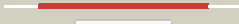



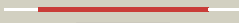







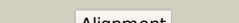




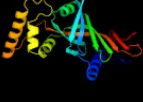









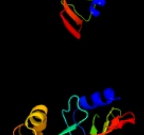
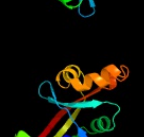

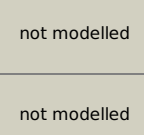


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2607_(pdxH)_2934208_2934882
 Date Wed Aug 7 12:50:25 BST 2019
 Unique Job ID ec2de9654be17e0e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2a2ja1	 Alignment		100.0	100	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
2	c2a2ja_	 Alignment		100.0	100	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
3	d1nrga_	 Alignment		100.0	39	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
4	c1nrgA_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: A; PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
5	d1ci0a_	 Alignment		100.0	37	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
6	d1dnja_	 Alignment		100.0	41	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
7	d1t9ma_	 Alignment		100.0	33	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
8	d1ty9a_	 Alignment		100.0	28	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
9	c4hmwB_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: B; PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phzg from burkholderia lata 383
10	c2i51B_	 Alignment		100.0	20	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
11	c2ou5B_	 Alignment		100.0	15	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

12	d2i02a1	Alignment		99.9	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
13	c3dmbA_	Alignment		99.9	16	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
14	d2hq7a1	Alignment		99.9	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
15	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
16	c2hhzA_	Alignment		99.9	17	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
17	d2fhqa1	Alignment		99.8	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
18	c3ec6A_	Alignment		99.8	18	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
19	c2iq6B_	Alignment		99.8	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
20	c3u34D_	Alignment		99.8	20	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
21	c3tgvD_	Alignment	not modelled	99.8	21	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
22	c3db0B_	Alignment	not modelled	99.8	18	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
23	d1vl7a_	Alignment	not modelled	99.8	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
24	c2iabB_	Alignment	not modelled	99.8	18	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
25	c2qeaB_	Alignment	not modelled	99.8	17	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
26	d2asfa1	Alignment	not modelled	99.7	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
27	d1rfea_	Alignment	not modelled	99.6	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
28	c3f7eB_	Alignment	not modelled	99.5	17	PDB header: unknown function Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeg_3380 f420 reductase

29	c2htdB_	Alignment	not modelled	99.5	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
30	d2htia1	Alignment	not modelled	99.5	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
31	c2htiA_	Alignment	not modelled	99.5	11	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
32	c5escD_	Alignment	not modelled	99.5	11	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
33	d1w9aa_	Alignment	not modelled	99.4	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
34	c2q9kA_	Alignment	not modelled	99.3	17	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
35	c4zkyB_	Alignment	not modelled	99.3	16	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5-phosphate oxidase; PDBTitle: structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis
36	d2arza1	Alignment	not modelled	99.2	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
37	d1flma_	Alignment	not modelled	99.1	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
38	c5bncB_	Alignment	not modelled	99.1	21	PDB header: heme binding protein Chain: B: PDB Molecule: heme binding protein msme_6519; PDBTitle: structure of heme binding protein msme_6519 from mycobacterium2 smegmatis
39	d2fg9a1	Alignment	not modelled	99.1	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
40	c3dnhB_	Alignment	not modelled	99.1	19	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
41	c3gasA_	Alignment	not modelled	99.0	14	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
42	d2hq9a1	Alignment	not modelled	98.9	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
43	c3ba3A_	Alignment	not modelled	98.9	19	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase-like protein; PDBTitle: crystal structure of pyridoxamine 5'-phosphate oxidase-like protein2 (np_78394.1) from lactobacillus plantarum at 1.55 a resolution
44	c3fkbB_	Alignment	not modelled	98.9	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 kitasato at3 2.51 a resolution
45	c6eciQ_	Alignment	not modelled	98.9	13	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
46	c3u0iA_	Alignment	not modelled	98.9	17	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
47	c3cp3A_	Alignment	not modelled	98.7	10	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
48	c4ybnB_	Alignment	not modelled	98.7	17	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
49	d2fura1	Alignment	not modelled	98.5	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
50	d1xhna1	Alignment	not modelled	98.4	23	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
51	d2vpaa1	Alignment	not modelled	98.1	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
52	c2ol5B_	Alignment	not modelled	98.0	15	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
53	c6rk0A_	Alignment	not modelled	97.8	13	PDB header: flavoprotein Chain: A: PDB Molecule: uncharacterized protein;

53	c0rkvA_	Alignment	not modelled	97.8	15	PDBTitle: structure of the flavocytochrome anf3 from azotobacter vinelandii PDB header: oxidoreductase/protein binding Chain: D: PDB Molecule: genomic dna, chromosome 3, p1 clone: mxl8;
54	c4n7rD_	Alignment	not modelled	97.2	17	PDBTitle: crystal structure of arabidopsis glutamyl-trna reductase in complex2 with its binding protein PDB header: unknown function Chain: C: PDB Molecule: putative uncharacterized protein;
55	c3r5yC_	Alignment	not modelled	96.8	17	PDBTitle: structure of a deazaflavin-dependent nitroreductase from nocardia2 farcinica, with co-factor f420 PDB header: unknown function
56	c3r5zB_	Alignment	not modelled	96.6	15	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	96.2	14	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	96.1	15	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	96.1	18	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
60	c2ptfB_	Alignment	not modelled	81.7	6	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
61	d2ptfa1	Alignment	not modelled	72.7	6	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
62	c3psqA_	Alignment	not modelled	40.9	18	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical exported protein; PDBTitle: crystal structure of spy0129, a streptococcus pyogenes class b sortase2 involved in pilus biogenesis
63	c5vb0E_	Alignment	not modelled	38.9	14	PDB header: transferase Chain: E: PDB Molecule: fosfomycin resistance protein fosa3; PDBTitle: crystal structure of fosfomycin resistance protein fosa3
64	c3bjqA_	Alignment	not modelled	35.3	16	PDB header: viral protein Chain: A: PDB Molecule: phage-related protein; PDBTitle: crystal structure of a phage-related protein (bb3626) from bordetella2 bronchiseptica rb50 at 2.05 a resolution
65	c5yfkA_	Alignment	not modelled	34.0	18	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein sortase b; PDBTitle: x-ray structure of a mutant form c232s of clostridium perfringens2 sortase b
66	c5b23B_	Alignment	not modelled	27.2	13	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein sortase b; PDBTitle: x-ray structure of clostridium perfringens sortase b
67	d2imla1	Alignment	not modelled	26.4	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
68	c3b5mD_	Alignment	not modelled	22.5	16	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
69	c6gf8B_	Alignment	not modelled	22.3	30	PDB header: cell adhesion Chain: B: PDB Molecule: zona pellucida sperm-binding protein 1,zona pellucida PDBTitle: molecular basis of egg coat filament cross-linking: structure of the2 glycosylated zp1 zp-n1 domain homodimer
70	c4ux7A_	Alignment	not modelled	21.7	22	PDB header: hydrolase Chain: A: PDB Molecule: putative peptidase c60b, sortase b; PDBTitle: structure of a clostridium difficile sortase
71	d1eoqa_	Alignment	not modelled	20.9	16	Fold: Acyl carrier protein-like Superfamily: Retrovirus capsid dimerization domain-like Family: Retrovirus capsid protein C-terminal domain
72	c4y4qA_	Alignment	not modelled	17.6	15	PDB header: hydrolase Chain: A: PDB Molecule: sortase, srtb family; PDBTitle: crystal structure of sortase b from type ii pilus of streptococcus2 pneumoniae
73	c5mrwG_	Alignment	not modelled	17.5	24	PDB header: hydrolase Chain: G: PDB Molecule: potassium-transporting atpase kdpc subunit; PDBTitle: structure of the kdpcfbc complex
74	d2oqza1	Alignment	not modelled	15.2	24	Fold: Sortase Superfamily: Sortase Family: Sortase
75	d1ejea_	Alignment	not modelled	14.6	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
76	c3lr4A_	Alignment	not modelled	14.3	16	PDB header: transferase Chain: A: PDB Molecule: sensor protein; PDBTitle: periplasmic domain of the riss sensor protein from burkholderia2 pseudomallei, barium phased at low ph
77	d1usca_	Alignment	not modelled	13.5	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
78	c4z85A_	Alignment	not modelled	12.8	8	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitrobenzoate nitroreductase; PDBTitle: crystal structur of pseudomonas fluorescens 2-nitrobenzoate 2-2 nitroreductase nbaa

79	d1in0a2	Alignment	not modelled	11.7	31	Fold: Ferredoxin-like Superfamily: YajQ-like Family: YajQ-like
80	c5cohA	Alignment	not modelled	11.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: frne protein; PDBTitle: crystal structure of a novel disulfide oxidoreductase from deinococcus2 radiodurans crystallized in presence of beta-mercaptoethanol
81	c5jcvA	Alignment	not modelled	10.9	24	PDB header: hydrolase Chain: A: PDB Molecule: lmo2181 protein; PDBTitle: sortase b from listeria monocytogenes.
82	d2nr4a1	Alignment	not modelled	10.5	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
83	c2kp7A	Alignment	not modelled	10.4	28	PDB header: hydrolase Chain: A: PDB Molecule: crossover junction endonuclease mus81; PDBTitle: solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
84	d2dbsa1	Alignment	not modelled	10.3	45	Fold: TTHC002-like Superfamily: TTHC002-like Family: TTHC002-like
85	c5ja9D	Alignment	not modelled	10.0	13	PDB header: toxin Chain: D: PDB Molecule: toxin higb-2; PDBTitle: crystal structure of the higb2 toxin in complex with nb6
86	d1qwza	Alignment	not modelled	9.8	22	Fold: Sortase Superfamily: Sortase Family: Sortase
87	c3bnkB	Alignment	not modelled	9.8	17	PDB header: electron transport Chain: B: PDB Molecule: flavoredoxin; PDBTitle: x-ray crystal structure of flavoredoxin from methanosarcina2 acetivorans
88	d1rz0a	Alignment	not modelled	9.3	9	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
89	c3sk7B	Alignment	not modelled	8.9	14	PDB header: replication inhibitor Chain: B: PDB Molecule: protein seqa; PDBTitle: crystal structure of v. cholerae seqa
90	c5fr7B	Alignment	not modelled	8.8	28	PDB header: signaling protein Chain: B: PDB Molecule: amyr; PDBTitle: erwinia amylovora amyr amylovoran repressor, a member of the ybjn2 protein family
91	c4l82D	Alignment	not modelled	8.7	7	PDB header: oxidoreductase Chain: D: PDB Molecule: rifea.00250.a; PDBTitle: structure of a putative oxidoreductase from rickettsia felis
92	c2yufA	Alignment	not modelled	8.5	24	PDB header: transcription Chain: A: PDB Molecule: ngfi-a-binding protein 1; PDBTitle: solution structure of the ncd2 domain in human2 transcriptional repressor nab1 protein
93	c4pl8H	Alignment	not modelled	8.2	20	PDB header: contractile protein/structural protein Chain: H: PDB Molecule: thymosin beta-4,protein cordon-bleu,thymosin beta-4; PDBTitle: structure of rabbit skeletal muscle actin in complex with a hybrid2 peptide comprising thymosin beta4 and the lysine-rich region of3 cordon-bleu
94	c1vw48	Alignment	not modelled	7.8	19	PDB header: ribosome Chain: 8: PDB Molecule: 54s ribosomal protein l13, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
95	c4aezC	Alignment	not modelled	7.6	14	PDB header: cell cycle Chain: C: PDB Molecule: mitotic spindle checkpoint component mad3; PDBTitle: crystal structure of mitotic checkpoint complex
96	d1i0ra	Alignment	not modelled	7.5	6	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
97	c1in0B	Alignment	not modelled	7.5	31	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: yajq protein; PDBTitle: yajq protein (hi1034)
98	c3fmtF	Alignment	not modelled	7.3	9	PDB header: replication inhibitor/dna Chain: F: PDB Molecule: protein seqa; PDBTitle: crystal structure of seqa bound to dna
99	c6raoF	Alignment	not modelled	7.1	21	PDB header: virus like particle Chain: F: PDB Molecule: afp5; PDBTitle: cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised