







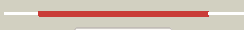










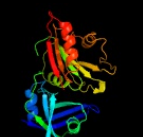




# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2895c_(viuB)_3204391_3205242
Date	Thu Aug 8 16:20:05 BST 2019
Unique Job ID	485c32a66bdb8079

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6k2IA_</a>	 Alignment		100.0	27	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> siderophore-interacting protein; <b>PDBTitle:</b> crystal structure of the siderophore-interacting protein sips from2 aeromonas hydrophila
2	<a href="#">c2gpiA_</a>	 Alignment		100.0	38	<b>PDB header:</b> fad-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> siderophore-interacting protein; <b>PDBTitle:</b> crystal structure of a siderophore-interacting protein (sputcn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
3	<a href="#">c6gehA_</a>	 Alignment		100.0	23	<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.
4	<a href="#">c4yhbA_</a>	 Alignment		100.0	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iron-chelator utilization protein; <b>PDBTitle:</b> crystal structure of a siderophore utilization protein from t. fusca
5	<a href="#">c4p6vF_</a>	 Alignment		100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> na(+)-translocating nadh-quinone reductase subunit f; <b>PDBTitle:</b> crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
6	<a href="#">c1gvhA_</a>	 Alignment		100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavoheomprotein; <b>PDBTitle:</b> the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unsuspected geometry of the3 distal heme pocket
7	<a href="#">c4u9uB_</a>	 Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> na(+)-translocating nadh-quinone reductase subunit f; <b>PDBTitle:</b> crystal structure of nqr fad-binding domain from vibrio cholerae
8	<a href="#">c2r6hC_</a>	 Alignment		100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh:ubiquinone oxidoreductase, na translocating, f <b>PDBTitle:</b> crystal structure of the domain comprising the nad binding and the fad2 binding regions of the nadh:ubiquinone oxidoreductase, na3 translocating, f subunit from porphyromonas gingivalis
9	<a href="#">c1krhA_</a>	 Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> benzoate 1,2-dioxygenase reductase; <b>PDBTitle:</b> x-ray structure of benzoate dioxygenase reductase
10	<a href="#">c3fpkB_</a>	 Alignment		100.0	13	<b>PDB header:</b> flavoprotein, oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin-nadp reductase; <b>PDBTitle:</b> crystal structure of ferredoxin-nadp reductase from salmonella2 typhimurium
11	<a href="#">c6o0aA_</a>	 Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavoheomoglobin; <b>PDBTitle:</b> crystal structure of flavohemoglobin from malassezia yamatoensis with2 bound fad and heme determined by iron sad phasing

12	<a href="#">c4wqmA_</a>	Alignment		100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> toluene-4-monooxygenase electron transfer component; <b>PDBTitle:</b> structure of the toluene 4-monooxygenase nadh oxidoreductase t4mof,2 k270s k271s variant
13	<a href="#">c6mv2A_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome b5 reductase 4; <b>PDBTitle:</b> 2.05a resolution structure of the cs-b5r domains of human ncb5or2 (nadp+ form)
14	<a href="#">c1cqxB_</a>	Alignment		100.0	12	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> flavohepmprotein; <b>PDBTitle:</b> crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
15	<a href="#">c2bgjB_</a>	Alignment		100.0	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin-nadp(h) reductase; <b>PDBTitle:</b> x-ray structure of the ferredoxin-nadp(h) reductase from rhodobacter2 capsulatus at 2.1 angstroms
16	<a href="#">c4eh1A_</a>	Alignment		100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavohepmprotein; <b>PDBTitle:</b> crystal structure of the flavohem-like-fad/nad binding domain of2 nitric oxide dioxygenase from vibrio cholerae o1 biovar el tor
17	<a href="#">c5ogxA_</a>	Alignment		100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome p450 reductase; <b>PDBTitle:</b> crystal structure of amycolatopsis cytochrome p450 reductase gcob.
18	<a href="#">c4g1bB_</a>	Alignment		100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavohepmpoglobin; <b>PDBTitle:</b> x-ray structure of yeast flavohemoglobin in complex with econazole
19	<a href="#">c2eixA_</a>	Alignment		100.0	12	<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
20	<a href="#">c1umkA_</a>	Alignment		100.0	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-cytochrome b5 reductase; <b>PDBTitle:</b> the structure of human erythrocyte nadh-cytochrome b52 reductase
21	<a href="#">c5tr9A_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-nadp reductase; <b>PDBTitle:</b> crystal structure of a ferredoxin nadp+ reductase from neisseria2 gonorrhoeae with bound fad
22	<a href="#">c2piaA_</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> reductase <b>Chain:</b> A: <b>PDB Molecule:</b> phthalate dioxygenase reductase; <b>PDBTitle:</b> phthalate dioxygenase reductase: a modular structure for electron2 transfer from pyridine nucleotides to [2fe-2s]
23	<a href="#">c5ylyB_</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> nitrate reductase; <b>PDBTitle:</b> crystal structure of the cytochrome b5 reductase domain of ulva2 prolifera nitrate reductase
24	<a href="#">c1a8pA_</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph\ferredoxin oxidoreductase; <b>PDBTitle:</b> ferredoxin reductase from azotobacter vinelandii
25	<a href="#">c1qgyA_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp+ reductase; <b>PDBTitle:</b> ferredoxin:nadp+ reductase mutant with lys 75 replaced by glu (k75e)
26	<a href="#">c1tvcA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methane monooxygenase component c; <b>PDBTitle:</b> fad and nadh binding domain of methane monooxygenase2 reductase from methylococcus capsulatus (bath)
27	<a href="#">c5thxA_</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of a ferredoxin nadp+ reductase from neisseria2 gonorrhoeae with bound nadp and fad
28	<a href="#">c4b4dA_</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-nadp reductase; <b>PDBTitle:</b> crystal structure of fad-containing ferredoxin-nadp reductase from2 xanthomonas axonopodis pv. citri
29	<a href="#">c5vi7B_</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin-nadp(+) reductase subunit

29	<a href="#">c3vj7B</a>	Alignment	not modelled	99.9	14	alpha; <b>PDBTitle:</b> ferredoxin nadp oxidoreductase (xfn)
30	<a href="#">c4f7dA</a>	Alignment	not modelled	99.9	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> crystal structure of ferredoxin-nadp reductase from burkholderia2 thailandensis e264
31	<a href="#">c1qfjD</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> protein (flavin reductase); <b>PDBTitle:</b> crystal structure of nad(p)h:flavin oxidoreductase from escherichia2 coli
32	<a href="#">c1fncA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> oxidoreductase (nadp+(a),ferredoxin(a)) <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-nadp+ reductase; <b>PDBTitle:</b> refined crystal structure of spinach ferredoxin reductase2 at 1.7 angstroms resolution: oxidized, reduced, and 2'-3 phospho-5'-amp bound states
33	<a href="#">c5jcaS</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> S: <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
34	<a href="#">c1jb9A</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin-nadp reductase; <b>PDBTitle:</b> crystal structure of the ferredoxin:nadp+ reductase from maize root at2 1.7 angstroms
35	<a href="#">c2rc5D</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> ferredoxin-nadp reductase; <b>PDBTitle:</b> refined structure of fnr from leptospira interrogans
36	<a href="#">c1cneA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitrate reductase; <b>PDBTitle:</b> structural studies on corn nitrate reductase: refined2 structure of the cytochrome b reductase fragment at 2.53 angstroms, its adp complex and an active site mutant and4 modeling of the cytochrome b domain
37	<a href="#">c2ok8D</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> putative ferredoxin--nadp reductase; <b>PDBTitle:</b> ferredoxin-nadp+ reductase from plasmodium falciparum
38	<a href="#">c4ylfA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydroorotate dehydrogenase b (nad(+)), electron transfer <b>PDBTitle:</b> insights into flavin-based electron bifurcation via the nadh-dependent2 reduced ferredoxin-nadp oxidoreductase structure
39	<a href="#">c1ep3B</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydroorotate dehydrogenase b (pyrk subunit); <b>PDBTitle:</b> crystal structure of lactococcus lactis dihydroorotate dehydrogenase2 b. data collected under cryogenic conditions.
40	<a href="#">c2b5oA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> ferredoxin-nadp reductase
41	<a href="#">c5o0xA</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putative ferric reductase; <b>PDBTitle:</b> crystal structure of dehydrogenase domain of cylindrospermum stagnale2 nadph-oxidase 5 (nox5)
42	<a href="#">c1ddiA</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase [nadph] flavoprotein alpha-component; <b>PDBTitle:</b> crystal structure of sir-fp60
43	<a href="#">c6efvA</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> sulfite reductase [nadph] flavoprotein alpha-component; <b>PDBTitle:</b> the nadph-dependent sulfite reductase flavoprotein adopts an extended2 conformation that is unique to this diflavin reductase
44	<a href="#">d2piaa1</a>	Alignment	not modelled	99.7	8	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
45	<a href="#">c4dqkA</a>	Alignment	not modelled	99.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional p-450/nadph-p450 reductase; <b>PDBTitle:</b> crystal structure of the fad binding domain of cytochrome p450 bm3
46	<a href="#">d1qx4a1</a>	Alignment	not modelled	99.7	17	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
47	<a href="#">d2cnda1</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
48	<a href="#">d1cqxa2</a>	Alignment	not modelled	99.6	11	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
49	<a href="#">d1gvha2</a>	Alignment	not modelled	99.6	13	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
50	<a href="#">c1f20A</a>	Alignment	not modelled	99.6	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric-oxide synthase; <b>PDBTitle:</b> crystal structure of rat neuronal nitric-oxide synthase fad/nadp+2 domain at 1.9a resolution.
51	<a href="#">c1tllA</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nitric-oxide synthase, brain; <b>PDBTitle:</b> crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
52	<a href="#">c1j9zB</a>	Alignment	not modelled	99.6	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh-pcytochrome p450 reductase; <b>PDBTitle:</b> cypor-w677g
53	<a href="#">d1ep3b1</a>	Alignment	not modelled	99.6	24	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like

54	<a href="#">d1ndha1</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
55	<a href="#">c5gxuA</a>	Alignment	not modelled	99.6	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph--cytochrome p450 reductase 2; <b>PDBTitle:</b> crystal structure of arabidopsis atr2
56	<a href="#">c3qftA</a>	Alignment	not modelled	99.6	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph--cytochrome p450 reductase; <b>PDBTitle:</b> crystal structure of nadph-cytochrome p450 reductase (fad/nadph domain2 and r457h mutant)
57	<a href="#">d1umka1</a>	Alignment	not modelled	99.6	20	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
58	<a href="#">d2bmwa1</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
59	<a href="#">d1krha1</a>	Alignment	not modelled	99.6	11	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
60	<a href="#">d1a8pa1</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
61	<a href="#">c2qtzA</a>	Alignment	not modelled	99.5	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methionine synthase reductase; <b>PDBTitle:</b> crystal structure of the nadp+-bound fad-containing fnr-like module of2 human methionine synthase reductase
62	<a href="#">d1sm4a1</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
63	<a href="#">d1fdra1</a>	Alignment	not modelled	99.5	14	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
64	<a href="#">d1tvca1</a>	Alignment	not modelled	99.5	18	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
65	<a href="#">c2bpoA</a>	Alignment	not modelled	99.5	11	<b>PDB header:</b> reductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph-cytochrom p450 reductase; <b>PDBTitle:</b> crystal structure of the yeast cpr triple mutant: d74g, y75f, k78a.
66	<a href="#">d1fnda1</a>	Alignment	not modelled	99.5	13	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
67	<a href="#">d1gawa1</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
68	<a href="#">d1qfza1</a>	Alignment	not modelled	99.4	14	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
69	<a href="#">d1qfja1</a>	Alignment	not modelled	99.4	20	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
70	<a href="#">c6j7aB</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> heme oxygenase 1,nadph--cytochrome p450 reductase; <b>PDBTitle:</b> fusion protein of heme oxygenase-1 and nadph cytochrome p450 reductase2 (17aa)
71	<a href="#">d1qfja2</a>	Alignment	not modelled	99.3	14	<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
72	<a href="#">d1qx4a2</a>	Alignment	not modelled	99.2	5	<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
73	<a href="#">d1umka2</a>	Alignment	not modelled	99.2	5	<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
74	<a href="#">d2cnda2</a>	Alignment	not modelled	99.2	12	<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="#">c3lrxC</a>	Alignment	not modelled	99.2	15	<b>PDB header:</b> oxidoreductase <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
76	<a href="#">d1jb9a1</a>	Alignment	not modelled	99.2	16	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
77	<a href="#">d1cqxa3</a>	Alignment	not modelled	99.2	11	<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
78	<a href="#">d1gvha3</a>	Alignment	not modelled	99.1	12	<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
79	<a href="#">d2piaa2</a>	Alignment	not modelled	99.1	16	<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
						<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> Ferredoxin reductase-like, C-terminal NADP-linked domain

80	<a href="#">d1tvca2</a>	Alignment	not modelled	99.1	8	<b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Aromatic dioxygenase reductase-like
81	<a href="#">d1krha2</a>	Alignment	not modelled	99.0	15	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Aromatic dioxygenase reductase-like
82	<a href="#">d1ndha2</a>	Alignment	not modelled	99.0	8	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
83	<a href="#">d1a8pa2</a>	Alignment	not modelled	99.0	9	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
84	<a href="#">d1fdra2</a>	Alignment	not modelled	98.9	14	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
85	<a href="#">c3a1fA_</a>	Alignment	not modelled	98.9	11	<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)
86	<a href="#">d1f20a2</a>	Alignment	not modelled	98.8	10	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> NADPH-cytochrome p450 reductase-like
87	<a href="#">d2bmwa2</a>	Alignment	not modelled	98.8	13	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
88	<a href="#">d1ddga2</a>	Alignment	not modelled	98.7	9	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> NADPH-cytochrome p450 reductase-like
89	<a href="#">d1qfza2</a>	Alignment	not modelled	98.7	9	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
90	<a href="#">d1ja1a3</a>	Alignment	not modelled	98.7	11	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> NADPH-cytochrome p450 reductase-like
91	<a href="#">d1gawa2</a>	Alignment	not modelled	98.7	11	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
92	<a href="#">d1fnda2</a>	Alignment	not modelled	98.7	10	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
93	<a href="#">d1ep3b2</a>	Alignment	not modelled	98.6	13	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Dihydroorotate dehydrogenase B, PyrK subunit
94	<a href="#">d1jb9a2</a>	Alignment	not modelled	98.5	11	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
95	<a href="#">d1sm4a2</a>	Alignment	not modelled	98.5	9	<b>Fold:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Supersfamily:</b> Ferredoxin reductase-like, C-terminal NADP-linked domain <b>Family:</b> Reductases
96	<a href="#">d1f20a1</a>	Alignment	not modelled	95.0	25	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Supersfamily:</b> Riboflavin synthase domain-like <b>Family:</b> NADPH-cytochrome p450 reductase FAD-binding domain-like
97	<a href="#">d1ddga1</a>	Alignment	not modelled	94.3	12	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Supersfamily:</b> Riboflavin synthase domain-like <b>Family:</b> NADPH-cytochrome p450 reductase FAD-binding domain-like
98	<a href="#">d1ja1a1</a>	Alignment	not modelled	85.4	12	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Supersfamily:</b> Riboflavin synthase domain-like <b>Family:</b> NADPH-cytochrome p450 reductase FAD-binding domain-like
99	<a href="#">c4he5A_</a>	Alignment	not modelled	61.7	17	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> peptidase family u32; <b>PDBTitle:</b> crystal structure of the selenomethionine variant of the c-terminal2 domain of geobacillus thermoleovorans putative u32 peptidase
100	<a href="#">c3ougA_</a>	Alignment	not modelled	55.8	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate 1-decarboxylase; <b>PDBTitle:</b> crystal structure of cleaved l-aspartate-alpha-decarboxylase from2 francisella tularensis
101	<a href="#">d2ffea1</a>	Alignment	not modelled	30.3	12	<b>Fold:</b> CofD-like <b>Supersfamily:</b> CofD-like <b>Family:</b> CofD-like
102	<a href="#">c3bmbB_</a>	Alignment	not modelled	25.0	29	<b>PDB header:</b> rna binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> regulator of nucleoside diphosphate kinase; <b>PDBTitle:</b> crystal structure of a new rna polymerase interacting2 protein
103	<a href="#">d2zoda2</a>	Alignment	not modelled	22.4	53	<b>Fold:</b> PurM C-terminal domain-like <b>Supersfamily:</b> PurM C-terminal domain-like <b>Family:</b> PurM C-terminal domain-like
104	<a href="#">c1pt1B_</a>	Alignment	not modelled	22.0	22	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate 1-decarboxylase; <b>PDBTitle:</b> unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
105	<a href="#">c2c45F_</a>	Alignment	not modelled	21.2	22	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> aspartate 1-decarboxylase; <b>PDBTitle:</b> native precursor of pyruvoyl dependent aspartate decarboxylase