Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0943c_(-)_1052700_1053740
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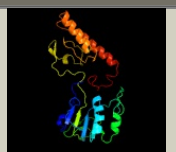
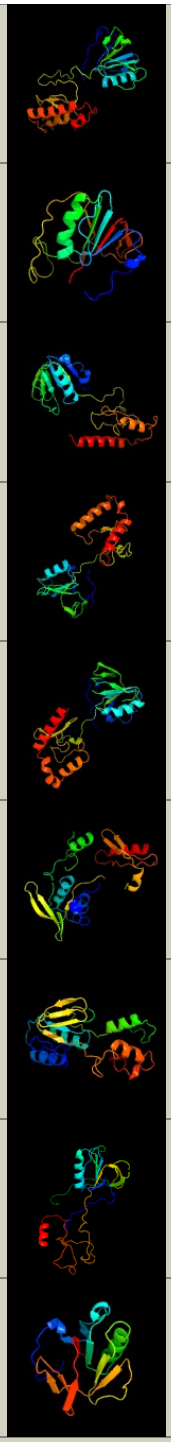
Unique Job ID	b9820de82adf4861

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5m0zA_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cyclohexanone monooxygenase from thermocrispum municipale.; **PDBTitle:** cyclohexanone monooxygenase from t. municipale: reduced enzyme bound2 to nadp+
2	c5mq6A_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyridine nucleotide-disulfide oxidoreductase-like protein; **PDBTitle:** polycyclic ketone monooxygenase from the thermophilic fungus2 thermothelomyces thermophila
3	c5j7xA_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dimethylaniline monooxygenase, putative; **PDBTitle:** baeyer-villiger monooxygenase bvmoafl838 from aspergillus flavus
4	c3gwdA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cyclohexanone monooxygenase; **PDBTitle:** closed crystal structure of cyclohexanone monooxygenase
5	c3uoyB_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**otemo; **PDBTitle:** crystal structure of otemo complex with fad and nadp (form 1)
6	c1w4xA_	Alignment		100.0	25	**PDB header:**oxygenase **Chain:** A: **PDB Molecule:**phenylacetone monooxygenase; **PDBTitle:** phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
7	c4ap3A_	Alignment		100.0	27	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**steroid monooxygenase; **PDBTitle:** oxidized steroid monooxygenase bound to nadp
8	c6a37A_	Alignment		100.0	25	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative flavin-binding monooxygenase; **PDBTitle:** x-ray structure of cyclohexanone monooxygenase from acinetobacter2 calcoaceticus
9	c3uclA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cyclohexanone monooxygenase; **PDBTitle:** cyclohexanone-bound crystal structure of cyclohexanone monooxygenase2 in the rotated conformation
10	c6jdkA_	Alignment		100.0	28	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**baeyer-villiger monooxygenase; **PDBTitle:** crystal structure of baeyer-villiger monooxygenase from parvibaculum2 lavamentivorans
11	d1w4xa1	Alignment		100.0	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains

12	c2vq7B_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**flavin-containing monooxygenase; **PDBTitle:** bacterial flavin-containing monooxygenase in complex with2 nadp: native data
13	d1w4xa2	Alignment		100.0	29	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
14	c5gsnD_	Alignment		99.9	18	**PDB header:**flavoprotein **Chain:** D: **PDB Molecule:**flavin-containing monooxygenase; **PDBTitle:** tmm in complex with methimazole
15	c1vqwB_	Alignment		99.9	11	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**protein with similarity to flavin-containing **PDBTitle:** crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine3 monooxygenases
16	c5nmwA_	Alignment		99.9	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavin-containing monooxygenase; **PDBTitle:** crystal structure of the pyrrolizidine alkaloid n-oxygenase from2 zonocerus variegatus in complex with fad
17	c3s5wB_	Alignment		99.7	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-ornithine 5-monooxygenase; **PDBTitle:** ornithine hydroxylase (pvda) from pseudomonas aeruginosa
18	c4d7eA_	Alignment		99.6	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lys monooxygenase; **PDBTitle:** an unprecedented nadph domain conformation in lysine2 monooxygenase nbtg from nocardia farcinica
19	c4b68A_	Alignment		99.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-ornithine n5 monooxygenase; **PDBTitle:** a. fumigatus ornithine hydroxylase (sida), re-oxidised state bound to2 nadp and arg
20	d2gv8a2	Alignment		99.6	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
21	d1ps9a2	Alignment	not modelled	99.6	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
22	c5cqfA_	Alignment	not modelled	99.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-lysine 6-monooxygenase; **PDBTitle:** crystal structure of l-lysine 6-monooxygenase from pseudomonas2 syringae
23	c5o8rA_	Alignment	not modelled	99.4	14	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**l-lysine 6-monooxygenase involved in desferrioxamine **PDBTitle:** the crystal structure of dfoa bound to fad and nadp; the2 desferrioxamine biosynthetic pathway cadaverine monooxygenase from3 the fire blight disease pathogen erwinia amylovora
24	c1lqtB_	Alignment	not modelled	99.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**fpra; **PDBTitle:** a covalent modification of nadp+ revealed by the atomic resolution2 structure of fpra, a mycobacterium tuberculosis oxidoreductase
25	c1cjcA_	Alignment	not modelled	99.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (adrenodoxin reductase); **PDBTitle:** structure of adrenodoxin reductase of mitochondrial p450 systems
26	c4tlxC_	Alignment	not modelled	99.2	17	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**ktzi; **PDBTitle:** kutzneria sp. 744 ornithine n-hydroxylase, ktzi-fadred-nadp+-l-orn
27	c3d1cA_	Alignment	not modelled	99.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavin-containing putative monooxygenase; **PDBTitle:** crystal structure of flavin-containing putative monooxygenase2 (np_373108.1) from staphylococcus aureus mu50 at 2.40 a resolution

28	c4usrA_	Alignment	not modelled	99.1	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**monooxygenase; **PDBTitle:** structure of flavin-containing monooxygenase from2 pseudomonas stutzeri nf13
29	d1cjca1	Alignment	not modelled	99.1	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
30	d1fl2a2	Alignment	not modelled	99.1	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
31	c4a9wB_	Alignment	not modelled	99.0	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**monooxygenase; **PDBTitle:** flavin-containing monooxygenase from stenotrophomonas maltophilia
32	d1fcda1	Alignment	not modelled	99.0	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
33	d1d7ya2	Alignment	not modelled	98.9	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
34	d2gv8a1	Alignment	not modelled	98.9	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
35	d1trba2	Alignment	not modelled	98.8	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
36	d1xhca2	Alignment	not modelled	98.8	7	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
37	d1q1ra2	Alignment	not modelled	98.7	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
38	d1gesa2	Alignment	not modelled	98.7	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
39	c4usqA_	Alignment	not modelled	98.6	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyridine nucleotide-disulfide oxidoreductase; **PDBTitle:** structure of flavin-containing monooxygenase from2 cellvibrio sp. br
40	d1gera2	Alignment	not modelled	98.6	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
41	d1onfa2	Alignment	not modelled	98.5	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
42	d1nhpa2	Alignment	not modelled	98.5	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
43	c1hyuA_	Alignment	not modelled	98.4	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** crystal structure of intact ahpf
44	d1m6ia2	Alignment	not modelled	98.4	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
45	d1xhca1	Alignment	not modelled	98.4	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
46	d1lvla2	Alignment	not modelled	98.4	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
47	c1fcdB_	Alignment	not modelled	98.4	15	**PDB header:**electron transport(flavocytochrome) **Chain:** B: **PDB Molecule:**flavocytochrome c sulfide dehydrogenase (flavin- **PDBTitle:** the structure of flavocytochrome c sulfide dehydrogenase2 from a purple phototrophic bacterium chromatium vinosum at3 2.5 angstroms resolution
48	d1ojta2	Alignment	not modelled	98.3	10	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
49	c3oc4A_	Alignment	not modelled	98.3	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase, pyridine nucleotide-disulfide family; **PDBTitle:** crystal structure of a pyridine nucleotide-disulfide family2 oxidoreductase from the enterococcus faecalis v583
50	c5jwcA_	Alignment	not modelled	98.3	14	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**nadh dehydrogenase, putative; **PDBTitle:** structure of ndh2 from plasmodium falciparum in complex with ryl-552
51	d3lada2	Alignment	not modelled	98.3	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
52	c6qkgB_	Alignment	not modelled	98.3	14	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**ncr a; **PDBTitle:** 2-naphthoyl-coa reductase(ncr)
53	d1lpfa2	Alignment	not modelled	98.3	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
						Fold:FAD/NAD(P)-binding domain

54	d3grsa2	Alignment	not modelled	98.2	16	**Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
55	d1feca2	Alignment	not modelled	98.2	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
56	d1gtea3	Alignment	not modelled	98.2	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
57	c4ylfD_	Alignment	not modelled	98.2	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase subunit a; **PDBTitle:** insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure
58	c3icrA_	Alignment	not modelled	98.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a-disulfide reductase; **PDBTitle:** crystal structure of oxidized bacillus anthracis coadr-rhd
59	c5jcaL_	Alignment	not modelled	98.1	18	**PDB header:**oxidoreductase **Chain:** L: **PDB Molecule:**nadh-dependent ferredoxin:nadp oxidoreductase (nfni) **PDBTitle:** nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfni)2 from pyrococcus furiosus
60	c2vdcI_	Alignment	not modelled	98.1	14	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**glutamate synthase [nadph] small chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
61	d1lqta1	Alignment	not modelled	98.1	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
62	d1dxla2	Alignment	not modelled	98.1	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
63	c4xdbC_	Alignment	not modelled	98.1	19	**PDB header:**oxidoreductase, membrane protein, flavop **Chain:** C: **PDB Molecule:**nadh dehydrogenase-like protein saouhsc_00878; **PDBTitle:** nadh:quinone oxidoreductase (ndh-ii) from staphylococcus aureus -2 holoprotein structure
64	c3ntaA_	Alignment	not modelled	98.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
65	d1djqa2	Alignment	not modelled	98.0	17	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**C-terminal domain of adrenodoxin reductase-like
66	c5w1jA_	Alignment	not modelled	98.0	10	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**thioredoxin glutathione reductase; **PDBTitle:** echinococcus granulosus thioredoxin glutathione reductas (egtgr)
67	c2bcpA_	Alignment	not modelled	98.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh oxidase; **PDBTitle:** structural analysis of streptococcus pyogenes nadh oxidase: c44s nox2 with azide
68	c1yqzA_	Alignment	not modelled	98.0	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a disulfide reductase; **PDBTitle:** structure of coenzyme a-disulfide reductase from2 staphylococcus aureus refined at 1.54 angstrom resolution
69	d1gv4a2	Alignment	not modelled	98.0	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
70	d1vdca2	Alignment	not modelled	98.0	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
71	c2gr2A_	Alignment	not modelled	98.0	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin reductase; **PDBTitle:** crystal structure of ferredoxin reductase, bpha4 (oxidized form)
72	d1d7ya1	Alignment	not modelled	97.9	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
73	d1mo9a2	Alignment	not modelled	97.9	10	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
74	c2v3aA_	Alignment	not modelled	97.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin reductase; **PDBTitle:** crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa.
75	d1aoga2	Alignment	not modelled	97.9	11	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
76	d1h6va2	Alignment	not modelled	97.9	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
77	c1gv4A_	Alignment	not modelled	97.8	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**programed cell death protein 8; **PDBTitle:** murine apoptosis-inducing factor (aif)
78	c4gapB_	Alignment	not modelled	97.8	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rotenone-insensitive nadh-ubiquinone oxidoreductase; **PDBTitle:** structure of the ndi1 protein from saccharomyces cerevisiae in complex2 with nad+
79	c1gthD_	Alignment	not modelled	97.8	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary

						complex with2 nadph and 5-iodouracil
80	c4g6gB_	Alignment	not modelled	97.8	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**rotenone-insensitive nadh-ubiquinone oxidoreductase, **PDBTitle:** crystal structure of ndh with trt
81	d1q1ra1	Alignment	not modelled	97.8	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
82	c4nwzA_	Alignment	not modelled	97.8	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulfide oxidoreductase; **PDBTitle:** structure of bacterial type ii nadh dehydrogenase from2 caldalkalibacillus thermarum at 2.5a resolution
83	d2v5za1	Alignment	not modelled	97.8	21	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
84	c1xdiA_	Alignment	not modelled	97.7	15	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**rv3303c-lpda; **PDBTitle:** crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
85	d1v59a2	Alignment	not modelled	97.7	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
86	d2cula1	Alignment	not modelled	97.6	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GidA-like
87	c3kpgA_	Alignment	not modelled	97.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfide-quinone reductase, putative; **PDBTitle:** crystal structure of sulfide:quinone oxidoreductase from2 acidithiobacillus ferrooxidans in complex with decylubiquinone
88	c2v6oA_	Alignment	not modelled	97.6	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin glutathione reductase; **PDBTitle:** structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
89	c1djnB_	Alignment	not modelled	97.6	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**trimethylamine dehydrogenase; **PDBTitle:** structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
90	c3cesB_	Alignment	not modelled	97.5	16	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl modification enzyme **PDBTitle:** crystal structure of e.coli mnmg (gida), a highly-conserved trna2 modifying enzyme
91	d1ebda2	Alignment	not modelled	97.5	11	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
92	c6gncA_	Alignment	not modelled	97.5	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of a ferredoxin-flavin thioredoxin reductase from2 clostridium acetobutylicum at 1.64 a resolution
93	c3g05B_	Alignment	not modelled	97.4	16	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl modification enzyme **PDBTitle:** crystal structure of n-terminal domain (2-550) of e.coli mnmg
94	c6mp5B_	Alignment	not modelled	97.4	16	**PDB header:**membrane protein, oxidoreductase **Chain:** B: **PDB Molecule:**sulfide:quinone oxidoreductase, mitochondrial; **PDBTitle:** crystal structure of native human sulfide:quinone oxidoreductase
95	c2zxiC_	Alignment	not modelled	97.4	20	**PDB header:**fad-binding protein **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl modification enzyme **PDBTitle:** structure of aquifex aeolicus gida in the form ii crystal
96	c3cp8C_	Alignment	not modelled	97.4	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** crystal structure of gida from chlorobium tepidum
97	c6du7C_	Alignment	not modelled	97.3	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glutathione reductase; **PDBTitle:** glutathione reductase from streptococcus pneumoniae
98	c3ic9D_	Alignment	not modelled	97.3	11	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
99	c4gcmB_	Alignment	not modelled	97.3	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of a thioredoxine reductase (trxb) from2 staphylococcus aureus subsp. aureus mu50 at 1.80 a resolution
100	c2eq7B_	Alignment	not modelled	97.2	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxoglutarate dehydrogenase e3 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
101	c1m6iA_	Alignment	not modelled	97.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**programmed cell death protein 8; **PDBTitle:** crystal structure of apoptosis inducing factor (aif)
102	c2cduB_	Alignment	not modelled	97.2	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph oxidase; **PDBTitle:** the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
103	c1ps9A_	Alignment	not modelled	97.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-dienoyl2 coa reductase
104	c3hwxC_	Alignment	not modelled	97.2	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**sulfide-quinone reductase;

104	c3hyxC_	Alignment	not modelled	97.2	15	**PDBTitle:** 3-d x-ray structure of the sulfide:quinone oxidoreductase from aquifex2 aeolicus in complex with aurachin c
105	c3l8kB_	Alignment	not modelled	97.2	9	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of a dihydrolipoyl dehydrogenase from sulfolobus2 solfataricus
106	c3lxdA_	Alignment	not modelled	97.2	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans
107	c1nhqA_	Alignment	not modelled	97.2	13	**PDB header:**oxidoreductase (h2o2(a)) **Chain:** A: **PDB Molecule:**nadh peroxidase; **PDBTitle:** crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303
108	c5twcA_	Alignment	not modelled	97.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** oxidoreductase iruo in the oxidized form
109	c1geuA_	Alignment	not modelled	97.1	17	**PDB header:**oxidoreductase(flavoenzyme) **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** anatomy of an engineered nad-binding site
110	c2weuD_	Alignment	not modelled	97.0	26	**PDB header:**antifungal protein **Chain:** D: **PDB Molecule:**tryptophan 5-halogenase; **PDBTitle:** crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
111	d1djqa3	Alignment	not modelled	97.0	15	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
112	c3iwaA_	Alignment	not modelled	97.0	26	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** crystal structure of a fad-dependent pyridine nucleotide-disulphide2 oxidoreductase from desulfovibrio vulgaris
113	c5uaoA_	Alignment	not modelled	97.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tryptophane-5-halogenase; **PDBTitle:** crystal structure of mibh, a lathipeptide tryptophan 5-halogenase
114	c6b4oB_	Alignment	not modelled	97.0	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**glutathione reductase; **PDBTitle:** 1.73 angstrom resolution crystal structure of glutathione reductase2 from enterococcus faecalis in complex with fad
115	c5n1tA_	Alignment	not modelled	96.9	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavin-binding subunit of sulfide dehydrogenase; **PDBTitle:** crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
116	c3fg2P_	Alignment	not modelled	96.9	21	**PDB header:**oxidoreductase **Chain:** P: **PDB Molecule:**putative rubredoxin reductase; **PDBTitle:** crystal structure of ferredoxin reductase for the cyp199a2 system from2 rhodopseudomonas palustris
117	c2eq8E_	Alignment	not modelled	96.9	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
118	c4jnqA_	Alignment	not modelled	96.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of a thioredoxin reductase from brucella melitensis
119	c1ndaD_	Alignment	not modelled	96.8	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**trypanothione oxidoreductase; **PDBTitle:** the structure of trypanosoma cruzi trypanothione reductase in the2 oxidized and nadph reduced state
120	c5jciA_	Alignment	not modelled	96.8	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**os09g0567300 protein; **PDBTitle:** structure and catalytic mechanism of monodehydroascorbate reductase,2 mdhar, from oryza sativa l. japonica