



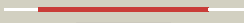



















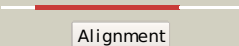
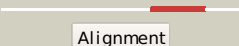
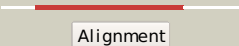


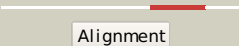


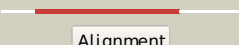

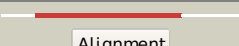
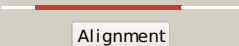
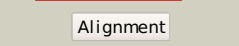
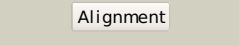
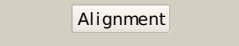

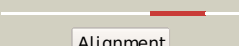
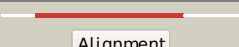
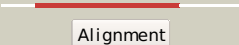

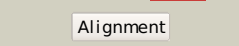


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1dxlC_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase of glycine decarboxylase2 from pisum sativum
2	<a href="#">c1ojtA_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> surface protein; <b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase
3	<a href="#">c2eq8E_</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
4	<a href="#">c2eq7B_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e3 component; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
5	<a href="#">c1zmcG_</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
6	<a href="#">c2qaeA_</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure analysis of trypanosoma cruzi lipoamide2 dehydrogenase
7	<a href="#">c1ebdB_</a>	 Alignment		100.0	29	<b>PDB header:</b> complex (oxidoreductase/transferase) <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase complexed with the binding2 domain of the dihydrolipoamide acetylase
8	<a href="#">c1lpfB_</a>	 Alignment		100.0	31	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> three-dimensional structure of lipoamide dehydrogenase from2 pseudomonas fluorescens at 2.8 angstroms resolution.3 analysis of redox and thermostability properties
9	<a href="#">c3urhB_</a>	 Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
10	<a href="#">c1bwcA_</a>	 Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (glutathione reductase); <b>PDBTitle:</b> structure of human glutathione reductase complexed with ajoene2 inhibitor and subversive substrate
11	<a href="#">c2a8xA_</a>	 Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from2 mycobacterium tuberculosis

12	<a href="#">c2r9zB_</a>	Alignment		100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione amide reductase; <b>PDBTitle:</b> glutathione amide reductase from chromatium gracile
13	<a href="#">c1v59B_</a>	Alignment		100.0	29	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of yeast lipoamide dehydrogenase2 complexed with nad+
14	<a href="#">c1zx9A_</a>	Alignment		100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> crystal structure of tn501 mera
15	<a href="#">c1xdia_</a>	Alignment		100.0	22	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> rv3303c-lpda; <b>PDBTitle:</b> crystal structure of lpda (rv3303c) from mycobacterium tuberculosis
16	<a href="#">c3ic9D_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> the structure of dihydrolipoamide dehydrogenase from colwellia2 psychrerythraea 34h.
17	<a href="#">c1tytA_</a>	Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trypanothione reductase, oxidized form; <b>PDBTitle:</b> crystal and molecular structure of crithidia fasciculata2 trypanothione reductase at 2.6 angstroms resolution
18	<a href="#">c2c3dB_</a>	Alignment		100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-oxopropyl-com reductase; <b>PDBTitle:</b> 2.15 angstrom crystal structure of 2-ketopropyl coenzyme m2 oxidoreductase carboxylase with a coenzyme m disulfide3 bound at the active site
19	<a href="#">c2w0hA_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> trypanothione reductase; <b>PDBTitle:</b> x ray structure of leishmania infantum trypanothione2 reductase in complex with antimony and nadph
20	<a href="#">c2v6oA_</a>	Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase; <b>PDBTitle:</b> structure of schistosoma mansoni thioredoxin-glutathione2 reductase (smtgr)
21	<a href="#">c3o0hA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of glutathione reductase from bartonella henselae
22	<a href="#">c1lvIA_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> the refined structure of pseudomonas putida lipoamide dehydrogenase2 complexed with nad+ at 2.45 angstroms resolution
23	<a href="#">c1geuA_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> oxidoreductase(flavoenzyme) <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> anatomy of an engineered nad-binding site
24	<a href="#">c1ndaD_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> trypanothione oxidoreductase; <b>PDBTitle:</b> the structure of trypanosoma cruzi trypanothione reductase2 in the oxidized and nadph reduced state
25	<a href="#">c3l8kB_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoyl dehydrogenase from2 sulfobolus solfataricus
26	<a href="#">c3dgzA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2; <b>PDBTitle:</b> crystal structure of mouse mitochondrial thioredoxin reductase, c-2 terminal 3-residue truncation
27	<a href="#">c1zkqA_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2, mitochondrial; <b>PDBTitle:</b> crystal structure of mouse thioredoxin reductase type 2
28	<a href="#">c2hqmB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of glutathione reductase glr1 from the yeast2 saccharomyces cerevisiae

29	<a href="#">c2nvkX</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> X: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase from drosophila2 melanogaster
30	<a href="#">c2bcpA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidase; <b>PDBTitle:</b> structural analysis of streptococcus pyogenes nadh oxidase:2 c44s nox with azide
31	<a href="#">c2cfyB</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1; <b>PDBTitle:</b> crystal structure of human thioredoxin reductase 1
32	<a href="#">c3kd9B</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> coenzyme a disulfide reductase; <b>PDBTitle:</b> crystal structure of pyridine nucleotide disulfide oxidoreductase from2 pyrococcus horikoshii
33	<a href="#">c3ntaA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide <b>PDBTitle:</b> structure of the shewanella loihica pv-4 nadh-dependent persulfide2 reductase
34	<a href="#">c3icrA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme a-disulfide reductase; <b>PDBTitle:</b> crystal structure of oxidized bacillus anthracis coadr-rhd
35	<a href="#">c1onfA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum glutathione reductase
36	<a href="#">c3cgdB</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase, class i; <b>PDBTitle:</b> pyridine nucleotide complexes with bacillus anthracis coenzyme a-2 disulfide reductase: a structural analysis of dual nad(p)h3 specificity
37	<a href="#">c2cduB</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh oxidase; <b>PDBTitle:</b> the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
38	<a href="#">c3oc4A</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxidoreductase, pyridine nucleotide-disulfide family; <b>PDBTitle:</b> crystal structure of a pyridine nucleotide-disulfide family2 oxidoreductase from the enterococcus faecalis v583
39	<a href="#">c1nhqA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase (h2o2(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> nadh peroxidase; <b>PDBTitle:</b> crystallographic analyses of nadh peroxidase cys42ala and cys42ser2 mutants: active site structure, mechanistic implications, and an3 unusual environment of arg303
40	<a href="#">c1yqzA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme a disulfide reductase; <b>PDBTitle:</b> structure of coenzyme a-disulfide reductase from2 staphylococcus aureus refined at 1.54 angstrom resolution
41	<a href="#">c3iwaA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide <b>PDBTitle:</b> crystal structure of a fad-dependent pyridine nucleotide-disulphide2 oxidoreductase from desulfovibrio vulgaris
42	<a href="#">c1gv4A</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> programed cell death protein 8; <b>PDBTitle:</b> murine apoptosis-inducing factor (aif)
43	<a href="#">c3fg2P</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> putative rubredoxin reductase; <b>PDBTitle:</b> crystal structure of ferredoxin reductase for the cyp199a2 system from2 rhodopseudomonas palustris
44	<a href="#">c3lxdA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide <b>PDBTitle:</b> crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans
45	<a href="#">c1m6iA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> programmed cell death protein 8; <b>PDBTitle:</b> crystal structure of apoptosis inducing factor (aif)
46	<a href="#">c2gr2A</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin reductase; <b>PDBTitle:</b> crystal structure of ferredoxin reductase, bpha4 (oxidized form)
47	<a href="#">c3kljA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad(fad)-dependent dehydrogenase, nirb-family (n-terminal <b>PDBTitle:</b> crystal structure of nadh:rubredoxin oxidoreductase from clostridium2 acetobutylicum
48	<a href="#">c1q1wA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putidaredoxin reductase; <b>PDBTitle:</b> crystal structure of putidaredoxin reductase from2 pseudomonas putida
49	<a href="#">c3ef6A</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> toluene 1,2-dioxygenase system ferredoxin--nad(+) <b>PDBTitle:</b> crystal structure of toluene 2,3-dioxygenase reductase
50	<a href="#">c2v3aA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin reductase; <b>PDBTitle:</b> crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa.
51	<a href="#">c1xhcA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidase /nitrite reductase; <b>PDBTitle:</b> nadh oxidase /nitrite reductase from pyrococcus furiosus pfu-1140779-2 001
52	<a href="#">c1hyuA</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> crystal structure of intact ahpf

53	<a href="#">c3hyxC</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfide-quinone reductase; <b>PDBTitle:</b> 3-d x-ray structure of the sulfide:quinone oxidoreductase from aquifex2 aeolicus in complex with aurachin c
54	<a href="#">c3kpgA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfide-quinone reductase, putative; <b>PDBTitle:</b> crystal structure of sulfide:quinone oxidoreductase from2 acidithiobacillus ferrooxidans in complex with decylubiquinone
55	<a href="#">c1gthD</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase; <b>PDBTitle:</b> dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
56	<a href="#">c2zbwA</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of thioredoxin reductase-like protein from thermus2 thermophilus hb8
57	<a href="#">c3ctyA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of t. acidophilum thioredoxin reductase
58	<a href="#">c1f12A</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alkyl hydroperoxide reductase subunit f; <b>PDBTitle:</b> catalytic core component of the alkylhydroperoxide reductase ahpf from2 e.coli
59	<a href="#">d3grsa1</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
60	<a href="#">c3r9uA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> thioredoxin-disulfide reductase from campylobacter jejuni.
61	<a href="#">c1fcdB</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> electron transport(flavocytochrome) <b>Chain:</b> B: <b>PDB Molecule:</b> flavocytochrome c sulfide dehydrogenase (flavin- <b>PDBTitle:</b> the structure of flavocytochrome c sulfide dehydrogenase2 from a purple phototrophic bacterium chromatium vinosum at3 2.5 angstroms resolution
62	<a href="#">c3fbsB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> the crystal structure of the oxidoreductase from agrobacterium2 tumefaciens
63	<a href="#">c1vdcA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph dependent thioredoxin reductase; <b>PDBTitle:</b> structure of nadph dependent thioredoxin reductase
64	<a href="#">c2vdcl</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> I: <b>PDB Molecule:</b> glutamate synthase [nadph] small chain; <b>PDBTitle:</b> the 9.5 a resolution structure of glutamate synthase from2 cryo-electron microscopy and its oligomerization behavior3 in solution: functional implications.
65	<a href="#">c3f8rD</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin reductase (trx3-3); <b>PDBTitle:</b> crystal structure of sulfobolus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
66	<a href="#">c2q7vA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans thioredoxin2 reductase
67	<a href="#">c1djnB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> trimethylamine dehydrogenase; <b>PDBTitle:</b> structural and biochemical characterization of recombinant wild type2 trimethylamine dehydrogenase from methylophilus methylotrophus (sp.3 w3a1)
68	<a href="#">c1ps9A</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
69	<a href="#">d1lpfa3</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
70	<a href="#">d3lada3</a>	Alignment	not modelled	100.0	32	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
71	<a href="#">d1xdia2</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
72	<a href="#">c2q0lA</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> helicobacter pylori thioredoxin reductase reduced by sodium dithionite2 in complex with nadp+
73	<a href="#">c3ab1B</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ferredoxin nadp+ oxidoreductase
74	<a href="#">c1f6mF</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a complex between thioredoxin2 reductase, thioredoxin, and the nadp+ analog, aadp+
75	<a href="#">d1v59a3</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
76	<a href="#">d1dxa3</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain



						<b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
77	<a href="#">c3d8xB</a>	 Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae nadph dependent2 thioredoxin reductase 1
78	<a href="#">d1ojta3</a>	 Alignment	not modelled	100.0	25	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
79	<a href="#">c3k30B</a>	 Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> histamine dehydrogenase from nocardioodes simplex
80	<a href="#">d1lvla3</a>	 Alignment	not modelled	100.0	22	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
81	<a href="#">c3lzxB</a>	 Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase 2; <b>PDBTitle:</b> crystal structure of ferredoxin-nadp+ oxidoreductase from bacillus2 subtilis (form ii)
82	<a href="#">d1ebda3</a>	 Alignment	not modelled	100.0	29	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
83	<a href="#">d1ojta1</a>	 Alignment	not modelled	100.0	23	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
84	<a href="#">c3h8lA</a>	 Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh oxidase; <b>PDBTitle:</b> the first x-ray structure of a sulfide:quinone2 oxidoreductase: insights into sulfide oxidation mechanism
85	<a href="#">c3d1cA</a>	 Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-containing putative monooxygenase; <b>PDBTitle:</b> crystal structure of flavin-containing putative monooxygenase2 (np_373108.1) from staphylococcus aureus mu50 at 2.40 a resolution
86	<a href="#">d3lada1</a>	 Alignment	not modelled	100.0	22	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
87	<a href="#">d1feca1</a>	 Alignment	not modelled	100.0	31	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
88	<a href="#">d1lpfa1</a>	 Alignment	not modelled	100.0	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
89	<a href="#">d1dxla1</a>	 Alignment	not modelled	100.0	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
90	<a href="#">c2a87A</a>	 Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of m. tuberculosis thioredoxin reductase
91	<a href="#">d3grsa3</a>	 Alignment	not modelled	100.0	25	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
92	<a href="#">c1lqtB</a>	 Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fprra; <b>PDBTitle:</b> a covalent modification of nadp+ revealed by the atomic resolution2 structure of fprra, a mycobacterium tuberculosis oxidoreductase
93	<a href="#">d1gesa3</a>	 Alignment	not modelled	100.0	24	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
94	<a href="#">d1mo9a1</a>	 Alignment	not modelled	99.9	31	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
95	<a href="#">c1y56A</a>	 Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ph1363; <b>PDBTitle:</b> crystal structure of l-proline dehydrogenase from p.horikoshii
96	<a href="#">d1aoga1</a>	 Alignment	not modelled	99.9	23	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
97	<a href="#">d1onfa3</a>	 Alignment	not modelled	99.9	18	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
98	<a href="#">d1h6va1</a>	 Alignment	not modelled	99.9	18	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
99	<a href="#">d1aoga3</a>	 Alignment	not modelled	99.9	23	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal)

						domain
100	<a href="#">c1cjcA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (adrenodoxin reductase); <b>PDBTitle:</b> structure of adrenodoxin reductase of mitochondrial p4502 systems
101	<a href="#">d1ebda1</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
102	<a href="#">d1v59a1</a>	Alignment	not modelled	99.9	31	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
103	<a href="#">d1mo9a3</a>	Alignment	not modelled	99.9	28	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
104	<a href="#">d1feca3</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
105	<a href="#">d1h6va3</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
106	<a href="#">d1lvla1</a>	Alignment	not modelled	99.9	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
107	<a href="#">d1gv4a1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
108	<a href="#">c1x31A</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sarcosine oxidase alpha subunit; <b>PDBTitle:</b> crystal structure of heterotetrameric sarcosine oxidase from <i>Corynebacterium sp. U-96</i>
109	<a href="#">d1m6ia1</a>	Alignment	not modelled	99.9	21	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
110	<a href="#">c3s5wB</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> L-ornithine 5-monooxygenase; <b>PDBTitle:</b> ornithine hydroxylase (pvda) from <i>Pseudomonas aeruginosa</i>
111	<a href="#">d1d4ca2</a>	Alignment	not modelled	99.9	25	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
112	<a href="#">d1nhpa3</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> CO dehydrogenase flavoprotein C-domain-like <b>Superfamily:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain <b>Family:</b> FAD/NAD-linked reductases, dimerisation (C-terminal) domain
113	<a href="#">d1y0pa2</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
114	<a href="#">d2bs2a2</a>	Alignment	not modelled	99.9	12	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
115	<a href="#">d1nhpa1</a>	Alignment	not modelled	99.9	23	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
116	<a href="#">d1qo8a2</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> Succinate dehydrogenase/fumarate reductase flavoprotein N-terminal domain
117	<a href="#">d1q1ra1</a>	Alignment	not modelled	99.9	29	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
118	<a href="#">d2gqfa1</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> HI0933 N-terminal domain-like
119	<a href="#">d2iida1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
120	<a href="#">d1ryia1</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain