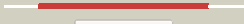



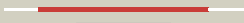



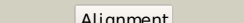
























Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	O52582
Date	Tue Jul 17 17:05:03 BST 2012
Unique Job ID	53fd2c8316765900

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1yqzA_	Alignment 		100.0	100	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
2	c3ntaA_	Alignment 		100.0	34	PDB header: oxidoreductase Chain: A; PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
3	c3icrA_	Alignment 		100.0	36	PDB header: oxidoreductase Chain: A; PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
4	c2bcpA_	Alignment 		100.0	24	PDB header: oxidoreductase Chain: A; PDB Molecule: nadh oxidase; PDBTitle: structural analysis of streptococcus pyogenes nadh oxidase:2 c44s nox with azide
5	c2cduB_	Alignment 		100.0	22	PDB header: oxidoreductase Chain: B; PDB Molecule: nadh oxidase; PDBTitle: the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
6	c3cgbB_	Alignment 		100.0	32	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
7	c1nhqA_	Alignment 		100.0	23	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
8	c3oc4A_	Alignment 		100.0	24	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
9	c3kd9B_	Alignment 		100.0	27	PDB header: oxidoreductase Chain: B; PDB Molecule: coenzyme a disulfide reductase; PDBTitle: crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
10	c3iwaA_	Alignment 		100.0	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
11	c1xdiA_	Alignment 		100.0	18	PDB header: unknown function Chain: A; PDB Molecule: rv3303c-lpda; PDBTitle: crystal structure of lpda (rv3303c) from mycobacterium tuberculosis

12	c2v6oA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansoni thioredoxin-gluthathione2 reductase (smtgr)
13	c2eq7B_	Alignment		100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoglutarate dehydrogenase e3 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
14	c2eq8E_	Alignment		100.0	22	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydroliipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
15	c2c3dB_	Alignment		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
16	c4dnaA_	Alignment		100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: probable glutathione reductase; PDBTitle: crystal structure of putative glutathione reductase from sinorhizobium2 meliloti 1021
17	c2w0hA_	Alignment		100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase; PDBTitle: x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
18	c1ndaD_	Alignment		100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: trypanothione oxidoreductase; PDBTitle: the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state
19	c3ic9D_	Alignment		100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydroliipoamide dehydrogenase; PDBTitle: the structure of dihydroliipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
20	c1ytA_	Alignment		100.0	18	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
21	c1zmcG_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: G: PDB Molecule: dihydroliipoyl dehydrogenase; PDBTitle: crystal structure of human dihydroliipoamide dehydrogenase2 complexed to nad+
22	c1lvIA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydroliipoamide dehydrogenase; PDBTitle: the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution
23	c1ojtA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: surface protein; PDBTitle: structure of dihydroliipoamide dehydrogenase
24	c3urhB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroliipoyl dehydrogenase; PDBTitle: crystal structure of a dihydroliipoamide dehydrogenase from2 sinorhizobium meliloti 1021
25	c1v59B_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroliipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
26	c1dxLC_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydroliipoamide dehydrogenase; PDBTitle: dihydroliipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
27	c3o0hA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae
28	c1lpfB_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydroliipoamide dehydrogenase; PDBTitle: three-dimensional structure of lipoamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3

						analysis of redox and thermostability properties
29	c3l8kB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoyl dehydrogenase from <i>Sulfolobus solfataricus</i>
30	c1ebdB_	Alignment	not modelled	100.0	20	PDB header: complex (oxidoreductase/transferase) Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
31	c2qaeA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure analysis of <i>Trypanosoma cruzi</i> lipoamide2 dehydrogenase
32	c1geuA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase (flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
33	c1zx9A_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: crystal structure of tn501 mera
34	c2r9zB_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione amide reductase; PDBTitle: glutathione amide reductase from <i>Chromatium gracile</i>
35	c2a8xA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of lipoamide dehydrogenase from <i>Mycobacterium tuberculosis</i>
36	c2nvkX_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from <i>Drosophila melanogaster</i>
37	c1onfA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of <i>Plasmodium falciparum</i> glutathione reductase
38	c2cfyB_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1
39	c3dgzA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
40	c1bwcA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
41	c1zkgA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
42	c2hqmB_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast <i>Saccharomyces cerevisiae</i>
43	c3fg2P_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: P: PDB Molecule: putative rubredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase for the cyp199a2 system from <i>Rhodospirillum rubrum</i>
44	c2gr2A_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase, bpha4 (oxidized form)
45	c1gv4A_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: programmed cell death protein 8; PDBTitle: murine apoptosis-inducing factor (aif)
46	c3lxdA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: crystal structure of ferredoxin reductase arr from <i>Novosphingobium aromaticivorans</i>
47	c3kljA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: nad(fad)-dependent dehydrogenase, nirb-family (n-terminal) PDBTitle: crystal structure of nadh:rubredoxin oxidoreductase from <i>Clostridium acetobutylicum</i>
48	c1q1wA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putidaredoxin reductase; PDBTitle: crystal structure of putidaredoxin reductase from <i>Pseudomonas putida</i>
49	c3ef6A_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: toluene 1,2-dioxygenase system ferredoxin--nad(+) PDBTitle: crystal structure of toluene 2,3-dioxygenase reductase
50	c2v3aA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin reductase; PDBTitle: crystal structure of rubredoxin reductase from <i>Pseudomonas aeruginosa</i>
51	c1m6iA_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: programmed cell death protein 8; PDBTitle: crystal structure of apoptosis inducing factor (aif)
52	c1xhcA_	Alignment	not modelled	100.0	23	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidase /nitrite reductase; PDBTitle: nadh oxidase /nitrite reductase from <i>Pyrococcus furiosus</i> pfu-1140779-2 001
53	c3kpgA_	Alignment	not modelled	100.0	13	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
						PDB header: oxidoreductase

54	c3hyxC_	Alignment	not modelled	100.0	14	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
55	c1hyuA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
56	c1fcdB_	Alignment	not modelled	100.0	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
57	c1gthD_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
58	c3h8IA_	Alignment	not modelled	100.0	21	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
59	d1nhpa3	Alignment	not modelled	100.0	24	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
60	c2zbwA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
61	c3k30B_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardiodes simplex
62	c3d8xB_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
63	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 methylphilus methylotrophus (sp.3 w3a1)
64	c1vdcA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dependent thioredoxin reductase; PDBTitle: structure of nadph dependent thioredoxin reductase
65	c3r9uA_	Alignment	not modelled	100.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: thioredoxin-disulfide reductase from campylobacter jejuni.
66	c1ps9A_	Alignment	not modelled	100.0	18	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
67	c3f8rD_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: thioredoxin reductase (trxb-3); PDBTitle: crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
68	c2q0IA_	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+
69	c2vdcl_	Alignment	not modelled	100.0	17	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.
70	c1fi2A_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: catalytic core component of the alkylhydroperoxide reductase ahpf from2 e.coli
71	c3ctyA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of t. acidophilum thioredoxin reductase
72	c3ab1B_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase
73	c3d1cA_	Alignment	not modelled	99.9	14	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
74	c3fbsB_	Alignment	not modelled	99.9	11	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
75	c3lzxB_	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase 2; PDBTitle: crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
76	d1gv4a1	Alignment	not modelled	99.9	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
77	c2a87A_	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of m. tuberculosis thioredoxin reductase
78	c1f6mF_	Alignment	not modelled	99.9	20	PDB header: oxidoreductase Chain: F: PDB Molecule: thioredoxin reductase;

78	c1rom1	Alignment	not modelled	99.9	20	PDBTitle: crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+ PDB header: oxidoreductase
79	c2q7vA	Alignment	not modelled	99.9	20	Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of deinococcus radiodurans thioredoxin2 reductase
80	c1y56A	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1363; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
81	c4a9wB	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: monooxygenase; PDBTitle: flavin-containing monooxygenase from stentrophomonas maltophilia
82	c1cjcA	Alignment	not modelled	99.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (adrenodoxin reductase); PDBTitle: structure of adrenodoxin reductase of mitochondrial p4502 systems
83	d1ojta3	Alignment	not modelled	99.9	16	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
84	d3lada3	Alignment	not modelled	99.9	16	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
85	d1ebda3	Alignment	not modelled	99.9	20	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
86	d1v59a3	Alignment	not modelled	99.9	18	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
87	c1lqtB	Alignment	not modelled	99.9	18	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
88	d1lpfa3	Alignment	not modelled	99.9	15	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
89	d1lvla3	Alignment	not modelled	99.9	18	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
90	d1m6ia1	Alignment	not modelled	99.9	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
91	d1dxla3	Alignment	not modelled	99.9	17	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
92	d3grsa3	Alignment	not modelled	99.9	12	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
93	d1xdia2	Alignment	not modelled	99.9	17	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
94	c2vq7B	Alignment	not modelled	99.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin-containing monooxygenase; PDBTitle: bacterial flavin-containing monooxygenase in complex with2 nadp: native data
95	d1gesa3	Alignment	not modelled	99.9	14	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
96	d1onfa3	Alignment	not modelled	99.9	14	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
97	c3s5wB	Alignment	not modelled	99.9	20	PDB header: oxidoreductase Chain: B: PDB Molecule: l-ornithine 5-monooxygenase; PDBTitle: ornithine hydroxylase (pvda) from pseudomonas aeruginosa
98	d1mo9a3	Alignment	not modelled	99.9	21	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
99	d3grsa1	Alignment	not modelled	99.9	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
100	d1feca3	Alignment	not modelled	99.9	7	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain

						domain
101	d1h6va3	Alignment	not modelled	99.9	11	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
102	d1aoga3	Alignment	not modelled	99.9	7	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: FAD/NAD-linked reductases, dimerisation (C-terminal) domain Family: FAD/NAD-linked reductases, dimerisation (C-terminal) domain
103	c1x31A	Alignment	not modelled	99.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from <i>Mycobacterium</i> sp. U-96
104	d1nhpa1	Alignment	not modelled	99.9	27	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
105	d1dxla1	Alignment	not modelled	99.9	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
106	c1vqwB	Alignment	not modelled	99.9	17	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
107	d1feca1	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
108	d1h6va1	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
109	d3lada1	Alignment	not modelled	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
110	d1lpfa1	Alignment	not modelled	99.8	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
111	d1mo9a1	Alignment	not modelled	99.8	18	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
112	d1qlra1	Alignment	not modelled	99.8	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
113	d1ebda1	Alignment	not modelled	99.8	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
114	d1d7ya1	Alignment	not modelled	99.8	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
115	d1ojta1	Alignment	not modelled	99.8	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
116	d1v59a1	Alignment	not modelled	99.8	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
117	d1aoga1	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
118	d1lvla1	Alignment	not modelled	99.8	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
119	d1fcda1	Alignment	not modelled	99.8	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
120	c3gwdA	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexanone monooxygenase; PDBTitle: closed crystal structure of cyclohexanone monooxygenase