





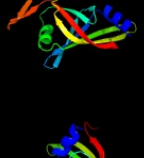
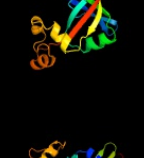
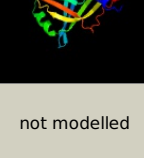


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2991 (-) _3347992_3348483
Date	Thu Aug 8 16:20:15 BST 2019
Unique Job ID	f1a7842d666c5567

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1rfea_	Alignment		100.0	96	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
2	c4zkyB_	Alignment		100.0	23	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5-phosphate oxidase; PDBTitle: structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis
3	d2fg9a1	Alignment		100.0	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
4	d2i02a1	Alignment		100.0	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
5	d2hq9a1	Alignment		100.0	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
6	d2fura1	Alignment		100.0	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
7	c3f7eB_	Alignment		99.9	24	PDB header: unknown function Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeg_3380 f420 reductase
8	c6rk0A_	Alignment		99.9	10	PDB header: flavoprotein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the flavocytochrome anf3 from azotobacter vinelandii
9	c3ec6A_	Alignment		99.9	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: general stress protein 26; PDBTitle: crystal structure of the general stress protein 26 from bacillus2 anthracis str. Sterne
10	c3u0iA_	Alignment		99.9	18	PDB header: unknown function Chain: A: PDB Molecule: probable fad-binding, putative uncharacterized protein; PDBTitle: crystal structure of a probable fad-binding, putative uncharacterized2 protein from brucella melitensis
11	d1w9aa_	Alignment		99.9	22	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like

12	d2asfa1	Alignment		99.9	26	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
13	c2iabB	Alignment		99.9	22	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a protein with fmn-binding split barrel fold2 (np_828636.1) from streptomyces avermitilis at 2.00 a resolution
14	d2fhqa1	Alignment		99.9	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
15	c2re7A	Alignment		99.9	18	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a pyridoxamine 5'-phosphate oxidase related2 protein (psyc_0186) from psychrobacter arcticus 273-4 at 2.50 a3 resolution
16	d2vpaa1	Alignment		99.9	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
17	c2htia	Alignment		99.9	19	PDB header: fmn-binding protein Chain: A: PDB Molecule: bh0577 protein; PDBTitle: crystal structure of a flavin-nucleotide-binding protein (bh_0577)2 from bacillus halodurans at 2.50 a resolution
18	d2htia1	Alignment		99.9	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
19	d2hq7a1	Alignment		99.9	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
20	c3fkhB	Alignment		99.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: putative pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_601736.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.51 a resolution
21	c3db0B	Alignment	not modelled	99.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: lin2891 protein; PDBTitle: crystal structure of putative pyridoxamine 5'-phosphate oxidase2 (np_472219.1) from listeria innocua at 2.00 a resolution
22	c4ybnB	Alignment	not modelled	99.9	14	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin-nucleotide-binding protein; PDBTitle: structure of the fad and heme binding protein msme_4975 from2 mycobacterium smegmatis
23	c3tgvD	Alignment	not modelled	99.9	22	PDB header: heme binding protein Chain: D: PDB Molecule: heme-binding protein hut2; PDBTitle: crystal structure of hut2,the heme storsge protein from vibrio2 cholerae
24	c6eciQ	Alignment	not modelled	99.9	22	PDB header: fad-binding protein Chain: Q: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn-binding PDBTitle: structure of the fad binding protein msme_5243 from mycobacterium2 smegmatis
25	c3u34D	Alignment	not modelled	99.9	18	PDB header: protein binding Chain: D: PDB Molecule: general stress protein; PDBTitle: crystal structure of the general stress fmn/fad binding protein from2 the phytopathogen xanthomonas citri
26	c3dmbA	Alignment	not modelled	99.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: putative general stress protein 26 with a pnp-oxidase like PDBTitle: crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution
27	c2ig6B	Alignment	not modelled	99.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: nimc/nima family protein; PDBTitle: crystal structure of a nimc/nima family protein (ca_c2569) from2 clostridium acetobutylicum at 1.80 a resolution
						Fold: Split barrel-like

28	d1vl7a_	Alignment	not modelled	99.9	17	Superfamily: FMN-binding split barrel Family: PNP-oxidase like
29	c3cp3A_	Alignment	not modelled	99.9	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved protein of unknown function dip18742 from corynebacterium diphtheriae
30	c2qeaB_	Alignment	not modelled	99.9	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative general stress protein 26; PDBTitle: crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution
31	c2hhzA_	Alignment	not modelled	99.9	20	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related; PDBTitle: crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution
32	c2htdB_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: predicted flavin-nucleotide-binding protein from cog3576 PDBTitle: crystal structure of a putative pyridoxamine 5'-phosphate oxidase2 (ldb0262) from lactobacillus delbrueckii subsp. at 1.60 a resolution
33	c5escD_	Alignment	not modelled	99.8	24	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
34	c2o15B_	Alignment	not modelled	99.8	11	PDB header: transcription regulator Chain: B: PDB Molecule: pai 2 protein; PDBTitle: crystal structure of a protease synthase and sporulation negative2 regulatory protein pai 2 from bacillus stearothermophilus
35	c3gasA_	Alignment	not modelled	99.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
36	d2arza1	Alignment	not modelled	99.8	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
37	c5bncB_	Alignment	not modelled	99.8	21	PDB header: heme binding protein Chain: B: PDB Molecule: heme binding protein msmeg_6519; PDBTitle: structure of heme binding protein msmeg_6519 from mycobacterium2 smegmatis
38	d1flma_	Alignment	not modelled	99.8	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
39	d1nrga_	Alignment	not modelled	99.7	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
40	c1nrgA_	Alignment	not modelled	99.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
41	c2q9kA_	Alignment	not modelled	99.7	16	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative oxidoreductase (exig_1997) from2 exiguobacterium sibiricum 255-15 at 1.59 a resolution
42	d1t9ma_	Alignment	not modelled	99.7	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
43	d1ty9a_	Alignment	not modelled	99.7	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
44	c2a2jA_	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis
45	c3dnhB_	Alignment	not modelled	99.7	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein atu2129; PDBTitle: the crystal structure of the protein atu2129 (unknown function) from2 agrobacterium tumefaciens str. c58
46	d2a2ja1	Alignment	not modelled	99.7	22	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
47	c2ou5B_	Alignment	not modelled	99.7	20	PDB header: flavoprotein Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn-binding; PDBTitle: crystal structure of a pyridoxamine 5'-phosphate oxidase-related fmn-2 binding protein (jann_0254) from jannaschia sp. ccs1 at 1.60 a3 resolution
48	d1dnla_	Alignment	not modelled	99.7	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
49	c4hmwB_	Alignment	not modelled	99.7	19	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phgz from burkholderia lata 383
50	c2i51B_	Alignment	not modelled	99.5	13	PDB header: flavoprotein Chain: B: PDB Molecule: uncharacterized conserved protein of cog5135; PDBTitle: crystal structure of a pyridoxamine 5'-phosphate oxidase-related, fmn2 binding protein (npun_f5749) from nostoc punctiforme pcc 73102 at3 1.40 a resolution
51	d1ci0a_	Alignment	not modelled	99.4	25	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
52	d1xhna1	Alignment	not modelled	99.4	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like

53	c4n7rD	Alignment	not modelled	99.3	19	PDB header: oxidoreductase/protein binding Chain: D: PDB Molecule: genomic dna, chromosome 3, p1 clone: mxl8; PDBTitle: crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein
54	c3ba3A	Alignment	not modelled	98.4	10	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase-like protein; PDBTitle: crystal structure of pyridoxamine 5'-phosphate oxidase-like protein2 (np_783940.1) from lactobacillus plantarum at 1.55 a resolution
55	c3r5yC	Alignment	not modelled	98.3	22	PDB header: unknown function Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420
56	c3r5zB	Alignment	not modelled	98.3	17	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of a deazaflavin-dependent reductase from nocardia2 farcinica, with co-factor f420
57	c3r5wO	Alignment	not modelled	98.3	16	PDB header: oxidoreductase Chain: O: PDB Molecule: deazaflavin-dependent nitroreductase; PDBTitle: structure of ddn, the deazaflavin-dependent nitroreductase from2 mycobacterium tuberculosis involved in bioreductive activation of pa-3 824, with co-factor f420
58	c4y9iA	Alignment	not modelled	98.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
59	c3h96B	Alignment	not modelled	98.0	15	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
60	d2ptfa1	Alignment	not modelled	97.0	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
61	c2ptfB	Alignment	not modelled	96.5	8	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein mth_863; PDBTitle: crystal structure of protein mth_863 from methanobacterium2 thermoautotrophicum bound to fmn
62	c3fgeA	Alignment	not modelled	95.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative flavin reductase with split barrel domain; PDBTitle: crystal structure of putative flavin reductase with split barrel2 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution
63	d2imla1	Alignment	not modelled	95.5	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
64	c3b5mD	Alignment	not modelled	95.0	17	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
65	c3e4vA	Alignment	not modelled	94.5	11	PDB header: flavoprotein Chain: A: PDB Molecule: nadh:fmn oxidoreductase like protein; PDBTitle: crystal structure of nadh:fmn oxidoreductase like protein in complex2 with fmn (yp_544701.1) from methylobacillus flagellatus kt at 1.40 a3 resolution
66	d1ejea	Alignment	not modelled	94.5	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
67	c4z85A	Alignment	not modelled	94.4	6	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitrobenzoate nitroreductase; PDBTitle: crystal structure of pseudomonas fluorescens 2-nitrobenzoate 2-2 nitroreductase nbaa
68	c3bpbB	Alignment	not modelled	94.3	9	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase component b; PDBTitle: crystal structure of nitrilotriacetate monooxygenase component b from2 bacillus cereus
69	d2nr4a1	Alignment	not modelled	92.7	8	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
70	c3pftA	Alignment	not modelled	89.1	13	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase; PDBTitle: crystal structure of untagged c54a mutant flavin reductase (dszd) in2 complex with fmn from mycobacterium goodii
71	c2d5mA	Alignment	not modelled	86.1	11	PDB header: electron transport Chain: A: PDB Molecule: flavoredoxin; PDBTitle: flavoredoxin of desulfovibrio vulgaris (miyazaki f)
72	c4l82D	Alignment	not modelled	85.6	10	PDB header: oxidoreductase Chain: D: PDB Molecule: rifea.00250.a; PDBTitle: structure of a putative oxidoreductase from rickettsia felis
73	c3hmzA	Alignment	not modelled	78.1	7	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase domain protein, fmn-binding; PDBTitle: crystal structure of a fmn-binding domain of flavin reductases-like2 enzyme (sba_0626) from shewanella baltica os155 at 1.50 a resolution
74	c3bnkB	Alignment	not modelled	77.2	11	PDB header: electron transport Chain: B: PDB Molecule: flavoredoxin; PDBTitle: x-ray crystal structure of flavoredoxin from methanosarcina2 acetivorans
75	c3cb0B	Alignment	not modelled	72.1	11	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxyphenylacetate 3-monooxygenase; PDBTitle: cobr
76	c4f07A	Alignment	not modelled	70.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: styrene monooxygenase component 2;

76	c4t07A	Alignment	not modelled	70.2	13	PDBTitle: structure of the styrene monooxygenase flavin reductase (smob) from2 pseudomonas putida s12 PDB header: oxidoreductase
77	c2r0xA	Alignment	not modelled	69.0	9	Chain: A: PDB Molecule: possible flavin reductase; PDBTitle: crystal structure of a putative flavin reductase (ycdh, hs_1225) from2 haemophilus somnus 129pt at 1.06 a resolution
78	c3rh7A	Alignment	not modelled	66.5	10	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution
79	d1rz0a	Alignment	not modelled	65.0	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
80	d1usca	Alignment	not modelled	63.9	8	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
81	c2qckA	Alignment	not modelled	59.9	9	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase domain protein; PDBTitle: crystal structure of flavin reductase domain protein (yp_831077.1)2 from arthrobacter sp. fb24 at 1.90 a resolution
82	c2d38A	Alignment	not modelled	58.2	6	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical nadh-dependent fmn oxidoreductase; PDBTitle: the crystal structure of flavin reductase hpac complexed with nadp+
83	c4xhyA	Alignment	not modelled	58.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase domain protein, fmn-binding protein; PDBTitle: nadh:fmn oxidoreductase from paracoccus denitrificans
84	c3nfwB	Alignment	not modelled	54.2	12	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin reductase-like, fmn-binding protein; PDBTitle: crystal structure of nitrilotriacetate monooxygenase component b2 (a0r521 homolog) from mycobacterium thermoresistibile
85	d1i0ra	Alignment	not modelled	52.2	6	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
86	c2r6vA	Alignment	not modelled	50.0	13	PDB header: flavoprotein Chain: A: PDB Molecule: uncharacterized protein ph0856; PDBTitle: crystal structure of fmn-binding protein (np_142786.1) from pyrococcus2 horikoshii at 1.35 a resolution
87	c3k87B	Alignment	not modelled	49.6	20	PDB header: oxidoreductase Chain: B: PDB Molecule: chlorophenol-4-monooxygenase component 1; PDBTitle: crystal structure of nadh:fad oxidoreductase (tftc) - fad2 complex
88	c4hx6D	Alignment	not modelled	44.5	9	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: streptomyces globisporus c-1027 nadh:fad oxidoreductase sgce6
89	d1wgba	Alignment	not modelled	41.1	9	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
90	d2bvca1	Alignment	not modelled	20.9	3	Fold: beta-Grasp (ubiquitin-like) Superfamily: Glutamine synthetase, N-terminal domain Family: Glutamine synthetase, N-terminal domain
91	c4p7xA	Alignment	not modelled	15.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: l-proline cis-4-hydroxylase; PDBTitle: l-pipecolic acid-bound l-proline cis-4-hydroxylase
92	c2ecrA	Alignment	not modelled	15.5	6	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase component (hpac) of 4-hydroxyphenylacetate PDBTitle: crystal structure of the ligand-free form of the flavin reductase2 component (hpac) of 4-hydroxyphenylacetate 3-monooxygenase
93	c4fmoB	Alignment	not modelled	15.5	11	PDB header: hydrolase Chain: B: PDB Molecule: dna mismatch repair protein pms1; PDBTitle: structure of the c-terminal domain of the saccharomyces cerevisiae2 mutl alpha (mlh1/pms1) heterodimer bound to a fragment of exo1
94	d1jlua	Alignment	not modelled	14.8	20	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Nucleotidyl transferase Family: Class I aminoacyl-tRNA synthetases (RS), catalytic domain
95	c5b42A	Alignment	not modelled	14.4	21	PDB header: dna binding protein Chain: A: PDB Molecule: dna mismatch repair protein mutl; PDBTitle: crystal structure of the c-terminal endonuclease domain of aquifex2 aeolicus mutl.
96	c3j21V	Alignment	not modelled	13.5	26	PDB header: ribosome Chain: V: PDB Molecule: 50s ribosomal protein l24e; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
97	d1e5ra	Alignment	not modelled	13.4	30	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Type II Proline 3-hydroxylase (proline oxidase)
98	c4a1eT	Alignment	not modelled	12.7	11	PDB header: ribosome Chain: T: PDB Molecule: rpl24; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
99	c3cr8C	Alignment	not modelled	12.3	16	PDB header: transferase Chain: C: PDB Molecule: sulfate adenylyltransferase, adenylylsulfate kinase; PDBTitle: hexameric aps kinase from thiobacillus denitrificans