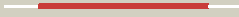






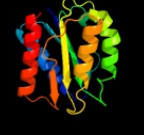






















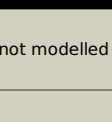


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2771c (- )_3080591_3081043
Date	Wed Aug 7 12:50:43 BST 2019
Unique Job ID	615853097831f5f5

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1ycga1</a>	 Alignment		100.0	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
2	<a href="#">c3fniA_</a>	 Alignment		100.0	12	<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
3	<a href="#">d1e5da1</a>	 Alignment		100.0	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
4	<a href="#">c5widB_</a>	 Alignment		100.0	18	<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
5	<a href="#">c3d7nA_</a>	 Alignment		100.0	19	<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
6	<a href="#">d2arka1</a>	 Alignment		100.0	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
7	<a href="#">c6h0cA_</a>	 Alignment		100.0	13	<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
8	<a href="#">c3hlyA_</a>	 Alignment		100.0	21	<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_synp6 protein. northeast structural genomics consortium target3 snr135d.
9	<a href="#">c2ohiB_</a>	 Alignment		100.0	18	<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
10	<a href="#">c1ychD_</a>	 Alignment		100.0	21	<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
11	<a href="#">d2a5la1</a>	 Alignment		100.0	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like

12	<a href="#">c2q9uB_</a>	Alignment		100.0	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> a-type flavoprotein; <b>PDBTitle:</b> crystal structure of the flavodiiron protein from giardia2 intestinalis
13	<a href="#">c5mp4C_</a>	Alignment		100.0	20	<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
14	<a href="#">c5f4bB_</a>	Alignment		100.0	20	<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)
15	<a href="#">d1vmea1</a>	Alignment		100.0	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
16	<a href="#">c4d02A_</a>	Alignment		100.0	17	<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
17	<a href="#">c3b6iB_</a>	Alignment		100.0	22	<b>PDB header:</b> flavoprotein <b>Chain:</b> B: <b>PDB Molecule:</b> flavoprotein wrba; <b>PDBTitle:</b> wrba from escherichia coli, native structure
18	<a href="#">c1vmeB_</a>	Alignment		99.9	8	<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
19	<a href="#">c4lafB_</a>	Alignment		99.9	25	<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
20	<a href="#">d5nula_</a>	Alignment		99.9	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
21	<a href="#">c6gagB_</a>	Alignment	not modelled	99.9	18	<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
22	<a href="#">c2zkiH_</a>	Alignment	not modelled	99.9	18	<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)
23	<a href="#">d1ydga_</a>	Alignment	not modelled	99.9	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> WrbA-like
24	<a href="#">c6fsiA_</a>	Alignment	not modelled	99.9	18	<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)
25	<a href="#">c5vegC_</a>	Alignment	not modelled	99.9	16	<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
26	<a href="#">c1e5dA_</a>	Alignment	not modelled	99.9	17	<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 desulfobivrio2 gigas
27	<a href="#">d2fz5a1</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
28	<a href="#">c5ljiA_</a>	Alignment	not modelled	99.9	20	<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

29	<a href="#">c3f6sl_</a>	Alignment	not modelled	99.9	20	<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
30	<a href="#">c3klbA_</a>	Alignment	not modelled	99.9	13	<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
31	<a href="#">c4iciA_</a>	Alignment	not modelled	99.9	11	<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) from2 bacteroides eggerthii dsm 20697 at 1.40 a resolution
32	<a href="#">c4heqB_</a>	Alignment	not modelled	99.9	19	<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
33	<a href="#">c4j8pA_</a>	Alignment	not modelled	99.9	12	<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) from2 bacteroides uniformis atcc 8492 at 1.50 a resolution
34	<a href="#">c2hnbA_</a>	Alignment	not modelled	99.9	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
35	<a href="#">d1f4pa_</a>	Alignment	not modelled	99.9	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
36	<a href="#">c3edoA_</a>	Alignment	not modelled	99.8	19	<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
37	<a href="#">c5b3kA_</a>	Alignment	not modelled	99.8	13	<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
38	<a href="#">c2m6rA_</a>	Alignment	not modelled	99.8	12	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> flavodoxin; <b>PDBTitle:</b> apo_yqca
39	<a href="#">c4oxxA_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> electron transport <b>Chain:</b> A; <b>PDB Molecule:</b> cindoxin; <b>PDBTitle:</b> crystal structure of cindoxin, surface entropy reduction mutant
40	<a href="#">c3u7iB_</a>	Alignment	not modelled	99.8	14	<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
41	<a href="#">d1ykga1</a>	Alignment	not modelled	99.8	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Cytochrome p450 reductase N-terminal domain-like
42	<a href="#">d1sqsa_</a>	Alignment	not modelled	99.8	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Hypothetical protein SP1951
43	<a href="#">c4r81C_</a>	Alignment	not modelled	99.8	15	<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
44	<a href="#">c4ptzC_</a>	Alignment	not modelled	99.8	17	<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
45	<a href="#">d1t5ba_</a>	Alignment	not modelled	99.8	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
46	<a href="#">c4h2dB_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> nadh-dependent diflavin oxidoreductase 1; <b>PDBTitle:</b> crystal structure of ndor1
47	<a href="#">c6dxdD_</a>	Alignment	not modelled	99.8	17	<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
48	<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
49	<a href="#">d1oboa_</a>	Alignment	not modelled	99.8	8	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
50	<a href="#">c1bvyF_</a>	Alignment	not modelled	99.8	10	<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)
51	<a href="#">d1bvyf_</a>	Alignment	not modelled	99.8	10	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
52	<a href="#">c3u7rB_</a>	Alignment	not modelled	99.8	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> nadh-dependent fmn reductase; <b>PDBTitle:</b> ferb - flavoenzyme nad(p)h:(acceptor) oxidoreductase (ferb) from2 paracoccus denitrificans
53	<a href="#">d1rlia_</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Hypothetical protein YwqN
54	<a href="#">c3e2uB_</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B; <b>PDB Molecule:</b> chromate reductase;

54	<a href="#">c5zyb</a>	Alignment	not modelled	99.7	15	<b>PDBTitle:</b> crystal structure of a chromate/uranium reductase from2 gluconacetobacter hansenii <b>PDB header:</b> oxidoreductase
55	<a href="#">c2hpaA</a>	Alignment	not modelled	99.7	15	<b>Chain:</b> A: <b>PDB Molecule:</b> fmn-dependent nadh-azoreductase; <b>PDBTitle:</b> crystal structure of fmn-dependent azoreductase from enterococcus2 faecalis
56	<a href="#">d1b1ca</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Cytochrome p450 reductase N-terminal domain-like
57	<a href="#">c2mtbA</a>	Alignment	not modelled	99.7	15	<b>PDB header:</b> electron transport <b>Chain:</b> A: <b>PDB Molecule:</b> flavodoxin-2; <b>PDBTitle:</b> solution structure of apo_fldb
58	<a href="#">c5mjiA</a>	Alignment	not modelled	99.7	20	<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)
59	<a href="#">c3svbB</a>	Alignment	not modelled	99.7	13	<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
60	<a href="#">c4c76A</a>	Alignment	not modelled	99.7	18	<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.
61	<a href="#">d1czna</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
62	<a href="#">d2fcra</a>	Alignment	not modelled	99.7	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
63	<a href="#">c3p0rA</a>	Alignment	not modelled	99.7	21	<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
64	<a href="#">c2wc1A</a>	Alignment	not modelled	99.7	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
65	<a href="#">c3fvwA</a>	Alignment	not modelled	99.7	13	<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.
66	<a href="#">c4n82B</a>	Alignment	not modelled	99.7	10	<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 nrdox
67	<a href="#">c3w7aD</a>	Alignment	not modelled	99.7	15	<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
68	<a href="#">d1ag9a</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
69	<a href="#">d1rtta</a>	Alignment	not modelled	99.7	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
70	<a href="#">c2q62A</a>	Alignment	not modelled	99.7	13	<b>PDB header:</b> flavoprotein <b>Chain:</b> A: <b>PDB Molecule:</b> arsh; <b>PDBTitle:</b> crystal structure of arsh from sinorhizobium meliloti
71	<a href="#">d1yoba1</a>	Alignment	not modelled	99.7	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
72	<a href="#">c4c0xA</a>	Alignment	not modelled	99.7	17	<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
73	<a href="#">c3lcmB</a>	Alignment	not modelled	99.7	16	<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
74	<a href="#">c3hr4C</a>	Alignment	not modelled	99.7	11	<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
75	<a href="#">c3k1yE</a>	Alignment	not modelled	99.7	13	<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 orthorhombic crystal form, northeast structural genomics consortium3 target cdr100d
76	<a href="#">c3rpeA</a>	Alignment	not modelled	99.7	17	<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.
77	<a href="#">d1ja1a2</a>	Alignment	not modelled	99.7	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Cytochrome p450 reductase N-terminal domain-like
78	<a href="#">c2v9cA</a>	Alignment	not modelled	99.7	20	<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.
79	<a href="#">c3f2vA</a>	Alignment	not modelled	99.6	14	<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.

80	<a href="#">d1tla2</a>	Alignment	not modelled	99.6	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Cytochrome p450 reductase N-terminal domain-like
81	<a href="#">d2z98a1</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
82	<a href="#">d1nni1</a>	Alignment	not modelled	99.6	17	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
83	<a href="#">d2qwxal</a>	Alignment	not modelled	99.6	14	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
84	<a href="#">d1t0ia_</a>	Alignment	not modelled	99.6	16	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
85	<a href="#">d1qrda_</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
86	<a href="#">d1fuea_</a>	Alignment	not modelled	99.6	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavodoxin-related
87	<a href="#">d1dxqa_</a>	Alignment	not modelled	99.6	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
88	<a href="#">c5lvaA</a>	Alignment	not modelled	99.6	12	<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.
89	<a href="#">c2vzha</a>	Alignment	not modelled	99.6	14	<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
90	<a href="#">c2fzvC</a>	Alignment	not modelled	99.5	13	<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
91	<a href="#">c4gi5B</a>	Alignment	not modelled	99.5	18	<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)
92	<a href="#">d1d4aa</a>	Alignment	not modelled	99.5	21	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Quinone reductase
93	<a href="#">c6efvA</a>	Alignment	not modelled	99.5	11	<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
94	<a href="#">d2fzva1</a>	Alignment	not modelled	99.5	12	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> NADPH-dependent FMN reductase
95	<a href="#">c2amjD</a>	Alignment	not modelled	99.4	16	<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
96	<a href="#">c5gxuA</a>	Alignment	not modelled	99.4	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh--cytochrome p450 reductase 2; <b>PDBTitle:</b> cystal structure of arabidopsis atr2
97	<a href="#">c1tla</a>	Alignment	not modelled	99.3	12	<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.
98	<a href="#">c3ha2B</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh-quinone reductase; <b>PDBTitle:</b> crystal structure of protein (nadh-quinone reductase) from2 p.pentosaceus, northeast structural genomics consortium target ptr24a
99	<a href="#">c2x2oA</a>	Alignment	not modelled	99.3	11	<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
100	<a href="#">c2bpoA</a>	Alignment	not modelled	99.3	8	<b>PDB header:</b> reductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadh-cytochrom p450 reductase; <b>PDBTitle:</b> crystal structure of the yeast cpr triple mutant: d74g, y75f, k78a.
101	<a href="#">c1j9zB</a>	Alignment	not modelled	99.3	12	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadh-cytochrome p450 reductase; <b>PDBTitle:</b> cypor-w677g
102	<a href="#">c6ebqB</a>	Alignment	not modelled	99.3	15	<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
103	<a href="#">d1rlja</a>	Alignment	not modelled	99.2	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Flavoproteins <b>Family:</b> Flavoprotein NrdI
104	<a href="#">c6j7aB</a>	Alignment	not modelled	99.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> heme oxygenase 1,nadh--cytochrome p450 reductase; <b>PDBTitle:</b> fusion protein of heme oxygenase-1 and nadph cytochrome p450 reductase2 (17aa)
105	<a href="#">c3eywA</a>	Alignment	not modelled	99.1	17	<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
106	<a href="#">c3n39D_</a>	Alignment	not modelled	99.1	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> protein nrdr; <b>PDBTitle:</b> ribonucleotide reductase dimanganese(ii)-nrdf from escherichia coli in2 complex with nrdr
107	<a href="#">c5gqsA_</a>	Alignment	not modelled	94.4	10	<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
108	<a href="#">d2r4qa1</a>	Alignment	not modelled	94.2	16	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Fructose specific IIB subunit-like
109	<a href="#">c3czcA_</a>	Alignment	not modelled	93.1	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> rmpb; <b>PDBTitle:</b> the crystal structure of a putative pts iib(ptxb) from streptococcus2 mutans
110	<a href="#">c5dleD_</a>	Alignment	not modelled	92.3	12	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> pts system, fructose-specific iibc component; <b>PDBTitle:</b> crystal structure from a domain (thr161-f265) from fructose-specific2 iibc component (pts system) from borrelia burgdorferi
111	<a href="#">c2m1zA_</a>	Alignment	not modelled	92.1	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lmo0427 protein; <b>PDBTitle:</b> solution structure of uncharacterized protein lmo0427
112	<a href="#">c2kyrA_</a>	Alignment	not modelled	91.9	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> fructose-like phosphotransferase enzyme iib component 1; <b>PDBTitle:</b> solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
113	<a href="#">c1tvmA_</a>	Alignment	not modelled	90.3	7	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, galactitol-specific iib component; <b>PDBTitle:</b> nmr structure of enzyme gatb of the galactitol-specific2 phosphoenolpyruvate-dependent phosphotransferase system
114	<a href="#">c4lruA_</a>	Alignment	not modelled	89.5	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> glyoxalase iii (glutathione-independent); <b>PDBTitle:</b> crystal structure of glyoxalase iii (orf 19.251) from candida albicans
115	<a href="#">c4p5pA_</a>	Alignment	not modelled	89.4	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> thij/pfpi family protein; <b>PDBTitle:</b> x-ray structure of francisella tularensis rapid encystment protein 242 kda (rep24), gene product of ftn_0841
116	<a href="#">c3nbmA_</a>	Alignment	not modelled	88.9	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pts system, lactose-specific iibc components; <b>PDBTitle:</b> the lactose-specific iib component domain structure of the2 phosphoenolpyruvate:carbohydrate phosphotransferase system (pts) from3 streptococcus pneumoniae.
117	<a href="#">d2r48a1</a>	Alignment	not modelled	87.1	18	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> PTS system IIB component-like <b>Family:</b> PTS system, Fructose specific IIB subunit-like
118	<a href="#">c3i3wB_</a>	Alignment	not modelled	86.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoglucosamine mutase; <b>PDBTitle:</b> structure of a phosphoglucosamine mutase from francisella tularensis
119	<a href="#">d1ccwa_</a>	Alignment	not modelled	84.8	11	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Cobalamin (vitamin B12)-binding domain <b>Family:</b> Cobalamin (vitamin B12)-binding domain
120	<a href="#">c1jvnB_</a>	Alignment	not modelled	84.0	13	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> bifunctional histidine biosynthesis protein hishf; <b>PDBTitle:</b> crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites