







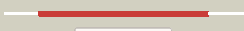














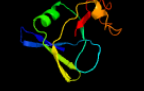


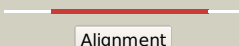

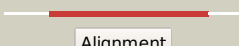

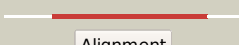
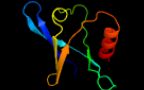
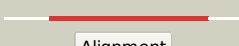


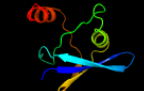




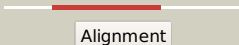

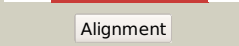



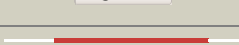
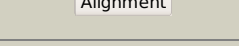


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0523c_(-)_614329_614724
Date	Fri Jul 26 01:50:07 BST 2019
Unique Job ID	000cb689e9950de7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h96B_	 Alignment		99.9	22	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
2	c4y9iA_	 Alignment		99.9	17	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
3	c3r5yC_	 Alignment		99.9	21	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
4	c3r5wO_	 Alignment		99.9	20	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	c3r5zB_	 Alignment		99.9	20	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
6	c2iabB_	 Alignment		97.3	12	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		97.2	14	PDB header: unknown function Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeg_3380 f420 reductase
8	d2asfa1	 Alignment		97.2	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
9	d1w9aa_	 Alignment		97.1	9	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
10	d1rfea_	 Alignment		97.0	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
11	c2q9kA_	 Alignment		96.5	11	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

12	d2hq7a1	 Alignment		96.5	8	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
13	c2htdB_	 Alignment		96.1	16	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
14	c5escD_	 Alignment		96.0	16	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
15	c3db0B_	 Alignment		95.6	6	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
16	c4zkyB_	 Alignment		95.6	14	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5-phosphate oxidase; PDBTitle: structure of f420 binding protein, msme_6526, from mycobacterium2 smegmatis
17	d2fhqa1	 Alignment		95.3	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
18	d1t9ma_	 Alignment		94.5	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
19	d2i02a1	 Alignment		94.4	8	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
20	c2re7A_	 Alignment		94.4	15	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
21	c2hhzA_	 Alignment	not modelled	94.1	9	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
22	d2a2ja1	 Alignment	not modelled	92.7	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
23	d1nrga_	 Alignment	not modelled	92.5	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
24	c1nrgA_	 Alignment	not modelled	92.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
25	d1vl7a_	 Alignment	not modelled	92.5	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
26	d2htia1	 Alignment	not modelled	92.5	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
27	c2htiA_	 Alignment	not modelled	92.5	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
28	c2a2ja_	 Alignment	not modelled	92.4	17	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

29	d2arza1	Alignment	not modelled	91.6	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
30	d2hq9a1	Alignment	not modelled	91.1	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
31	c2ig6B_	Alignment	not modelled	90.9	8	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	d1ty9a_	Alignment	not modelled	90.3	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
33	c3dnhB_	Alignment	not modelled	89.8	16	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
34	d1ci0a_	Alignment	not modelled	89.5	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
35	c3cp3A_	Alignment	not modelled	89.3	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
36	c3ec6A_	Alignment	not modelled	88.5	15	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
37	c3tgvD_	Alignment	not modelled	86.6	17	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
38	c3dmbA_	Alignment	not modelled	86.0	8	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
39	c4hmwB_	Alignment	not modelled	84.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phzg from burkholderia lata 383
40	c6eciQ_	Alignment	not modelled	82.7	9	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
41	d2fura1	Alignment	not modelled	81.9	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
42	c3u0iA_	Alignment	not modelled	80.2	11	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
43	c3fkhB_	Alignment	not modelled	76.2	18	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
44	d1dnla_	Alignment	not modelled	75.1	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
45	c4ybnB_	Alignment	not modelled	72.3	15	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
46	c3u34D_	Alignment	not modelled	71.5	11	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	c5bncB_	Alignment	not modelled	65.7	8	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
48	d2vpaa1	Alignment	not modelled	62.4	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
49	d2ptfa1	Alignment	not modelled	60.5	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
50	d2fg9a1	Alignment	not modelled	60.1	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
51	c2i51B_	Alignment	not modelled	55.6	10	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
52	d2imla1	Alignment	not modelled	53.4	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
53	c2ntfB_	Alignment	not modelled	49.1	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein mth_863;

53	c2pud_	Alignment	not modelled	48.1	10	PDBTitle: crystal structure of protein mth_863 from methanobacterium2 thermoautotrophicum bound to fmn
54	d1flma_	Alignment	not modelled	45.7	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
55	c2qeaB_	Alignment	not modelled	39.7	16	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
56	c2levA_	Alignment	not modelled	39.3	28	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ler; PDBTitle: structure of the dna complex of the c-terminal domain of ler
57	c3gasA_	Alignment	not modelled	31.0	10	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
58	c4n7rD_	Alignment	not modelled	28.5	13	PDB header: oxidoreductase/protein binding Chain: D: PDB Molecule: genomic dna, chromosome 3, p1 clone: mx18; PDBTitle: crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein
59	d1hnra_	Alignment	not modelled	26.9	17	Fold: H-NS histone-like proteins Superfamily: H-NS histone-like proteins Family: H-NS histone-like proteins
60	c2ou5B_	Alignment	not modelled	18.6	11	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
61	c2w8xB_	Alignment	not modelled	12.1	29	PDB header: membrane protein Chain: B: PDB Molecule: ion-channel modulator raklp; PDBTitle: structure of the tick ion-channel modulator ra-klp
62	c1worA_	Alignment	not modelled	9.7	13	PDB header: transferase Chain: A: PDB Molecule: aminomethyltransferase; PDBTitle: crystal structure of t-protein of the glycine cleavage2 system
63	c6mk1V_	Alignment	not modelled	9.3	33	PDB header: protein fibril Chain: V: PDB Molecule: PDBTitle: cryo-em of self-assembly peptide filament heat_r1
64	c1ztnA_	Alignment	not modelled	8.4	67	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
65	d1khba2	Alignment	not modelled	7.9	26	Fold: PEP carboxykinase N-terminal domain Superfamily: PEP carboxykinase N-terminal domain Family: PEP carboxykinase N-terminal domain