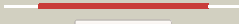



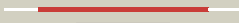






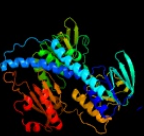












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0462_(lpd)_552617_554011
Date	Tue Jul 23 14:50:54 BST 2019
Unique Job ID	d66a476d7f6a3d2a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2a8xA_</a>	Alignment 		100.0	98	<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
2	<a href="#">c1ojtA_</a>	Alignment 		100.0	36	<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="#">c6bz0C_</a>	Alignment 		100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> 1.83 angstrom resolution crystal structure of dihydrolipoyl2 dehydrogenase from acinetobacter baumannii in complex with fad.
4	<a href="#">c2eq8E_</a>	Alignment 		100.0	37	<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
5	<a href="#">c6aonB_</a>	Alignment 		100.0	37	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> 1.72 angstrom resolution crystal structure of 2-oxoglutarate2 dehydrogenase complex subunit dihydrolipoamide dehydrogenase from3 bordetella pertussis in complex with fad
6	<a href="#">c5w1jA_</a>	Alignment 		100.0	25	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase; <b>PDBTitle:</b> echinococcus granulosus thioredoxin glutathione reductas (egtgr)
7	<a href="#">c2qaeA_</a>	Alignment 		100.0	39	<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
8	<a href="#">c1dxlC_</a>	Alignment 		100.0	37	<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
9	<a href="#">c1lpfB_</a>	Alignment 		100.0	37	<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
10	<a href="#">c3ic9D_</a>	Alignment 		100.0	23	<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.
11	<a href="#">c2v6oA_</a>	Alignment 		100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase; <b>PDBTitle:</b> structure of schistosoma mansoni thioredoxin-gluthathione2 reductase (smtgr)

12	<a href="#">c1lvA_</a>	Alignment		100.0	33	<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
13	<a href="#">c1v59B_</a>	Alignment		100.0	37	<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="#">c1ebdB_</a>	Alignment		100.0	38	<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
15	<a href="#">c3urhB_</a>	Alignment		100.0	38	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
16	<a href="#">c1zmcG_</a>	Alignment		100.0	35	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> crystal structure of human dihydrolipoamide dehydrogenase2 complexed to nad+
17	<a href="#">c4dnaA_</a>	Alignment		100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable glutathione reductase; <b>PDBTitle:</b> crystal structure of putative glutathione reductase from sinorhizobium2 meliloti 1021
18	<a href="#">c4jdrB_</a>	Alignment		100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoamide dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase of pyruvate dehydrogenase from2 escherichia coli
19	<a href="#">c1xdiA_</a>	Alignment		100.0	28	<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
20	<a href="#">c1bwcA_</a>	Alignment		100.0	28	<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
21	<a href="#">c6du7C_</a>	Alignment	not modelled	100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> glutathione reductase from streptococcus pneumoniae
22	<a href="#">c2eq7B_</a>	Alignment	not modelled	100.0	35	<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
23	<a href="#">c2r9zB_</a>	Alignment	not modelled	100.0	28	<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
24	<a href="#">c5x1yC_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> structure of mercuric reductase from lysinibacillus sphaericus
25	<a href="#">c3o0hA_</a>	Alignment	not modelled	100.0	27	<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
26	<a href="#">c1zx9A_</a>	Alignment	not modelled	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
27	<a href="#">c2c3dB_</a>	Alignment	not modelled	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
28	<a href="#">c5v36A_</a>	Alignment	not modelled	100.0	27	<b>PDB header:</b> hydrolase,oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> 1.88 angstrom resolution crystal structure of glutathione

					reductase2 from streptococcus mutans ua159 in complex with fad <b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> 1.73 angstrom resolution crystal structure of glutathione reductase2 from enterococcus faecalis in complex with fad
29	<a href="#">c6b4oB_</a>	Alignment	not modelled	100.0	27
30	<a href="#">c1geuA_</a>	Alignment	not modelled	100.0	28
31	<a href="#">c1tytA_</a>	Alignment	not modelled	100.0	25
32	<a href="#">c2hqmB_</a>	Alignment	not modelled	100.0	25
33	<a href="#">c2w0hA_</a>	Alignment	not modelled	100.0	25
34	<a href="#">c3dgzA_</a>	Alignment	not modelled	100.0	24
35	<a href="#">c1zkgA_</a>	Alignment	not modelled	100.0	24
36	<a href="#">c3l8kB_</a>	Alignment	not modelled	100.0	28
37	<a href="#">c4j56A_</a>	Alignment	not modelled	100.0	21
38	<a href="#">c4ywoA_</a>	Alignment	not modelled	100.0	31
39	<a href="#">c1ndaD_</a>	Alignment	not modelled	100.0	24
40	<a href="#">c2nvkX_</a>	Alignment	not modelled	100.0	25
41	<a href="#">c2cfyB_</a>	Alignment	not modelled	100.0	22
42	<a href="#">c1onfA_</a>	Alignment	not modelled	100.0	26
43	<a href="#">c2bcpA_</a>	Alignment	not modelled	100.0	22
44	<a href="#">c3ntaA_</a>	Alignment	not modelled	100.0	20
45	<a href="#">c3kd9B_</a>	Alignment	not modelled	100.0	26
46	<a href="#">c3oc4A_</a>	Alignment	not modelled	100.0	19
47	<a href="#">c3cgdB_</a>	Alignment	not modelled	100.0	20
48	<a href="#">c2cduB_</a>	Alignment	not modelled	100.0	19
49	<a href="#">c3icrA_</a>	Alignment	not modelled	100.0	22
50	<a href="#">c1nhqA_</a>	Alignment	not modelled	100.0	21
51	<a href="#">c4b1bB_</a>	Alignment	not modelled	100.0	21
52	<a href="#">c5er0D_</a>	Alignment	not modelled	100.0	22
53	<a href="#">c1vgtA_</a>	Alignment	not modelled	100.0	20

53	<a href="#">c1y4aA_</a>	Alignment	not modelled	100.0	20	<b>PDBTitle:</b> structure of coenzyme a-disulfide reductase from2 staphylococcus aureus refined at 1.54 angstrom resolution <b>PDB header:</b> oxidoreductase
54	<a href="#">c3iwaA_</a>	Alignment	not modelled	100.0	25	<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
55	<a href="#">c1gv4A_</a>	Alignment	not modelled	100.0	17	<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)
56	<a href="#">c3fg2P_</a>	Alignment	not modelled	100.0	23	<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
57	<a href="#">c1m6iA_</a>	Alignment	not modelled	100.0	14	<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)
58	<a href="#">c5jciA_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> os09g0567300 protein; <b>PDBTitle:</b> structure and catalytic mechanism of monodehydroascorbate reductase,2 mdhar, from oryza sativa l. japonica
59	<a href="#">c3lxdA_</a>	Alignment	not modelled	100.0	24	<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
60	<a href="#">c2gr2A_</a>	Alignment	not modelled	100.0	21	<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)
61	<a href="#">c1q1wA_</a>	Alignment	not modelled	100.0	20	<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
62	<a href="#">c3kijA_</a>	Alignment	not modelled	100.0	20	<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
63	<a href="#">c2v3aA_</a>	Alignment	not modelled	100.0	20	<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.
64	<a href="#">c3ef6A_</a>	Alignment	not modelled	100.0	18	<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
65	<a href="#">c1hyuA_</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> crystal structure of intact ahpf
66	<a href="#">c5jwcA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> membrane protein <b>Chain:</b> A; <b>PDB Molecule:</b> nadh dehydrogenase, putative; <b>PDBTitle:</b> structure of ndh2 from plasmodium falciparum in complex with ryl-552
67	<a href="#">c6mp5B_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> membrane protein, oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> sulfide:quinone oxidoreductase, mitochondrial; <b>PDBTitle:</b> crystal structure of native human sulfide:quinone oxidoreductase
68	<a href="#">c1xhcA_</a>	Alignment	not modelled	100.0	23	<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
69	<a href="#">c4g6gB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> rotenone-insensitive nadh-ubiquinone oxidoreductase, <b>PDBTitle:</b> crystal structure of ndh with trt
70	<a href="#">c4gapB_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> rotenone-insensitive nadh-ubiquinone oxidoreductase; <b>PDBTitle:</b> structure of the ndi1 protein from saccharomyces cerevisiae in complex2 with nad+
71	<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, ternary complex with2 nadph and 5-iodouracil
72	<a href="#">c2zbwA_</a>	Alignment	not modelled	100.0	16	<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
73	<a href="#">c5w4cA_</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 thioredoxin reductase from cryptococcus2 neoformans in complex with fad (fo conformation)
74	<a href="#">c4xdbC_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase, membrane protein, flavop <b>Chain:</b> C; <b>PDB Molecule:</b> nadh dehydrogenase-like protein saouhsc_00878; <b>PDBTitle:</b> nadh:quinone oxidoreductase (ndh-ii) from staphylococcus aureus -2 holoprotein structure
75	<a href="#">c3kpgA_</a>	Alignment	not modelled	100.0	21	<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
76	<a href="#">d3grsa1</a>	Alignment	not modelled	100.0	35	<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
77	<a href="#">c3ctyA_</a>	Alignment	not modelled	100.0	23	<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



78	<a href="#">c4gcmB</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a thioredoxine reductase (trxb) from2 staphylococcus aureus subsp. aureus mu50 at 1.80 a resolution
79	<a href="#">c6gndG</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of the complex of a ferredoxin-flavin thioredoxin2 reductase and a thioredoxin from clostridium acetobutylicum at 2.9 a3 resolution
80	<a href="#">d3lada3</a>	Alignment	not modelled	100.0	37	<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="#">c4jmqA</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a thioredoxin reductase from brucella melitensis
82	<a href="#">c5jcaL</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> nadh-dependent ferredoxin:nadp oxidoreductase (fnfi) <b>PDBTitle:</b> nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (fnfi)2 from pyrococcus furiosus
83	<a href="#">c4ntdA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of hlmi
84	<a href="#">c1fl2A</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> catalytic core component of the alkylhydroperoxide reductase ahpf from2 e.coli
85	<a href="#">d1lpfa3</a>	Alignment	not modelled	100.0	37	<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
86	<a href="#">c6garB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of oxidised ferredoxin/flavodoxin nadp+2 oxidoreductase 1 (fnr1) from bacillus cereus
87	<a href="#">d1v59a3</a>	Alignment	not modelled	100.0	36	<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
88	<a href="#">c6gncA</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 a ferredoxin-flavin thioredoxin reductase from2 clostridium acetobutylicum at 1.64 a resolution
89	<a href="#">d1dxla3</a>	Alignment	not modelled	100.0	34	<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
90	<a href="#">c3r9uA</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> thioredoxin-disulfide reductase from campylobacter jejuni.
91	<a href="#">d1ojta3</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
92	<a href="#">c3hyxC</a>	Alignment	not modelled	100.0	20	<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
93	<a href="#">c5odeA</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gll2934 protein; <b>PDBTitle:</b> structure of a novel oxidoreductase from gloeobacter violaceus
94	<a href="#">c4nwaA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulfide oxidoreductase; <b>PDBTitle:</b> structure of bacterial type ii nadh dehydrogenase from2 caldalkalibacillus therrmarum at 2.5a resolution
95	<a href="#">c5twcA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> oxidoreductase iruo in the oxidized form
96	<a href="#">d1vla3</a>	Alignment	not modelled	100.0	33	<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
97	<a href="#">c4a5lB</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of the thioredoxin reductase from entamoeba2 histolytica
98	<a href="#">c4fk1D</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative thioredoxin reductase; <b>PDBTitle:</b> crystal structure of putative thioredoxin reductase trxb from bacillus2 anthracis
99	<a href="#">c5mjkC</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of lactococcus lactis thioredoxin reductase (fo2 conformation)
100	<a href="#">c2q7vA</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of deinococcus radiodurans thioredoxin reductase
101	<a href="#">c5i6pB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase;

101	<a href="#">c9j9bB_</a>	Alignment	not modelled	100.0	19	<b>PDBTitle:</b> structure of a thioredoxin reductase from gloeobacter violaceus <b>PDB header:</b> oxidoreductase
102	<a href="#">c4y1fD_</a>	Alignment	not modelled	100.0	20	<b>Chain:</b> D: <b>PDB Molecule:</b> dihydropyrimidine dehydrogenase subunit a; <b>PDBTitle:</b> insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure
103	<a href="#">c6qkqB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> ncr a; <b>PDBTitle:</b> 2-naphthoyl-coa reductase(ncr)
104	<a href="#">c1vdcA_</a>	Alignment	not modelled	100.0	18	<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
105	<a href="#">c3fbsB_</a>	Alignment	not modelled	100.0	16	<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
106	<a href="#">c5jriA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase; <b>PDBTitle:</b> structure of an oxidoreductase semet-labelled from synechocystis sp.2 pcc6803
107	<a href="#">c5uwya_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> the crystal structure of thioredoxin reductase from streptococcus2 pyogenes mgas5005
108	<a href="#">c4a9wB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> flavin-containing monooxygenase from stentrophomonas maltophilia
109	<a href="#">c5m5jA_</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> thioredoxin reductase from giardia duodenalis
110	<a href="#">c5xhuA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ycgf from bacillus subtilis
111	<a href="#">c4jnaA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> oxidoreductase/oxidoreductase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> deph; <b>PDBTitle:</b> crystal structure of the deph complex with dimethyl-fk228
112	<a href="#">d1xdia2</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
113	<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
114	<a href="#">c2vdcl_</a>	Alignment	not modelled	100.0	19	<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 from cryo-2 electron microscopy and its oligomerization behavior in solution:3 functional implications.
115	<a href="#">c3f8rD_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin reductase (trxb-3); <b>PDBTitle:</b> crystal structure of sulfolobus solfataricus thioredoxin2 reductase b3 in complex with two nadp molecules
116	<a href="#">c3d8xB_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae ndpph dependent2 thioredoxin reductase 1
117	<a href="#">c3ab1B_</a>	Alignment	not modelled	100.0	22	<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
118	<a href="#">c3lzb_</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)
119	<a href="#">c1f6mF_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of a complex between thioredoxin reductase,2 thioredoxin, and the nadp+ analog, aadp+
120	<a href="#">c6bwtD_</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> 2.45 angstrom resolution crystal structure thioredoxin reductase from2 francisella tularensis.