

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ef6A_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: toluene 1,2-dioxygenase system ferredoxin--nad(+) PDBTitle: crystal structure of toluene 2,3-dioxygenase reductase
2	c2gr2A_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase, bpha4 (oxidized form)
3	c3lxdA_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans
4	c1qlwA_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: putidaredoxin reductase; PDBTitle: crystal structure of putidaredoxin reductase from2 pseudomonas putida
5	c3fg2P_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: P: PDB Molecule: putative rubredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase for the cyp199a2 system from2 rhodospseudomonas palustris
6	c3ntaA_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
7	c3icrA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
8	c1gv4A_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: programmed cell death protein 8; PDBTitle: murine apoptosis-inducing factor (aif)
9	c3oc4A_	 Alignment		100.0	17	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
10	c1nhqA_	 Alignment		100.0	18	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
11	c1m6iA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: programmed cell death protein 8; PDBTitle: crystal structure of apoptosis inducing factor (aif)

12	c2bcpA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidase; PDBTitle: structural analysis of streptococcus pyogenes nadh oxidase:2 c44s nox with azide
13	c2cduB_	Alignment		100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh oxidase; PDBTitle: the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
14	c3kljA_	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: nad(fad)-dependent dehydrogenase, nirb-family (n-terminal PDBTitle: crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum
15	c3iwaA_	Alignment		100.0	22	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
16	c3kd9B_	Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: coenzyme a disulfide reductase; PDBTitle: crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
17	c1yqzA_	Alignment		100.0	18	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
18	c2v3aA_	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin reductase; PDBTitle: crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa.
19	c3cgdB_	Alignment		100.0	18	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
20	c2v6oA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
21	c2c3dB_	Alignment	not modelled	100.0	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
22	c3urhB_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
23	c2eq7B_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoglutarate dehydrogenase e3 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
24	c1zmcG_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: G: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
25	c1ojtA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: surface protein; PDBTitle: structure of dihydrolipoamide dehydrogenase
26	c2qaeA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
27	c1xdia_	Alignment	not modelled	100.0	22	PDB header: unknown function Chain: A: PDB Molecule: rv3303c-lpda; PDBTitle: crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
28	c1zx9A_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase;

						PDBTitle: crystal structure of tn501 mera
29	c2eq8E_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
30	c1dxlC_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
31	c1lvIA_	Alignment	not modelled	100.0	18	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
32	c1tytA_	Alignment	not modelled	100.0	14	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
33	c3l8kB_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoyl dehydrogenase from2 sulfolobus solfataricus
34	c1lpfB_	Alignment	not modelled	100.0	15	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
35	c1ebdB_	Alignment	not modelled	100.0	22	PDB header: complex (oxidoreductase/transferase) Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
36	c1v59B_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
37	c3o0hA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae
38	c1geuA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
39	c1ndaD_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: D: PDB Molecule: trypanothione oxidoreductase; PDBTitle: the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state
40	c2w0hA_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase; PDBTitle: x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
41	c2r9zB_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione amide reductase; PDBTitle: glutathione amide reductase from chromatium gracile
42	c1bwcA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
43	c2nvkX_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
44	c3ic9D_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
45	c2a8xA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
46	c3dgzA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
47	c1zkqA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
48	c1onfA_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of plasmodium falciparum glutathione reductase
49	c2hqmB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
50	c1xhcA_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidase /nitrite reductase; PDBTitle: nadh oxidase /nitrite reductase from pyrococcus furiosus pfu-1140779-2 001
51	c2cfyB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1
52	c3hyxC_	Alignment	not modelled	100.0	14	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
53	c1fcdB_	Alignment	not modelled	100.0	18	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 at 3.25 angstroms resolution
54	c3kpgA	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfide-quinone reductase, putative; PDBTitle: crystal structure of sulfide:quinone oxidoreductase from <i>acidithiobacillus ferrooxidans</i> in complex with decylubiquinone
55	c1hyuA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
56	c1gthD	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpg) from pig, ternary2 complex with nadph and 5-iodouracil
57	c3k30B	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from <i>nocardioides simplex</i>
58	c1ps9A	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4-dienoyl-coa reductase; PDBTitle: the crystal structure and reaction mechanism of <i>e. coli</i> 2,4-2 dienoyl coa reductase
59	c1djnB	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: trimethylamine dehydrogenase; PDBTitle: structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from <i>methylophilus methylotrophus</i> (sp.3 w3a1)
60	c2zbwA	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase-like protein from <i>thermus2 thermophilus</i> hb8
61	c2vdcI	Alignment	not modelled	100.0	18	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.
62	c3h8lA	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidase; PDBTitle: the first x-ray structure of a sulfide:quinone2 oxidoreductase: insights into sulfide oxidation mechanism
63	d1gv4a1	Alignment	not modelled	100.0	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
64	c1vdcA	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dependent thioredoxin reductase; PDBTitle: structure of nadph dependent thioredoxin reductase
65	c3r9uA	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: thioredoxin-disulfide reductase from <i>campylobacter jejuni</i> .
66	c3ctyA	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of <i>t. acidophilum</i> thioredoxin reductase
67	c3ab1B	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase
68	c1f6mF	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: F: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
69	c1fl2A	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: catalytic core component of the alkylhydroperoxide reductase ahpf from2 <i>e.coli</i>
70	c3d1cA	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing putative monooxygenase; PDBTitle: crystal structure of flavin-containing putative monooxygenase2 (np_373108.1) from <i>staphylococcus aureus</i> mu50 at 2.40 a resolution
71	d1m6ia1	Alignment	not modelled	100.0	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
72	c3f8rD	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase (trxb-3); PDBTitle: crystal structure of <i>sulfolobus solfataricus</i> thioredoxin2 reductase b3 in complex with two nadp molecules
73	c3lzxB	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase 2; PDBTitle: crystal structure of ferredoxin-nadp+ oxidoreductase from <i>bacillus2 subtilis</i> (form ii)
74	c3d8xB	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of <i>saccharomyces cerevisiae</i> nadph dependent2 thioredoxin reductase 1
75	c3fbsB	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of the oxidoreductase from <i>agrobacterium2 tumefaciens</i>
76	c1cjcA	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (adrenodoxin reductase); PDBTitle: structure of adrenodoxin reductase of mitochondrial p4502 systems
77	c2q0lA	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
						PDB header: oxidoreductase

78	c2q7vA	Alignment	not modelled	100.0	17	Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of deinococcus radiodurans thioredoxin2 reductase
79	c1y56A	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1363; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
80	c2a87A	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of m. tuberculosis thioredoxin reductase
81	c1lqtB	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: fprra; PDBTitle: a covalent modification of nadp+ revealed by the atomic resolution2 structure of fprra, a mycobacterium tuberculosis oxidoreductase
82	c1x31A	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
83	d3grsa1	Alignment	not modelled	99.9	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
84	d1dxla1	Alignment	not modelled	99.9	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
85	d1lpfa1	Alignment	not modelled	99.9	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
86	c3s5wB	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: l-ornithine 5-monooxygenase; PDBTitle: ornithine hydroxylase (pvda) from pseudomonas aeruginosa
87	d1mo9a1	Alignment	not modelled	99.9	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
88	d3lada1	Alignment	not modelled	99.9	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
89	d1ojta1	Alignment	not modelled	99.9	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
90	d1nhpa1	Alignment	not modelled	99.9	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
91	d1h6va1	Alignment	not modelled	99.9	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
92	c2vq7B	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin-containing monooxygenase; PDBTitle: bacterial flavin-containing monooxygenase in complex with2 nadp: native data
93	c1vqwB	Alignment	not modelled	99.9	16	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
94	d1xhca1	Alignment	not modelled	99.9	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
95	d1fecal	Alignment	not modelled	99.9	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
96	d1lvla1	Alignment	not modelled	99.9	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
97	d1ebda1	Alignment	not modelled	99.9	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
98	d1fcda1	Alignment	not modelled	99.9	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
99	d1d7ya1	Alignment	not modelled	99.9	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
100	d1v59a1	Alignment	not modelled	99.9	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
101	d1qlra1	Alignment	not modelled	99.9	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
102	d1aoga1	Alignment	not modelled	99.9	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
						PDB header: oxidoreductase

103	c3gwdA	Alignment	not modelled	99.9	22	Chain: A: PDB Molecule: cyclohexanone monooxygenase; PDBTitle: closed crystal structure of cyclohexanone monooxygenase
104	c1w4xA	Alignment	not modelled	99.9	16	PDB header: oxygenase Chain: A: PDB Molecule: phenylacetone monooxygenase; PDBTitle: phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
105	d1d4ca2	Alignment	not modelled	99.8	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
106	d1y0pa2	Alignment	not modelled	99.8	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
107	c1chuA	Alignment	not modelled	99.8	14	PDB header: flavoenzyme Chain: A: PDB Molecule: protein (l-aspartate oxidase); PDBTitle: structure of l-aspartate oxidase: implications for the2 succinate dehydrogenase/ fumarate reductase family
108	d1qo8a2	Alignment	not modelled	99.8	14	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
109	d1kf6a2	Alignment	not modelled	99.8	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
110	d1xdia1	Alignment	not modelled	99.8	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
111	d2iida1	Alignment	not modelled	99.8	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
112	d2bs2a2	Alignment	not modelled	99.8	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
113	d1reoa1	Alignment	not modelled	99.8	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
114	c3p4rM	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol:fumarate oxidoreductase in complex2 with glutarate
115	c2e5vA	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate oxidase; PDBTitle: crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfolobus tokodaii
116	d2gqfa1	Alignment	not modelled	99.7	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
117	d1seza1	Alignment	not modelled	99.7	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
118	c1kf6A	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno
119	d1ryia1	Alignment	not modelled	99.7	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
120	d1trba1	Alignment	not modelled	99.7	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains