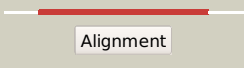

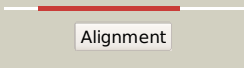

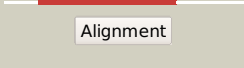

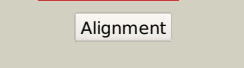

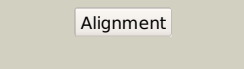
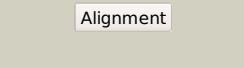


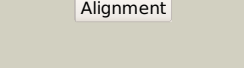

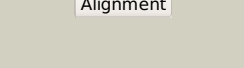

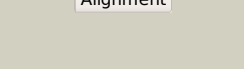

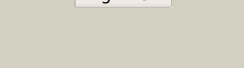












# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3571_(hmp)_4012596_4013672
Date	Fri Aug 9 18:20:25 BST 2019
Unique Job ID	9d29617dad1807e6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2piaA_</a>			100.0	28	<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="#">c1gvhA_</a>			100.0	27	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavoheмоprotein; <b>PDBTitle:</b> the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unsuspected geometry of the3 distal heme pocket
3	<a href="#">c4g1bB_</a>			100.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> flavoheмоglobin; <b>PDBTitle:</b> x-ray structure of yeast flavohemoglobin in complex with econazole
4	<a href="#">c4p6vF_</a>			100.0	20	<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
5	<a href="#">c6o0aA_</a>			100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavoheмоglobin; <b>PDBTitle:</b> crystal structure of flavohemoglobin from malassezia yamatoensis with2 bound fad and heme determined by iron sad phasing
6	<a href="#">c1cqxB_</a>			100.0	29	<b>PDB header:</b> lipid binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> flavoheмоprotein; <b>PDBTitle:</b> crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
7	<a href="#">c1krhA_</a>			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
8	<a href="#">c6mv2A_</a>			100.0	26	<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)
9	<a href="#">c2r6hC_</a>			100.0	20	<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
10	<a href="#">c5ogxA_</a>			100.0	24	<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="#">c4eh1A_</a>			100.0	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavoheмоprotein; <b>PDBTitle:</b> crystal structure of the flavohem-like-fad/nad binding domain of2 nitric oxide dioxygenase from vibrio cholerae o1 biovar el tor

12	<a href="#">c1ep3B_</a>	Alignment		100.0	16	<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.
13	<a href="#">c5ylyB_</a>	Alignment		100.0	22	<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
14	<a href="#">c4wqmA_</a>	Alignment		100.0	21	<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
15	<a href="#">c4u9uB_</a>	Alignment		100.0	21	<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
16	<a href="#">c5jcaS_</a>	Alignment		100.0	22	<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
17	<a href="#">c4yifa_</a>	Alignment		100.0	24	<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
18	<a href="#">c1tvcA_</a>	Alignment		100.0	21	<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)
19	<a href="#">c2eixA_</a>	Alignment		100.0	18	<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="#">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
21	<a href="#">c1umkA_</a>	Alignment	not modelled	100.0	25	<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
22	<a href="#">c3fpkB_</a>	Alignment	not modelled	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
23	<a href="#">c5vj7B_</a>	Alignment	not modelled	100.0	21	<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)
24	<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
25	<a href="#">c1fncA_</a>	Alignment	not modelled	100.0	24	<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
26	<a href="#">c4b4dA_</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> crystal structure of fad-containing ferredoxin-nadp reductase from2 xanthomonas axonopodis pv. citri
27	<a href="#">c5tr9A_</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 fad
28	<a href="#">c1qgyA_</a>	Alignment	not modelled	100.0	25	<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)

29	<a href="#">c1a8pA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph\;ferredoxin oxidoreductase; <b>PDBTitle:</b> ferredoxin reductase from azotobacter vinelandii
30	<a href="#">c1qfjD</a>	Alignment	not modelled	100.0	18	<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
31	<a href="#">c2b5oA</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin--nadp reductase; <b>PDBTitle:</b> ferredoxin-nadp reductase
32	<a href="#">c5thxA</a>	Alignment	not modelled	100.0	17	<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
33	<a href="#">c1jb9A</a>	Alignment	not modelled	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 the ferredoxin:nadp+ reductase from maize root at2 1.7 angstroms
34	<a href="#">c1cneA</a>	Alignment	not modelled	100.0	24	<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
35	<a href="#">c4f7dA</a>	Alignment	not modelled	100.0	17	<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
36	<a href="#">c5o0xA</a>	Alignment	not modelled	100.0	22	<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)
37	<a href="#">c4yhbA</a>	Alignment	not modelled	100.0	18	<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
38	<a href="#">c2rc5D</a>	Alignment	not modelled	100.0	24	<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
39	<a href="#">c6gehA</a>	Alignment	not modelled	100.0	13	<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.
40	<a href="#">c6k2IA</a>	Alignment	not modelled	100.0	12	<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="#">c2gpjA</a>	Alignment	not modelled	100.0	16	<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="#">c1ddiA</a>	Alignment	not modelled	99.9	26	<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	99.9	23	<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="#">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
45	<a href="#">c1tllA</a>	Alignment	not modelled	99.9	20	<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.
46	<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
47	<a href="#">c1f20A</a>	Alignment	not modelled	99.9	21	<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.
48	<a href="#">d1tvca2</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> Aromatic dioxygenase reductase-like
49	<a href="#">d1cqxa3</a>	Alignment	not modelled	99.9	29	<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
50	<a href="#">d1gvha3</a>	Alignment	not modelled	99.9	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> Flavo-hemoglobin, C-terminal domain
51	<a href="#">d1ep3b2</a>	Alignment	not modelled	99.9	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> Dihydroorotate dehydrogenase B, PyrK subunit
52	<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
53	<a href="#">c3oftA</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadph--cytochrome p450 reductase;

53	<a href="#">c3qf1A</a>	Alignment	not modelled	99.9	18	<b>PDBTitle:</b> crystal structure of nadph-cytochrome p450 reductase (fad/nadph domain2 and r457h mutant)
54	<a href="#">d1qfja2</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
55	<a href="#">c4n58A</a>	Alignment	not modelled	99.9	28	<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
56	<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
57	<a href="#">d2piaa2</a>	Alignment	not modelled	99.9	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> Aromatic dioxygenase reductase-like
58	<a href="#">d1doia</a>	Alignment	not modelled	99.9	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
59	<a href="#">d2piaa3</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
60	<a href="#">d1umka2</a>	Alignment	not modelled	99.9	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="#">d1krha2</a>	Alignment	not modelled	99.9	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> Aromatic dioxygenase reductase-like
62	<a href="#">d1a70a</a>	Alignment	not modelled	99.9	30	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
63	<a href="#">d1qx4a2</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> Reductases
64	<a href="#">d2cnda2</a>	Alignment	not modelled	99.9	33	<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="#">d1fxia</a>	Alignment	not modelled	99.9	27	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
66	<a href="#">d1e0za</a>	Alignment	not modelled	99.8	27	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
67	<a href="#">d1iuea</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
68	<a href="#">d1frra</a>	Alignment	not modelled	99.8	30	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
69	<a href="#">c2bpoA</a>	Alignment	not modelled	99.8	20	<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.
70	<a href="#">d1awda</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
71	<a href="#">d1offa</a>	Alignment	not modelled	99.8	29	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
72	<a href="#">d1pfda</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
73	<a href="#">d1czpa</a>	Alignment	not modelled	99.8	35	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
74	<a href="#">d1wria</a>	Alignment	not modelled	99.8	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
75	<a href="#">d1frda</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
76	<a href="#">d1gaqb</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
77	<a href="#">c4itkA</a>	Alignment	not modelled	99.8	29	<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
78	<a href="#">d2cjoa</a>	Alignment	not modelled	99.8	33	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
79	<a href="#">d1a8pa2</a>	Alignment	not modelled	99.8	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
80	<a href="#">d4fxca</a>	Alignment	not modelled	99.8	33	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like

				Family:2Fe-2S ferredoxin-related		
81	<a href="#">d1gvha2</a>	Alignment	not modelled	99.8	31	<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
82	<a href="#">d1ndha2</a>	Alignment	not modelled	99.8	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
83	<a href="#">d2bmwa2</a>	Alignment	not modelled	99.8	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
84	<a href="#">c6j7aB_</a>	Alignment	not modelled	99.8	17	<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)
85	<a href="#">d2piaa1</a>	Alignment	not modelled	99.8	32	<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
86	<a href="#">d1jq4a_</a>	Alignment	not modelled	99.8	22	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin domains from multidomain proteins
87	<a href="#">c3a1fA_</a>	Alignment	not modelled	99.8	25	<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)
88	<a href="#">d1fdra2</a>	Alignment	not modelled	99.8	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
89	<a href="#">d1jb9a2</a>	Alignment	not modelled	99.7	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
90	<a href="#">d1qfza2</a>	Alignment	not modelled	99.7	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
91	<a href="#">d1gawa2</a>	Alignment	not modelled	99.7	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
92	<a href="#">d1krha3</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 domains from multidomain proteins
93	<a href="#">d1fnda2</a>	Alignment	not modelled	99.7	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
94	<a href="#">c5frtC_</a>	Alignment	not modelled	99.7	24	<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
95	<a href="#">d1fdra1</a>	Alignment	not modelled	99.7	33	<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
96	<a href="#">d1cqxa2</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
97	<a href="#">c3lrxC_</a>	Alignment	not modelled	99.7	19	<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
98	<a href="#">d1f20a2</a>	Alignment	not modelled	99.7	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> NADPH-cytochrome p450 reductase-like
99	<a href="#">d1qx4a1</a>	Alignment	not modelled	99.7	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
100	<a href="#">d1krha1</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
101	<a href="#">d2bmwa1</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
102	<a href="#">c3zyyX_</a>	Alignment	not modelled	99.7	26	<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
103	<a href="#">d1ddga2</a>	Alignment	not modelled	99.7	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> NADPH-cytochrome p450 reductase-like
104	<a href="#">d1a8pa1</a>	Alignment	not modelled	99.7	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
105	<a href="#">d1umka1</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
106	<a href="#">d1sm4a2</a>	Alignment	not modelled	99.7	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
107	<a href="#">d1tvca1</a>	Alignment	not modelled	99.7	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
108	<a href="#">d1ja1a3</a>	Alignment	not modelled	99.7	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> NADPH-cytochrome p450 reductase-like
109	<a href="#">d2cnda1</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
110	<a href="#">d1sm4a1</a>	Alignment	not modelled	99.6	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
111	<a href="#">d1ndha1</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
112	<a href="#">d1gawa1</a>	Alignment	not modelled	99.6	28	<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
113	<a href="#">d1ep3b1</a>	Alignment	not modelled	99.6	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
114	<a href="#">d1fnda1</a>	Alignment	not modelled	99.6	28	<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="#">d1qfja1</a>	Alignment	not modelled	99.6	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
116	<a href="#">c3ah7A</a>	Alignment	not modelled	99.6	19	<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) from <i>Pseudomonas putida</i> JCM 20004
117	<a href="#">d1qfza1</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
118	<a href="#">d1i7ha</a>	Alignment	not modelled	99.5	21	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> 2Fe-2S ferredoxin-like <b>Family:</b> 2Fe-2S ferredoxin-related
119	<a href="#">c2mjdA</a>	Alignment	not modelled	99.4	24	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> adrenodoxin homolog, mitochondrial; <b>PDBTitle:</b> oxidized yeast adrenodoxin homolog 1
120	<a href="#">c2y5cB</a>	Alignment	not modelled	99.4	23	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> adrenodoxin-like protein, mitochondrial; <b>PDBTitle:</b> structure of human ferredoxin 2 (fdx2) in complex with 2Fe2S2 cluster