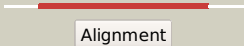

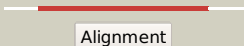

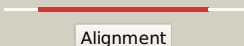







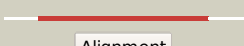




















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3369 (-)_3781158_3781592
Date	Fri Aug 9 18:20:03 BST 2019
Unique Job ID	cc89dfe7dd3f596e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3f7eB_	 Alignment		99.9	23	PDB header: unknown function Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeg_3380 f420 reductase
2	d1w9aa_	 Alignment		99.9	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
3	d1rfea_	 Alignment		99.9	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
4	d2asfa1	 Alignment		99.9	23	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
5	c2iabB_	 Alignment		99.9	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
6	c3tgvD_	 Alignment		99.9	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
7	c4zkyB_	 Alignment		99.9	18	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5-phosphate oxidase; PDBTitle: structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis
8	c3db0B_	 Alignment		99.9	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
9	d2i02a1	 Alignment		99.9	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
10	d2fhqa1	 Alignment		99.9	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
11	c3ec6A_	 Alignment		99.9	20	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

12	d2hq7a1	Alignment		99.9	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
13	d2fg9a1	Alignment		99.9	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
14	c2re7A_	Alignment		99.9	12	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
15	d2hq9a1	Alignment		99.9	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
16	d1vl7a_	Alignment		99.9	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
17	c3u0iA_	Alignment		99.9	10	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
18	c2htdB_	Alignment		99.9	21	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
19	d2htia1	Alignment		99.8	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
20	c2htiA_	Alignment		99.8	16	PDB header: fmn-binding protein Chain: A: PDB Molecule: bh0577 protein; PDBTitle: crystal structure of a putative general stress protein (bh_0577)2 from bacillus halodurans at 2.50 a resolution
21	c5escD_	Alignment	not modelled	99.8	16	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
22	c3fkhB_	Alignment	not modelled	99.8	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
23	c6eciQ_	Alignment	not modelled	99.8	15	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
24	d2arza1	Alignment	not modelled	99.8	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
25	c3u34D_	Alignment	not modelled	99.8	13	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
26	c2qeaB_	Alignment	not modelled	99.8	18	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
27	c2ig6B_	Alignment	not modelled	99.8	12	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
28	c5hncB_	Alignment	not modelled	99.8	14	PDB header: heme binding protein Chain: B: PDB Molecule: heme binding protein msmeq_6519;

28	c3unrB	Alignment	not modelled	99.8	14	PDBTitle: structure of heme binding protein msmeg_6519 from mycobacterium2 smegmatis PDB header: oxidoreductase Chain: A: PDB Molecule: putative general stress protein 26 with a pnp-oxidase like
29	c3dmbA	Alignment	not modelled	99.8	12	PDBTitle: crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related;
30	c2hhzA	Alignment	not modelled	99.8	14	PDBTitle: crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution
31	d2fura1	Alignment	not modelled	99.8	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
32	d1flma	Alignment	not modelled	99.8	23	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
33	c2q9kA	Alignment	not modelled	99.8	16	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
34	c3gasA	Alignment	not modelled	99.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
35	c3cp3A	Alignment	not modelled	99.8	18	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	c3dnhB	Alignment	not modelled	99.8	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
37	c4ybnB	Alignment	not modelled	99.8	15	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
38	d2vpaa1	Alignment	not modelled	99.7	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
39	c6rk0A	Alignment	not modelled	99.7	11	PDB header: flavoprotein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the flavocytochrome anf3 from azotobacter vinelandii
40	d1t9ma	Alignment	not modelled	99.7	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
41	d1ty9a	Alignment	not modelled	99.7	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
42	c4hmwB	Alignment	not modelled	99.6	17	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phzg from burkholderia lata 383
43	d1dnla	Alignment	not modelled	99.6	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
44	c1nrgA	Alignment	not modelled	99.6	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
45	d1nrga	Alignment	not modelled	99.6	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
46	d2a2ja1	Alignment	not modelled	99.6	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
47	c2a2jA	Alignment	not modelled	99.6	21	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	c2ou5B	Alignment	not modelled	99.6	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
49	c2o15B	Alignment	not modelled	99.5	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
50	d1xhna1	Alignment	not modelled	99.5	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
51	c2i51B	Alignment	not modelled	99.4	19	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	d1ci0a	Alignment	not modelled	99.3	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like

53	c4n7rD_	Alignment	not modelled	99.1	14	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
54	c3r5zB_	Alignment	not modelled	98.7	19	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
55	c3r5yC_	Alignment	not modelled	98.6	19	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
56	c3r5wO_	Alignment	not modelled	98.6	18	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
57	c3h96B_	Alignment	not modelled	98.6	14	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
58	c3ba3A_	Alignment	not modelled	98.4	11	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase-like protein; PDBTitle: crystal structure of pyridoxamine 5'-phosphate oxidase-like protein2 (np_783940.1) from lactobacillus plantarum at 1.55 a resolution
59	c4y9iA_	Alignment	not modelled	98.3	16	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
60	d2ptfa1	Alignment	not modelled	97.0	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
61	c2ptfB_	Alignment	not modelled	96.5	13	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
62	d2imla1	Alignment	not modelled	95.7	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
63	c3b5mD_	Alignment	not modelled	94.6	9	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
64	c3fgeA_	Alignment	not modelled	93.8	13	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
65	d2nr4a1	Alignment	not modelled	93.0	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
66	d1ejea_	Alignment	not modelled	92.9	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
67	c3bpbB_	Alignment	not modelled	92.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nitritotriacetate monooxygenase component b; PDBTitle: crystal structure of nitritotriacetate monooxygenase component b from2 bacillus cereus
68	c3e4vA_	Alignment	not modelled	92.4	11	PDB header: flavoprotein Chain: A: PDB Molecule: nadh:fmn oxidoreductase like protein; PDBTitle: crystal structure of nadh:fmn oxidoreductase like protein in complex2 with fmn (yp_544701.1) from methylobacillus flagellatus kt at 1.40 a3 resolution
69	c4z85A_	Alignment	not modelled	91.6	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitrobenzoate nitroreductase; PDBTitle: crystal structur of pseudomonas fluorescens 2-nitrobenzoate 2-2 nitroreductase nbaa
70	c2d5mA_	Alignment	not modelled	83.9	13	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: flavodoxin of desulfovibrio vulgaris (miyazaki f)
71	c4f07A_	Alignment	not modelled	80.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: styrene monooxygenase component 2; PDBTitle: structure of the styrene monooxygenase flavin reductase (smob) from2 pseudomonas putida s12
72	c4l82D_	Alignment	not modelled	77.3	3	PDB header: oxidoreductase Chain: D: PDB Molecule: rifea.00250.a; PDBTitle: structure of a putative oxidoreductase from rickettsia felis
73	c3bnkB_	Alignment	not modelled	76.5	15	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: x-ray crystal structure of flavodoxin from methanosarcina2 acetivorans
74	c3hzmA_	Alignment	not modelled	72.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase domain protein, fmn-binding; PDBTitle: crystal structure of a fmn-binding domain of flavin reductases-like2 enzyme (sba1_0626) from shewanella baltica os155 at 1.50 a resolution
75	c2d38A_	Alignment	not modelled	69.5	9	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical nadh-dependent fmn oxidoreductase; PDBTitle: the crystal structure of flavin reductase hpac complexed with nadp+
						PDB header: oxidoreductase

76	c2qckA	Alignment	not modelled	68.6	9	Chain: A: PDB Molecule: flavin reductase domain protein; PDBTitle: crystal structure of flavin reductase domain protein (yp_831077.1)2 from arthrobacter sp. fb24 at 1.90 a resolution
77	c4xhyA	Alignment	not modelled	68.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase domain protein, fmn-binding protein; PDBTitle: nadh:fmn oxidoreductase from paracoccus denitrificans
78	c3pftA	Alignment	not modelled	68.4	4	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase; PDBTitle: crystal structure of untaged c54a mutant flavin reductase (dszd) in2 complex with fmn from mycobacterium goodii
79	c3rh7A	Alignment	not modelled	64.8	13	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical oxidoreductase; PDBTitle: crystal structure of a putative oxidoreductase (sma0793) from2 sinorhizobium meliloti 1021 at 3.00 a resolution
80	c3cb0B	Alignment	not modelled	62.9	8	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxyphenylacetate 3-monoxygenase; PDBTitle: cobr
81	d1lusca	Alignment	not modelled	59.3	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
82	c2r6vA	Alignment	not modelled	57.2	11	PDB header: flavoprotein Chain: A: PDB Molecule: uncharacterized protein ph0856; PDBTitle: crystal structure of fmn-binding protein (np_142786.1) from pyrococcus2 horikoshii at 1.35 a resolution
83	d1i0ra	Alignment	not modelled	55.2	8	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
84	d1rz0a	Alignment	not modelled	54.3	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
85	c3k87B	Alignment	not modelled	50.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: chlorophenol-4-monoxygenase component 1; PDBTitle: crystal structure of nadh:fad oxidoreductase (tftc) - fad2 complex
86	c2r0xA	Alignment	not modelled	47.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: possible flavin reductase; PDBTitle: crystal structure of a putative flavin reductase (ycdh_hs_1225) from2 haemophilus somnus 129pt at 1.06 a resolution
87	c3ipzA	Alignment	not modelled	47.2	16	PDB header: electron transport, oxidoreductase Chain: A: PDB Molecule: monothiol glutaredoxin-s14, chloroplastic; PDBTitle: crystal structure of arabidopsis monothiol glutaredoxin atgrxcp
88	c2ecrA	Alignment	not modelled	43.4	6	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase component (hpac) of 4-hydroxyphenylacetate PDBTitle: crystal structure of the ligand-free form of the flavin reductase2 component (hpac) of 4-hydroxyphenylacetate 3-monoxygenase
89	d2d9ra1	Alignment	not modelled	42.3	13	Fold: Double-split beta-barrel Superfamily: AF2212/PG0164-like Family: PG0164-like
90	d1wgba	Alignment	not modelled	36.9	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
91	c3nfwB	Alignment	not modelled	36.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin reductase-like, fmn-binding protein; PDBTitle: crystal structure of nitrilotriacetate monoxygenase component b2 (a0r521 homolog) from mycobacterium thermoresistibile
92	d1e5ra	Alignment	not modelled	28.6	9	Fold: Double-stranded beta-helix Superfamily: Clavaminatase synthase-like Family: Type II Proline 3-hydroxylase (proline oxidase)
93	c4p7xA	Alignment	not modelled	24.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: l-proline cis-4-hydroxylase; PDBTitle: l-pipecolic acid-bound l-proline cis-4-hydroxylase
94	c4hx6D	Alignment	not modelled	24.7	9	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: streptomyces globisporus c-1027 nadh:fad oxidoreductase sgce6
95	c3zywB	Alignment	not modelled	19.8	10	PDB header: metal binding protein Chain: B: PDB Molecule: glutaredoxin-3; PDBTitle: crystal structure of the first glutaredoxin domain of human2 glutaredoxin 3 (glrx3)
96	d1qnaa2	Alignment	not modelled	18.2	22	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
97	d1lisa2	Alignment	not modelled	17.8	25	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
98	d1nh2a2	Alignment	not modelled	16.8	19	Fold: TBP-like Superfamily: TATA-box binding protein-like Family: TATA-box binding protein (TBP), C-terminal domain
99	d2es2a1	Alignment	not modelled	15.1	16	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like