


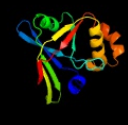




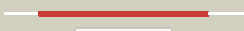















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2061c (-)_2316689_2317093
Date	Mon Aug 5 13:25:17 BST 2019
Unique Job ID	a5ad0d79f1fbfeb1

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f7eB_	 Alignment		99.9	21	PDB header: unknown function Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeq_3380 f420 reductase
2	d1rfea_	 Alignment		99.9	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
3	d2asfa1	 Alignment		99.9	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
4	c2iabB_	 Alignment		99.9	23	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
5	c4zkyB_	 Alignment		99.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5-phosphate oxidase; PDBTitle: structure of f420 binding protein, msmeq_6526, from mycobacterium2 smegmatis
6	d1w9aa_	 Alignment		99.9	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
7	d2fg9a1	 Alignment		99.9	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
8	c5escD_	 Alignment		99.9	20	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
9	c2re7A_	 Alignment		99.9	16	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
10	c3tgvD_	 Alignment		99.9	14	PDB header: heme binding protein Chain: D: PDB Molecule: heme-binding protein hutz; PDBTitle: crystal structure of hutz,the heme storsge protein from vibrio2 cholerae
11	d2i02a1	 Alignment		99.8	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like

12	c3db0B_	Alignment		99.8	15	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
13	c3u0iA_	Alignment		99.8	13	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
14	d2hq7a1	Alignment		99.8	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
15	d2htia1	Alignment		99.8	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
16	c2htiA_	Alignment		99.8	15	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
17	d1vl7a_	Alignment		99.8	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
18	d2hq9a1	Alignment		99.8	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
19	d2fhqa1	Alignment		99.8	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
20	c4ybnB_	Alignment		99.8	20	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin-nucleotide-binding protein; PDBTitle: structure of the fad and heme binding protein msmeq_4975 from2 mycobacterium smegmatis
21	d2fura1	Alignment	not modelled	99.8	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
22	c3fkbB_	Alignment	not modelled	99.8	13	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
23	c6eciQ_	Alignment	not modelled	99.8	16	PDB header: fad-binding protein Chain: Q: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn-binding PDBTitle: structure of the fad binding protein msmeq_5243 from mycobacterium2 smegmatis
24	c3ec6A_	Alignment	not modelled	99.8	19	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
25	c2hhzA_	Alignment	not modelled	99.8	15	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
26	c2htdB_	Alignment	not modelled	99.8	19	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
						PDB header: protein binding

27	c3u34D_	Alignment	not modelled	99.8	16	Chain: D; PDB Molecule: general stress protein; PDBTitle: crystal structure of the general stress fmn/fad binding protein from2 the phytopathogen xanthomonas citri
28	c3dmbA_	Alignment	not modelled	99.8	15	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
29	c6rk0A_	Alignment	not modelled	99.8	17	PDB header: flavoprotein Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: structure of the flavocytochrome anf3 from azotobacter vinelandii
30	c2ig6B_	Alignment	not modelled	99.7	14	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
31	d2vpaa1	Alignment	not modelled	99.7	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
32	c3cp3A_	Alignment	not modelled	99.7	14	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
33	d1t9ma_	Alignment	not modelled	99.7	22	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
34	d1nrga_	Alignment	not modelled	99.7	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
35	c1nrgA_	Alignment	not modelled	99.7	20	PDB header: oxidoreductase Chain: A; PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
36	c2qeaB_	Alignment	not modelled	99.7	14	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
37	d1ty9a_	Alignment	not modelled	99.7	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
38	c2q9kA_	Alignment	not modelled	99.7	18	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
39	d2arza1	Alignment	not modelled	99.7	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
40	c5bncB_	Alignment	not modelled	99.7	15	PDB header: heme binding protein Chain: B; PDB Molecule: heme binding protein msmeq_6519; PDBTitle: structure of heme binding protein msmeq_6519 from mycobacterium2 smegmatis
41	d2a2ja1	Alignment	not modelled	99.7	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
42	d1dnla_	Alignment	not modelled	99.7	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
43	c2ou5B_	Alignment	not modelled	99.6	19	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
44	c4hmwB_	Alignment	not modelled	99.6	24	PDB header: oxidoreductase Chain: B; PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phzg from burkholderia lata 383
45	d1flma_	Alignment	not modelled	99.6	22	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
46	c2a2jA_	Alignment	not modelled	99.6	12	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
47	c3dnhB_	Alignment	not modelled	99.6	10	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
48	c2ol5B_	Alignment	not modelled	99.6	10	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
49	c3gasA_	Alignment	not modelled	99.5	13	PDB header: oxidoreductase Chain: A; PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hgz2 in complex with heme
50	c2i51B_	Alignment	not modelled	99.5	16	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	99.5	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
						PDB header: flavoprotein

52	c3h96B_	Alignment	not modelled	99.3	19	Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
53	d1xhna1	Alignment	not modelled	99.2	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
54	c3r5yC_	Alignment	not modelled	99.1	19	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
55	c3r5zB_	Alignment	not modelled	99.1	19	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
56	c3r5wO_	Alignment	not modelled	99.0	21	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
57	c4y9iA_	Alignment	not modelled	99.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
58	c3ba3A_	Alignment	not modelled	98.8	11	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
59	c4n7rD_	Alignment	not modelled	98.5	17	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
60	d2ptfa1	Alignment	not modelled	96.6	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
61	c2ptfB_	Alignment	not modelled	95.8	17	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	d2imla1	Alignment	not modelled	95.1	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
63	d1ejea_	Alignment	not modelled	95.0	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
64	c3b5mD_	Alignment	not modelled	93.8	18	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
65	c3fgeA_	Alignment	not modelled	90.8	12	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
66	c2d5mA_	Alignment	not modelled	88.3	19	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: flavodoxin of desulfovibrio vulgaris (miyazaki f)
67	c3e4vA_	Alignment	not modelled	87.5	17	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
68	c4z85A_	Alignment	not modelled	87.4	18	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitrobenzoate nitroreductase; PDBTitle: crystal structur of pseudomonas fluorescens 2-nitrobenzoate 2-2 nitroreductase nbaa
69	c3bpbK_	Alignment	not modelled	87.2	12	PDB header: oxidoreductase Chain: B: PDB Molecule: nitrilotriacetate monooxygenase component b; PDBTitle: crystal structure of nitrilotriacetate monooxygenase component b from2 bacillus cereus
70	c4f07A_	Alignment	not modelled	83.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: styrene monooxygenase component 2; PDBTitle: structure of the styrene monooxygenase flavin reductase (smob) from2 pseudomonas putida s12
71	c3bnkB_	Alignment	not modelled	82.6	12	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: x-ray crystal structure of flavodoxin from methanosarcina2 acetivorans
72	c4xhyA_	Alignment	not modelled	70.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase domain protein, fmn-binding protein; PDBTitle: nadh:fmn oxidoreductase from paracoccus denitrificans
73	d1usca_	Alignment	not modelled	66.9	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
74	d2nr4a1	Alignment	not modelled	66.3	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
75	c3cb0B_	Alignment	not modelled	61.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxyphenylacetate 3-monooxygenase; PDBTitle: cobr
						Fold: Split barrel-like

76	d1i0ra_	Alignment	not modelled	57.3	12	Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
77	d1rz0a_	Alignment	not modelled	45.2	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
78	c2qckA_	Alignment	not modelled	44.8	16	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
79	c3nfwB_	Alignment	not modelled	42.3	18	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
80	c3rh7A_	Alignment	not modelled	36.4	16	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
81	c3hmzA_	Alignment	not modelled	36.0	14	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 (sbal_0626) from shewanella baltica os155 at 1.50 a resolution
82	c2d38A_	Alignment	not modelled	34.5	4	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical nadh-dependent fmn oxidoreductase; PDBTitle: the crystal structure of flavin reductase hpac complexed with nadp+
83	c3pftA_	Alignment	not modelled	34.2	6	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
84	c3k87B_	Alignment	not modelled	32.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: chlorophenol-4-monooxygenase component 1; PDBTitle: crystal structure of nadh:fad oxidoreductase (tftc) - fad2 complex
85	c2r0xA_	Alignment	not modelled	30.6	18	PDB header: oxidoreductase 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
86	d2z1ca1	Alignment	not modelled	26.4	21	Fold: OB-fold Superfamily: HupF/HypC-like Family: HupF/HypC-like
87	c2r6vA_	Alignment	not modelled	20.6	10	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
88	d1wgba_	Alignment	not modelled	18.8	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
89	c4l82D_	Alignment	not modelled	15.8	9	PDB header: oxidoreductase Chain: D: PDB Molecule: rifea.00250.a; PDBTitle: structure of a putative oxidoreductase from rickettsia felis
90	c2ecrA_	Alignment	not modelled	14.7	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
91	c5vfkA_	Alignment	not modelled	13.7	17	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of an archaeal duf61 family protein sso0941
92	c1ksia_	Alignment	not modelled	10.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: copper amine oxidase; PDBTitle: crystal structure of a eukaryotic (pea seedling) copper-containing2 amine oxidase at 2.2a resolution
93	c2ytxA_	Alignment	not modelled	10.6	8	PDB header: rna binding protein Chain: A: PDB Molecule: cold shock domain-containing protein e1; PDBTitle: solution structure of the second cold-shock domain of the human2 kiaa0885 protein (unr protein)
94	c1ztgD_	Alignment	not modelled	10.5	16	PDB header: dna, rna binding protein/dna Chain: D: PDB Molecule: poly(rc)-binding protein 1; PDBTitle: human alpha polyc binding protein kh1
95	d1mzga_	Alignment	not modelled	9.9	10	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
96	d2axya1	Alignment	not modelled	9.4	12	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
97	c6mdxA_	Alignment	not modelled	8.6	14	PDB header: dna binding protein/dna Chain: A: PDB Molecule: spirt-like domain-containing protein spartan; PDBTitle: mechanism of protease dependent dpc repair
98	d1ni7a_	Alignment	not modelled	8.3	7	Fold: SufE/NifU Superfamily: SufE/NifU Family: SufE-like
99	c2wshC_	Alignment	not modelled	7.9	18	PDB header: hydrolase Chain: C: PDB Molecule: endonuclease ii; PDBTitle: structure of bacteriophage t4 endoi e118a mutant