

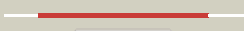




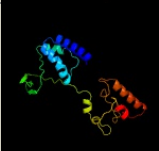



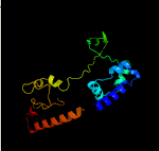

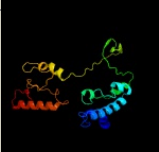

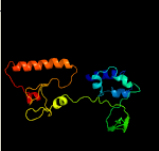







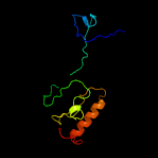
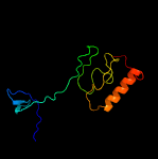

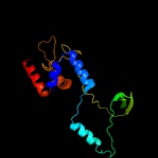
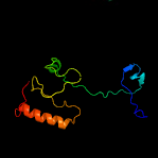

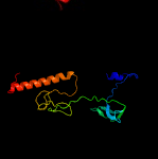



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3741c_(-)_4192357_4193031
Date	Fri Aug 9 18:20:44 BST 2019
Unique Job ID	103382ca83aedd5d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5mq6A_</a>	 Alignment		100.0	14	<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 thermotheomyces thermophila
2	<a href="#">c3uoyB_</a>	 Alignment		100.0	12	<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)
3	<a href="#">c1w4xA_</a>	 Alignment		100.0	21	<b>PDB header:</b> oxygenase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetone monooxygenase; <b>PDBTitle:</b> phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
4	<a href="#">c4ap3A_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> steroid monooxygenase; <b>PDBTitle:</b> oxidized steroid monooxygenase bound to nadp
5	<a href="#">c3gwdA_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexanone monooxygenase; <b>PDBTitle:</b> closed crystal structure of cyclohexanone monooxygenase
6	<a href="#">c5m0zA_</a>	 Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexanone monooxygenase from thermocrisum municipale.; <b>PDBTitle:</b> cyclohexanone monooxygenase from t. municipale: reduced enzyme bound2 to nadp+
7	<a href="#">c5j7xA_</a>	 Alignment		100.0	14	<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="#">c6jdkA_</a>	 Alignment		100.0	15	<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
9	<a href="#">c3uclA_</a>	 Alignment		100.0	14	<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
10	<a href="#">c6a37A_</a>	 Alignment		100.0	15	<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="#">d1w4xa2</a>	 Alignment		99.7	23	<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

12	<a href="#">d1w4xa1</a>	Alignment		99.5	18	<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
13	<a href="#">c2vq7B_</a>	Alignment		99.3	13	<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
14	<a href="#">c5gsnD_</a>	Alignment		99.1	15	<b>PDB header:</b> flavoprotein <b>Chain:</b> D: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> tmm in complex with methimazole
15	<a href="#">c5nmwA_</a>	Alignment		98.8	11	<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="#">c5cqaA_</a>	Alignment		98.6	13	<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
17	<a href="#">c1vqwB_</a>	Alignment		98.4	15	<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
18	<a href="#">c3s5wB_</a>	Alignment		98.3	9	<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
19	<a href="#">c1lqtB_</a>	Alignment		98.1	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fpfa; <b>PDBTitle:</b> a covalent modification of nadp+ revealed by the atomic resolution2 structure of fpfa, a mycobacterium tuberculosis oxidoreductase
20	<a href="#">c4b68A_</a>	Alignment		98.0	16	<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
21	<a href="#">c5o8rA_</a>	Alignment	not modelled	98.0	8	<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
22	<a href="#">c1cjcA_</a>	Alignment	not modelled	97.7	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (adrenodoxin reductase); <b>PDBTitle:</b> structure of adrenodoxin reductase of mitochondrial p450 systems
23	<a href="#">c4tixC_</a>	Alignment	not modelled	97.6	12	<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
24	<a href="#">d1ps9a2</a>	Alignment	not modelled	97.5	11	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> C-terminal domain of adrenodoxin reductase-like
25	<a href="#">c4a9wB_</a>	Alignment	not modelled	97.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> flavin-containing monooxygenase from stentrophomonas maltophilia
26	<a href="#">c4usrA_</a>	Alignment	not modelled	97.2	18	<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
27	<a href="#">d2gv8a1</a>	Alignment	not modelled	97.0	8	<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
28	<a href="#">d1d7ya2</a>	Alignment	not modelled	96.6	14	<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

29	<a href="#">c4usqA</a>	Alignment	not modelled	96.4	23	<b>PDB header:</b> oxidoreductase <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="#">c1ndaD</a>	Alignment	not modelled	96.2	19	<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
31	<a href="#">c3hyxC</a>	Alignment	not modelled	96.1	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
32	<a href="#">c1geuA</a>	Alignment	not modelled	96.0	16	<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
33	<a href="#">c1yqzA</a>	Alignment	not modelled	95.8	19	<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="#">c4j56A</a>	Alignment	not modelled	95.8	9	<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
35	<a href="#">c1xdia</a>	Alignment	not modelled	95.7	11	<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
36	<a href="#">c4b1bB</a>	Alignment	not modelled	95.6	10	<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
37	<a href="#">c5jwcA</a>	Alignment	not modelled	95.6	17	<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
38	<a href="#">c2eq7B</a>	Alignment	not modelled	95.5	14	<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 psbd0
39	<a href="#">d1xhca2</a>	Alignment	not modelled	95.5	14	<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
40	<a href="#">c6du7C</a>	Alignment	not modelled	95.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> glutathione reductase from streptococcus pneumoniae
41	<a href="#">c3o0hA</a>	Alignment	not modelled	95.4	20	<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
42	<a href="#">c3icrA</a>	Alignment	not modelled	95.4	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 coadr-rhd
43	<a href="#">c2w0hA</a>	Alignment	not modelled	95.1	19	<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
44	<a href="#">c1tytA</a>	Alignment	not modelled	95.1	19	<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
45	<a href="#">c3oc4A</a>	Alignment	not modelled	95.1	19	<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
46	<a href="#">d1fcdal</a>	Alignment	not modelled	95.0	17	<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
47	<a href="#">c6mp5B</a>	Alignment	not modelled	95.0	12	<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
48	<a href="#">c6qkgB</a>	Alignment	not modelled	94.9	18	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> ncr a; <b>PDBTitle:</b> 2-naphthoyl-coa reductase(ncr)
49	<a href="#">c2ardA</a>	Alignment	not modelled	94.6	22	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase prna; <b>PDBTitle:</b> the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination
50	<a href="#">c3ntaA</a>	Alignment	not modelled	94.5	18	<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="#">c3d1cA</a>	Alignment	not modelled	94.4	18	<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
52	<a href="#">c5hy5A</a>	Alignment	not modelled	94.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan 6-halogenase; <b>PDBTitle:</b> crystal structure of a tryptophan 6-halogenase (stth) from2 streptomyces toxytricini <b>PDB header:</b> oxidoreductase

53	<a href="#">c3urhB_</a>	Alignment	not modelled	94.1	14	<b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoamide dehydrogenase from <i>Sinorhizobium meliloti</i> 1021
54	<a href="#">c5uaoA_</a>	Alignment	not modelled	93.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan 5-halogenase; <b>PDBTitle:</b> crystal structure of mibh, a lathipeptide tryptophan 5-halogenase
55	<a href="#">c4dnaA_</a>	Alignment	not modelled	93.6	15	<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 <i>Sinorhizobium meliloti</i> 1021
56	<a href="#">c6b4oB_</a>	Alignment	not modelled	93.5	12	<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 <i>Enterococcus faecalis</i> in complex with fad
57	<a href="#">c6ib5B_</a>	Alignment	not modelled	93.5	21	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan 6-halogenase; <b>PDBTitle:</b> mutant of flavin-dependent tryptophan halogenase thal with altered2 regioselectivity (thal-rbh5)
58	<a href="#">c2gr2A_</a>	Alignment	not modelled	93.5	13	<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)
59	<a href="#">c2bcpA_</a>	Alignment	not modelled	93.5	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidase; <b>PDBTitle:</b> structural analysis of <i>Streptococcus pyogenes</i> nadh oxidase: c44s nox2 with azide
60	<a href="#">c1ps9A_</a>	Alignment	not modelled	93.4	11	<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 <i>E. coli</i> 2,4-dienoyl2 coa reductase
61	<a href="#">c2weuD_</a>	Alignment	not modelled	93.3	14	<b>PDB header:</b> antifungal protein <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan 5-halogenase; <b>PDBTitle:</b> crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
62	<a href="#">c1m6iA_</a>	Alignment	not modelled	93.2	24	<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)
63	<a href="#">c4xdbC_</a>	Alignment	not modelled	93.2	14	<b>PDB header:</b> oxidoreductase, membrane protein, flavoprotein <b>Chain:</b> C: <b>PDB Molecule:</b> nadh dehydrogenase-like protein saouhsc_00878; <b>PDBTitle:</b> nadh:quinone oxidoreductase (ndh-ii) from <i>Staphylococcus aureus</i> -2 holoprotein structure
64	<a href="#">d1q1ra2</a>	Alignment	not modelled	93.2	18	<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
65	<a href="#">c2cduB_</a>	Alignment	not modelled	93.1	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 from <i>Lactobacillus sanfranciscensis</i>
66	<a href="#">c2v3aA_</a>	Alignment	not modelled	93.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin reductase; <b>PDBTitle:</b> crystal structure of rubredoxin reductase from <i>Pseudomonas aeruginosa</i> .
67	<a href="#">c1gv4A_</a>	Alignment	not modelled	93.0	27	<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)
68	<a href="#">d2cula1</a>	Alignment	not modelled	93.0	15	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> GidA-like
69	<a href="#">c1lvA_</a>	Alignment	not modelled	93.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> the refined structure of <i>Pseudomonas putida</i> lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution
70	<a href="#">d1ryia1</a>	Alignment	not modelled	92.9	17	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
71	<a href="#">c2pyxA_</a>	Alignment	not modelled	92.9	15	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase; <b>PDBTitle:</b> crystal structure of tryptophan halogenase (yp_750003.1) from <i>Shewanella frigidimarina</i> ncimb 400 at 1.50 a resolution
72	<a href="#">c1zx9A_</a>	Alignment	not modelled	92.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> crystal structure of tn501 mera
73	<a href="#">c4d7eA_</a>	Alignment	not modelled	92.9	20	<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 <i>Nocardia farcinica</i>
74	<a href="#">c5jciA_</a>	Alignment	not modelled	92.9	19	<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 <i>Oryza sativa</i> l. japonica
75	<a href="#">c5n1tA_</a>	Alignment	not modelled	92.8	11	<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 <i>T. paradoxus</i>
76	<a href="#">d1m6ia2</a>	Alignment	not modelled	92.7	28	<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
77	<a href="#">c3k30B_</a>	Alignment	not modelled	92.6	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> histamine dehydrogenase from <i>Nocardiothes simplex</i>
78	<a href="#">c1nhqA_</a>	Alignment	not modelled	92.6	16	<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
79	<a href="#">c2e4gB_</a>	Alignment	not modelled	92.6	23	<b>PDB header:</b> biosynthetic protein, flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan halogenase; <b>PDBTitle:</b> rebh with bound l-trp
80	<a href="#">c6de6B_</a>	Alignment	not modelled	92.6	4	<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
81	<a href="#">c6fr1A_</a>	Alignment	not modelled	92.6	23	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase superfamily; <b>PDBTitle:</b> brvh, a flavin-dependent halogenase from brevundimonas sp. bal3
82	<a href="#">c4nwzA_</a>	Alignment	not modelled	92.5	11	<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
83	<a href="#">d1gesa2</a>	Alignment	not modelled	92.0	23	<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
84	<a href="#">c4g6gB_</a>	Alignment	not modelled	91.9	15	<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
85	<a href="#">c4ywoA_</a>	Alignment	not modelled	91.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> mercuric reductase from metallosphaera sedula
86	<a href="#">c2zxiC_</a>	Alignment	not modelled	91.8	17	<b>PDB header:</b> fad-binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> structure of aquifex aeolicus gida in the form ii crystal
87	<a href="#">c1zkqA_</a>	Alignment	not modelled	91.8	8	<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
88	<a href="#">c3cp8C_</a>	Alignment	not modelled	91.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> crystal structure of gida from chlorobium tepidum
89	<a href="#">c2hqmB_</a>	Alignment	not modelled	91.6	14	<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
90	<a href="#">d1feca2</a>	Alignment	not modelled	91.5	28	<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
91	<a href="#">d1gera2</a>	Alignment	not modelled	91.4	23	<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
92	<a href="#">c3cesB_</a>	Alignment	not modelled	91.3	17	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl modification enzyme <b>PDBTitle:</b> crystal structure of e.coli mnmg (gida), a highly-conserved trna2 modifying enzyme
93	<a href="#">c5v36A_</a>	Alignment	not modelled	91.3	16	<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
94	<a href="#">c2eq8E_</a>	Alignment	not modelled	91.2	18	<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
95	<a href="#">c3ef6A_</a>	Alignment	not modelled	91.2	11	<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
96	<a href="#">c1fcdB_</a>	Alignment	not modelled	90.8	19	<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
97	<a href="#">c4gapB_</a>	Alignment	not modelled	90.7	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 ndi1 protein from saccharomyces cerevisiae in complex2 with nad+
98	<a href="#">d1lva2</a>	Alignment	not modelled	90.7	12	<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
99	<a href="#">d1nhpa2</a>	Alignment	not modelled	90.5	15	<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
100	<a href="#">c3dgzA_</a>	Alignment	not modelled	90.4	8	<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="#">c1q1wA_</a>	Alignment	not modelled	90.2	16	<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
102	<a href="#">c3kd9B_</a>	Alignment	not modelled	90.1	15	<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
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase;



103	<a href="#">c6bz0C_</a>	Alignment	not modelled	89.9	13	<b>PDBTitle:</b> 1.83 angstrom resolution crystal structure of dihydrolipoyl2 dehydrogenase from acinetobacter baumannii in complex with fad.
104	<a href="#">c1ebdB_</a>	Alignment	not modelled	89.8	18	<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
105	<a href="#">c3cgdB_</a>	Alignment	not modelled	89.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase, class i; <b>PDBTitle:</b> pyridine nucleotide complexes with bacillus anthracis coenzyme a-2 disulfide reductase: a structural analysis of dual nad(p)h3 specificity
106	<a href="#">c3kpgA_</a>	Alignment	not modelled	89.5	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
107	<a href="#">c1v59B_</a>	Alignment	not modelled	89.5	13	<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+
108	<a href="#">d1gv4a2</a>	Alignment	not modelled	89.3	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
109	<a href="#">d1d7ya1</a>	Alignment	not modelled	89.3	14	<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
110	<a href="#">c4dggA_</a>	Alignment	not modelled	89.2	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phytoene dehydrogenase; <b>PDBTitle:</b> crystal structure of phytoene desaturase crti from pantoea ananatis
111	<a href="#">d1aoga2</a>	Alignment	not modelled	89.1	20	<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
112	<a href="#">c3djeA_</a>	Alignment	not modelled	89.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fructosyl amine: oxygen oxidoreductase; <b>PDBTitle:</b> crystal structure of the deglycating enzyme fructosamine2 oxidase from aspergillus fumigatus (amadoriase ii) in3 complex with fsa
113	<a href="#">c2cfyB_</a>	Alignment	not modelled	88.9	12	<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
114	<a href="#">c3iwaA_</a>	Alignment	not modelled	88.9	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 a fad-dependent pyridine nucleotide-disulphide2 oxidoreductase from desulfovibrio vulgaris
115	<a href="#">c1dxlC_</a>	Alignment	not modelled	88.6	12	<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
116	<a href="#">c2a8xA_</a>	Alignment	not modelled	87.5	20	<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
117	<a href="#">d1mo9a1</a>	Alignment	not modelled	87.3	15	<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
118	<a href="#">c3h8IA_</a>	Alignment	not modelled	87.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidase; <b>PDBTitle:</b> the first x-ray structure of a sulfide:quinone2 oxidoreductase: insights into sulfide oxidation mechanism
119	<a href="#">c5jcaL_</a>	Alignment	not modelled	86.9	20	<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
120	<a href="#">c3cp2A_</a>	Alignment	not modelled	86.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trna uridine 5-carboxymethylaminomethyl <b>PDBTitle:</b> crystal structure of gida from e. coli