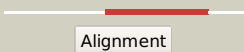

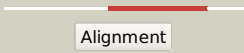



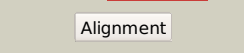



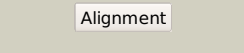

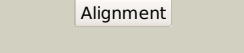



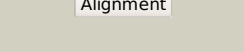

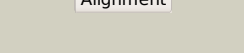

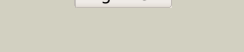






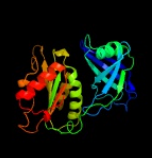





# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3554_(fdxB)_3992864_3994921
Date	Fri Aug 9 18:20:23 BST 2019
Unique Job ID	6c70a4b14a02ba25

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2piaA_</a>	 Alignment		100.0	27	<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]
2	<a href="#">c6o0aA_</a>	 Alignment		100.0	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavoheemoglobin; <b>PDBTitle:</b> crystal structure of flavohemoglobin from malassezia yamatoensis with2 bound fad and heme determined by iron sad phasing
3	<a href="#">c4g1bB_</a>	 Alignment		100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavoheemoglobin; <b>PDBTitle:</b> x-ray structure of yeast flavohemoglobin in complex with econazole
4	<a href="#">c1gvhA_</a>	 Alignment		100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavoheemoprotein; <b>PDBTitle:</b> the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unsuspected geometry of the3 distal heme pocket
5	<a href="#">c1cqxB_</a>	 Alignment		100.0	23	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> flavoheemoprotein; <b>PDBTitle:</b> crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
6	<a href="#">c6mv2A_</a>	 Alignment		100.0	23	<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)
7	<a href="#">c4p6vF_</a>	 Alignment		100.0	23	<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
8	<a href="#">c1krhA_</a>	 Alignment		100.0	23	<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
9	<a href="#">c4wqmA_</a>	 Alignment		100.0	25	<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
10	<a href="#">c5ogxA_</a>	 Alignment		100.0	26	<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.
11	<a href="#">c2r6hC_</a>	 Alignment		100.0	21	<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

12	<a href="#">c5ylyB</a>	Alignment		100.0	25	<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 proliferans nitrate reductase
13	<a href="#">c3fpkB</a>	Alignment		100.0	21	<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
14	<a href="#">c4eh1A</a>	Alignment		100.0	25	<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 of 2 nitric oxide dioxygenase from vibrio cholerae o1 biovar el tor
15	<a href="#">c1ep3B</a>	Alignment		100.0	19	<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.
16	<a href="#">c5tr9A</a>	Alignment		100.0	22	<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
17	<a href="#">c2eixA</a>	Alignment		100.0	23	<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
18	<a href="#">c2ok8D</a>	Alignment		100.0	21	<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
19	<a href="#">c1umkA</a>	Alignment		100.0	21	<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
20	<a href="#">c4u9uB</a>	Alignment		100.0	24	<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
21	<a href="#">c1a8pA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh\;ferredoxin oxidoreductase; <b>PDBTitle:</b> ferredoxin reductase from azotobacter vinelandii
22	<a href="#">c1fncA</a>	Alignment	not modelled	100.0	21	<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
23	<a href="#">c5thxA</a>	Alignment	not modelled	100.0	23	<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
24	<a href="#">c1tvcA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> methane monoxygenase component c; <b>PDBTitle:</b> fad and nadh binding domain of methane monoxygenase2 reductase from methylococcus capsulatus (bath)
25	<a href="#">c2bgjB</a>	Alignment	not modelled	100.0	21	<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
26	<a href="#">c4b4dA</a>	Alignment	not modelled	100.0	20	<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
27	<a href="#">c1qgyA</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp+ reductase; <b>PDBTitle:</b> ferredoxin:nadp+ reductase mutant with lys 75 replaced by glu (k75e)
28	<a href="#">c5jcaS</a>	Alignment	not modelled	100.0	21	<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 (fnf1)2 from pyrococcus furiosus
29	<a href="#">c1jb9A_</a>	Alignment	not modelled	100.0	18	<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
30	<a href="#">c2b5oA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> ferredoxin-nadp reductase
31	<a href="#">c2rc5D_</a>	Alignment	not modelled	100.0	23	<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
32	<a href="#">c4f7dA_</a>	Alignment	not modelled	100.0	20	<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
33	<a href="#">c1cneA_</a>	Alignment	not modelled	100.0	21	<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
34	<a href="#">c4ylfA_</a>	Alignment	not modelled	100.0	19	<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
35	<a href="#">c5o0xA_</a>	Alignment	not modelled	100.0	20	<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)
36	<a href="#">c5vj7B_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ferredoxin-nadp(+) reductase subunit alpha; <b>PDBTitle:</b> ferredoxin nadp oxidoreductase (xfn)
37	<a href="#">c1qfjD_</a>	Alignment	not modelled	100.0	21	<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
38	<a href="#">c6gehA_</a>	Alignment	not modelled	100.0	14	<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.
39	<a href="#">c4yhbA_</a>	Alignment	not modelled	100.0	19	<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
40	<a href="#">c6k2lA_</a>	Alignment	not modelled	100.0	20	<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
41	<a href="#">c2gpiA_</a>	Alignment	not modelled	100.0	13	<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
42	<a href="#">c6efvA_</a>	Alignment	not modelled	100.0	20	<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
43	<a href="#">c1ddiA_</a>	Alignment	not modelled	100.0	22	<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
44	<a href="#">c1tilA_</a>	Alignment	not modelled	100.0	18	<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.
45	<a href="#">c5gxuA_</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph--cytochrome p450 reductase 2; <b>PDBTitle:</b> cystal structure of arabidopsis atr2
46	<a href="#">c1f20A_</a>	Alignment	not modelled	99.9	19	<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.
47	<a href="#">d1tvca2</a>	Alignment	not modelled	99.9	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> Aromatic dioxygenase reductase-like
48	<a href="#">d1gvha3</a>	Alignment	not modelled	99.9	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> Flavo-hemoglobin, C-terminal domain
49	<a href="#">c1j9zB_</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph-cytochrome p450 reductase; <b>PDBTitle:</b> cypor-w677g
50	<a href="#">c4dqkA_</a>	Alignment	not modelled	99.9	22	<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
51	<a href="#">d1qfja2</a>	Alignment	not modelled	99.9	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
52	<a href="#">c3qftA_</a>	Alignment	not modelled	99.9	21	<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)
53	<a href="#">d2cnda2</a>	Alignment	not modelled	99.9	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
54	<a href="#">c2qtzA</a>	Alignment	not modelled	99.9	19	<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
55	<a href="#">d1cqxa3</a>	Alignment	not modelled	99.9	19	<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> Flavoheemoglobin, C-terminal domain
56	<a href="#">d1krha2</a>	Alignment	not modelled	99.9	23	<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
57	<a href="#">d1umka2</a>	Alignment	not modelled	99.9	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
58	<a href="#">d1qx4a2</a>	Alignment	not modelled	99.9	19	<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
59	<a href="#">c2bpoA</a>	Alignment	not modelled	99.9	24	<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.
60	<a href="#">d1ep3b2</a>	Alignment	not modelled	99.9	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> Dihydroorotate dehydrogenase B, PyrK subunit
61	<a href="#">d1a8pa2</a>	Alignment	not modelled	99.9	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
62	<a href="#">c4n58A</a>	Alignment	not modelled	99.8	26	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> pectocin m2; <b>PDBTitle:</b> crystal structure of pectocin m2 at 1.86 angstroms
63	<a href="#">d2piaa2</a>	Alignment	not modelled	99.8	28	<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
64	<a href="#">d1ndha2</a>	Alignment	not modelled	99.8	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> Reductases
65	<a href="#">c3a1fA</a>	Alignment	not modelled	99.8	22	<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)
66	<a href="#">d2bmwa2</a>	Alignment	not modelled	99.8	19	<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
67	<a href="#">d1fdra2</a>	Alignment	not modelled	99.8	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> Reductases
68	<a href="#">d1doia</a>	Alignment	not modelled	99.8	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
69	<a href="#">d2piaa3</a>	Alignment	not modelled	99.8	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
70	<a href="#">d1gvha2</a>	Alignment	not modelled	99.8	26	<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
71	<a href="#">d1cqxa2</a>	Alignment	not modelled	99.8	25	<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
72	<a href="#">d1f20a2</a>	Alignment	not modelled	99.8	19	<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
73	<a href="#">d1e0za</a>	Alignment	not modelled	99.8	25	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
74	<a href="#">d1qfza2</a>	Alignment	not modelled	99.8	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> Reductases
75	<a href="#">d1gawa2</a>	Alignment	not modelled	99.8	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> Reductases
76	<a href="#">d1jb9a2</a>	Alignment	not modelled	99.8	19	<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
77	<a href="#">d1fnda2</a>	Alignment	not modelled	99.8	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
78	<a href="#">d1ddga2</a>	Alignment	not modelled	99.8	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> NADPH-cytochrome p450 reductase-like

79	<a href="#">c6j7aB</a>	Alignment	not modelled	99.8	21	<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)
80	<a href="#">d1fdra1</a>	Alignment	not modelled	99.7	25	<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
81	<a href="#">d1sm4a2</a>	Alignment	not modelled	99.7	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> Reductases
82	<a href="#">d1a70a</a>	Alignment	not modelled	99.7	29	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
83	<a href="#">d1a8pa1</a>	Alignment	not modelled	99.7	27	<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
84	<a href="#">c4zyoA</a>	Alignment	not modelled	99.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa desaturase; <b>PDBTitle:</b> crystal structure of human integral membrane stearyl-coa desaturase2 with substrate
85	<a href="#">c3lrxC</a>	Alignment	not modelled	99.7	18	<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
86	<a href="#">d1ja1a3</a>	Alignment	not modelled	99.7	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> NADPH-cytochrome p450 reductase-like
87	<a href="#">d1offa</a>	Alignment	not modelled	99.7	30	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
88	<a href="#">d1qx4a1</a>	Alignment	not modelled	99.7	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
89	<a href="#">d1frra</a>	Alignment	not modelled	99.7	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
90	<a href="#">d1frda</a>	Alignment	not modelled	99.7	23	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
91	<a href="#">d2bmwa1</a>	Alignment	not modelled	99.7	19	<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
92	<a href="#">d1fxia</a>	Alignment	not modelled	99.7	31	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
93	<a href="#">d1lumka1</a>	Alignment	not modelled	99.7	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
94	<a href="#">d1krha1</a>	Alignment	not modelled	99.7	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
95	<a href="#">d1iuea</a>	Alignment	not modelled	99.7	28	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
96	<a href="#">d1awda</a>	Alignment	not modelled	99.7	30	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
97	<a href="#">d1czpa</a>	Alignment	not modelled	99.7	35	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
98	<a href="#">d2cnda1</a>	Alignment	not modelled	99.7	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
99	<a href="#">d2cjoa</a>	Alignment	not modelled	99.7	31	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
100	<a href="#">d2piaa1</a>	Alignment	not modelled	99.7	29	<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
101	<a href="#">d1wrja</a>	Alignment	not modelled	99.7	30	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
102	<a href="#">d1pfda</a>	Alignment	not modelled	99.7	28	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
103	<a href="#">d1sm4a1</a>	Alignment	not modelled	99.7	25	<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
104	<a href="#">d1gaqb</a>	Alignment	not modelled	99.7	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
105	<a href="#">d1ndha1</a>	Alignment	not modelled	99.7	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

106	<a href="#">d1gawa1</a>	Alignment	not modelled	99.7	26	<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
107	<a href="#">d4fxca_</a>	Alignment	not modelled	99.6	31	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
108	<a href="#">c4itkA_</a>	Alignment	not modelled	99.6	31	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> apoferreredoxin; <b>PDBTitle:</b> the structure of c.reinhardtii ferredoxin 2
109	<a href="#">d1tvca1</a>	Alignment	not modelled	99.6	23	<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
110	<a href="#">d1fnda1</a>	Alignment	not modelled	99.6	29	<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
111	<a href="#">d1ep3b1</a>	Alignment	not modelled	99.6	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
112	<a href="#">c5frc_</a>	Alignment	not modelled	99.6	25	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> dimeric (2fe-2s) protein; <b>PDBTitle:</b> structure of the fesii (shethna) protein of azotobacter vinelandii
113	<a href="#">d1jq4a_</a>	Alignment	not modelled	99.6	25	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
114	<a href="#">d1qfza1</a>	Alignment	not modelled	99.6	23	<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
115	<a href="#">d1krha3</a>	Alignment	not modelled	99.6	31	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
116	<a href="#">d1qfja1</a>	Alignment	not modelled	99.5	25	<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
117	<a href="#">c4ymkA_</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> acyl-coa desaturase 1; <b>PDBTitle:</b> crystal structure of stearyl-coenzyme a desaturase 1
118	<a href="#">c3zyyX_</a>	Alignment	not modelled	99.4	18	<b>PDB header:</b> iron-sulfur-binding protein <b>Chain:</b> X: <b>PDB Molecule:</b> iron-sulfur cluster binding protein; <b>PDBTitle:</b> reductive activator for corrinoid,iron-sulfur protein
119	<a href="#">d1jb9a1</a>	Alignment	not modelled	99.4	22	<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
120	<a href="#">c3ah7A_</a>	Alignment	not modelled	99.3	24	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> [2fe-2s]ferredoxin; <b>PDBTitle:</b> crystal structure of the isc-like [2fe-2s] ferredoxin (fdxb) from2 pseudomonas putida jcm 20004