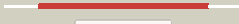



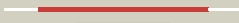



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3403c_(-)_3822442_3824043
Date	Fri Aug 9 18:20:07 BST 2019
Unique Job ID	70c6ca4b31f8a965

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c5j7xA_</a>	 Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dimethylaniline monooxygenase, putative; <b>PDBTitle:</b> baeyer-villiger monooxygenase bvmoaf1838 from aspergillus flavus
2	<a href="#">c5mq6A_</a>	 Alignment		100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridine nucleotide-disulfide oxidoreductase-like protein; <b>PDBTitle:</b> polycyclic ketone monooxygenase from the thermophilic fungus2 thermothelomyces thermophila
3	<a href="#">c5m0zA_</a>	 Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexanone monooxygenase from thermocrispum municipale.; <b>PDBTitle:</b> cyclohexanone monooxygenase from t. municipale: reduced enzyme bound2 to nadp+
4	<a href="#">c3uoyB_</a>	 Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> otemo; <b>PDBTitle:</b> crystal structure of otemo complex with fad and nadp (form 1)
5	<a href="#">c3gwdA_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexanone monooxygenase; <b>PDBTitle:</b> closed crystal structure of cyclohexanone monooxygenase
6	<a href="#">c6jdkA_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> baeyer-villiger monooxygenase; <b>PDBTitle:</b> crystal structure of baeyer-villiger monooxygenase from parvibaculum2 lavamentivorans
7	<a href="#">c1w4xA_</a>	 Alignment		100.0	16	<b>PDB header:</b> oxygenase <b>Chain:</b> A: <b>PDB Molecule:</b> phenylacetone monooxygenase; <b>PDBTitle:</b> phenylacetone monooxygenase, a baeyer-villiger2 monooxygenase
8	<a href="#">c6a37A_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative flavin-binding monooxygenase; <b>PDBTitle:</b> x-ray structure of cyclohexanone monooxygenase from acinetobacter2 calcoaceticus
9	<a href="#">c4ap3A_</a>	 Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> steroid monooxygenase; <b>PDBTitle:</b> oxidized steroid monooxygenase bound to nadp
10	<a href="#">c3uclA_</a>	 Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cyclohexanone monooxygenase; <b>PDBTitle:</b> cyclohexanone-bound crystal structure of cyclohexanone monooxygenase2 in the rotated conformation
11	<a href="#">c3s5wB_</a>	 Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> l-ornithine 5-monooxygenase; <b>PDBTitle:</b> ornithine hydroxylase (pvda) from pseudomonas aeruginosa

12	<a href="#">c1vqwB_</a>	Alignment		100.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein with similarity to flavin-containing <b>PDBTitle:</b> crystal structure of a protein with similarity to flavin-2 containing monooxygenases and to mammalian dimethylalanine3 monooxygenases
13	<a href="#">c5cqfA_</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lysine 6-monooxygenase; <b>PDBTitle:</b> crystal structure of l-lysine 6-monooxygenase from pseudomonas2 syringae
14	<a href="#">c2vq7B_</a>	Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> bacterial flavin-containing monooxygenase in complex with2 nadp: native data
15	<a href="#">c5gsnD_</a>	Alignment		100.0	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> D: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> tmm in complex with methimazole
16	<a href="#">c4b68A_</a>	Alignment		100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-ornithine n5 monooxygenase; <b>PDBTitle:</b> a. fumigatus ornithine hydroxylase (sida), re-oxidised state bound to2 nadp and arg
17	<a href="#">c4tlxC_</a>	Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> ktzi; <b>PDBTitle:</b> kutzneria sp. 744 ornithine n-hydroxylase, ktzi-fadred-nadp+-l-orn
18	<a href="#">c4d7eA_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-lys monooxygenase; <b>PDBTitle:</b> an unprecedented nadph domain conformation in lysine2 monooxygenase nbtg from nocardia farcinica
19	<a href="#">c5nmwA_</a>	Alignment		100.0	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavin-containing monooxygenase; <b>PDBTitle:</b> crystal structure of the pyrrolizidine alkaloid n-oxygenase from2 zonocerus variegatus in complex with fad
20	<a href="#">c5o8rA_</a>	Alignment		100.0	12	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-lysine 6-monooxygenase involved in desferrioxamine <b>PDBTitle:</b> the crystal structure of dfoa bound to fad and nadp; the2 desferrioxamine biosynthetic pathway cadaverine monooxygenase from3 the fire blight disease pathogen erwinia amylovora
21	<a href="#">c3d1cA_</a>	Alignment	not modelled	99.9	18	<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
22	<a href="#">c1lqtB_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fpfa; <b>PDBTitle:</b> a covalent modification of nadp+ revealed by the atomic resolution2 structure of fpfa, a mycobacterium tuberculosis oxidoreductase
23	<a href="#">c1hyuA_</a>	Alignment	not modelled	99.9	16	<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
24	<a href="#">c1cjcA_</a>	Alignment	not modelled	99.9	13	<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 p450 systems
25	<a href="#">c4usrA_</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> monooxygenase; <b>PDBTitle:</b> structure of flavin-containing monooxygenase from2 pseudomonas stutzeri nf13
26	<a href="#">c5w1jA_</a>	Alignment	not modelled	99.8	21	<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)
27	<a href="#">d1w4xa1</a>	Alignment	not modelled	99.8	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
28	<a href="#">c4a9wB_</a>	Alignment	not modelled	99.8	19	<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 <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin glutathione reductase; <b>PDBTitle:</b> structure of schistosoma mansoni thioredoxin-gluthathione2 reductase (smtgr)
29	<a href="#">c2v6oA_</a>	Alignment	not modelled	99.8	15
30	<a href="#">d2gv8a1</a>	Alignment	not modelled	99.8	10
31	<a href="#">c1gthD_</a>	Alignment	not modelled	99.8	18
32	<a href="#">c4usqA_</a>	Alignment	not modelled	99.8	18
33	<a href="#">c1gv4A_</a>	Alignment	not modelled	99.8	14
34	<a href="#">c3ntaA_</a>	Alignment	not modelled	99.8	19
35	<a href="#">c3oc4A_</a>	Alignment	not modelled	99.8	17
36	<a href="#">c3icrA_</a>	Alignment	not modelled	99.8	16
37	<a href="#">c5twcA_</a>	Alignment	not modelled	99.7	17
38	<a href="#">c4gapB_</a>	Alignment	not modelled	99.7	19
39	<a href="#">c4g6gB_</a>	Alignment	not modelled	99.7	18
40	<a href="#">c2c3dB_</a>	Alignment	not modelled	99.7	19
41	<a href="#">c1xdia_</a>	Alignment	not modelled	99.7	19
42	<a href="#">c5jcaL_</a>	Alignment	not modelled	99.7	16
43	<a href="#">c6qkaB_</a>	Alignment	not modelled	99.7	18
44	<a href="#">c5jwcA_</a>	Alignment	not modelled	99.7	15
45	<a href="#">c3urhB_</a>	Alignment	not modelled	99.7	15
46	<a href="#">c5jciA_</a>	Alignment	not modelled	99.7	19
47	<a href="#">c6garB_</a>	Alignment	not modelled	99.7	19
48	<a href="#">c6du7C_</a>	Alignment	not modelled	99.7	16
49	<a href="#">c3iwaA_</a>	Alignment	not modelled	99.7	20
50	<a href="#">c3dgzA_</a>	Alignment	not modelled	99.7	17
51	<a href="#">c2eq8E_</a>	Alignment	not modelled	99.7	18
52	<a href="#">c6mp5B_</a>	Alignment	not modelled	99.7	15

						<b>PDBTitle:</b> crystal structure of native human sulfide:quinone oxidoreductase
53	<a href="#">c4yifD_</a>	Alignment	not modelled	99.7	16	<b>PDB header:</b> oxidoreductase <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
54	<a href="#">c1ojtA_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> surface protein; <b>PDBTitle:</b> structure of dihydrolipoamide dehydrogenase
55	<a href="#">c1zqkA_</a>	Alignment	not modelled	99.7	17	<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
56	<a href="#">c1v59B_</a>	Alignment	not modelled	99.7	12	<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+
57	<a href="#">c1tytA_</a>	Alignment	not modelled	99.7	14	<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
58	<a href="#">c2gr2A_</a>	Alignment	not modelled	99.7	20	<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)
59	<a href="#">c2qaeA_</a>	Alignment	not modelled	99.7	15	<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
60	<a href="#">c2eq7B_</a>	Alignment	not modelled	99.7	17	<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
61	<a href="#">c1yqzA_</a>	Alignment	not modelled	99.7	21	<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
62	<a href="#">c2a8xA_</a>	Alignment	not modelled	99.7	17	<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
63	<a href="#">c2vdcI_</a>	Alignment	not modelled	99.7	18	<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.
64	<a href="#">c1dxlC_</a>	Alignment	not modelled	99.7	15	<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
65	<a href="#">c3r9uA_</a>	Alignment	not modelled	99.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> thioredoxin-disulfide reductase from campylobacter jejuni.
66	<a href="#">c1m6iA_</a>	Alignment	not modelled	99.7	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)
67	<a href="#">c2w0hA_</a>	Alignment	not modelled	99.7	12	<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
68	<a href="#">d1w4xa2</a>	Alignment	not modelled	99.7	11	<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
69	<a href="#">c1ps9A_</a>	Alignment	not modelled	99.7	14	<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-dienoyl2 coa reductase
70	<a href="#">c1zx9A_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> crystal structure of tn501 mera
71	<a href="#">c1zmcG_</a>	Alignment	not modelled	99.7	14	<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+
72	<a href="#">c3kd9B_</a>	Alignment	not modelled	99.7	20	<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
73	<a href="#">c2zbwA_</a>	Alignment	not modelled	99.7	18	<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
74	<a href="#">c2bcpA_</a>	Alignment	not modelled	99.7	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
75	<a href="#">c3k30B_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> histamine dehydrogenase; <b>PDBTitle:</b> histamine dehydrogenase from nocardioes simplex
76	<a href="#">c1bwcA_</a>	Alignment	not modelled	99.7	15	<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
77	<a href="#">c3fg2P_</a>	Alignment	not modelled	99.6	21	<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 rhodospseudomonas palustris

78	<a href="#">c3ic9D</a>	Alignment	not modelled	99.6	19	<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.
79	<a href="#">c1ndaD</a>	Alignment	not modelled	99.6	16	<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
80	<a href="#">c1q1wA</a>	Alignment	not modelled	99.6	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
81	<a href="#">c2hqmB</a>	Alignment	not modelled	99.6	13	<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
82	<a href="#">c6b4oB</a>	Alignment	not modelled	99.6	14	<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
83	<a href="#">c5n1tA</a>	Alignment	not modelled	99.6	17	<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
84	<a href="#">c5w4cA</a>	Alignment	not modelled	99.6	18	<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)
85	<a href="#">c1geuA</a>	Alignment	not modelled	99.6	16	<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
86	<a href="#">c3o0hA</a>	Alignment	not modelled	99.6	16	<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
87	<a href="#">c2r9zB</a>	Alignment	not modelled	99.6	17	<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
88	<a href="#">c1djnB</a>	Alignment	not modelled	99.6	12	<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)
89	<a href="#">c4j56A</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase 2; <b>PDBTitle:</b> structure of plasmidom falciparum thioredoxin reductase-thioredoxin2 complex
90	<a href="#">c5jriA</a>	Alignment	not modelled	99.6	14	<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
91	<a href="#">c4dnaA</a>	Alignment	not modelled	99.6	17	<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
92	<a href="#">c1ebdB</a>	Alignment	not modelled	99.6	14	<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
93	<a href="#">c1fcdB</a>	Alignment	not modelled	99.6	13	<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
94	<a href="#">c5odeA</a>	Alignment	not modelled	99.6	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
95	<a href="#">c2v3aA</a>	Alignment	not modelled	99.6	18	<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.
96	<a href="#">c4xdbC</a>	Alignment	not modelled	99.6	17	<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
97	<a href="#">c5uwvA</a>	Alignment	not modelled	99.6	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
98	<a href="#">c3l8kB</a>	Alignment	not modelled	99.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyl dehydrogenase; <b>PDBTitle:</b> crystal structure of a dihydrolipoyl dehydrogenase from sulfolobus2 solfataricus
99	<a href="#">c4gcmB</a>	Alignment	not modelled	99.6	19	<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
100	<a href="#">c5v36A</a>	Alignment	not modelled	99.6	13	<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
101	<a href="#">c2nvkX</a>	Alignment	not modelled	99.6	15	<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
						<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoovl dehydrogenase:

102	<a href="#">c6aonB_</a>	Alignment	not modelled	99.6	19	<b>PDBTitle:</b> 1.72 angstrom resolution crystal structure of 2-oxoglutarate2 dehydrogenase complex subunit dihydrolipoamide dehydrogenase from3 bordetella pertussis in complex with fad <b>PDB header:</b> oxidoreductase
103	<a href="#">c3kpgA_</a>	Alignment	not modelled	99.6	14	<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
104	<a href="#">c2cfyB_</a>	Alignment	not modelled	99.6	15	<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
105	<a href="#">c1lVA_</a>	Alignment	not modelled	99.6	13	<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
106	<a href="#">c4jmqA_</a>	Alignment	not modelled	99.6	19	<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
107	<a href="#">c4jnaA_</a>	Alignment	not modelled	99.6	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
108	<a href="#">c4ntdA_</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> crystal structure of hImi
109	<a href="#">c2ywlA_</a>	Alignment	not modelled	99.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase related protein; <b>PDBTitle:</b> crystal structure of thioredoxin reductase-related protein ttha03702 from thermus thermophilus hb8
110	<a href="#">c5yggB_</a>	Alignment	not modelled	99.6	21	<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 rhodopseudomonas palustris
111	<a href="#">c4ywoA_</a>	Alignment	not modelled	99.6	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> mercuric reductase; <b>PDBTitle:</b> mercuric reductase from metallosphaera sedula
112	<a href="#">c4nzwA_</a>	Alignment	not modelled	99.6	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 thermarum at 2.5a resolution
113	<a href="#">c3lzxB_</a>	Alignment	not modelled	99.6	15	<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)
114	<a href="#">c6bz0C_</a>	Alignment	not modelled	99.6	16	<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.
115	<a href="#">c1vdcA_</a>	Alignment	not modelled	99.6	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
116	<a href="#">c4jdrB_</a>	Alignment	not modelled	99.6	21	<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
117	<a href="#">c1lpfB_</a>	Alignment	not modelled	99.6	20	<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
118	<a href="#">c4b1bB_</a>	Alignment	not modelled	99.6	13	<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
119	<a href="#">c3lxdA_</a>	Alignment	not modelled	99.6	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
120	<a href="#">c1x31A_</a>	Alignment	not modelled	99.6	25	<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 from2 corynebacterium sp. u-96