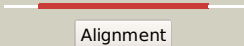

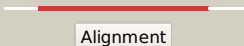

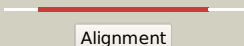







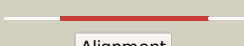











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1261c_(-)_1409490_1409939
Date	Wed Jul 31 22:05:35 BST 2019
Unique Job ID	b1b1eca897da1a2c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r5zB_	 Alignment		100.0	37	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	30	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	29	PDB header: flavoprotein Chain: B; PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeq_3358 f420 reductase
4	c3r5wO_	 Alignment		100.0	42	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	37	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		98.9	19	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		98.8	20	PDB header: unknown function Chain: B; PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeq_3380 f420 reductase
8	d1rfea_	 Alignment		98.7	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
9	c3tgvD_	 Alignment		98.6	18	PDB header: heme binding protein Chain: D; PDB Molecule: heme-binding protein hutz; PDBTitle: crystal structure of hutz, the heme storage protein from vibrio2 cholerae
10	d2asfa1	 Alignment		98.6	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
11	d1vl7a_	 Alignment		98.5	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like

12	c4zkyB_	Alignment		98.5	17	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5-phosphate oxidase; PDBTitle: structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis
13	d1w9aa_	Alignment		98.5	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
14	d2htia1	Alignment		98.4	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
15	c2htiA_	Alignment		98.4	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
16	c3db0B_	Alignment		98.4	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
17	d2fg9a1	Alignment		98.4	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
18	d2i02a1	Alignment		98.3	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
19	d2hq7a1	Alignment		98.1	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
20	d2hq9a1	Alignment		98.1	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
21	c3ec6A_	Alignment	not modelled	98.0	11	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
22	c2ig6B_	Alignment	not modelled	98.0	19	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
23	c2re7A_	Alignment	not modelled	98.0	9	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
24	d2fura1	Alignment	not modelled	98.0	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
25	d2fhqa1	Alignment	not modelled	97.9	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
26	c3fkhB_	Alignment	not modelled	97.8	15	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
27	c3gasA_	Alignment	not modelled	97.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hug2 in complex with heme
						PDB header: unknown function Chain: A: PDB Molecule: probable fad-binding, putative

28	c3u0IA_	Alignment	not modelled	97.6	11	uncharacterized protein; PDBTitle: crystal structure of a probable fad-binding, putative uncharacterized2 protein from brucella melitensis
29	c2hhzA_	Alignment	not modelled	97.6	11	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
30	c5escD_	Alignment	not modelled	97.5	19	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
31	c6eciQ_	Alignment	not modelled	97.5	14	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
32	c2q9kA_	Alignment	not modelled	97.4	14	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
33	c4ybnB_	Alignment	not modelled	97.3	19	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
34	c3cp3A_	Alignment	not modelled	97.3	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
35	c3u34D_	Alignment	not modelled	97.2	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
36	c2qeaB_	Alignment	not modelled	97.1	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
37	c3dmbA_	Alignment	not modelled	97.0	9	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
38	c3dnhB_	Alignment	not modelled	97.0	12	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
39	d2arza1	Alignment	not modelled	96.8	23	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
40	c2htdB_	Alignment	not modelled	96.8	22	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
41	c5bncB_	Alignment	not modelled	96.7	20	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
42	c6rk0A_	Alignment	not modelled	96.7	15	PDB header: flavoprotein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the flavocytochrome anf3 from azotobacter vinelandii
43	d2a2ja1	Alignment	not modelled	96.6	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
44	d1t9ma_	Alignment	not modelled	96.6	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
45	c1nrgA_	Alignment	not modelled	96.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
46	d1nrga_	Alignment	not modelled	96.5	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
47	c2a2jA_	Alignment	not modelled	96.2	13	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
48	d1ty9a_	Alignment	not modelled	95.9	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
49	c4hmwB_	Alignment	not modelled	95.7	12	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phgz from burkholderia lata 383
50	d1flma_	Alignment	not modelled	94.9	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
51	d1ci0a_	Alignment	not modelled	94.0	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
52	d1dnla_	Alignment	not modelled	93.8	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like

53	d2vpaa1	Alignment	not modelled	89.3	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
54	d2ptfa1	Alignment	not modelled	87.7	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
55	c2ptfB	Alignment	not modelled	86.9	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
56	c2ou5B	Alignment	not modelled	85.0	24	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
57	d1xhna1	Alignment	not modelled	84.7	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
58	c2ol5B	Alignment	not modelled	78.2	12	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
59	c4n7rD	Alignment	not modelled	61.4	12	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
60	c2i51B	Alignment	not modelled	36.9	17	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	c4a2nB	Alignment	not modelled	29.0	26	PDB header: transferase Chain: B: PDB Molecule: isoprenylcysteine carboxyl methyltransferase; PDBTitle: crystal structure of ma-icmt
62	d2imla1	Alignment	not modelled	25.3	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
63	c5v7pA	Alignment	not modelled	24.9	19	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
64	c4u65A	Alignment	not modelled	22.0	17	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
65	d2nr4a1	Alignment	not modelled	10.5	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
66	c4wt5A	Alignment	not modelled	10.5	26	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
67	c5d5pC	Alignment	not modelled	9.4	32	PDB header: transferase Chain: C: PDB Molecule: hcgB; PDBTitle: hcgB from methanococcus maripaludis
68	c3brcA	Alignment	not modelled	7.9	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein of unknown function; PDBTitle: crystal structure of a conserved protein of unknown function from2 methanobacterium thermoautotrophicum
69	c2levA	Alignment	not modelled	7.3	29	PDB header: transcription regulator/dna Chain: A: PDB Molecule: ler; PDBTitle: structure of the dna complex of the c-terminal domain of ler
70	d1kb0a2	Alignment	not modelled	7.3	36	Fold: 8-bladed beta-propeller Superfamily: Quinoprotein alcohol dehydrogenase-like Family: Quinoprotein alcohol dehydrogenase-like
71	c6mk1V	Alignment	not modelled	7.0	50	PDB header: protein fibril Chain: V: PDB Molecule: PDBTitle: cryo-em of self-assembly peptide filament heat_r1
72	c3fgeA	Alignment	not modelled	6.3	9	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
73	c3b5mD	Alignment	not modelled	6.1	24	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
74	c4fprC	Alignment	not modelled	6.0	43	PDB header: protein binding Chain: C: PDB Molecule: avirulence effector avrlm4-7; PDBTitle: structure of a fungal protein
75	c1ztnA	Alignment	not modelled	5.2	33	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
76	c6d10A	Alignment	not modelled	5.1	20	PDB header: cell adhesion Chain: A: PDB Molecule: alginate biosynthesis protein algf;

