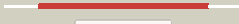



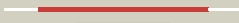








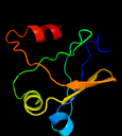














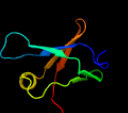




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1871c (-)_2121502_2121891
Date	Fri Aug 2 13:30:48 BST 2019
Unique Job ID	b0b6ae33644088e1

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r5yC_	 Alignment		100.0	20	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
2	c3r5zB_	 Alignment		100.0	21	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
3	c3h96B_	 Alignment		100.0	14	PDB header: flavoprotein Chain: B; PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeq_3358 f420 reductase
4	c3r5wO_	 Alignment		100.0	26	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
5	c4y9iA_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: A; PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeq_2027
6	c2iabB_	 Alignment		98.6	20	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
7	c3f7eB_	 Alignment		98.4	22	PDB header: unknown function Chain: B; PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeq_3380 f420 reductase
8	d1w9aa_	 Alignment		98.2	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
9	d2hq9a1	 Alignment		98.2	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
10	d1rfea_	 Alignment		98.2	25	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
11	d2asfa1	 Alignment		98.1	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like

12	d2htia1	Alignment		98.1	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
13	c2htiA	Alignment		98.1	13	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
14	c3tgvD	Alignment		98.1	15	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
15	d2i02a1	Alignment		98.1	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
16	c4zkyB	Alignment		98.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5-phosphate oxidase; PDBTitle: structure of f420 binding protein, msmeq_6526, from mycobacterium2 smegmatis
17	c6eciQ	Alignment		98.0	10	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
18	c2q9kA	Alignment		98.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative oxidoreductase (exig_1997) from2 exigubacterium sibiricum 255-15 at 1.59 a resolution
19	c5escD	Alignment		97.9	15	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
20	c3db0B	Alignment		97.8	23	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
21	c2htdB	Alignment	not modelled	97.7	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
22	c3u0iA	Alignment	not modelled	97.7	14	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
23	d2hq7a1	Alignment	not modelled	97.7	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
24	c2hhzA	Alignment	not modelled	97.5	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
25	c3fkhB	Alignment	not modelled	97.5	11	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 kitasafo at3 2.51 a resolution
26	d2fhqa1	Alignment	not modelled	97.4	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
						Fold: Split barrel-like

27	d1vl7a_	Alignment	not modelled	97.4	21	Superfamily: FMN-binding split barrel Family: PNP-oxidase like
28	c3ec6A_	Alignment	not modelled	97.3	21	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
29	c2re7A_	Alignment	not modelled	97.2	13	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
30	d2fg9a1	Alignment	not modelled	97.1	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
31	c2ig6B_	Alignment	not modelled	97.1	16	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
32	d1flma_	Alignment	not modelled	97.0	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
33	d2arza1	Alignment	not modelled	96.9	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
34	c4ybnB_	Alignment	not modelled	96.8	20	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin-nucleotide-binding protein; PDBTitle: structure of the fad and heme binding protein msmeg_4975 from2 mycobacterium smegmatis
35	c3dnhB_	Alignment	not modelled	96.8	14	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
36	d1t9ma_	Alignment	not modelled	96.8	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
37	c3gasA_	Alignment	not modelled	96.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
38	d2fura1	Alignment	not modelled	96.6	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
39	c3cp3A_	Alignment	not modelled	96.5	12	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
40	c5bncB_	Alignment	not modelled	96.4	15	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
41	c1nrgA_	Alignment	not modelled	96.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
42	d1nrga_	Alignment	not modelled	96.3	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
43	d1ty9a_	Alignment	not modelled	96.3	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
44	c2qeaB_	Alignment	not modelled	96.2	12	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
45	d2a2ja1	Alignment	not modelled	96.0	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
46	c3u34D_	Alignment	not modelled	95.9	16	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
47	d1ci0a_	Alignment	not modelled	95.5	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
48	c2a2jA_	Alignment	not modelled	95.4	15	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
49	c4hmwB_	Alignment	not modelled	95.4	14	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phzg from burkholderia lata 383
50	c3dmbA_	Alignment	not modelled	95.4	14	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
51	d1dnja_	Alignment	not modelled	94.9	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
52	d2ptfa1	Alignment	not modelled	90.1	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
						PDB header: structural genomics, unknown function

53	c2ptfB_	Alignment	not modelled	89.9	14	Chain: B: PDB Molecule: uncharacterized protein mth_863; PDBTitle: crystal structure of protein mth_863 from methanobacterium2 thermoautotrophicum bound to fmn
54	c6rk0A_	Alignment	not modelled	87.4	13	PDB header: flavoprotein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the flavocytochrome anf3 from azotobacter vinelandii
55	c2ou5B_	Alignment	not modelled	86.1	18	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
56	d2vpaa1	Alignment	not modelled	85.3	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
57	c4n7rD_	Alignment	not modelled	77.7	16	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
58	d1xhna1	Alignment	not modelled	49.6	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
59	c2i51B_	Alignment	not modelled	43.6	23	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
60	d2imla1	Alignment	not modelled	41.3	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
61	c2ol5B_	Alignment	not modelled	36.3	6	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
62	c2levA_	Alignment	not modelled	30.5	23	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ler; PDBTitle: structure of the dna complex of the c-terminal domain of ler
63	d2nr4a1	Alignment	not modelled	16.0	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
64	d1hnra_	Alignment	not modelled	11.5	3	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
65	c6mk1V_	Alignment	not modelled	8.3	17	PDB header: protein fibril Chain: V: PDB Molecule: ; PDBTitle: cryo-em of self-assembly peptide filament heat_r1
66	c1ztnA_	Alignment	not modelled	7.5	57	PDB header: transport protein Chain: A: PDB Molecule: potassium voltage-gated channel subfamily c member 4; PDBTitle: inactivation gate of potassium channel raw3, nmr, 8 structures
67	c4wt5A_	Alignment	not modelled	5.1	13	PDB header: chaperone Chain: A: PDB Molecule: rubisco accumulation factor 1, isoform 2; PDBTitle: the c-terminal domain of rubisco accumulation factor 1 from2 arabidopsis thaliana, crystal form ii