase from thermocrisium municipale.; <b>PDBTitle:</b> cyclohexanone monooxygenase from t. municipale: reduced enzyme bound2 to nadp+
2	<a href="#">c5mq6A_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase-like protein; <b>PDBTitle:</b> polycyclic ketone monooxygenase from the thermophilic fungus2 thermothelomyces thermophila
3	<a href="#">c3gwdA_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexanone monooxygenase; <b>PDBTitle:</b> closed crystal structure of cyclohexanone monooxygenase
4	<a href="#">c3uoyB_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> otemo; <b>PDBTitle:</b> crystal structure of otemo complex with fad and nadp (form 1)
5	<a href="#">c1w4xA_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxygenase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetone monooxygenase; <b>PDBTitle:</b> phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
6	<a href="#">c4ap3A_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> steroid monooxygenase; <b>PDBTitle:</b> oxidized steroid monooxygenase bound to nadp
7	<a href="#">c5j7xA_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethylaniline monooxygenase, putative; <b>PDBTitle:</b> baeyer-villiger monooxygenase bmoafl838 from aspergillus flavus
8	<a href="#">c3uclA_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexanone monooxygenase; <b>PDBTitle:</b> cyclohexanone-bound crystal structure of cyclohexanone monooxygenase2 in the rotated conformation
9	<a href="#">c6jdkA_</a>	 Alignment		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> baeyer-villiger monooxygenase; <b>PDBTitle:</b> crystal structure of baeyer-villiger monooxygenase from parvibaculum2 lavamentivorans
10	<a href="#">c6a37A_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative flavin-binding monooxygenase; <b>PDBTitle:</b> x-ray structure of cyclohexanone monooxygenase from acinetobacter2 calcoaceticus
11	<a href="#">c2vq7B_</a>	 Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> bacterial flavin-containing monooxygenase in complex with2 nadp: native data

12	<a href="#">c5gsnD</a>	Alignment		100.0	19	<b>PDB header:</b> flavoprotein <b>Chain:</b> D: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> tmm in complex with methimazole
13	<a href="#">c1vqwB</a>	Alignment		100.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein with similarity to flavin-containing <b>PDBTitle:</b> crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine3 monooxygenases
14	<a href="#">d1w4xa1</a>	Alignment		100.0	27	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
15	<a href="#">c5nmwA</a>	Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> crystal structure of the pyrrolizidine alkaloid n-oxygenase from2 zonocerus variegatus in complex with fad
16	<a href="#">c3s5wB</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-ornithine 5-monooxygenase; <b>PDBTitle:</b> ornithine hydroxylase (pvda) from pseudomonas aeruginosa
17	<a href="#">c5cqaA</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lysine 6-monooxygenase; <b>PDBTitle:</b> crystal structure of l-lysine 6-monooxygenase from pseudomonas2 syringae
18	<a href="#">c4b68A</a>	Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-ornithine n5 monooxygenase; <b>PDBTitle:</b> a. fumigatus ornithine hydroxylase (sida), re-oxidised state bound to2 nadp and arg
19	<a href="#">c5o8rA</a>	Alignment		100.0	11	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-lysine 6-monooxygenase involved in desferrioxamine <b>PDBTitle:</b> the crystal structure of dfoa bound to fad and nadp; the2 desferrioxamine biosynthetic pathway cadaverine monooxygenase from3 the fire blight disease pathogen erwinia amylovora
20	<a href="#">c4tlxC</a>	Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> ktzi; <b>PDBTitle:</b> kutzneria sp. 744 ornithine n-hydroxylase, ktzi-fadred-nadp+-l-orn
21	<a href="#">c4d7eA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lys monooxygenase; <b>PDBTitle:</b> an unprecedented nadph domain conformation in lysine2 monooxygenase nbtg from nocardia farcinica
22	<a href="#">d2qv8a1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
23	<a href="#">c4usrA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> structure of flavin-containing monooxygenase from2 pseudomonas stutzeri nf13
24	<a href="#">c3d1cA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-containing putative monooxygenase; <b>PDBTitle:</b> crystal structure of flavin-containing putative monooxygenase2 (np_373108.1) from staphylococcus aureus mu50 at 2.40 a resolution
25	<a href="#">c1lqtB</a>	Alignment	not modelled	100.0	18	<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
26	<a href="#">d1w4xa2</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
27	<a href="#">c4a9wB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> flavin-containing monooxygenase from stentrophomonas maltophilia
28	<a href="#">c1cicA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (adrenodoxin reductase);

28	<a href="#">c4qjA</a>	Alignment	not modelled	100.0	15	<b>PDBTitle:</b> structure of adrenodoxin reductase of mitochondrial p450 systems <b>PDB header:</b> oxidoreductase
29	<a href="#">c4usqA</a>	Alignment	not modelled	100.0	17	<b>Chain:</b> A; <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase; <b>PDBTitle:</b> structure of flavin-containing monooxygenase from2 cellvibrio sp. br
30	<a href="#">c1hyuA</a>	Alignment	not modelled	99.9	17	<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
31	<a href="#">c3ntaA</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> structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
32	<a href="#">c3icrA</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> crystal structure of oxidized bacillus anthracis coadr-rhd
33	<a href="#">c1yqzA</a>	Alignment	not modelled	99.9	17	<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
34	<a href="#">c6qkgB</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> flavoprotein <b>Chain:</b> B; <b>PDB Molecule:</b> ncr a; <b>PDBTitle:</b> 2-naphthoyl-coa reductase(ncr)
35	<a href="#">c1qv4A</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> programed cell death protein 8; <b>PDBTitle:</b> murine apoptosis-inducing factor (aif)
36	<a href="#">c5w1jA</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> signaling protein <b>Chain:</b> A; <b>PDB Molecule:</b> thioredoxin glutathione reductase; <b>PDBTitle:</b> echinococcus granulosus thioredoxin glutathione reductas (egtgr)
37	<a href="#">c3oc4A</a>	Alignment	not modelled	99.9	18	<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
38	<a href="#">c1ps9A</a>	Alignment	not modelled	99.9	15	<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
39	<a href="#">c2v6oA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> thioredoxin glutathione reductase; <b>PDBTitle:</b> structure of schistosoma mansoni thioredoxin-gluthatione2 reductase (smtgr)
40	<a href="#">c6garB</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of oxidised ferredoxin/flavodoxin nadp+2 oxidoreductase 1 (fnr1) from bacillus cereus
41	<a href="#">c1xdia</a>	Alignment	not modelled	99.9	16	<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
42	<a href="#">c5twcA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> oxidoreductase iruo in the oxidized form
43	<a href="#">c1gthD</a>	Alignment	not modelled	99.9	16	<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
44	<a href="#">c6du7C</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C; <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> glutathione reductase from streptococcus pneumoniae
45	<a href="#">c5jciA</a>	Alignment	not modelled	99.8	16	<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
46	<a href="#">c2bcpA</a>	Alignment	not modelled	99.8	18	<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
47	<a href="#">c4g6gB</a>	Alignment	not modelled	99.8	19	<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
48	<a href="#">c4gapB</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> rotenone-insensitive nadh-ubiquinone oxidoreductase; <b>PDBTitle:</b> structure of the ndi1 protein from saccharomyces cerevisiae in complex2 with nad+
49	<a href="#">c2cduB</a>	Alignment	not modelled	99.8	17	<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
50	<a href="#">c1tytA</a>	Alignment	not modelled	99.8	16	<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
51	<a href="#">c3r9uA</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> thioredoxin-disulfide reductase from campylobacter jejuni.
52	<a href="#">c1nhqA</a>	Alignment	not modelled	99.8	18	<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 <b>PDB header:</b> oxidoreductase

53	<a href="#">c2eq7B_</a>	Alignment	not modelled	99.8	17	<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
54	<a href="#">c5w4cA_</a>	Alignment	not modelled	99.8	19	<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)
55	<a href="#">c5jwcA_</a>	Alignment	not modelled	99.8	14	<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
56	<a href="#">c2zwbA_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
57	<a href="#">c5jriA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase; <b>PDBTitle:</b> structure of an oxidoreductase semet-labelled from synechocystis sp.2 pcc6803
58	<a href="#">c3iwaA_</a>	Alignment	not modelled	99.8	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
59	<a href="#">c2gr2A_</a>	Alignment	not modelled	99.8	16	<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)
60	<a href="#">c2w0hA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trypanothione reductase; <b>PDBTitle:</b> x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
61	<a href="#">c1m6iA_</a>	Alignment	not modelled	99.8	16	<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)
62	<a href="#">c2vdcI_</a>	Alignment	not modelled	99.8	18	<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.
63	<a href="#">c4jmqA_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a thioredoxin reductase from brucella melitensis
64	<a href="#">c5ygaB_</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ferredoxin nadp+ oxidoreductase from2 rhodopseudomonas palustris
65	<a href="#">c6mp5B_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> membrane protein, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> sulfide:quinone oxidoreductase, mitochondrial; <b>PDBTitle:</b> crystal structure of native human sulfide:quinone oxidoreductase
66	<a href="#">c4yIfD_</a>	Alignment	not modelled	99.8	14	<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-nadp oxidoreductase structure
67	<a href="#">c1djnB_</a>	Alignment	not modelled	99.8	20	<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 methylphilus methylotrophus (sp.3 w3a1)
68	<a href="#">c5v36A_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> hydrolase,oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> 1.88 angstrom resolution crystal structure of glutathione reductase2 from streptococcus mutans ua159 in complex with fad
69	<a href="#">c6gncA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a ferredoxin-flavin thioredoxin reductase from2 clostridium acetobutylicum at 1.64 a resolution
70	<a href="#">c6b4oB_</a>	Alignment	not modelled	99.8	15	<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
71	<a href="#">c1ojtA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> surface protein; <b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase
72	<a href="#">c5odeA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gll2934 protein; <b>PDBTitle:</b> structure of a novel oxidoreductase from gloebacter violaceus
73	<a href="#">c4j56A_</a>	Alignment	not modelled	99.8	14	<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
74	<a href="#">c4gcmB_</a>	Alignment	not modelled	99.8	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a thioredoxine reductase (trxb) from2 staphylococcus aureus subsp. aureus mu50 at 1.80 a resolution
75	<a href="#">c5niiB_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of the atypical thioredoxin reductase tri from2 desulfovibrio vulgaris hildenborough
76	<a href="#">c5uwyA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> the crystal structure of thioredoxin reductase from streptococcus2 pyogenes mgas5005

77	<a href="#">c1v59B_</a>	Alignment	not modelled	99.8	15	<b>Chain:</b> B: <b>PDB Molecule:</b> dihydroliipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
78	<a href="#">c5jcaL_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> nadh-dependent ferredoxin:nadp oxidoreductase (nfni) <b>PDBTitle:</b> nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfni)2 from pyrococcus furiosus
79	<a href="#">c4dnaA_</a>	Alignment	not modelled	99.8	16	<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 melliloti 1021
80	<a href="#">c4b1bB_</a>	Alignment	not modelled	99.8	15	<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
81	<a href="#">c4ntdA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of hlm1
82	<a href="#">c3k30B_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> histamine dehydrogenase from nocardiodes simplex
83	<a href="#">c4fk1D_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative thioredoxin reductase; <b>PDBTitle:</b> crystal structure of putative thioredoxin reductase trxb from bacillus2 anthracis
84	<a href="#">c1dxlC_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydroliipoamide dehydrogenase; <b>PDBTitle:</b> dihydroliipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
85	<a href="#">c5n1tA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-binding subunit of sulfide dehydrogenase; <b>PDBTitle:</b> crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
86	<a href="#">c2qaeA_</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroliopoyl dehydrogenase; <b>PDBTitle:</b> crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
87	<a href="#">c1geuA_</a>	Alignment	not modelled	99.8	17	<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
88	<a href="#">c2hqmB_</a>	Alignment	not modelled	99.8	17	<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
89	<a href="#">c4xdbC_</a>	Alignment	not modelled	99.8	16	<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
90	<a href="#">c4nwaA_</a>	Alignment	not modelled	99.8	19	<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 thermanum at 2.5a resolution
91	<a href="#">c1ndaD_</a>	Alignment	not modelled	99.8	14	<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
92	<a href="#">c3ic9D_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydroliipoamide dehydrogenase; <b>PDBTitle:</b> the structure of dihydroliipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
93	<a href="#">c3lxdA_</a>	Alignment	not modelled	99.8	18	<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
94	<a href="#">c3lzxB_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase 2; <b>PDBTitle:</b> crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
95	<a href="#">c3kd9B_</a>	Alignment	not modelled	99.8	22	<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
96	<a href="#">c3urhB_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroliopoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydroliipoamide dehydrogenase from2 sinorhizobium melliloti 1021
97	<a href="#">c2eq8E_</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydroliipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
98	<a href="#">c4jnaA_</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> deph; <b>PDBTitle:</b> crystal structure of the deph complex with dimethyl-fk228
99	<a href="#">c2ywlA_</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase related protein; <b>PDBTitle:</b> crystal structure of thioredoxin reductase-related protein ttha03702 from thermus thermophilus hb8
100	<a href="#">c3dgzA_</a>	Alignment	not modelled	99.8	15	<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
101	<a href="#">c3cqdB_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase, class i;

101	<a href="#">c3c9bB</a>	Alignment	not modelled	99.8	15	<b>PDBTitle:</b> pyridine nucleotide complexes with bacillus anthracis coenzyme a-2 disulfide reductase: a structural analysis of dual nad(p)h3 specificity
102	<a href="#">c2c3dB</a>	Alignment	not modelled	99.8	17	<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
103	<a href="#">c3o0hA</a>	Alignment	not modelled	99.8	15	<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
104	<a href="#">c3l8kB</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoyl dehydrogenase from sulfolobus2 solfataricus
105	<a href="#">c2a8xA</a>	Alignment	not modelled	99.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
106	<a href="#">c5j60B</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> structure of a thioredoxin reductase from gloeobacter violaceus
107	<a href="#">c2v3aA</a>	Alignment	not modelled	99.8	13	<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.
108	<a href="#">c3fbsB</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
109	<a href="#">c1lvIA</a>	Alignment	not modelled	99.8	14	<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
110	<a href="#">c1zkqA</a>	Alignment	not modelled	99.8	15	<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
111	<a href="#">c1zx9A</a>	Alignment	not modelled	99.8	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> crystal structure of tn501 mera
112	<a href="#">c4ntcA</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glit; <b>PDBTitle:</b> crystal structure of glit
113	<a href="#">c1q1wA</a>	Alignment	not modelled	99.8	17	<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
114	<a href="#">c1lpfB</a>	Alignment	not modelled	99.8	18	<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
115	<a href="#">c5m5jA</a>	Alignment	not modelled	99.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> thioredoxin reductase from giardia duodenalis
116	<a href="#">c4ywoA</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> mercuric reductase from metallosphaera sedula
117	<a href="#">c6aonB</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl 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
118	<a href="#">c3f8rD</a>	Alignment	not modelled	99.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin reductase (trxb-3); <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
119	<a href="#">c1fcdB</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> electron transport(flavocytochrome) <b>Chain:</b> B: <b>PDB Molecule:</b> flavocytochrome c sulfide dehydrogenase (flavin- <b>PDBTitle:</b> the structure of flavocytochrome c sulfide dehydrogenase2 from a purple phototrophic bacterium chromatium vinosum at3 2.5 angstroms resolution
120	<a href="#">c6gndG</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of the complex of a ferredoxin-flavin thioredoxin2 reductase and a thioredoxin from clostridium acetobutylicum at 2.9 a3 resolution