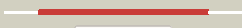
















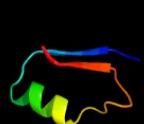

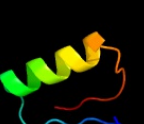




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1422_(-)_1596887_1597915
Date	Wed Jul 31 22:05:53 BST 2019
Unique Job ID	a3f3d69e621a2944

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2ppvA</a>	 Alignment		100.0	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a protein belonging to the upf0052 (se_0549) from2 staphylococcus epidermidis atcc 12228 at 2.00 a resolution
2	<a href="#">d2hzba1</a>	 Alignment		100.0	35	<b>Fold:</b> CofD-like <b>Superfamily:</b> CofD-like <b>Family:</b> CofD-like
3	<a href="#">c2q7xA</a>	 Alignment		100.0	33	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> upf0052 protein sp_1565; <b>PDBTitle:</b> crystal structure of a putative phospho transferase (sp_1565) from2 streptococcus pneumoniae tigr4 at 2.00 a resolution
4	<a href="#">d2ffea1</a>	 Alignment		100.0	16	<b>Fold:</b> CofD-like <b>Superfamily:</b> CofD-like <b>Family:</b> CofD-like
5	<a href="#">c2p0yA</a>	 Alignment		100.0	33	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein lp_0780; <b>PDBTitle:</b> crystal structure of q88yi3_lacpl from lactobacillus plantarum.2 northeast structural genomics consortium target lpr6
6	<a href="#">d1rlia</a>	 Alignment		84.5	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Hypothetical protein YwqN
7	<a href="#">c2gr2A</a>	 Alignment		80.2	19	<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)
8	<a href="#">c3n8kG</a>	 Alignment		78.7	44	<b>PDB header:</b> lyase <b>Chain:</b> G: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
9	<a href="#">c5jwcA</a>	 Alignment		78.1	27	<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
10	<a href="#">d1d7ya1</a>	 Alignment		77.9	19	<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
11	<a href="#">d1pj5a2</a>	 Alignment		76.3	21	<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

12	<a href="#">c3dzcA_</a>	Alignment		76.2	10	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine 2-epimerase; <b>PDBTitle:</b> 2.35 angstrom resolution structure of wecb (vc0917), a udp-n-2 acetylglucosamine 2-epimerase from vibrio cholerae.
13	<a href="#">c3kpgA_</a>	Alignment		75.5	30	<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
14	<a href="#">d1ryia1</a>	Alignment		75.0	16	<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
15	<a href="#">c2uygF_</a>	Alignment		73.6	31	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> crystallographic structure of the typeii 3-dehydroquinase from thermus2 thermophilus
16	<a href="#">c2weuD_</a>	Alignment		73.4	32	<b>PDB header:</b> antifungal protein <b>Chain:</b> D: <b>PDB Molecule:</b> tryptophan 5-halogenase; <b>PDBTitle:</b> crystal structure of tryptophan 5-halogenase (pyrh) complex2 with substrate tryptophan
17	<a href="#">d1cjca2</a>	Alignment		72.3	16	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
18	<a href="#">c4rhcH_</a>	Alignment		71.9	38	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> 3-dehydroquinate dehydratase; <b>PDBTitle:</b> crystal structure of 3-dehydroquinate dehydratase from acinetobacter2 baumannii at 2.68 a resolution
19	<a href="#">d1h05a_</a>	Alignment		70.6	44	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Type II 3-dehydroquinate dehydratase <b>Family:</b> Type II 3-dehydroquinate dehydratase
20	<a href="#">d1p3da1</a>	Alignment		69.5	17	<b>Fold:</b> MurCD N-terminal domain <b>Superfamily:</b> MurCD N-terminal domain <b>Family:</b> MurCD N-terminal domain
21	<a href="#">c1phhA_</a>	Alignment	not modelled	69.0	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> p-hydroxybenzoate hydroxylase; <b>PDBTitle:</b> crystal structure of p-hydroxybenzoate hydroxylase complexed with its2 reaction product 3,4-dihydroxybenzoate
22	<a href="#">d1uqra_</a>	Alignment	not modelled	68.4	39	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Type II 3-dehydroquinate dehydratase <b>Family:</b> Type II 3-dehydroquinate dehydratase
23	<a href="#">c3lzxB_</a>	Alignment	not modelled	68.3	23	<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)
24	<a href="#">c3kljA_</a>	Alignment	not modelled	68.3	23	<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
25	<a href="#">c5uaoA_</a>	Alignment	not modelled	68.3	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophane-5-halogenase; <b>PDBTitle:</b> crystal structure of mibh, a lathipeptide tryptophan 5-halogenase
26	<a href="#">c4dgcA_</a>	Alignment	not modelled	68.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> phytoene dehydrogenase; <b>PDBTitle:</b> crystal structure of phytoene desaturase crt1 from pantoea ananatis
27	<a href="#">d1vmea1</a>	Alignment	not modelled	68.0	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
28	<a href="#">c4jinqA_</a>	Alignment	not modelled	67.8	23	<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

29	<a href="#">d1fmta2</a>	Alignment	not modelled	67.1	19	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
30	<a href="#">d1gqoa_</a>	Alignment	not modelled	66.8	25	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Type II 3-dehydroquininate dehydratase <b>Family:</b> Type II 3-dehydroquininate dehydratase
31	<a href="#">d2blna2</a>	Alignment	not modelled	66.0	21	<b>Fold:</b> Formyltransferase <b>Superfamily:</b> Formyltransferase <b>Family:</b> Formyltransferase
32	<a href="#">c5twcA_</a>	Alignment	not modelled	65.1	23	<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
33	<a href="#">c3cwcB_</a>	Alignment	not modelled	64.3	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative glycerate kinase 2; <b>PDBTitle:</b> crystal structure of putative glycerate kinase 2 from salmonella2 typhimurium lt2
34	<a href="#">c5n1tA_</a>	Alignment	not modelled	63.2	23	<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
35	<a href="#">c5tukC_</a>	Alignment	not modelled	62.7	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tetracycline destructase tet(51); <b>PDBTitle:</b> crystal structure of tetracycline destructase tet(51)
36	<a href="#">c4l8lA_</a>	Alignment	not modelled	62.7	39	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquininate dehydratase 1; <b>PDBTitle:</b> crystal structure of the type ii dehydroquinase from pseudomonas2 aeruginosa
37	<a href="#">c3lwzC_</a>	Alignment	not modelled	62.4	31	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-dehydroquininate dehydratase; <b>PDBTitle:</b> 1.65 angstrom resolution crystal structure of type ii 3-dehydroquininate2 dehydratase (aroq) from yersinia pestis
38	<a href="#">d1hya1</a>	Alignment	not modelled	62.2	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
39	<a href="#">c2qx7A_</a>	Alignment	not modelled	62.2	19	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> eugenol synthase 1; <b>PDBTitle:</b> structure of eugenol synthase from ocimum basilicum
40	<a href="#">c3kd9B_</a>	Alignment	not modelled	62.1	29	<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
41	<a href="#">c1yrwA_</a>	Alignment	not modelled	61.8	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> protein arna; <b>PDBTitle:</b> crystal structure of e.coli arna transformylase domain
42	<a href="#">c1v59B_</a>	Alignment	not modelled	61.7	26	<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+
43	<a href="#">c3d8xB_</a>	Alignment	not modelled	60.0	10	<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
44	<a href="#">c5t57A_</a>	Alignment	not modelled	59.9	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> semialdehyde dehydrogenase nad-binding protein; <b>PDBTitle:</b> crystal structure of a semialdehyde dehydrogenase nad-binding protein2 from cupriavidus necator in complex with calcium and nad
45	<a href="#">c4jdrB_</a>	Alignment	not modelled	59.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoal dehydrogenase; <b>PDBTitle:</b> dihydrolipoamide dehydrogenase of pyruvate dehydrogenase from2 escherichia coli
46	<a href="#">c4g6gB_</a>	Alignment	not modelled	59.2	20	<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
47	<a href="#">c6cv6L_</a>	Alignment	not modelled	59.0	25	<b>PDB header:</b> lyase <b>Chain:</b> L: <b>PDB Molecule:</b> 3-dehydroquininate dehydratase; <b>PDBTitle:</b> crystal structure of 3-dehydroquininate dehydratase, type ii, from2 burkholderia phymatum stm815
48	<a href="#">d1fcda1</a>	Alignment	not modelled	58.7	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
49	<a href="#">c5v36A_</a>	Alignment	not modelled	58.7	29	<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
50	<a href="#">c3kipU_</a>	Alignment	not modelled	58.5	39	<b>PDB header:</b> lyase <b>Chain:</b> U: <b>PDB Molecule:</b> 3-dehydroquinase, type ii; <b>PDBTitle:</b> crystal structure of type-ii 3-dehydroquinase from c. albicans
51	<a href="#">c3a1fA_</a>	Alignment	not modelled	58.4	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome b-245 heavy chain; <b>PDBTitle:</b> the crystal structure of nadph binding domain of gp91(phox)
52	<a href="#">c6gncA_</a>	Alignment	not modelled	58.4	23	<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
53	<a href="#">c4nwzA_</a>	Alignment	not modelled	58.2	30	<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
						<b>PDB header:</b> hydrolase

54	<a href="#">c3i3lA_</a>	Alignment	not modelled	57.7	26	<b>Chain:</b> A: <b>PDB Molecule:</b> alkylhalidase cmls; <b>PDBTitle:</b> crystal structure of cmls, a flavin-dependent halogenase
55	<a href="#">d1ep3b2</a>	Alignment	not modelled	57.6	39	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Dihydroorotate dehydrogenase B, PyrK subunit <b>PDB header:</b> oxidoreductase
56	<a href="#">c3lrxC_</a>	Alignment	not modelled	57.5	23	<b>Chain:</b> C: <b>PDB Molecule:</b> putative hydrogenase; <b>PDBTitle:</b> crystal structure of the c-terminal domain (residues 78-226) of pf19112 hydrogenase from pyrococcus furiosus, northeast structural genomics3 consortium target pfr246a
57	<a href="#">c5tulA_</a>	Alignment	not modelled	57.4	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> tetracycline destructase tet(55); <b>PDBTitle:</b> crystal structure of tetracycline destructase tet(55)
58	<a href="#">c1xdia_</a>	Alignment	not modelled	57.2	40	<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
59	<a href="#">d1k0ia1</a>	Alignment	not modelled	56.9	10	<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
60	<a href="#">d1fdra2</a>	Alignment	not modelled	56.9	21	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
61	<a href="#">c4j33B_</a>	Alignment	not modelled	56.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> kynurenine 3-monooxygenase; <b>PDBTitle:</b> crystal structure of kynurenine 3-monooxygenase (kmo-394)
62	<a href="#">d2piaa2</a>	Alignment	not modelled	56.6	35	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Aromatic dioxygenase reductase-like
63	<a href="#">c6gehA_</a>	Alignment	not modelled	56.5	15	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> fad-binding 9, siderophore-interacting domain protein; <b>PDBTitle:</b> structure and reactivity of a siderophore-interacting protein from the2 marine bacterium shewanella reveals unanticipated functional3 versatility.
64	<a href="#">d1gvha3</a>	Alignment	not modelled	56.3	17	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Flavo-hemoglobin, C-terminal domain
65	<a href="#">d1qfja2</a>	Alignment	not modelled	56.2	18	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
66	<a href="#">c3fg2P_</a>	Alignment	not modelled	56.2	16	<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
67	<a href="#">c3icrA_</a>	Alignment	not modelled	56.0	23	<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
68	<a href="#">d1ndha2</a>	Alignment	not modelled	56.0	25	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
69	<a href="#">c3s2uA_</a>	Alignment	not modelled	55.8	23	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine--n-acetylmuramyl-(pentapeptide) <b>PDBTitle:</b> crystal structure of the pseudomonas aeruginosa murg:udp-glcna2 substrate complex
70	<a href="#">c2e4gB_</a>	Alignment	not modelled	55.8	29	<b>PDB header:</b> biosynthetic protein, flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan halogenase; <b>PDBTitle:</b> rebh with bound l-trp
71	<a href="#">c1fcdB_</a>	Alignment	not modelled	55.5	19	<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
72	<a href="#">c3ef6A_</a>	Alignment	not modelled	55.2	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
73	<a href="#">c6bpyA_</a>	Alignment	not modelled	55.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> aspergillus fumigatus thioredoxin reductase
74	<a href="#">d1qfza2</a>	Alignment	not modelled	54.9	25	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
75	<a href="#">c3u80A_</a>	Alignment	not modelled	54.9	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinatase, type ii; <b>PDBTitle:</b> 1.60 angstrom resolution crystal structure of a 3-dehydroquinatase2 dehydratase-like protein from bifidobacterium longum
76	<a href="#">d1ddga2</a>	Alignment	not modelled	54.7	13	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> NADPH-cytochrome p450 reductase-like
77	<a href="#">d1qx4a2</a>	Alignment	not modelled	54.6	24	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
78	<a href="#">c3uteB_</a>	Alignment	not modelled	54.3	23	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> crystal structure of aspergillus fumigatus udp

						galactopyranose mutase2 sulfate complex <b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
79	<a href="#">d1umka2</a>	Alignment	not modelled	54.3	20	<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
80	<a href="#">c1lvIA</a>	Alignment	not modelled	54.3	26	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
81	<a href="#">d2cnda2</a>	Alignment	not modelled	54.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> tetx2 protein; <b>PDBTitle:</b> structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
82	<a href="#">c2xdoC</a>	Alignment	not modelled	53.5	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> udp-galactopyranose mutase; <b>PDBTitle:</b> crystal structure of reduced udp-galactopyranose mutase
83	<a href="#">c4dshB</a>	Alignment	not modelled	52.9	20	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
84	<a href="#">d2bmwa2</a>	Alignment	not modelled	52.8	25	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> tryptophan 6-halogenase; <b>PDBTitle:</b> mutant of flavin-dependent tryptophan halogenase thal with altered2 regioselectivity (thal-rebh5)
85	<a href="#">c6ib5B</a>	Alignment	not modelled	52.7	29	<b>Fold:</b> Glycerate kinase I <b>Superfamily:</b> Glycerate kinase I <b>Family:</b> Glycerate kinase I
86	<a href="#">d1to6a</a>	Alignment	not modelled	52.5	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> spermidine synthase; <b>PDBTitle:</b> crystal structure of spermidine synthase from helicobacter2 pylori
87	<a href="#">c2cmgA</a>	Alignment	not modelled	52.4	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamine amidotransferase subunit pdxt; <b>PDBTitle:</b> crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
88	<a href="#">c2ywjA</a>	Alignment	not modelled	52.2	14	<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+
89	<a href="#">c4gapB</a>	Alignment	not modelled	52.2	20	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase superfamily; <b>PDBTitle:</b> brvh, a flavin-dependent halogenase from brevundimonas sp. bal3
90	<a href="#">c6frIA</a>	Alignment	not modelled	52.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> up1; <b>PDBTitle:</b> structure of up1 protein
91	<a href="#">c2ivoC</a>	Alignment	not modelled	51.8	22	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> NADPH-cytochrome p450 reductase-like
92	<a href="#">d1f20a2</a>	Alignment	not modelled	51.6	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 (lbnx)
93	<a href="#">c5er0D</a>	Alignment	not modelled	51.3	17	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> cobyric acid synthase; <b>PDBTitle:</b> murt/gatd peptidoglycan amidotransferase complex from streptococcus2 pneumoniae r6
94	<a href="#">c6fqbE</a>	Alignment	not modelled	51.2	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> precorrin-2 dehydrogenase; <b>PDBTitle:</b> sirc, precorrin-2 dehydrogenase
95	<a href="#">c3dfzB</a>	Alignment	not modelled	51.1	15	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
96	<a href="#">d1sm4a2</a>	Alignment	not modelled	50.4	25	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
97	<a href="#">d1a8pa2</a>	Alignment	not modelled	50.3	24	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
98	<a href="#">d1e9yb2</a>	Alignment	not modelled	50.2	31	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Metallo-dependent hydrolases <b>Family:</b> alpha-subunit of urease, catalytic domain
99	<a href="#">c1nhqA</a>	Alignment	not modelled	50.1	27	<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
100	<a href="#">d1tvca2</a>	Alignment	not modelled	50.0	26	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Aromatic dioxygenase reductase-like
101	<a href="#">c2bcpA</a>	Alignment	not modelled	49.9	16	<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
102	<a href="#">c2ardA</a>	Alignment	not modelled	49.6	32	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan halogenase prna; <b>PDBTitle:</b> the structure of tryptophan 7-halogenase (prna) suggests a mechanism2 for regioselective chlorination
103	<a href="#">c1kyqC</a>	Alignment	not modelled	49.5	20	<b>PDB header:</b> oxidoreductase, lyase <b>Chain:</b> C: <b>PDB Molecule:</b> siroheme biosynthesis protein met8; <b>PDBTitle:</b> met8p: a bifunctional nad-dependent dehydrogenase and2 ferrochelataase involved in siroheme synthesis.
						<b>PDB header:</b> oxidoreductase



104	<a href="#">c1yqzA</a>	Alignment	not modelled	49.5	21	<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
105	<a href="#">c5w4cA</a>	Alignment	not modelled	49.0	19	<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)
106	<a href="#">c2a87A</a>	Alignment	not modelled	48.9	20	<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
107	<a href="#">d1gtza</a>	Alignment	not modelled	48.8	31	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Type II 3-dehydroquinate dehydratase <b>Family:</b> Type II 3-dehydroquinate dehydratase
108	<a href="#">d1cqxa3</a>	Alignment	not modelled	48.6	27	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Flavo-hemoglobin, C-terminal domain
109	<a href="#">c2eixA</a>	Alignment	not modelled	48.5	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-cytochrome b5 reductase; <b>PDBTitle:</b> the structure of physarum polycephalum cytochrome b5 reductase
110	<a href="#">d1gawa2</a>	Alignment	not modelled	48.2	22	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
111	<a href="#">d2c4va1</a>	Alignment	not modelled	48.1	23	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Type II 3-dehydroquinate dehydratase <b>Family:</b> Type II 3-dehydroquinate dehydratase
112	<a href="#">c3vewA</a>	Alignment	not modelled	47.4	39	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> o-carbamoyltransferase tobz; <b>PDBTitle:</b> crystal structure of the o-carbamoyltransferase tobz in complex with2 adp
113	<a href="#">c2eq8E</a>	Alignment	not modelled	47.2	33	<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
114	<a href="#">c5eowA</a>	Alignment	not modelled	47.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-hydroxynicotinate 3-monooxygenase; <b>PDBTitle:</b> crystal structure of 6-hydroxynicotinic acid 3-monooxygenase from2 pseudomonas putida kt2440
115	<a href="#">c6aioA</a>	Alignment	not modelled	46.6	26	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> pnpa; <b>PDBTitle:</b> crystal structure of p-nitrophenol 4-monooxygenase pnpa from2 pseudomonas putida dll-e4
116	<a href="#">d1jb9a2</a>	Alignment	not modelled	46.4	20	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Superfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
117	<a href="#">c1ryiB</a>	Alignment	not modelled	45.3	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glycine oxidase; <b>PDBTitle:</b> structure of glycine oxidase with bound inhibitor glycolate
118	<a href="#">c3iwaA</a>	Alignment	not modelled	45.1	17	<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
119	<a href="#">c5m5jA</a>	Alignment	not modelled	44.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> thioredoxin reductase; <b>PDBTitle:</b> thioredoxin reductase from giardia duodenalis
120	<a href="#">c3hyxC</a>	Alignment	not modelled	44.8	36	<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