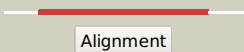

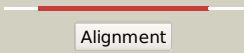



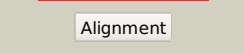



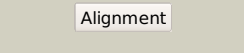

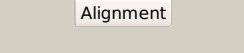



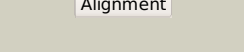

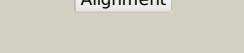

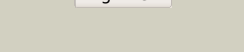
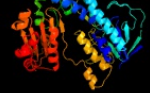


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2855_(mtr)_3165215_3166594
Date	Wed Aug 7 12:50:52 BST 2019
Unique Job ID	f02f3cb1b392708e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2eq8E_</a>			100.0	28	<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
2	<a href="#">c1xdiA_</a>			100.0	25	<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
3	<a href="#">c6aonB_</a>			100.0	26	<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
4	<a href="#">c5w1jA_</a>			100.0	26	<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)
5	<a href="#">c4jdrB_</a>			100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase of pyruvate dehydrogenase from2 escherichia coli
6	<a href="#">c1zx9A_</a>			100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> crystal structure of tn501 mera
7	<a href="#">c2eq7B_</a>			100.0	28	<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 psbdp
8	<a href="#">c3o0hA_</a>			100.0	28	<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
9	<a href="#">c1lvA_</a>			100.0	25	<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
10	<a href="#">c4dnaA_</a>			100.0	30	<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
11	<a href="#">c1ojtA_</a>			100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> surface protein; <b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase

12	<a href="#">c3ic9D_</a>	Alignment		100.0	25	<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.
13	<a href="#">c1ebdB_</a>	Alignment		100.0	28	<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
14	<a href="#">c6bz0C_</a>	Alignment		100.0	25	<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.
15	<a href="#">c1lpfB_</a>	Alignment		100.0	28	<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
16	<a href="#">c1dxlC_</a>	Alignment		100.0	25	<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
17	<a href="#">c5x1yC_</a>	Alignment		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
18	<a href="#">c2r9zB_</a>	Alignment		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
19	<a href="#">c1zmcG_</a>	Alignment		100.0	24	<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+
20	<a href="#">c6du7C_</a>	Alignment		100.0	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> glutathione reductase; <b>PDBTitle:</b> glutathione reductase from streptococcus pneumoniae
21	<a href="#">c2v6oA_</a>	Alignment	not modelled	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)
22	<a href="#">c2a8xA_</a>	Alignment	not modelled	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
23	<a href="#">c2qaeA_</a>	Alignment	not modelled	100.0	25	<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
24	<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
25	<a href="#">c3urhB_</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 dihydrolipoamide dehydrogenase from2 sinorhizobium meliloti 1021
26	<a href="#">c1bwcA_</a>	Alignment	not modelled	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
27	<a href="#">c1v59B_</a>	Alignment	not modelled	100.0	22	<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+
28	<a href="#">c4ywoA_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> mercuric reductase from metallosphaera sedula

29	<a href="#">c1ndaD_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> trypanothione oxidoreductase; <b>PDBTitle:</b> the structure of trypanosoma cruzi trypanothione reductase in the2 oxidized and nadph reduced state
30	<a href="#">c4j56A_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2; <b>PDBTitle:</b> structure of plasmodium falciparum thioredoxin reductase-thioredoxin2 complex
31	<a href="#">c3l8kB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydropolyl dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydropolyl dehydrogenase from sulfobolus2 solfataricus
32	<a href="#">c2w0hA_</a>	Alignment	not modelled	100.0	22	<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
33	<a href="#">c1tytA_</a>	Alignment	not modelled	100.0	24	<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
34	<a href="#">c1geuA_</a>	Alignment	not modelled	100.0	27	<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
35	<a href="#">c6b4oB_</a>	Alignment	not modelled	100.0	27	<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
36	<a href="#">c5v36A_</a>	Alignment	not modelled	100.0	28	<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
37	<a href="#">c2hqmB_</a>	Alignment	not modelled	100.0	25	<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
38	<a href="#">c1zkgA_</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
39	<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
40	<a href="#">c2nvkX_</a>	Alignment	not modelled	100.0	24	<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
41	<a href="#">c1onfA_</a>	Alignment	not modelled	100.0	25	<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
42	<a href="#">c2cfyB_</a>	Alignment	not modelled	100.0	24	<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
43	<a href="#">c2cduB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph oxidase; <b>PDBTitle:</b> the crystal structure of water-forming nad(p)h oxidase from2 lactobacillus sanfranciscensis
44	<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
45	<a href="#">c2bcpA_</a>	Alignment	not modelled	100.0	18	<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: c44s nox2 with azide
46	<a href="#">c3kd9B_</a>	Alignment	not modelled	100.0	22	<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
47	<a href="#">c3cgdB_</a>	Alignment	not modelled	100.0	20	<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
48	<a href="#">c3oc4A_</a>	Alignment	not modelled	100.0	18	<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
49	<a href="#">c1nhqA_</a>	Alignment	not modelled	100.0	19	<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
50	<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
51	<a href="#">c5er0D_</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nadh oxidase; <b>PDBTitle:</b> water-forming nadh oxidase from lactobacillus brevis (lbnox)
52	<a href="#">c4b1bB_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of plasmodium falciparum oxidised2 thioredoxin reductase at 2.9 angstrom
53	<a href="#">c1yqzA_</a>	Alignment	not modelled	100.0	15	<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
54	<a href="#">c3iwaA_</a>	Alignment	not modelled	100.0	20 <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
55	<a href="#">c1gv4A_</a>	Alignment	not modelled	100.0	14 <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="#">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)
57	<a href="#">c5jciA_</a>	Alignment	not modelled	100.0	18 <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
58	<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
59	<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
60	<a href="#">c3kijA_</a>	Alignment	not modelled	100.0	15 <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
61	<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)
62	<a href="#">c1q1wA_</a>	Alignment	not modelled	100.0	17 <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
63	<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
64	<a href="#">c2v3aA_</a>	Alignment	not modelled	100.0	17 <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.
65	<a href="#">c1hyuA_</a>	Alignment	not modelled	100.0	19 <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="#">c1xhcA_</a>	Alignment	not modelled	100.0	19 <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
67	<a href="#">c6mp5B_</a>	Alignment	not modelled	100.0	14 <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="#">c5jwcA_</a>	Alignment	not modelled	100.0	14 <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
69	<a href="#">d3grsa1</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
70	<a href="#">c4g6gB_</a>	Alignment	not modelled	100.0	14 <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
71	<a href="#">c6gndG_</a>	Alignment	not modelled	100.0	18 <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
72	<a href="#">c2zbwA_</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 thioredoxin reductase-like protein from thermus2 thermophilus hb8
73	<a href="#">c3kpgA_</a>	Alignment	not modelled	100.0	16 <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
74	<a href="#">c3ctyA_</a>	Alignment	not modelled	100.0	18 <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
75	<a href="#">c4gapB_</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> structure of the ndi1 protein from saccharomyces cerevisiae in complex2 with nad+
76	<a href="#">c1gthD_</a>	Alignment	not modelled	100.0	17 <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
77	<a href="#">c5jcaL_</a>	Alignment	not modelled	100.0	17 <b>PDB header:</b> oxidoreductase <b>Chain:</b> L: <b>PDB Molecule:</b> nadh-dependent ferredoxin:nadp oxidoreductase (nfni) <b>PDBTitle:</b> nadp(h) bound nadh-dependent ferredoxin:nadp



					oxidoreductase (nfni)2 from pyrococcus furiosus <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> gll2934 protein; <b>PDBTitle:</b> structure of a novel oxidoreductase from gloebacter violaceus
78	<a href="#">c5odeA_</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 hlm1
79	<a href="#">c4ntdA_</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> crystal structure of lactococcus lactis thioredoxin reductase (fo2 conformation)
80	<a href="#">c6gncA_</a>	Alignment	not modelled	100.0	18 <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
81	<a href="#">c3hyxC_</a>	Alignment	not modelled	100.0	13 <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
82	<a href="#">c5mjkC_</a>	Alignment	not modelled	100.0	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of putative thioredoxin reductase trxb from bacillus2 anthracis
83	<a href="#">c4gcmB_</a>	Alignment	not modelled	100.0	18 <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
84	<a href="#">c4fk1D_</a>	Alignment	not modelled	100.0	13 <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
85	<a href="#">c5w4cA_</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 from cryptococcus2 neoformans in complex with fad (fo conformation)
86	<a href="#">c5jriA_</a>	Alignment	not modelled	100.0	15 <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
87	<a href="#">c1fl2A_</a>	Alignment	not modelled	100.0	18 <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
88	<a href="#">c2q7vA_</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 deinococcus radiodurans thioredoxin reductase
89	<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.
90	<a href="#">c5n1tA_</a>	Alignment	not modelled	100.0	13 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-binding subunit of sulfide dehydrogenase; <b>PDBTitle:</b> crystal structure of complex between flavocytochrome c and copper2 chaperone copc from t. paradoxus
91	<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
92	<a href="#">c4jmqA_</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 a thioredoxin reductase from brucella mellitensis
93	<a href="#">c4usqA_</a>	Alignment	not modelled	100.0	14 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase; <b>PDBTitle:</b> structure of flavin-containing monooxygenase from2 cellvibrio sp. br
94	<a href="#">c5j60B_</a>	Alignment	not modelled	100.0	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> structure of a thioredoxin reductase from gloebacter violaceus
95	<a href="#">c4xdbC_</a>	Alignment	not modelled	100.0	13 <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
96	<a href="#">d3lada3</a>	Alignment	not modelled	100.0	35 <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="#">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
98	<a href="#">c4nwzA_</a>	Alignment	not modelled	100.0	19 <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 thermanum at 2.5a resolution
99	<a href="#">c4a5lB_</a>	Alignment	not modelled	100.0	21 <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
100	<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 <b>PDB header:</b> oxidoreductase

101	<a href="#">c4yIfD</a>	Alignment	not modelled	100.0	17	<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
102	<a href="#">c6garB</a>	Alignment	not modelled	100.0	18	<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
103	<a href="#">c5niiB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of the atypical thioredoxin reductase tri from2 desulfovibrio vulgaris hildenborough
104	<a href="#">c5uwyA</a>	Alignment	not modelled	100.0	19	<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
105	<a href="#">d1dxa3</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
106	<a href="#">c1vdcA</a>	Alignment	not modelled	100.0	15	<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
107	<a href="#">d1oita3</a>	Alignment	not modelled	100.0	27	<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
108	<a href="#">d1xdia2</a>	Alignment	not modelled	100.0	30	<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
109	<a href="#">c4jnaA</a>	Alignment	not modelled	100.0	18	<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
110	<a href="#">c6qkgB</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> ncr a; <b>PDBTitle:</b> 2-naphthoyl-coa reductase(ncr)
111	<a href="#">c3fbsB</a>	Alignment	not modelled	100.0	18	<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
112	<a href="#">d1v59a3</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
113	<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 thioredoxin reductase,2 thioredoxin, and the nadp+ analog, aadp+
114	<a href="#">c5xhuA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ycgT from bacillus subtilis
115	<a href="#">c1fcdB</a>	Alignment	not modelled	100.0	15	<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
116	<a href="#">d1lva3</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
117	<a href="#">c5m5jA</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 reductase from giardia duodenalis
118	<a href="#">c3d8xB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> thioredoxin reductase 1; <b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae ndph dependent2 thioredoxin reductase 1
119	<a href="#">c5yggB</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 from2 rhodospseudomonas palustris
120	<a href="#">d1ebda3</a>	Alignment	not modelled	100.0	35	<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