Phyre^2

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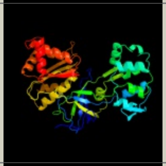
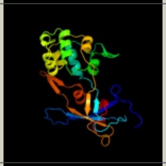
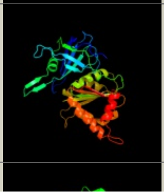
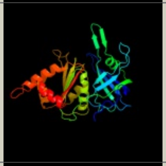
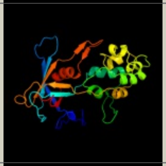
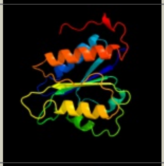
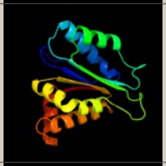
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1j9zB_	Alignment		100.0	33	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nadph-cytochrome p450 reductase; **PDBTitle:** cypor-w677g
2	c2bpoA_	Alignment		100.0	32	**PDB header:**reductase **Chain:** A: **PDB Molecule:**nadph-cytochrom p450 reductase; **PDBTitle:** crystal structure of the yeast cpr triple mutant: d74g,2 y75f, k78a.
3	c1tllA_	Alignment		100.0	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase, brain; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
4	c1ddiA_	Alignment		100.0	99	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**sulfite reductase [nadph] flavoprotein alpha- **PDBTitle:** crystal structure of sir-fp60
5	c3qftA_	Alignment		100.0	34	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph--cytochrome p450 reductase; **PDBTitle:** crystal structure of nadph-cytochrome p450 reductase (fad/nadph domain2 and r457h mutant)
6	c2qtzA_	Alignment		100.0	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methionine synthase reductase; **PDBTitle:** crystal structure of the nadp+-bound fad-containing fnr-like module of2 human methionine synthase reductase
7	c1f20A_	Alignment		100.0	35	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitric-oxide synthase; **PDBTitle:** crystal structure of rat neuronal nitric-oxide synthase fad/nadp+2 domain at 1.9a resolution.
8	c1jb9A_	Alignment		100.0	32	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** crystal structure of the ferredoxin:nadp+ reductase from maize root at2 1.7 angstroms
9	c2rc5D_	Alignment		100.0	26	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** refined structure of fnr from leptospira interrogans
10	d1ddga1	Alignment		100.0	100	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
11	c2b5oA_	Alignment		100.0	30	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp reductase; **PDBTitle:** ferredoxin-nadp reductase

12	c1fncA_	Alignment		100.0	31	**PDB header:**oxidoreductase (nadp+(a),ferredoxin(a)) **Chain:** A: **PDB Molecule:**ferredoxin-nadp+ reductase; **PDBTitle:** refined crystal structure of spinach ferredoxin reductase2 at 1.7 angstroms resolution: oxidized, reduced, and 2'-3 phospho-5'-amp bound states
13	c1qgyA_	Alignment		100.0	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ferredoxin--nadp+ reductase; **PDBTitle:** ferredoxin:nadp+ reductase mutant with lys 75 replaced by glu (k75e)
14	d1ja1a1	Alignment		100.0	28	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
15	d1f20a1	Alignment		100.0	29	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**NADPH-cytochrome p450 reductase FAD-binding domain-like
16	c3hr4C_	Alignment		100.0	30	**PDB header:**oxidoreductase/metal binding protein **Chain:** C: **PDB Molecule:**nitric oxide synthase, inducible; **PDBTitle:** human inos reductase and calmodulin complex
17	d1ja1a2	Alignment		100.0	26	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
18	d1ddga2	Alignment		100.0	99	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
19	d1tlla2	Alignment		100.0	33	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
20	d1ja1a3	Alignment		100.0	47	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
21	c2ok8D_	Alignment	not modelled	100.0	27	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**putative ferredoxin--nadp reductase; **PDBTitle:** ferredoxin-nadp+ reductase from plasmodium falciparum
22	d1b1ca_	Alignment	not modelled	100.0	26	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
23	d1f20a2	Alignment	not modelled	100.0	43	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**NADPH-cytochrome p450 reductase-like
24	d1ykga1	Alignment	not modelled	100.0	99	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Cytochrome p450 reductase N-terminal domain-like
25	c1bvyF_	Alignment	not modelled	100.0	19	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**protein (cytochrome p450 bm-3); **PDBTitle:** complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
26	d1bvyf_	Alignment	not modelled	100.0	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
27	d1jb9a2	Alignment	not modelled	100.0	38	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
28	d1fnda2	Alignment	not modelled	100.0	34	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
29	d1gawa2	Alignment	not modelled	100.0	33	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain

						Family: Reductases
30	d2bmwa2	Alignment	not modelled	100.0	33	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
31	d1sm4a2	Alignment	not modelled	100.0	33	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
32	c1krhA_	Alignment	not modelled	100.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**benzoate 1,2-dioxygenase reductase; **PDBTitle:** x-ray stucture of benzoate dioxygenase reductase
33	d1qfza2	Alignment	not modelled	100.0	34	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
34	c1cqxB_	Alignment	not modelled	100.0	20	**PDB header:**lipid binding protein **Chain:** B: **PDB Molecule:**flavohemoprotein; **PDBTitle:** crystal structure of the flavohemoglobin from alcaligenes eutrophus at2 1.75 a resolution
35	c2hnbA_	Alignment	not modelled	100.0	25	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**protein mioc; **PDBTitle:** solution structure of a bacterial holo-flavodoxin
36	c1gvhA_	Alignment	not modelled	100.0	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**flavohemoprotein; **PDBTitle:** the x-ray structure of ferric escherichia coli2 flavohemoglobin reveals an unespected geometry of the3 distal heme pocket
37	d1jb9a1	Alignment	not modelled	99.9	27	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
38	c2r6hC_	Alignment	not modelled	99.9	16	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**nadh:ubiquinone oxidoreductase, na translocating, f **PDBTitle:** 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
39	c2eixA_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-cytochrome b5 reductase; **PDBTitle:** the structure of physarum polycephalum cytochrome b5 reductase
40	c2bgjB_	Alignment	not modelled	99.9	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp(h) reductase; **PDBTitle:** x-ray structure of the ferredoxin-nadp(h) reductase from2 rhodobacter capsulatus at 2.1 angstroms
41	d1qfza1	Alignment	not modelled	99.9	28	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
42	d1yoba1	Alignment	not modelled	99.9	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
43	c1a8pA_	Alignment	not modelled	99.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadph\:ferredoxin oxidoreductase; **PDBTitle:** ferredoxin reductase from azotobacter vinelandii
44	d1f4pa_	Alignment	not modelled	99.9	24	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
45	c1qfjD_	Alignment	not modelled	99.9	22	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein (flavin reductase); **PDBTitle:** crystal structure of nad(p)h:flavin oxidoreductase from escherichia2 coli
46	c3f6sI_	Alignment	not modelled	99.9	22	**PDB header:**electron transport **Chain:** I: **PDB Molecule:**flavodoxin; **PDBTitle:** desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin2 alternate conformers
47	c1umkA_	Alignment	not modelled	99.9	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nadh-cytochrome b5 reductase; **PDBTitle:** the structure of human erythrocyte nadh-cytochrome b52 reductase
48	c1tvcA_	Alignment	not modelled	99.9	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**methane monooxygenase component c; **PDBTitle:** fad and nadh binding domain of methane monooxygenase2 reductase from methylococcus capsulatus (bath)
49	c2wc1A_	Alignment	not modelled	99.9	20	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin; **PDBTitle:** three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
50	d2fcra_	Alignment	not modelled	99.9	22	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
51	c3fpkB_	Alignment	not modelled	99.9	19	**PDB header:**flavoprotein, oxidoreductase **Chain:** B: **PDB Molecule:**ferredoxin-nadp reductase; **PDBTitle:** crystal structure of ferredoxin-nadp reductase from salmonella2 typhimurium
52	d1czna_	Alignment	not modelled	99.9	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
53	c1ep3B_	Alignment	not modelled	99.9	22	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dihydroorotate dehydrogenase b (pyrk subunit); **PDBTitle:** crystal structure of lactococcus lactis dihydroorotate dehydrogenase2 b. data collected under cryogenic conditions.
54	d1ag9a_	Alignment	not modelled	99.9	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related

55	d1oboa_	Alignment	not modelled	99.9	21	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
56	d1rlja_	Alignment	not modelled	99.9	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavoprotein NrdI
57	c1cneA_	Alignment	not modelled	99.9	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**nitrate reductase; **PDBTitle:** 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
58	c2piaA_	Alignment	not modelled	99.9	23	**PDB header:**reductase **Chain:** A: **PDB Molecule:**phthalate dioxygenase reductase; **PDBTitle:** phthalate dioxygenase reductase: a modular structure for2 electron transfer from pyridine nucleotides to [2fe-2s]
59	d1fuea_	Alignment	not modelled	99.9	24	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
60	c2x2oA_	Alignment	not modelled	99.9	20	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**nrdi protein; **PDBTitle:** the flavoprotein nrdi from bacillus cereus with the2 initially oxidized fmn cofactor in an intermediate3 radiation reduced state
61	d1gawa1	Alignment	not modelled	99.8	28	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
62	c3n39D_	Alignment	not modelled	99.8	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**protein nrdi; **PDBTitle:** ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdi
63	d1tvca2	Alignment	not modelled	99.8	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
64	d1sm4a1	Alignment	not modelled	99.8	26	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
65	d1fdra2	Alignment	not modelled	99.8	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
66	d1qfja2	Alignment	not modelled	99.8	16	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
67	d1a8pa2	Alignment	not modelled	99.8	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
68	d1cqxa3	Alignment	not modelled	99.7	14	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
69	d1umka2	Alignment	not modelled	99.7	17	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
70	d1krha2	Alignment	not modelled	99.7	21	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
71	d1gvha3	Alignment	not modelled	99.7	14	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Flavohemoglobin, C-terminal domain
72	d2bmwa1	Alignment	not modelled	99.7	26	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
73	d5nula_	Alignment	not modelled	99.7	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
74	d2fz5a1	Alignment	not modelled	99.7	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
75	d2piaa2	Alignment	not modelled	99.7	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Aromatic dioxygenase reductase-like
76	d2cnda2	Alignment	not modelled	99.7	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
77	d1fnda1	Alignment	not modelled	99.7	29	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
78	d1qx4a2	Alignment	not modelled	99.7	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
79	d1ndha2	Alignment	not modelled	99.6	17	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Reductases
80	c3hlyA_	Alignment	not modelled	99.6	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2

						synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
81	d1e5da1	Alignment	not modelled	99.5	16	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
82	c2gpjA_	Alignment	not modelled	99.5	15	**PDB header:**fad-binding protein **Chain:** A: **PDB Molecule:**siderophore-interacting protein; **PDBTitle:** crystal structure of a siderophore-interacting protein (sputcn32_0076)2 from shewanella putrefaciens cn-32 at 2.20 a resolution
83	d1ep3b2	Alignment	not modelled	99.5	18	**Fold:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Superfamily:**Ferredoxin reductase-like, C-terminal NADP-linked domain **Family:**Dihydroorotate dehydrogenase B, PyrK subunit
84	d1vmea1	Alignment	not modelled	99.5	19	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
85	c1vmeB_	Alignment	not modelled	99.5	19	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**flavoprotein; **PDBTitle:** crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
86	c2ohiB_	Alignment	not modelled	99.5	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**type a flavoprotein fpra; **PDBTitle:** crystal structure of coenzyme f420h2 oxidase (fpra), a diiron2 flavoprotein, reduced state
87	c3a1fA_	Alignment	not modelled	99.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome b-245 heavy chain; **PDBTitle:** the crystal structure of nadph binding domain of gp91(phox)
88	c3lrxC_	Alignment	not modelled	99.4	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**putative hydrogenase; **PDBTitle:** crystal structure of the c-terminal domain (residues 78-226)2 of pf1911 hydrogenase from pyrococcus furiosus, northeast3 structural genomics consortium target pfr246a
89	d1ycga1	Alignment	not modelled	99.4	18	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Flavodoxin-related
90	c2q9uB_	Alignment	not modelled	99.3	13	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**a-type flavoprotein; **PDBTitle:** crystal structure of the flavodiiron protein from giardia2 intestinalis
91	c1ychD_	Alignment	not modelled	99.3	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**nitric oxide reductase; **PDBTitle:** x-ray crystal structures of moorella thermoacetica fpra.2 novel diiron site structure and mechanistic insights into3 a scavenging nitric oxide reductase
92	c3fniA_	Alignment	not modelled	99.2	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
93	d2arka1	Alignment	not modelled	99.2	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
94	c1e5dA_	Alignment	not modelled	99.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubredoxin\:oxygen oxidoreductase; **PDBTitle:** rubredoxin oxygen:oxidoreductase (roo) from anaerobe2 desulfovibrio gigas
95	d2a5la1	Alignment	not modelled	98.9	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
96	c3d7nA_	Alignment	not modelled	98.7	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**flavodoxin, wrba-like protein; **PDBTitle:** the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
97	d1ydga_	Alignment	not modelled	98.7	17	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**WrbA-like
98	c2zkiH_	Alignment	not modelled	98.6	12	**PDB header:**transcription **Chain:** H: **PDB Molecule:**199aa long hypothetical trp repressor binding **PDBTitle:** crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
99	c3b6iB_	Alignment	not modelled	98.6	19	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**flavoprotein wrba; **PDBTitle:** wrba from escherichia coli, native structure
100	c3klbA_	Alignment	not modelled	98.5	15	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative flavoprotein; **PDBTitle:** crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
101	d1fdra1	Alignment	not modelled	98.2	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
102	d1ep3b1	Alignment	not modelled	98.2	26	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
103	d2cnda1	Alignment	not modelled	98.1	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
104	d1a8pa1	Alignment	not modelled	98.1	21	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
105	d2piaa1	Alignment	not modelled	98.1	27	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like

						Family: Ferredoxin reductase FAD-binding domain-like
106	c3edoA_	Alignment	not modelled	98.0	16	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**putative trp repressor binding protein; **PDBTitle:** crystal structure of flavoprotein in complex with fmn2 (yp_193882.1) from lactobacillus acidophilus ncfm at 1.203 a resolution
107	d1krha1	Alignment	not modelled	98.0	25	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
108	d1tvca1	Alignment	not modelled	97.9	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
109	d1cqxa2	Alignment	not modelled	97.9	27	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
110	c2q62A_	Alignment	not modelled	97.9	17	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**arsh; **PDBTitle:** crystal structure of arsh from sinorhizobium meliloti
111	d1qfja1	Alignment	not modelled	97.9	31	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
112	d1qx4a1	Alignment	not modelled	97.8	20	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
113	d1gvha2	Alignment	not modelled	97.7	24	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
114	d1umka1	Alignment	not modelled	97.7	19	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Riboflavin synthase domain-like **Family:**Ferredoxin reductase FAD-binding domain-like
115	c3f2vA_	Alignment	not modelled	97.7	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**general stress protein 14; **PDBTitle:** crystal structure of the general stress protein 142 (tde0354) in complex with fmn from treponema denticola,3 northeast structural genomics consortium target tdr58.
116	d2qwxa1	Alignment	not modelled	97.6	13	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
117	d1t5ba_	Alignment	not modelled	97.6	8	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
118	d1rtta_	Alignment	not modelled	97.6	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase
119	c3k1yE_	Alignment	not modelled	97.5	14	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**oxidoreductase; **PDBTitle:** x-ray structure of oxidoreductase from corynebacterium2 diphtheriae. orthorombic crystal form, northeast structural3 genomics consortium target cdr100d
120	d1t0ia_	Alignment	not modelled	97.5	12	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**NADPH-dependent FMN reductase