Phyre^2

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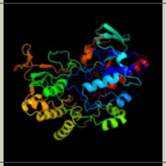
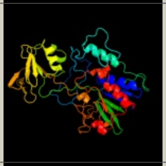
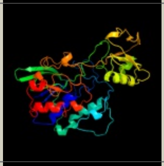
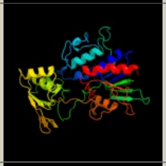
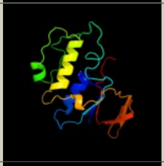
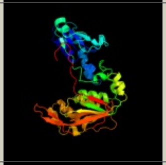
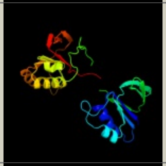
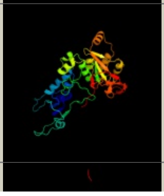
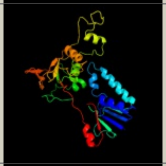
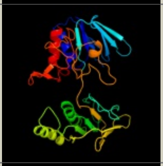
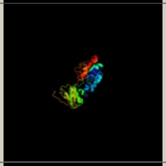
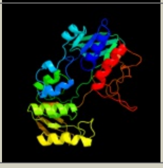
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3gwdA_	Alignment		100.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cyclohexanone monooxygenase; **PDBTitle:** closed crystal structure of cyclohexanone monooxygenase
2	c1w4xA_	Alignment		100.0	12	**PDB header:**oxygenase **Chain:** A: **PDB Molecule:**phenylacetone monooxygenase; **PDBTitle:** phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
3	c1vqwB_	Alignment		100.0	22	**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
4	c2vq7B_	Alignment		100.0	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**flavin-containing monooxygenase; **PDBTitle:** bacterial flavin-containing monooxygenase in complex with2 nadp: native data
5	c3s5wB_	Alignment		100.0	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**l-ornithine 5-monooxygenase; **PDBTitle:** ornithine hydroxylase (pvda) from pseudomonas aeruginosa
6	d2gv8a1	Alignment		99.9	24	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
7	c3d1cA_	Alignment		99.9	18	**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
8	d1w4xa1	Alignment		99.9	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
9	c1lqtB_	Alignment		99.8	16	**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
10	c3oc4A_	Alignment		99.7	26	**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
11	c1cjcA_	Alignment		99.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (adrenodoxin reductase); **PDBTitle:** structure of adrenodoxin reductase of mitochondrial p4502 systems

12	c3ntaA_	Alignment		99.7	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
13	c3icrA_	Alignment		99.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**coenzyme a-disulfide reductase; **PDBTitle:** crystal structure of oxidized bacillus anthracis coadr-rhd
14	c3kd9B_	Alignment		99.6	25	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**coenzyme a disulfide reductase; **PDBTitle:** crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
15	c1ps9A_	Alignment		99.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2,4-dienoyl-coa reductase; **PDBTitle:** the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
16	c3iwaA_	Alignment		99.6	20	**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
17	c1hyuA_	Alignment		99.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** crystal structure of intact ahpf
18	c1gv4A_	Alignment		99.6	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**programed cell death protein 8; **PDBTitle:** murine apoptosis-inducing factor (aif)
19	c1gthD_	Alignment		99.6	23	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
20	c1yqzA_	Alignment		99.5	19	**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
21	d1w4xa2	Alignment	not modelled	99.5	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
22	c2bcpA_	Alignment	not modelled	99.5	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh oxidase; **PDBTitle:** structural analysis of streptococcus pyogenes nadh oxidase:2 c44s nox with azide
23	d1djqa3	Alignment	not modelled	99.5	17	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
24	c1xdiA_	Alignment	not modelled	99.5	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**rv3303c-lpda; **PDBTitle:** crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
25	c1nhqA_	Alignment	not modelled	99.5	22	**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
26	c1zx9A_	Alignment	not modelled	99.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mercuric reductase; **PDBTitle:** crystal structure of tn501 mera
27	c2gr2A_	Alignment	not modelled	99.5	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin reductase; **PDBTitle:** crystal structure of ferredoxin reductase, bpha4 (oxidized form)
28	d2gqfa1	Alignment	not modelled	99.4	11	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
						PDB header:oxidoreductase

29	c1ojtA_	Alignment	not modelled	99.4	17	**Chain:** A: **PDB Molecule:**surface protein; **PDBTitle:** structure of dihydrolipoamide dehydrogenase
30	c3lxdA_	Alignment	not modelled	99.4	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**fad-dependent pyridine nucleotide-disulphide **PDBTitle:** crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans
31	c2ywlA_	Alignment	not modelled	99.4	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase related protein; **PDBTitle:** crystal structure of thioredoxin reductase-related protein ttha03702 from thermus thermophilus hb8
32	c2v3aA_	Alignment	not modelled	99.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin reductase; **PDBTitle:** crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa.
33	c1q1wA_	Alignment	not modelled	99.4	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putidaredoxin reductase; **PDBTitle:** crystal structure of putidaredoxin reductase from2 pseudomonas putida
34	d2voua1	Alignment	not modelled	99.4	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
35	c3nlcA_	Alignment	not modelled	99.4	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein vp0956; **PDBTitle:** crystal structure of the vp0956 protein from vibrio parahaemolyticus.2 northeast structural genomics consortium target vpr147
36	c2eq7B_	Alignment	not modelled	99.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxoglutarate dehydrogenase e3 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
37	c2qaeA_	Alignment	not modelled	99.4	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
38	c3k30B_	Alignment	not modelled	99.4	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**histamine dehydrogenase; **PDBTitle:** histamine dehydrogenase from nocardiodes simplex
39	c1v59B_	Alignment	not modelled	99.4	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
40	c2e4gB_	Alignment	not modelled	99.4	17	**PDB header:**biosynthetic protein, flavoprotein **Chain:** B: **PDB Molecule:**tryptophan halogenase; **PDBTitle:** rebh with bound l-trp
41	c1fcdB_	Alignment	not modelled	99.4	17	**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
42	c3cp8C_	Alignment	not modelled	99.4	15	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** crystal structure of gida from chlorobium tepidum
43	c2vdcI_	Alignment	not modelled	99.4	21	**PDB header:**oxidoreductase **Chain:** I: **PDB Molecule:**glutamate synthase [nadph] small chain; **PDBTitle:** the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
44	c2eq8E_	Alignment	not modelled	99.4	17	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**pyruvate dehydrogenase complex, dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
45	c2zxiC_	Alignment	not modelled	99.4	15	**PDB header:**fad-binding protein **Chain:** C: **PDB Molecule:**trna uridine 5-carboxymethylaminomethyl **PDBTitle:** structure of aquifex aeolicus gida in the form ii crystal
46	d2i0za1	Alignment	not modelled	99.4	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
47	c2a8xA_	Alignment	not modelled	99.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
48	c1tytA_	Alignment	not modelled	99.4	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trypanothione reductase, oxidized form; **PDBTitle:** crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution
49	c3urhB_	Alignment	not modelled	99.3	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
50	c2ardA_	Alignment	not modelled	99.3	22	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**tryptophan halogenase prna; **PDBTitle:** the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination
51	c2weuD_	Alignment	not modelled	99.3	18	**PDB header:**antifungal protein **Chain:** D: **PDB Molecule:**tryptophan 5-halogenase; **PDBTitle:** crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
52	c1djnB_	Alignment	not modelled	99.3	21	**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)
53	c3dgzA	Alignment	not modelled	99.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase 2;

53	c3dgzA_	Alignment	not modelled	99.3	14	**PDBTitle:** crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
54	c3ka7A_	Alignment	not modelled	99.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of an oxidoreductase from methanosarcina2 mazei. northeast structural genomics consortium target id3 mar208
55	c3g05B_	Alignment	not modelled	99.3	14	**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
56	c2v6oA_	Alignment	not modelled	99.3	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin glutathione reductase; **PDBTitle:** structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
57	c3i6dA_	Alignment	not modelled	99.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** crystal structure of ppo from bacillus subtilis with af
58	d1o5wa1	Alignment	not modelled	99.3	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
59	c2w0hA_	Alignment	not modelled	99.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**trypanothione reductase; **PDBTitle:** x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
60	c2cduB_	Alignment	not modelled	99.3	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph oxidase; **PDBTitle:** the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
61	c3o0hA_	Alignment	not modelled	99.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** crystal structure of glutathione reductase from bartonella henselae
62	c3ic9D_	Alignment	not modelled	99.3	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
63	c1zkqA_	Alignment	not modelled	99.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase 2, mitochondrial; **PDBTitle:** crystal structure of mouse thioredoxin reductase type 2
64	d1gesa1	Alignment	not modelled	99.3	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
65	c1m6iA_	Alignment	not modelled	99.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**programmed cell death protein 8; **PDBTitle:** crystal structure of apoptosis inducing factor (aif)
66	c3fg2P_	Alignment	not modelled	99.3	21	**PDB header:**oxidoreductase **Chain:** P: **PDB Molecule:**putative rubredoxin reductase; **PDBTitle:** crystal structure of ferredoxin reductase for the cyp199a2 system from2 rhodopseudomonas palustris
67	d1rp0a1	Alignment	not modelled	99.3	18	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**Thi4-like
68	c2pyxA_	Alignment	not modelled	99.3	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**tryptophan halogenase; **PDBTitle:** crystal structure of tryptophan halogenase (yp_750003.1) from2 shewanella frigidimarina ncimb 400 at 1.50 a resolution
69	c2b9yA_	Alignment	not modelled	99.3	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative aminooxidase; **PDBTitle:** crystal structure of cla-producing fatty acid isomerase2 from p. acnes
70	c3r9uA_	Alignment	not modelled	99.3	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** thioredoxin-disulfide reductase from campylobacter jejuni.
71	c2hqmB_	Alignment	not modelled	99.3	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione reductase; **PDBTitle:** crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
72	c3jskN_	Alignment	not modelled	99.3	25	**PDB header:**biosynthetic protein **Chain:** N: **PDB Molecule:**cypbp37 protein; **PDBTitle:** thiazole synthase from neurospora crassa
73	c3cesB_	Alignment	not modelled	99.3	17	**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
74	c3v76A_	Alignment	not modelled	99.3	12	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavoprotein; **PDBTitle:** the crystal structure of a flavoprotein from sinorhizobium meliloti
75	d2cula1	Alignment	not modelled	99.3	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GidA-like
76	c1dxlC_	Alignment	not modelled	99.3	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
77	d1k0ia1	Alignment	not modelled	99.3	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
78	c3hyxC_	Alignment	not modelled	99.3	20	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**sulfide-quinone reductase; **PDBTitle:** 3-d x-ray structure of the sulfide:quinone oxidoreductase from aquifex2 aeolicus in complex with aurachin c

79	c1ltxR_	Alignment	not modelled	99.2	11	**PDB header:**transferase/protein binding **Chain:** R: **PDB Molecule:**rab escort protein 1; **PDBTitle:** structure of rab escort protein-1 in complex with rab2 geranylgeranyl transferase and isoprenoid
80	d1pj5a2	Alignment	not modelled	99.2	14	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
81	c1ndaD_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**trypanothione oxidoreductase; **PDBTitle:** the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state
82	d1ps9a3	Alignment	not modelled	99.2	23	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
83	c3i3lA_	Alignment	not modelled	99.2	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylhalidase cmls; **PDBTitle:** crystal structure of cmls, a flavin-dependent halogenase
84	c1ebdB_	Alignment	not modelled	99.2	15	**PDB header:**complex (oxidoreductase/transferase) **Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
85	c1zmcG_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**dihydrolipoyl dehydrogenase; **PDBTitle:** crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
86	d1ryia1	Alignment	not modelled	99.2	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
87	c3ps9A_	Alignment	not modelled	99.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of mnmc from e. coli
88	d2bcgg1	Alignment	not modelled	99.2	12	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
89	c2c3dB_	Alignment	not modelled	99.2	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**2-oxopropyl-com reductase; **PDBTitle:** 2.15 angstrom crystal structure of 2-ketopropyl coenzyme m2 oxidoreductase carboxylase with a coenzyme m disulfide3 bound at the active site
90	c2a87A_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of m. tuberculosis thioredoxin reductase
91	d3c96a1	Alignment	not modelled	99.2	16	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
92	c3ef6A_	Alignment	not modelled	99.2	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**toluene 1,2-dioxygenase system ferredoxin--nad(+) **PDBTitle:** crystal structure of toluene 2,3-dioxygenase reductase
93	c3ab1B_	Alignment	not modelled	99.2	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** crystal structure of ferredoxin nadp+ oxidoreductase
94	c2cfyB_	Alignment	not modelled	99.2	16	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin reductase 1; **PDBTitle:** crystal structure of human thioredoxin reductase 1
95	c3nrnA_	Alignment	not modelled	99.2	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein pf1083; **PDBTitle:** crystal structure of pf1083 protein from pyrococcus furiosus,2 northeast structural genomics consortium target pfr223
96	c3cgdB_	Alignment	not modelled	99.2	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyridine nucleotide-disulfide oxidoreductase, class i; **PDBTitle:** pyridine nucleotide complexes with bacillus anthracis coenzyme a-2 disulfide reductase: a structural analysis of dual nad(p)h3 specificity
97	c1pj6A_	Alignment	not modelled	99.2	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**n,n-dimethylglycine oxidase; **PDBTitle:** crystal structure of dimethylglycine oxidase of arthrobacter2 globiformis in complex with folic acid
98	c2ivdA_	Alignment	not modelled	99.2	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protoporphyrinogen oxidase; **PDBTitle:** structure of protoporphyrinogen oxidase from myxococcus2 xanthus with acifluorfen
99	c1x31A_	Alignment	not modelled	99.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sarcosine oxidase alpha subunit; **PDBTitle:** crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
100	c1geuA_	Alignment	not modelled	99.2	17	**PDB header:**oxidoreductase(flavoenzyme) **Chain:** A: **PDB Molecule:**glutathione reductase; **PDBTitle:** anatomy of an engineered nad-binding site
101	d2gf3a1	Alignment	not modelled	99.1	20	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
102	c1f8sA_	Alignment	not modelled	99.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-amino acid oxidase; **PDBTitle:** crystal structure of l-amino acid oxidase from calloselasma2 rhodostoma, complexed with three molecules of o-aminobenzoate.
103	c2gmhA_	Alignment	not modelled	99.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**electron transfer flavoprotein-ubiquinone **PDBTitle:** structure of porcine electron transfer flavoprotein-2 ubiquinone oxidoreductase in complexed with ubiquinone
104	c3fbsB_	Alignment	not modelled	99.1	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase;

104	[illegible]	Alignment	not modelled	99.1	14	**PDBTitle:** the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
105	c3qj4A_	Alignment	not modelled	99.1	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**renalase; **PDBTitle:** crystal structure of human renalase (isoform 1)
106	c2r9zB_	Alignment	not modelled	99.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutathione amide reductase; **PDBTitle:** glutathione amide reductase from chromatium gracile
107	c1bwcA_	Alignment	not modelled	99.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein (glutathione reductase); **PDBTitle:** structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
108	c1lpfB_	Alignment	not modelled	99.1	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** three-dimensional structure of lipoamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties
109	c2bryA_	Alignment	not modelled	99.1	19	**PDB header:**transport **Chain:** A: **PDB Molecule:**nedd9 interacting protein with calponin homology **PDBTitle:** crystal structure of the native monooxygenase domain of2 mical at 1.45 a resolution
110	d1d5ta1	Alignment	not modelled	99.1	11	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**GDI-like N domain
111	c3dmeB_	Alignment	not modelled	99.1	12	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**conserved exported protein; **PDBTitle:** crystal structure of conserved exported protein from2 bordetella pertussis. northeast structural genomics target3 ber141
112	c3kpgA_	Alignment	not modelled	99.1	18	**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
113	c3pvcA_	Alignment	not modelled	99.1	15	**PDB header:**oxidoreductase, transferase **Chain:** A: **PDB Molecule:**trna 5-methylaminomethyl-2-thiouridine biosynthesis **PDBTitle:** crystal structure of apo mnmc from yersinia pestis
114	c1lvlA_	Alignment	not modelled	99.1	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dihydrolipoamide dehydrogenase; **PDBTitle:** the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution
115	c2i0zA_	Alignment	not modelled	99.1	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nad(fad)-utilizing dehydrogenases; **PDBTitle:** crystal structure of a fad binding protein from bacillus2 cereus, a putative nad(fad)-utilizing dehydrogenases
116	d1gtea4	Alignment	not modelled	99.1	22	**Fold:**Nucleotide-binding domain **Superfamily:**Nucleotide-binding domain **Family:**N-terminal domain of adrenodoxin reductase-like
117	d1b5qa1	Alignment	not modelled	99.1	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD-linked reductases, N-terminal domain
118	c2nvkX_	Alignment	not modelled	99.1	15	**PDB header:**oxidoreductase **Chain:** X: **PDB Molecule:**thioredoxin reductase; **PDBTitle:** crystal structure of thioredoxin reductase from drosophila2 melanogaster
119	c1qo8A_	Alignment	not modelled	99.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c3 fumarate reductase; **PDBTitle:** the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
120	c1jrxA_	Alignment	not modelled	99.1	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavocytochrome c; **PDBTitle:** crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina