



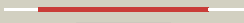



















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1kf6A_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: A: PDB Molecule: fumarate reductase flavoprotein; PDBTitle: e. coli quinol-fumarate reductase with bound inhibitor hqno
2	c3p4rM_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: M: PDB Molecule: fumarate reductase flavoprotein subunit; PDBTitle: crystal structure of menaquinol: fumarate oxidoreductase in complex2 with glutarate
3	c1yq4A_	 Alignment		100.0	42	PDB header: oxidoreductase Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: avian respiratory complex ii with 3-nitropropionate and ubiquinone
4	c2bs3A_	 Alignment		100.0	38	PDB header: oxidoreductase Chain: A: PDB Molecule: quinol-fumarate reductase flavoprotein subunit a; PDBTitle: glu c180 -> gln variant quinol: fumarate reductase from2 wollinella succinogenes
5	c2aczA_	 Alignment		100.0	44	PDB header: oxidoreductase/electron transport Chain: A: PDB Molecule: succinate dehydrogenase flavoprotein subunit; PDBTitle: complex ii (succinate dehydrogenase) from e. coli with atpenin a52 inhibitor co-crystallized at the ubiquinone binding site
6	c2fjaC_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: adenylylsulfate reductase, subunit a; PDBTitle: adenosine 5'-phosphosulfate reductase in complex with2 substrate
7	c3gyxA_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: adenylylsulfate reductase; PDBTitle: crystal structure of adenylylsulfate reductase from2 desulfovibrio gigas
8	c1chuA_	 Alignment		100.0	34	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
9	c2e5vA_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate oxidase; PDBTitle: crystal structure of l-aspartate oxidase from2 hyperthermophilic archaeon sulfobolus tokodaii
10	c1qo8A_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c3 fumarate reductase; PDBTitle: the structure of the open conformation of a flavocytochrome2 c3 fumarate reductase
11	c1d4cB_	 Alignment		100.0	29	PDB header: oxidoreductase Chain: B: PDB Molecule: flavocytochrome c fumarate reductase; PDBTitle: crystal structure of the uncomplexed form of the2 flavocytochrome c fumarate reductase of shewanella3 putrefaciens strain mr-1

12	c1jrxA_	Alignment		100.0	30	PDB header: oxidoreductase Chain: A: PDB Molecule: flavocytochrome c; PDBTitle: crystal structure of arg402ala mutant flavocytochrome c32 from shewanella frigidimarina
13	d1chua2	Alignment		100.0	37	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
14	d1kf6a2	Alignment		100.0	100	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
15	d2bs2a1	Alignment		100.0	31	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
16	d1qo8a2	Alignment		100.0	31	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
17	d1y0pa2	Alignment		100.0	32	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
18	d1kf6a1	Alignment		100.0	100	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
19	d1neka2	Alignment		100.0	45	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
20	c2gqfA_	Alignment		100.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein hi0933; PDBTitle: crystal structure of flavoprotein hi0933 from haemophilus influenzae2 rd
21	d2bs2a2	Alignment	not modelled	100.0	39	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
22	c2i0za_	Alignment	not modelled	100.0	18	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
23	d1neka1	Alignment	not modelled	100.0	34	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
24	d1d4ca2	Alignment	not modelled	100.0	34	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
25	d1jnra2	Alignment	not modelled	100.0	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
26	d1jnra1	Alignment	not modelled	100.0	21	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
27	c3cesB_	Alignment	not modelled	100.0	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 PDB header: rna binding protein

28	c3g05B_	Alignment	not modelled	100.0	15	Chain: B: PDB Molecule: trna uridine 5-carboxymethylaminomethyl modification enzyme PDBTitle: crystal structure of n-terminal domain (2-550) of e.coli mnmg
29	c3cp8C_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
30	d2qqfa1	Alignment	not modelled	99.9	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
31	c3nlcA_	Alignment	not modelled	99.9	16	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
32	d2bs2a3	Alignment	not modelled	99.9	45	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
33	d1kf6a3	Alignment	not modelled	99.9	100	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
34	d1neka3	Alignment	not modelled	99.9	53	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
35	c2zxiC_	Alignment	not modelled	99.9	20	PDB header: fad-binding protein Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: structure of aquifex aeolicus gida in the form ii crystal
36	d1chua1	Alignment	not modelled	99.9	29	Fold: Spectrin repeat-like Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein C-terminal domain
37	d1chua3	Alignment	not modelled	99.9	39	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
38	d2i0za1	Alignment	not modelled	99.9	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
39	c2v6oA_	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansoni thioredoxin-gluthathione2 reductase (smtgr)
40	c1hyuA_	Alignment	not modelled	99.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
41	c3dgzA_	Alignment	not modelled	99.8	32	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2; PDBTitle: crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
42	c1zkqA_	Alignment	not modelled	99.8	32	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase 2, mitochondrial; PDBTitle: crystal structure of mouse thioredoxin reductase type 2
43	c1zmcG_	Alignment	not modelled	99.8	24	PDB header: oxidoreductase Chain: G: PDB Molecule: dihydrolipoal dehydrogenase; PDBTitle: crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
44	c1tytA_	Alignment	not modelled	99.8	15	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
45	c2nvkX_	Alignment	not modelled	99.8	34	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
46	c1ojtA_	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: surface protein; PDBTitle: structure of dihydrolipoamide dehydrogenase
47	c1ndaD_	Alignment	not modelled	99.8	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
48	c2c3dB_	Alignment	not modelled	99.8	16	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
49	c2w0hA_	Alignment	not modelled	99.8	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
50	c3atrA_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand
51	c1v50B_	Alignment	not modelled	99.8	27	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase;

51	c1v39B	Alignment	not modelled	99.8	27	PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
52	c2cfyB	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1
53	c2eq8E	Alignment	not modelled	99.8	31	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
54	c3l8kB	Alignment	not modelled	99.8	14	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoyl dehydrogenase from2 sulfolobus solfataricus
55	c3o0hA	Alignment	not modelled	99.8	26	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase from bartonella henselae
56	c1lv1A	Alignment	not modelled	99.7	17	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
57	c3jskN	Alignment	not modelled	99.7	24	PDB header: biosynthetic protein Chain: N: PDB Molecule: cybpb37 protein; PDBTitle: thiazole synthase from neurospora crassa
58	c2hqmB	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
59	c3r9uA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: thioredoxin-disulfide reductase from campylobacter jejuni.
60	c1onfA	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of plasmodium falciparum glutathione reductase
61	d3grsa1	Alignment	not modelled	99.7	28	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
62	c2qaeA	Alignment	not modelled	99.7	12	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
63	c3urhB	Alignment	not modelled	99.7	23	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
64	c1dx1C	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
65	c1geuA	Alignment	not modelled	99.7	25	PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
66	d1h6va1	Alignment	not modelled	99.7	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
67	c2a8xA	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
68	d1jnra3	Alignment	not modelled	99.7	14	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
69	c1ebdB	Alignment	not modelled	99.7	22	PDB header: complex (oxidoreductase/transferase) Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
70	c3f8rD	Alignment	not modelled	99.7	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
71	c3icrA	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
72	d1rp0a1	Alignment	not modelled	99.7	23	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Thi4-like
73	c2eq7B	Alignment	not modelled	99.7	28	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoglutarate dehydrogenase e3 component; PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
74	c1lpfB	Alignment	not modelled	99.7	20	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
75	c2rghA	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3

						glycerophosphate dehydrogenase
76	c1bwcA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
77	c3fbsB_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
78	c2rgoA_	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-glycerophosphate oxidase; PDBTitle: structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
79	c1fl2A_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: catalytic core component of the alkylhydroperoxide reductase ahpF from2 e.coli
80	c2zbwA_	Alignment	not modelled	99.7	15	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
81	c3ic9D_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: the structure of dihydropyrimidine dehydrogenase from colwellia2 psychrerythraea 34h.
82	c3da1A_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: glycerol-3-phosphate dehydrogenase; PDBTitle: x-ray structure of the glycerol-3-phosphate dehydrogenase2 from bacillus halodurans complexed with fad. northeast3 structural genomics consortium target bhr167.
83	c1yqzA_	Alignment	not modelled	99.7	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
84	c1f6mF_	Alignment	not modelled	99.7	22	PDB header: oxidoreductase Chain: F: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
85	c1gthD_	Alignment	not modelled	99.7	25	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
86	c2r4iA_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: aerobic glycerol-3-phosphate dehydrogenase; PDBTitle: crystal structure of escherichia coli semet substituted2 glycerol-3-phosphate dehydrogenase in complex with dhap
87	d3lada1	Alignment	not modelled	99.7	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
88	c2r9zB_	Alignment	not modelled	99.7	21	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione amide reductase; PDBTitle: glutathione amide reductase from chromatium gracile
89	d1lvia1	Alignment	not modelled	99.7	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
90	c2q7vA_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of deinococcus radiodurans thioredoxin2 reductase
91	c1x31A_	Alignment	not modelled	99.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
92	d1lpfa1	Alignment	not modelled	99.7	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
93	c3kd9B_	Alignment	not modelled	99.7	18	PDB header: oxidoreductase Chain: B: PDB Molecule: coenzyme a disulfide reductase; PDBTitle: crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
94	c2q0lA_	Alignment	not modelled	99.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
95	c1y56A_	Alignment	not modelled	99.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical protein ph1363; PDBTitle: crystal structure of l-proline dehydrogenase from p.horikoshii
96	c1m6iA_	Alignment	not modelled	99.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: programmed cell death protein 8; PDBTitle: crystal structure of apoptosis inducing factor (aif)
97	d1dxa1	Alignment	not modelled	99.6	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
98	c3cgdB_	Alignment	not modelled	99.6	17	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
99	c1gv4A_	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: programmed cell death protein 8; PDBTitle: murine apoptosis-inducing factor (aif)
100	d1v59a1	Alignment	not modelled	99.6	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain

100	d1v39a1	Alignment	not modelled	99.6	10	Family: FAD/NAD-linked reductases, N-terminal and central domains Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
101	d1ojta1	Alignment	not modelled	99.6	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
102	d1fecal	Alignment	not modelled	99.6	24	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
103	c3ntaA	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
104	c2gmhA	Alignment	not modelled	99.6	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
105	d1ebda1	Alignment	not modelled	99.6	22	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
106	c3ab1B	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase
107	c1vdcA	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nadph dependent thioredoxin reductase; PDBTitle: structure of nadph dependent thioredoxin reductase
108	c3d8xB	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
109	c2gewA	Alignment	not modelled	99.6	11	PDB header: oxidoreductase Chain: A: PDB Molecule: cholesterol oxidase; PDBTitle: atomic resolution structure of cholesterol oxidase @ ph 9.02 (streptomyces sp. sa-coo)
110	c2gr2A	Alignment	not modelled	99.6	12	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase, bpha4 (oxidized form)
111	c3ctyA	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of t. acidophilum thioredoxin reductase
112	d2gmha1	Alignment	not modelled	99.6	16	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
113	c1xdia	Alignment	not modelled	99.6	17	PDB header: unknown function Chain: A: PDB Molecule: rv3303c-lpda; PDBTitle: crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
114	c3lxdA	Alignment	not modelled	99.6	14	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans
115	c1q1wA	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: putidaredoxin reductase; PDBTitle: crystal structure of putidaredoxin reductase from2 pseudomonas putida
116	c1zx9A	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: crystal structure of tn501 mera
117	c3i3IA	Alignment	not modelled	99.5	16	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
118	d1ryia1	Alignment	not modelled	99.5	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
119	c3iwaA	Alignment	not modelled	99.5	17	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
120	d1aoga1	Alignment	not modelled	99.5	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains