



























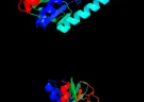
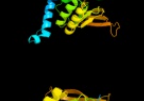



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1f6mF_	 Alignment		100.0	100	PDB header: oxidoreductase Chain: F; PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
2	c1hyuA_	 Alignment		100.0	34	PDB header: oxidoreductase Chain: A; PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: crystal structure of intact ahpf
3	c3r9uA_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin reductase; PDBTitle: thioredoxin-disulfide reductase from campylobacter jejuni.
4	c2q7vA_	 Alignment		100.0	42	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of deinococcus radiodurans thioredoxin2 reductase
5	c2v6oA_	 Alignment		100.0	17	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin glutathione reductase; PDBTitle: structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
6	c1vdcA_	 Alignment		100.0	45	PDB header: oxidoreductase Chain: A; PDB Molecule: nadph dependent thioredoxin reductase; PDBTitle: structure of nadph dependent thioredoxin reductase
7	c3ctvA_	 Alignment		100.0	28	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of t. acidophilum thioredoxin reductase
8	c1fi2A_	 Alignment		100.0	32	PDB header: oxidoreductase Chain: A; PDB Molecule: alkyl hydroperoxide reductase subunit f; PDBTitle: catalytic core component of the alkylhydroperoxide reductase ahpf from e.coli
9	c2a87A_	 Alignment		100.0	47	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of m. tuberculosis thioredoxin reductase
10	c2zbwA_	 Alignment		100.0	25	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
11	c1gthD_	 Alignment		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

12	c3d8xB_	Alignment		100.0	51	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
13	c3f8rD_	Alignment		100.0	35	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
14	c2q0lA_	Alignment		100.0	33	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
15	c2r9zB_	Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione amide reductase; PDBTitle: glutathione amide reductase from chromatium gracile
16	c1ojtA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: surface protein; PDBTitle: structure of dihydrolipoamide dehydrogenase
17	c1geuA_	Alignment		100.0	19	PDB header: oxidoreductase(flavoenzyme) Chain: A: PDB Molecule: glutathione reductase; PDBTitle: anatomy of an engineered nad-binding site
18	c2a8xA_	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis
19	c3dgzA_	Alignment		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
20	c1ebdB_	Alignment		100.0	21	PDB header: complex (oxidoreductase/transferase) Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
21	c2nvkX_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: X: PDB Molecule: thioredoxin reductase; PDBTitle: crystal structure of thioredoxin reductase from drosophila2 melanogaster
22	c3urhB_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
23	c2eq8E_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: E: PDB Molecule: pyruvate dehydrogenase complex, dihydrolipoamide PDBTitle: crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
24	c3lzxB_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase 2; PDBTitle: crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
25	c1zkqA_	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
26	c1bwcA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (glutathione reductase); PDBTitle: structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
27	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.
28	c3lxdA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: crystal structure of ferredoxin reductase arr from

						novosphingobium2 aromaticivorans
29	c2hqmB_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae
30	c1lpfB_	Alignment	not modelled	100.0	21	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
31	c2c3dB_	Alignment	not modelled	100.0	18	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
32	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
33	c3ab1B_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin--nadp reductase; PDBTitle: crystal structure of ferredoxin nadp+ oxidoreductase
34	c1v59B_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
35	c3l8kB_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure of a dihydrolipoyl dehydrogenase from2 sulfolobus solfataricus
36	c1lvIA_	Alignment	not modelled	100.0	22	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
37	c1zx9A_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: mercuric reductase; PDBTitle: crystal structure of tn501 mera
38	c3ntaA_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: A: PDB Molecule: fad-dependent pyridine nucleotide-disulphide PDBTitle: structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
39	c2eq7B_	Alignment	not modelled	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
40	c2bcpA_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidase; PDBTitle: structural analysis of streptococcus pyogenes nadh oxidase:2 c44s nox with azide
41	c2w0hA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: trypanothione reductase; PDBTitle: x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
42	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+
43	c3oc4A_	Alignment	not modelled	100.0	22	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
44	c1qlwA_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putidaredoxin reductase; PDBTitle: crystal structure of putidaredoxin reductase from2 pseudomonas putida
45	c2qaeA_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: dihydrolipoyl dehydrogenase; PDBTitle: crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
46	c1dxlC_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: C: PDB Molecule: dihydrolipoamide dehydrogenase; PDBTitle: dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
47	c1gv4A_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: programed cell death protein 8; PDBTitle: murine apoptosis-inducing factor (aif)
48	c1bytA_	Alignment	not modelled	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
49	c2cfyB_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin reductase 1; PDBTitle: crystal structure of human thioredoxin reductase 1
50	c3fg2P_	Alignment	not modelled	100.0	20	PDB header: oxidoreductase Chain: P: PDB Molecule: putative rubredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase for the cyp199a2 system from2 rhodospseudomonas palustris
51	c3lcrA_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: coenzyme a-disulfide reductase; PDBTitle: crystal structure of oxidized bacillus anthracis coadr-rhd
52	c1onfA_	Alignment	not modelled	100.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione reductase; PDBTitle: crystal structure of plasmodium falciparum glutathione reductase
						PDB header: oxidoreductase

53	c3fbsB_	Alignment	not modelled	100.0	19	Chain: B: PDB Molecule: oxidoreductase; PDBTitle: the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
54	c1ndaD_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: D: PDB Molecule: trypanothione oxidoreductase; PDBTitle: the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state
55	c1xdiA_	Alignment	not modelled	100.0	19	PDB header: unknown function Chain: A: PDB Molecule: rv3303c-lpda; PDBTitle: crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
56	c1yqzA_	Alignment	not modelled	100.0	20	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
57	c2vdcl_	Alignment	not modelled	100.0	19	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.
58	c2gr2A_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin reductase; PDBTitle: crystal structure of ferredoxin reductase, bpha4 (oxidized form)
59	c3ef6A_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: toluene 1,2-dioxygenase system ferredoxin--nad(+) PDBTitle: crystal structure of toluene 2,3-dioxygenase reductase
60	c2cduB_	Alignment	not modelled	100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: nadh oxidase; PDBTitle: the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
61	c1m6iA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: programmed cell death protein 8; PDBTitle: crystal structure of apoptosis inducing factor (aif)
62	c3kd9B_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: coenzyme a disulfide reductase; PDBTitle: crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
63	c1nhqA_	Alignment	not modelled	100.0	24	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
64	c2v3aA_	Alignment	not modelled	100.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: rubredoxin reductase; PDBTitle: crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa.
65	c3iwaA_	Alignment	not modelled	99.9	21	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
66	c1xhcA_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh oxidase /nitrite reductase; PDBTitle: nadh oxidase /nitrite reductase from pyrococcus furiosus pfu-1140779-2 001
67	c3cgdB_	Alignment	not modelled	99.9	21	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
68	c3kpgA_	Alignment	not modelled	99.9	17	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
69	c3kljA_	Alignment	not modelled	99.9	20	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
70	c3h8lA_	Alignment	not modelled	99.9	16	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
71	c1djnb_	Alignment	not modelled	99.9	17	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)
72	c3hyxC_	Alignment	not modelled	99.9	12	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
73	c1fcdB_	Alignment	not modelled	99.9	16	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
74	c3k30B_	Alignment	not modelled	99.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: histamine dehydrogenase; PDBTitle: histamine dehydrogenase from nocardiodies simplex
75	c3d1cA_	Alignment	not modelled	99.9	15	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
						PDB header: oxidoreductase

76	c1ps9A	Alignment	not modelled	99.9	20	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
77	c1x31A	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: sarcosine oxidase alpha subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
78	c1cjcA	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (adrenodoxin reductase); PDBTitle: structure of adrenodoxin reductase of mitochondrial p4502 systems
79	c1lqtB	Alignment	not modelled	99.9	17	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
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	d3grsa1	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
82	d1trba1	Alignment	not modelled	99.9	98	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
83	d3lada1	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
84	d1ojta1	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
85	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
86	d1h6va1	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
87	d1d4ca2	Alignment	not modelled	99.9	21	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
88	d1ebda1	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
89	d1lpfa1	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
90	c3s5wB	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: l-ornithine 5-monooxygenase; PDBTitle: ornithine hydroxylase (pvda) from pseudomonas aeruginosa
91	d1qo8a2	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
92	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
93	d1aoga1	Alignment	not modelled	99.8	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
94	d1y0pa2	Alignment	not modelled	99.8	20	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
95	d1dxla1	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
96	d1fecal	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
97	d2bs2a2	Alignment	not modelled	99.8	12	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
98	d1vdca1	Alignment	not modelled	99.8	37	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
99	d1seza1	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
100	d1jnra2	Alignment	not modelled	99.8	19	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
101	c3cesB	Alignment	not modelled	99.8	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
102	c3g05B_	Alignment	not modelled	99.8	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
103	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
104	c1w4xA_	Alignment	not modelled	99.8	20	PDB header: oxygenase Chain: A: PDB Molecule: phenylacetone monooxygenase; PDBTitle: phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
105	c3gwdA_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexanone monooxygenase; PDBTitle: closed crystal structure of cyclohexanone monooxygenase
106	d2gmha1	Alignment	not modelled	99.8	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
107	c2vq7B_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin-containing monooxygenase; PDBTitle: bacterial flavin-containing monooxygenase in complex with2 nadp: native data
108	d1mo9a1	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
109	d2gqfa1	Alignment	not modelled	99.7	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: HI0933 N-terminal domain-like
110	d2iida1	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
111	d1reoa1	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
112	c2zxiC_	Alignment	not modelled	99.7	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
113	d1neka2	Alignment	not modelled	99.7	15	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
114	c1vqwB_	Alignment	not modelled	99.7	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
115	c3cp8C_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: C: PDB Molecule: trna uridine 5-carboxymethylaminomethyl PDBTitle: crystal structure of gida from chlorobium tepidum
116	c1chuA_	Alignment	not modelled	99.7	12	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
117	c2gmhA_	Alignment	not modelled	99.7	13	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
118	d1gv4a1	Alignment	not modelled	99.7	17	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
119	c1yvvB_	Alignment	not modelled	99.7	14	PDB header: oxidoreductase Chain: B: PDB Molecule: amine oxidase, flavin-containing; PDBTitle: x-ray structure of p. syringae q888a4 oxidoreductase at2 resolution 2.5a. northeast structural genomics consortium3 target psr10.
120	c3atrA_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: conserved archaeal protein; PDBTitle: geranylgeranyl reductase (ggr) from sulfolobus acidocaldarius co-2 crystallized with its ligand