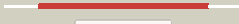



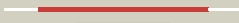



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0580c (-) _677128_677619
Date	Fri Jul 26 01:50:13 BST 2019
Unique Job ID	2c3a1497ca41abf4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r5yC_	 Alignment		100.0	22	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
2	c3r5zB_	 Alignment		100.0	16	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
3	c3h96B_	 Alignment		100.0	19	PDB header: flavoprotein Chain: B; PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
4	c3r5wO_	 Alignment		100.0	19	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		99.9	19	PDB header: oxidoreductase Chain: A; PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
6	c2iabB_	 Alignment		98.9	17	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	d1rfea_	 Alignment		98.8	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
8	d1w9aa_	 Alignment		98.6	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
9	c3f7eB_	 Alignment		98.6	17	PDB header: unknown function Chain: B; PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeg_3380 f420 reductase
10	d2asfa1	 Alignment		98.6	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
11	d2i02a1	 Alignment		98.4	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like

12	c3db0B_	Alignment		98.4	16	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
13	c3tgvD_	Alignment		98.3	10	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
14	c4zkyB_	Alignment		98.2	14	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5-phosphate oxidase; PDBTitle: structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis
15	d2hq7a1	Alignment		98.1	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
16	c3ec6A_	Alignment		98.1	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
17	c2htia_	Alignment		98.0	12	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
18	d2htia1	Alignment		98.0	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
19	c2re7A_	Alignment		97.9	20	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
20	d2fg9a1	Alignment		97.9	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
21	d2fura1	Alignment	not modelled	97.9	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
22	d1vl7a_	Alignment	not modelled	97.9	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
23	d2fhqa1	Alignment	not modelled	97.9	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
24	d2hq9a1	Alignment	not modelled	97.8	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
25	c2ig6B_	Alignment	not modelled	97.7	11	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	c3gasA_	Alignment	not modelled	97.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
27	c3fkhB_	Alignment	not modelled	97.5	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
28	c3u0iA_	Alignment	not modelled	97.4	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
29	c4ybnB_	Alignment	not modelled	97.4	25 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
30	c5escD_	Alignment	not modelled	97.4	17 PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
31	c3cp3A_	Alignment	not modelled	97.3	11 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
32	c2qeaB_	Alignment	not modelled	97.3	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
33	d2arza1	Alignment	not modelled	97.2	16 Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
34	c2q9kA_	Alignment	not modelled	97.2	4 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	c6eciQ_	Alignment	not modelled	97.2	15 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
36	c3u34D_	Alignment	not modelled	97.1	17 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
37	c3dmbA_	Alignment	not modelled	97.1	19 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	97.1	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
39	d1t9ma_	Alignment	not modelled	97.1	12 Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
40	c2htdB_	Alignment	not modelled	96.8	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
41	c2hhzA_	Alignment	not modelled	96.8	8 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
42	c5bncB_	Alignment	not modelled	96.7	11 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
43	c6rk0A_	Alignment	not modelled	96.5	20 PDB header: flavoprotein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the flavocytochrome anf3 from azotobacter vinelandii
44	c4n7rD_	Alignment	not modelled	96.1	11 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
45	d1ty9a_	Alignment	not modelled	95.6	10 Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
46	c1nrgA_	Alignment	not modelled	95.4	12 PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
47	d1nrga_	Alignment	not modelled	95.4	12 Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
48	c4hmwB_	Alignment	not modelled	94.9	13 PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phgz from burkholderia lata 383
49	c2ou5B_	Alignment	not modelled	93.7	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
50	d1ci0a_	Alignment	not modelled	93.5	18 Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
51	d2a2ja1	Alignment	not modelled	93.4	12 Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
52	c2a2ja1	Alignment	not modelled	93.4	12 PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase;

52	c4azjA	Alignment	not modelled	92.8	12	PDBTitle: crystal structure of a putative pyridoxine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis
53	d2vpaa1	Alignment	not modelled	91.7	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
54	d1xhna1	Alignment	not modelled	88.8	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
55	d1dnla	Alignment	not modelled	87.6	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
56	d1flma	Alignment	not modelled	84.0	9	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
57	c2ol5B	Alignment	not modelled	81.0	13	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
58	c2ptfB	Alignment	not modelled	72.6	15	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
59	d2ptfa1	Alignment	not modelled	71.2	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
60	c2i51B	Alignment	not modelled	33.0	15	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	d1aopa2	Alignment	not modelled	23.0	25	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
62	c3opyG	Alignment	not modelled	11.3	16	PDB header: transferase Chain: G: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
63	c5zdcL	Alignment	not modelled	11.2	19	PDB header: hydrolase Chain: L: PDB Molecule: poly adp-ribose glycohydrolase; PDBTitle: crystal structure of poly(adp-ribose) glycohydrolase (parg) from2 deinococcus radiodurans in complex with adp-ribose (p32)
64	d2nr4a1	Alignment	not modelled	10.1	7	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
65	d1zj8a1	Alignment	not modelled	10.1	24	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
66	c1ztnA	Alignment	not modelled	10.0	38	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
67	c3zfnA	Alignment	not modelled	10.0	26	PDB header: hydrolase Chain: A: PDB Molecule: n-terminal protease npro; PDBTitle: crystal structure of product-like, processed n-terminal protease npro
68	d1w7ca3	Alignment	not modelled	9.1	24	Fold: Cystatin-like Superfamily: Amine oxidase N-terminal region Family: Amine oxidase N-terminal region
69	c2cqyA	Alignment	not modelled	8.8	8	PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, PDBTitle: solution structure of b domain from human propionyl-coa2 carboxylase alpha subunit
70	c3opyE	Alignment	not modelled	7.8	16	PDB header: transferase Chain: E: PDB Molecule: 6-phosphofructo-1-kinase alpha-subunit; PDBTitle: crystal structure of pichia pastoris phosphofructokinase in the t-2 state
71	d2imla1	Alignment	not modelled	7.2	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
72	d1ku2a1	Alignment	not modelled	6.4	50	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Sigma3 and sigma4 domains of RNA polymerase sigma factors Family: Sigma3 domain
73	d1v7wa2	Alignment	not modelled	5.5	23	Fold: Supersandwich Superfamily: Galactose mutarotase-like Family: Glycosyltransferase family 36 N-terminal domain
74	c4wt5A	Alignment	not modelled	5.5	12	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
75	c1vi7A	Alignment	not modelled	5.5	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein yigz; PDBTitle: crystal structure of an hypothetical protein