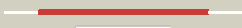



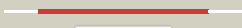
















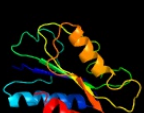






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3052c_(nrdI)_3414243_3414695
Date	Thu Aug 8 16:20:22 BST 2019
Unique Job ID	affa421d3e1da686

Detailed template information

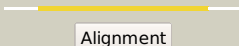
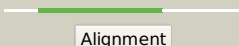
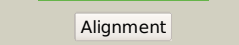


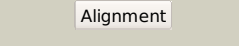
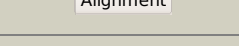
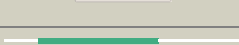


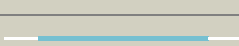


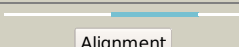

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c6ebqB_</a>	 Alignment		100.0	48	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> protein nrdi; <b>PDBTitle:</b> crystal structure of the flavoprotein nrdi from aerococcus urinae in2 oxidized form
2	<a href="#">d1rlja_</a>	 Alignment		100.0	28	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavoprotein NrdI
3	<a href="#">c3n39D_</a>	 Alignment		100.0	57	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> protein nrdi; <b>PDBTitle:</b> ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdi
4	<a href="#">c2x2oA_</a>	 Alignment		100.0	36	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> nrdi protein; <b>PDBTitle:</b> the flavoprotein nrdi from bacillus cereus with the initially oxidized2 fmn cofactor in an intermediate radiation reduced state
5	<a href="#">c4n82B_</a>	 Alignment		100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> ribonucleotide reductase; <b>PDBTitle:</b> x-ray crystal structure of streptococcus sanguinis nrdiox
6	<a href="#">c6j7aB_</a>	 Alignment		99.9	18	<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)
7	<a href="#">c1tIIA_</a>	 Alignment		99.9	13	<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.
8	<a href="#">c6efvA_</a>	 Alignment		99.9	14	<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
9	<a href="#">c3hr4C_</a>	 Alignment		99.9	16	<b>PDB header:</b> oxidoreductase/metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> nitric oxide synthase, inducible; <b>PDBTitle:</b> human inos reductase and calmodulin complex
10	<a href="#">c2bpoA_</a>	 Alignment		99.9	15	<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.
11	<a href="#">c1j9zB_</a>	 Alignment		99.9	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph-cytochrome p450 reductase; <b>PDBTitle:</b> cypor-w677g

12	<a href="#">d1tlla2</a>	Alignment		99.9	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Cytochrome p450 reductase N-terminal domain-like
13	<a href="#">c5gxuA</a>	Alignment		99.9	17	<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
14	<a href="#">d1bvyf</a>	Alignment		99.9	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
15	<a href="#">c1bvvyF</a>	Alignment		99.9	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> protein (cytochrome p450 bm-3); <b>PDBTitle:</b> complex of the heme and fmn-binding domains of the2 cytochrome p450(bm-3)
16	<a href="#">c2m6rA</a>	Alignment		99.9	13	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> apo_yqca
17	<a href="#">d1ja1a2</a>	Alignment		99.9	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Cytochrome p450 reductase N-terminal domain-like
18	<a href="#">d1b1ca</a>	Alignment		99.9	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Cytochrome p450 reductase N-terminal domain-like
19	<a href="#">c4h2dB</a>	Alignment		99.9	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph-dependent diflavin oxidoreductase 1; <b>PDBTitle:</b> crystal structure of ndor1
20	<a href="#">d1yoba1</a>	Alignment		99.9	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
21	<a href="#">c5b3kA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pa3435; <b>PDBTitle:</b> c101a mutant of flavodoxin from pseudomonas aeruginosa
22	<a href="#">d1czna</a>	Alignment	not modelled	99.9	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
23	<a href="#">d1ykga1</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Cytochrome p450 reductase N-terminal domain-like
24	<a href="#">d2fcra</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
25	<a href="#">c2wc1A</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> three-dimensional structure of the nitrogen fixation2 flavodoxin (niff) from rhodobacter capsulatus at 2.2 a
26	<a href="#">d1oboa</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
27	<a href="#">c5vegC</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> electron transport <b>Chain:</b> C: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> structure of a short-chain flavodoxin associated with a non-canonical2 pdu bacterial microcompartment
28	<a href="#">c5ljiA</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> streptococcus pneumonia tigr4 flavodoxin: structural and biophysical2 characterization of a novel drug target
						<b>PDB header:</b> electron transport

29	<a href="#">c4oxxA</a>	Alignment	not modelled	99.8	11	<b>Chain:</b> A; <b>PDB Molecule:</b> cindoxin; <b>PDBTitle:</b> crystal structure of cindoxin, surface entropy reduction mutant
30	<a href="#">c2hnbA</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> protein mioc; <b>PDBTitle:</b> solution structure of a bacterial holo-flavodoxin
31	<a href="#">c6ohkA</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> crystal structure of fusobacterium nucleatum flavodoxin mutant k13g2 bound to flavin mononucleotide
32	<a href="#">c6fsiA</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> crystal structure of semiquinone flavodoxin 1 from bacillus cereus2 (1.32 a resolution)
33	<a href="#">d1fuea</a>	Alignment	not modelled	99.8	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
34	<a href="#">d1ag9a</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
35	<a href="#">c6gaqB</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> crystal structure of oxidised flavodoxin 2 from bacillus cereus
36	<a href="#">c2mtbA</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> flavodoxin-2; <b>PDBTitle:</b> solution structure of apo_fldb
37	<a href="#">c3f6sl</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> electron transport <b>Chain:</b> I; <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> desulfovibrio desulfuricans (atcc 29577) oxidized flavodoxin alternate2 conformers
38	<a href="#">c4heqB</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> the crystal structure of flavodoxin from desulfovibrio gigas
39	<a href="#">d1f4pa</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
40	<a href="#">d2fz5a1</a>	Alignment	not modelled	99.6	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
41	<a href="#">d1e5da1</a>	Alignment	not modelled	99.5	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
42	<a href="#">d1vmea1</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
43	<a href="#">c5widB</a>	Alignment	not modelled	99.5	10	<b>PDB header:</b> flavoprotein <b>Chain:</b> B; <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> structure of a flavodoxin from the domain archaea
44	<a href="#">c4icia</a>	Alignment	not modelled	99.5	17	<b>PDB header:</b> flavoprotein <b>Chain:</b> A; <b>PDB Molecule:</b> putative flavoprotein; <b>PDBTitle:</b> crystal structure of a putative flavoprotein (bacegg_01620) from bacteroides eggerthii dsm 20697 at 1.40 a resolution
45	<a href="#">d5nula</a>	Alignment	not modelled	99.5	5	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
46	<a href="#">c3hlyA</a>	Alignment	not modelled	99.5	10	<b>PDB header:</b> flavoprotein <b>Chain:</b> A; <b>PDB Molecule:</b> flavodoxin-like domain; <b>PDBTitle:</b> crystal structure of the flavodoxin-like domain from synechococcus sp2 q5mzp6_sypn6 protein. northeast structural genomics consortium target3 snr135d.
47	<a href="#">c1vmeB</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> electron transport <b>Chain:</b> B; <b>PDB Molecule:</b> flavoprotein; <b>PDBTitle:</b> crystal structure of flavoprotein (tm0755) from thermotoga maritima at2 1.80 a resolution
48	<a href="#">c3kibA</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> flavoprotein <b>Chain:</b> A; <b>PDB Molecule:</b> putative flavoprotein; <b>PDBTitle:</b> crystal structure of putative flavoprotein in complex with fmn2 (yp_213683.1) from bacteroides fragilis nctc 9343 at 1.75 a3 resolution
49	<a href="#">c3fniA</a>	Alignment	not modelled	99.4	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> putative diflavin flavoprotein a 3; <b>PDBTitle:</b> crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
50	<a href="#">c6h0cA</a>	Alignment	not modelled	99.4	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> putative diflavin flavoprotein a 3; <b>PDBTitle:</b> flv1 flavodiiron core from synechocystis sp. pcc6803
51	<a href="#">c4j8pA</a>	Alignment	not modelled	99.4	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> A; <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> crystal structure of a putative flavoprotein (bacuni_04544) from bacteroides uniformis atcc 8492 at 1.50 a resolution
52	<a href="#">d1ycga1</a>	Alignment	not modelled	99.4	5	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
53	<a href="#">c1ychD</a>	Alignment	not modelled	99.3	6	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> nitric oxide reductase; <b>PDBTitle:</b> x-ray crystal structures of moorella thermoacetica fpra. novel diiron2 site structure and mechanistic insights into a scavenging nitric3 oxide reductase
54	<a href="#">c2ohiB</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> type a flavoprotein fpra; <b>PDBTitle:</b> crystal structure of coenzyme f420h2 oxidase (fpra), a

						diiron2 flavoprotein, reduced state
55	<a href="#">d2arka1</a>	Alignment	not modelled	99.3	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
56	<a href="#">c2q9uB</a>	Alignment	not modelled	99.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> α-type flavoprotein; <b>PDBTitle:</b> crystal structure of the flavodiiron protein from giardia2 intestinalis
57	<a href="#">c3edoA</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> putative trp repressor binding protein; <b>PDBTitle:</b> crystal structure of flavoprotein in complex with fmn (yp_193882.1)2 from lactobacillus acidophilus ncmf at 1.20 a resolution
58	<a href="#">c1e5dA</a>	Alignment	not modelled	99.2	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin\oxygen oxidoreductase; <b>PDBTitle:</b> rubredoxin oxygen:oxidoreductase (roo) from anaerobe desulfovibrio2 gigas
59	<a href="#">c4d02A</a>	Alignment	not modelled	99.2	9	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> anaerobic nitric oxide reductase flavorubredoxin; <b>PDBTitle:</b> the crystallographic structure of flavorubredoxin from escherichia2 coli
60	<a href="#">c3d7nA</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin, wrba-like protein; <b>PDBTitle:</b> the crystal structure of the flavodoxin, wrba-like protein from2 agrobacterium tumefaciens
61	<a href="#">d2a5la1</a>	Alignment	not modelled	99.2	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
62	<a href="#">c5f4bB</a>	Alignment	not modelled	99.1	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p)h dehydrogenase (quinone); <b>PDBTitle:</b> structure of b. abortus wrba-related protein a (wrpa)
63	<a href="#">c3b6iB</a>	Alignment	not modelled	99.0	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> flavoprotein wrba; <b>PDBTitle:</b> wrba from escherichia coli, native structure
64	<a href="#">c5mp4C</a>	Alignment	not modelled	98.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> protoplast secreted protein 2; <b>PDBTitle:</b> the structure of pst2p from saccharomyces cerevisiae
65	<a href="#">c4lafB</a>	Alignment	not modelled	98.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad(p)h dehydrogenase (quinone); <b>PDBTitle:</b> crystal structure of pnbp complex with fmn
66	<a href="#">c2zkiH</a>	Alignment	not modelled	98.8	14	<b>PDB header:</b> transcription <b>Chain:</b> H: <b>PDB Molecule:</b> 199aa long hypothetical trp repressor binding <b>PDBTitle:</b> crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
67	<a href="#">d1ydga</a>	Alignment	not modelled	98.7	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
68	<a href="#">c4ptzC</a>	Alignment	not modelled	97.7	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> fmn reductase ssue; <b>PDBTitle:</b> crystal structure of the escherichia coli alkanesulfonate fmn2 reductase ssue in fmn-bound form
69	<a href="#">d1t5ba</a>	Alignment	not modelled	97.6	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
70	<a href="#">d1rlia</a>	Alignment	not modelled	97.6	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Hypothetical protein YwqN
71	<a href="#">c4c0xA</a>	Alignment	not modelled	97.5	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase 1; <b>PDBTitle:</b> the crystal structure of ppazor in complex with anthraquinone-2-2 sulfonate
72	<a href="#">c3svlB</a>	Alignment	not modelled	97.4	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> protein yief; <b>PDBTitle:</b> structural basis of the improvement of chrr - a multi-purpose enzyme
73	<a href="#">c2hpaA</a>	Alignment	not modelled	97.4	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase; <b>PDBTitle:</b> crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
74	<a href="#">c2q62A</a>	Alignment	not modelled	97.4	10	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> arsh; <b>PDBTitle:</b> crystal structure of arsh from sinorhizobium meliloti
75	<a href="#">c6dxdD</a>	Alignment	not modelled	97.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase; <b>PDBTitle:</b> the crystal structure of an fmn-dependent nadh-azoreductase from2 klebsiella pneumoniae
76	<a href="#">c3u7rB</a>	Alignment	not modelled	97.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph-dependent fmn reductase; <b>PDBTitle:</b> ferb - flavoenzyme nad(p)h:(acceptor) oxidoreductase (ferb) from2 paracoccus denitrificans
77	<a href="#">c3f2vA</a>	Alignment	not modelled	97.2	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> general stress protein 14; <b>PDBTitle:</b> crystal structure of the general stress protein 14 (tde0354) in2 complex with fmn from treponema denticola, northeast structural3 genomics consortium target tdr58.
78	<a href="#">c3lcmB</a>	Alignment	not modelled	97.2	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> putative oxidoreductase; <b>PDBTitle:</b> crystal structure of smu.1420 from streptococcus mutans ua159
79	<a href="#">c4c76A</a>	Alignment	not modelled	97.1	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fmn reductase (nadph); <b>PDBTitle:</b> crystal structure of the fmn-reductase msue from pseudomonas putida2 kt2440.
						<b>Fold:</b> Flavodoxin-like

80	<a href="#">d1sqsa_</a>	Alignment	not modelled	97.1	8	<b>Superfamily:</b> Flavoproteins <b>Family:</b> Hypothetical protein SP1951
81	<a href="#">c3u7iB_</a>	Alignment	not modelled	97.0	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase 1; <b>PDBTitle:</b> the crystal structure of fmn-dependent nadh-azoreductase 1 (gbaa0966)2 from bacillus anthracis str. ames ancestor
82	<a href="#">c2v9cA_</a>	Alignment	not modelled	96.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase 1; <b>PDBTitle:</b> x-ray crystallographic structure of a pseudomonas2 aeruginosa azoreductase in complex with methyl red.
83	<a href="#">d1t0ia_</a>	Alignment	not modelled	96.8	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
84	<a href="#">d2z98a1</a>	Alignment	not modelled	96.7	9	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
85	<a href="#">c3w7aD_</a>	Alignment	not modelled	96.7	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase; <b>PDBTitle:</b> crystal structure of azoreductase azrc fin complex with sulfone-2 modified azo dye acid red 88
86	<a href="#">d1rtta_</a>	Alignment	not modelled	96.7	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
87	<a href="#">c4r81C_</a>	Alignment	not modelled	96.6	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nadh dehydrogenase; <b>PDBTitle:</b> nad(p)h:quinone oxidoreductase from methanothermobacter marburgensis
88	<a href="#">c3p0rA_</a>	Alignment	not modelled	96.6	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> azoreductase; <b>PDBTitle:</b> crystal structure of azoreductase from bacillus anthracis str. sterne
89	<a href="#">c3s2yB_</a>	Alignment	not modelled	96.4	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> chromate reductase; <b>PDBTitle:</b> crystal structure of a chromate/uranium reductase from2 gluconacetobacter hansenii
90	<a href="#">d2qwxal</a>	Alignment	not modelled	96.3	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
91	<a href="#">d1nni1_</a>	Alignment	not modelled	96.0	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
92	<a href="#">d1qrda_</a>	Alignment	not modelled	95.9	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
93	<a href="#">c3rpeA_</a>	Alignment	not modelled	95.9	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> modulator of drug activity b; <b>PDBTitle:</b> 1.1 angstrom crystal structure of putative modulator of drug activity2 (mdab) from yersinia pestis co92.
94	<a href="#">c5mjiA_</a>	Alignment	not modelled	95.6	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> bramp domain protein; <b>PDBTitle:</b> crystal structure of rosb with bound intermediate ohc-rp (8-demethyl-2 8-formylriboflavin-5'-phosphate)
95	<a href="#">c5lvaA_</a>	Alignment	not modelled	95.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad(p)h-fmn oxidoreductase; <b>PDBTitle:</b> crystal structure of thermophilic tryptophan halogenase (th-hal)2 enzyme from streptomycin violaceusniger.
96	<a href="#">d1dxqa_</a>	Alignment	not modelled	94.3	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
97	<a href="#">c4gi5B_</a>	Alignment	not modelled	94.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> quinone reductase; <b>PDBTitle:</b> crystal structure of a putative quinone reductase from klebsiella2 pneumoniae (target psi-013613)
98	<a href="#">c2amjD_</a>	Alignment	not modelled	93.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> modulator of drug activity b; <b>PDBTitle:</b> crystal structure of modulator of drug activity b from escherichia2 coli o157:h7
99	<a href="#">c2fzvC_</a>	Alignment	not modelled	93.2	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> putative arsenical resistance protein; <b>PDBTitle:</b> crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
100	<a href="#">c3k1yE_</a>	Alignment	not modelled	93.1	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> oxidoreductase; <b>PDBTitle:</b> x-ray structure of oxidoreductase from corynebacterium diphtheriae.2 orthorombic crystal form, northeast structural genomics consortium3 target cdr100d
101	<a href="#">c3fwvA_</a>	Alignment	not modelled	92.6	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative nad(p)h-dependent fmn reductase; <b>PDBTitle:</b> crystal structure of the q8dwd8_strmu protein from streptococcus2 mutans. northeast structural genomics consortium target smr99.
102	<a href="#">d2fzva1</a>	Alignment	not modelled	88.4	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
103	<a href="#">c2vzha_</a>	Alignment	not modelled	83.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-dependent fmn reductase; <b>PDBTitle:</b> structures of nadh:fmn oxidoreductase (emob)-fmn complex
104	<a href="#">d1d4aa_</a>	Alignment	not modelled	83.3	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
105	<a href="#">c5c4iA_</a>	Alignment	not modelled	77.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> oxalate oxidoreductase subunit alpha; <b>PDBTitle:</b> structure of an oxalate oxidoreductase

106	<a href="#">c3ha2B_</a>	 Alignment	not modelled	72.3	9	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadph-quinone reductase; <b>PDBTitle:</b> crystal structure of protein (nadph-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
107	<a href="#">c3s40C_</a>	 Alignment	not modelled	59.3	13	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> diacylglycerol kinase; <b>PDBTitle:</b> the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
108	<a href="#">d2c42a3</a>	 Alignment	not modelled	50.2	17	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Pyruvate-ferredoxin oxidoreductase, PFOR, domain II
109	<a href="#">c5gqsA_</a>	 Alignment	not modelled	48.0	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> pts galactitol transporter subunit iib; <b>PDBTitle:</b> nmr based solution structure of pts system, galactitol-specific iib2 component from methicillin resistant staphylococcus aureus
110	<a href="#">c2iz6A_</a>	 Alignment	not modelled	45.1	13	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> molybdenum cofactor carrier protein; <b>PDBTitle:</b> structure of the chlamydomonas reinhardtii moco carrier2 protein
111	<a href="#">c4kjeA_</a>	 Alignment	not modelled	42.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glutaredoxin; <b>PDBTitle:</b> atomic resolution structure of pfgrx1
112	<a href="#">d1t1va_</a>	 Alignment	not modelled	41.9	18	<b>Fold:</b> Thioredoxin fold <b>Superfamily:</b> Thioredoxin-like <b>Family:</b> SH3BGR (SH3-binding, glutamic acid-rich protein-like)
113	<a href="#">d1ik6a2</a>	 Alignment	not modelled	40.9	15	<b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Branched-chain alpha-keto acid dehydrogenase beta-subunit, C-terminal-domain
114	<a href="#">c2qv7A_</a>	 Alignment	not modelled	40.1	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diacylglycerol kinase dgkb; <b>PDBTitle:</b> crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
115	<a href="#">d1ozha1</a>	 Alignment	not modelled	40.0	7	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
116	<a href="#">c3c3jA_</a>	 Alignment	not modelled	36.6	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative tagatose-6-phosphate ketose/aldose isomerase; <b>PDBTitle:</b> crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
117	<a href="#">c3eywA_</a>	 Alignment	not modelled	36.2	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> c-terminal domain of glutathione-regulated potassium-efflux <b>PDBTitle:</b> crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
118	<a href="#">c4gmfD_</a>	 Alignment	not modelled	35.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> yersiniabactin biosynthetic protein ybtu; <b>PDBTitle:</b> apo structure of a thiazolinyil imine reductase from yersinia2 enterocolitica (irp3)
119	<a href="#">d2ji7a1</a>	 Alignment	not modelled	34.6	11	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
120	<a href="#">d1ybha1</a>	 Alignment	not modelled	32.0	8	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain