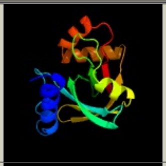
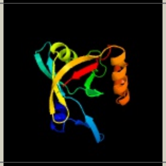
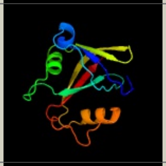
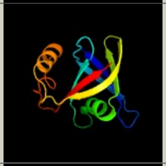
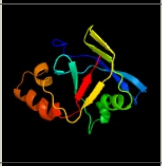
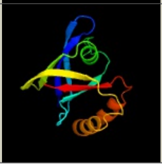
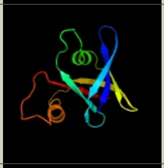
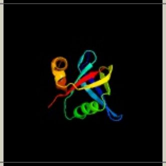
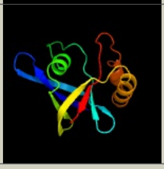
Email	mdejesus@rockefeller.edu
Description	RVBD3547_(-)_3987023_3987478
Date	Fri Aug 9 18:20:22 BST 2019
Unique Job ID	a9f0604c5d95243e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r5zB_	Alignment		100.0	41	**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
2	c3r5yC_	Alignment		100.0	40	**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
3	c3h96B_	Alignment		100.0	33	**PDB header:**flavoprotein **Chain:** B: **PDB Molecule:**f420-h2 dependent reductase a; **PDBTitle:** msmeg_3358 f420 reductase
4	c4y9iA_	Alignment		100.0	45	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**mycobacterium tuberculosis paralogous family 11; **PDBTitle:** structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
5	c3r5wO_	Alignment		100.0	100	**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
6	c3f7eB_	Alignment		99.0	24	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related, fmn- **PDBTitle:** msmeg_3380 f420 reductase
7	c2iabB_	Alignment		98.9	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
8	d1rfea_	Alignment		98.7	16	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
9	d2asfa1	Alignment		98.6	17	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
10	c4zkyB_	Alignment		98.5	24	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyridoxamine 5-phosphate oxidase; **PDBTitle:** structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis
11	c3tgvD_	Alignment		98.5	22	**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

12	d1w9aa_	Alignment		98.4	14	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
13	c3db0B_	Alignment		98.4	22	**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
14	d1vl7a_	Alignment		98.4	20	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
15	c2htiA_	Alignment		98.2	21	**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
16	d2htia1	Alignment		98.2	21	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
17	d2i02a1	Alignment		98.2	15	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
18	d2fg9a1	Alignment		98.2	16	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
19	d2hq9a1	Alignment		98.1	23	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
20	c3dnhB_	Alignment		98.1	18	**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
21	c5bncB_	Alignment	not modelled	98.0	18	**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
22	c2hhzA_	Alignment	not modelled	98.0	19	**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
23	d2arza1	Alignment	not modelled	98.0	27	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
24	c3ec6A_	Alignment	not modelled	97.9	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
25	c2ig6B_	Alignment	not modelled	97.9	22	**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
26	c2re7A_	Alignment	not modelled	97.9	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
27	c3gasA_	Alignment	not modelled	97.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**heme oxygenase; **PDBTitle:** crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
						Fold: Split barrel-like

28	d2hq7a1	Alignment	not modelled	97.8	14	**Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
29	d2a2ja1	Alignment	not modelled	97.8	11	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
30	d2fura1	Alignment	not modelled	97.7	20	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
31	c2a2jA_	Alignment	not modelled	97.7	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
32	d2fhqa1	Alignment	not modelled	97.6	24	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
33	c4ybnB_	Alignment	not modelled	97.6	24	**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
34	d1ty9a_	Alignment	not modelled	97.6	14	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
35	d1t9ma_	Alignment	not modelled	97.6	21	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
36	c3fkhB_	Alignment	not modelled	97.6	20	**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
37	c6eciQ_	Alignment	not modelled	97.6	21	**PDB header:**fad-binding protein **Chain:** Q: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase-related, fmn-binding **PDBTitle:** structure of the fad binding protein msmeg_5243 from mycobacterium2 smegmatis
38	c5escD_	Alignment	not modelled	97.5	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**hupz; **PDBTitle:** crystal structure of group a streptococcus hupz
39	c3u0iA_	Alignment	not modelled	97.4	19	**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
40	c2q9kA_	Alignment	not modelled	97.4	15	**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
41	c3cp3A_	Alignment	not modelled	97.3	19	**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
42	c2htdB_	Alignment	not modelled	97.3	23	**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
43	c1nrgA_	Alignment	not modelled	97.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**pyridoxine 5'-phosphate oxidase; **PDBTitle:** structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
44	d1nrga_	Alignment	not modelled	97.3	16	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
45	d1dnla_	Alignment	not modelled	97.3	15	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
46	c4hmwB_	Alignment	not modelled	97.3	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**pyridoxamine 5'-phosphate oxidase; **PDBTitle:** crystal structure of phzg from burkholderia lata 383
47	c3dmbA_	Alignment	not modelled	97.2	18	**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
48	c3u34D_	Alignment	not modelled	97.1	19	**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
49	c2qeaB_	Alignment	not modelled	96.8	21	**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
50	d1ci0a_	Alignment	not modelled	96.6	12	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
51	c6rk0A_	Alignment	not modelled	96.4	27	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** structure of the flavocytochrome anf3 from azotobacter vinelandii
52	d1xhna1	Alignment	not modelled	96.1	17	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like

53	d1flma_	Alignment	not modelled	95.8	21	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
54	d2vpaa1	Alignment	not modelled	94.3	19	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**PNP-oxidase like
55	d2ptfa1	Alignment	not modelled	88.1	16	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**MTH863-like
56	c2ptfB_	Alignment	not modelled	84.9	16	**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
57	c4n7rD_	Alignment	not modelled	84.4	12	**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	c2ou5B_	Alignment	not modelled	79.9	12	**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
59	c2ol5B_	Alignment	not modelled	79.7	17	**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
60	c2i51B_	Alignment	not modelled	71.4	9	**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
61	d2imla1	Alignment	not modelled	20.9	15	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**MTH863-like
62	c3fgeA_	Alignment	not modelled	17.6	8	**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	d1kb0a2	Alignment	not modelled	13.8	27	**Fold:**8-bladed beta-propeller **Superfamily:**Quinoprotein alcohol dehydrogenase-like **Family:**Quinoprotein alcohol dehydrogenase-like
64	c4a2nB_	Alignment	not modelled	13.0	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**isoprenylcysteine carboxyl methyltransferase; **PDBTitle:** crystal structure of ma-icmt
65	d1zq1c1	Alignment	not modelled	12.3	42	**Fold:**GatB/YqeY motif **Superfamily:**GatB/YqeY motif **Family:**GatB/GatE C-terminal domain-like
66	d1qrda_	Alignment	not modelled	12.0	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
67	c4z85A_	Alignment	not modelled	11.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-nitrobenzoate nitroreductase; **PDBTitle:** crystal structur of pseudomonas fluorescens 2-nitrobenzoate 2-2 nitroreductase nbaa
68	c3bpkB_	Alignment	not modelled	11.2	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase component b; **PDBTitle:** crystal structure of nitrilotriacetate monooxygenase component b from2 bacillus cereus
69	c4wt5A_	Alignment	not modelled	10.7	16	**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
70	c4u65A_	Alignment	not modelled	10.5	20	**PDB header:**transferase/hydrolase **Chain:** A: **PDB Molecule:**two component histidine kinase, ggdef domain protein/eal **PDBTitle:** structure of the periplasmic output domain of the legionella2 pneumophila lapd ortholog cdgs9 in complex with pseudomonas3 fluorescens lapg
71	d1dxqa_	Alignment	not modelled	9.6	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
72	c5v7pA_	Alignment	not modelled	9.2	32	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein-s-isoprenylcysteine o-methyltransferase; **PDBTitle:** atomic structure of the eukaryotic intramembrane ras methyltransferase2 icmt (isoprenylcysteine carboxyl methyltransferase), in complex with3 a monobody
73	d1dgsa3	Alignment	not modelled	9.0	14	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
74	d2nr4a1	Alignment	not modelled	8.7	21	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**MTH863-like
75	d1d4aa_	Alignment	not modelled	8.6	20	**Fold:**Flavodoxin-like **Superfamily:**Flavoproteins **Family:**Quinone reductase
76	c2dhyA_	Alignment	not modelled	8.1	24	**PDB header:**immune system **Chain:** A: **PDB Molecule:**cue domain-containing protein 1; **PDBTitle:** solution structure of the cue domain in the human cue2

						domain containing protein 1 (cuedc1)
77	d1k3ra1	Alignment	not modelled	7.1	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Hypothetical protein MTH1 (MT0001), insert domain
78	c2levA_	Alignment	not modelled	6.8	24	**PDB header:**transcription regulator/dna **Chain:** A: **PDB Molecule:**ler; **PDBTitle:** structure of the dna complex of the c-terminal domain of ler
79	c6mk1V_	Alignment	not modelled	6.8	67	**PDB header:**protein fibril **Chain:** V: **PDB Molecule:** **PDBTitle:** cryo-em of self-assembly peptide filament heat_r1
80	c2amjD_	Alignment	not modelled	6.7	17	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**modulator of drug activity b; **PDBTitle:** crystal structure of modulator of drug activity b from escherichia2 coli o157:h7
81	c3gr1A_	Alignment	not modelled	5.8	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein prgh; **PDBTitle:** periplasmic domain of the t3ss inner membrane protein prgh from2 s.typhimurium (fragment 170-392)
82	d3cx5g1	Alignment	not modelled	5.7	15	**Fold:**14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Superfamily:**14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**14 kDa protein of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
83	c3b5mD_	Alignment	not modelled	5.5	22	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
84	c5jfzB_	Alignment	not modelled	5.2	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uncharacterized protein yhfg; **PDBTitle:** e. coli ecfict in complex with ecfica mutant e28g
85	c5jfzF_	Alignment	not modelled	5.2	18	**PDB header:**transferase **Chain:** F: **PDB Molecule:**uncharacterized protein yhfg; **PDBTitle:** e. coli ecfict in complex with ecfica mutant e28g
86	c1zauA_	Alignment	not modelled	5.2	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** adenylation domain of nad+ dependent dna ligase from m.tuberculosis
87	c1cpbA_	Alignment	not modelled	5.1	21	**PDB header:**hydrolase (c-terminal peptidase) **Chain:** A: **PDB Molecule:**carboxypeptidase b; **PDBTitle:** structure of carboxypeptidase b at 2.8 angstroms resolution
88	d1v9pa3	Alignment	not modelled	5.0	15	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase