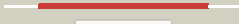



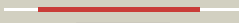
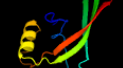











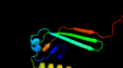

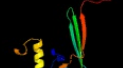




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3129 (-)_3494657_3494989
Date	Thu Aug 8 16:20:31 BST 2019
Unique Job ID	3b501ce3b0e0aeb8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fkhB_	 Alignment		100.0	41	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
2	c6eciQ_	 Alignment		99.9	61	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
3	c3cp3A_	 Alignment		99.9	37	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
4	c3u0iA_	 Alignment		99.9	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
5	d2hq9a1	 Alignment		99.8	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
6	d2fg9a1	 Alignment		99.7	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
7	c2htiA_	 Alignment		99.7	22	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
8	d2htia1	 Alignment		99.7	22	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
9	d2fura1	 Alignment		99.7	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
10	c6rk0A_	 Alignment		99.6	14	PDB header: flavoprotein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the flavocytochrome anf3 from azotobacter vinelandii
11	d2vpaa1	 Alignment		99.5	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like

12	d1rfea_	Alignment		99.5	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
13	c4ybnB_	Alignment		99.4	9	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
14	c4zkyB_	Alignment		99.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5-phosphate oxidase; PDBTitle: structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis
15	c3db0B_	Alignment		99.3	11	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
16	c3ec6A_	Alignment		99.2	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
17	d2asfa1	Alignment		99.2	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
18	d2i02a1	Alignment		99.1	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
19	c3f7eB_	Alignment		99.1	16	PDB header: unknown function Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeg_3380 f420 reductase
20	c2re7A_	Alignment		99.1	14	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
21	c2ol5B_	Alignment	not modelled	99.0	11	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
22	c3dmbA_	Alignment	not modelled	98.9	14	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
23	d2hq7a1	Alignment	not modelled	98.9	4	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
24	d2fhqa1	Alignment	not modelled	98.9	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
25	c2iabB_	Alignment	not modelled	98.8	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
26	c3u34D_	Alignment	not modelled	98.7	14	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
27	c2qeaB_	Alignment	not modelled	98.7	15	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
28	c2iq6B_	Alignment	not modelled	98.6	8	PDB header: oxidoreductase Chain: B: PDB Molecule: nimc/nima family protein;

28	c2tqub_	Alignment	not modelled	98.8	8	PDBTitle: crystal structure of a nimc/nima family protein (ca_c2569) from2 clostridium acetobutylicum at 1.80 a resolution
29	d1w9aa_	Alignment	not modelled	98.5	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
30	c5escD_	Alignment	not modelled	98.4	8	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
31	c2htdB_	Alignment	not modelled	98.4	18	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
32	c3tgvD_	Alignment	not modelled	98.4	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
33	d1vl7a_	Alignment	not modelled	98.1	9	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
34	c2ou5B_	Alignment	not modelled	98.0	20	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
35	d2arza1	Alignment	not modelled	97.9	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
36	d1flma_	Alignment	not modelled	97.9	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
37	c2hhzA_	Alignment	not modelled	97.8	13	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
38	c5bncB_	Alignment	not modelled	97.7	7	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
39	c1nrgA_	Alignment	not modelled	97.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
40	d1nrga_	Alignment	not modelled	97.6	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
41	d1ty9a_	Alignment	not modelled	97.5	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
42	d1dnla_	Alignment	not modelled	97.5	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
43	d1t9ma_	Alignment	not modelled	97.3	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
44	d2a2ja1	Alignment	not modelled	97.3	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
45	c2q9kA_	Alignment	not modelled	97.2	6	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
46	c2a2jA_	Alignment	not modelled	97.1	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
47	c3dnhB_	Alignment	not modelled	97.1	10	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
48	c3gasA_	Alignment	not modelled	96.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
49	c4hmwB_	Alignment	not modelled	96.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phzg from burkholderia lata 383
50	d1xhna1	Alignment	not modelled	96.6	5	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
51	c2i51B_	Alignment	not modelled	95.3	10	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	95.1	8	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
						PDB header: oxidoreductase/protein binding

53	c4n7rD_	Alignment	not modelled	91.2	7	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	d2es2a1	Alignment	not modelled	28.9	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
55	c3ba3A_	Alignment	not modelled	26.2	16	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
56	c3r5wO_	Alignment	not modelled	25.3	17	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	c3a0jB_	Alignment	not modelled	22.3	17	PDB header: transcription Chain: B: PDB Molecule: cold shock protein; PDBTitle: crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
58	d1c9oa_	Alignment	not modelled	18.3	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
59	c3r5yC_	Alignment	not modelled	17.3	20	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
60	c2k5nA_	Alignment	not modelled	17.1	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative cold-shock protein; PDBTitle: solution nmr structure of the n-terminal domain of protein eca15802 from erwinia carotovora, northeast structural genomics consortium3 target ewr156a
61	c1wrgA_	Alignment	not modelled	14.3	16	PDB header: membrane protein Chain: A: PDB Molecule: light-harvesting protein b-880, beta chain; PDBTitle: light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
62	c2mqhA_	Alignment	not modelled	14.3	19	PDB header: dna binding protein Chain: A: PDB Molecule: nucleic acid binding protein; PDBTitle: solution structure of the chlamydomonas reinhardtii nab1 cold shock2 domain, csd1
63	c2l55A_	Alignment	not modelled	13.9	17	PDB header: metal binding protein Chain: A: PDB Molecule: silb,silver efflux protein, mfp component of the three PDBTitle: solution structure of the c-terminal domain of silb from cupriavidus2 metallidurans
64	c4j5iH_	Alignment	not modelled	13.2	26	PDB header: oxidoreductase Chain: H: PDB Molecule: alpha-ketoglutarate-dependent taurine dioxygenase; PDBTitle: crystal structure of an alpha-ketoglutarate-dependent taurine2 dioxygenase from mycobacterium smegmatis
65	c1zeqX_	Alignment	not modelled	13.1	20	PDB header: metal binding protein Chain: X: PDB Molecule: cation efflux system protein cusf; PDBTitle: 1.5 a structure of apo-cusf residues 6-88 from escherichia2 coli
66	d1wfga_	Alignment	not modelled	11.8	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
67	c2ytxA_	Alignment	not modelled	11.4	14	PDB header: rna binding protein Chain: A: PDB Molecule: cold shock domain-containing protein e1; PDBTitle: solution structure of the second cold-shock domain of the human2 kiaa0885 protein (unr protein)
68	c2kcmA_	Alignment	not modelled	11.1	14	PDB header: nucleic acid binding protein Chain: A: PDB Molecule: cold shock domain family protein; PDBTitle: solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a.
69	d1mjca_	Alignment	not modelled	10.8	19	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
70	c4a4iA_	Alignment	not modelled	10.7	13	PDB header: rna binding protein Chain: A: PDB Molecule: protein lin-28 homolog b; PDBTitle: crystal structure of the human lin28b cold shock domain
71	c3camB_	Alignment	not modelled	10.5	14	PDB header: gene regulation Chain: B: PDB Molecule: cold-shock domain family protein; PDBTitle: crystal structure of the cold shock domain protein from neisseria2 meningitidis
72	d1g6pa_	Alignment	not modelled	10.2	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
73	c2ytyA_	Alignment	not modelled	9.6	15	PDB header: rna binding protein Chain: A: PDB Molecule: cold shock domain-containing protein e1; PDBTitle: solution structure of the fourth cold-shock domain of the human2 kiaa0885 protein (unr protein)
74	c4k0dB_	Alignment	not modelled	8.0	32	PDB header: signaling protein Chain: B: PDB Molecule: periplasmic sensor hybrid histidine kinase; PDBTitle: periplasmic sensor domain of sensor histidine kinase, adeh_2942
75	c1n0wB_	Alignment	not modelled	8.0	56	PDB header: gene regulation/antitumor protein Chain: B: PDB Molecule: breast cancer type 2 susceptibility protein; PDBTitle: crystal structure of a rad51-brca2 brc repeat complex
76	c3qr5B_	Alignment	not modelled	6.7	15	PDB header: signaling protein Chain: B: PDB Molecule: cardiac ca2+ release channel; PDBTitle: structure of the first domain of a cardiac ryanodine receptor mutant2 with exon 3 deleted
						PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogue

77	c4y9IA_	Alignment	not modelled	6.7	13	family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeg_2027
78	c1kjkA_	Alignment	not modelled	6.6	35	PDB header: viral protein Chain: A; PDB Molecule: integrase; PDBTitle: solution structure of the lambda integrase amino-terminal2 domain
79	d1z1ba1	Alignment	not modelled	6.6	35	Fold: DNA-binding domain Superfamily: DNA-binding domain Family: lambda integrase N-terminal domain
80	c2lssA_	Alignment	not modelled	6.3	28	PDB header: rna binding protein, dna binding protein Chain: A; PDB Molecule: cold shock-like protein; PDBTitle: solution structure of the r. rickettsii cold shock-like protein
81	c5aj1A_	Alignment	not modelled	6.1	57	PDB header: structural protein Chain: A; PDB Molecule: swi/snf-related matrix-associated actin-dependent regulator PDBTitle: solution structure of the smarc domain
82	c6et5u_	Alignment	not modelled	6.0	21	PDB header: photosynthesis Chain: U; PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
83	c2yvtA_	Alignment	not modelled	5.8	19	PDB header: rna binding protein Chain: A; PDB Molecule: cold shock domain-containing protein e1; PDBTitle: solution structure of the fifth cold-shock domain of the human2 kiaa0885 protein (unr protein)
84	c3hr1A_	Alignment	not modelled	5.6	21	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: endonuclease-like protein; PDBTitle: crystal structure of a putative endonuclease-like protein (ngo0050)2 from neisseria gonorrhoeae
85	c5o6fA_	Alignment	not modelled	5.5	17	PDB header: dna binding protein Chain: A; PDB Molecule: cold-shock protein; PDBTitle: nmr structure of cold shock protein a from corynebacterium2 pseudotuberculosis
86	c3c66C_	Alignment	not modelled	5.5	40	PDB header: transferase Chain: C; PDB Molecule: pre-mrna polyadenylation factor fip1; PDBTitle: yeast poly(a) polymerase in complex with fip1 residues 80-105
87	c3c66D_	Alignment	not modelled	5.5	40	PDB header: transferase Chain: D; PDB Molecule: pre-mrna polyadenylation factor fip1; PDBTitle: yeast poly(a) polymerase in complex with fip1 residues 80-105
88	c2oq9A_	Alignment	not modelled	5.4	45	PDB header: structural protein Chain: A; PDB Molecule: minicollagen-5; PDBTitle: structure of the non-canonical mcol5 of hydra nematocysts
89	c3mb2J_	Alignment	not modelled	5.3	64	PDB header: isomerase Chain: J; PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - beta subunit; PDBTitle: kinetic and structural characterization of a heterohexameric 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily