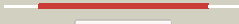



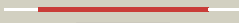



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1558 (-) _1762953_1763399
Date	Fri Aug 2 13:30:14 BST 2019
Unique Job ID	c689430666ad509c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r5yC_	 Alignment		100.0	53	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	76	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	33	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeg_3358 f420 reductase
4	c4y9iA_	 Alignment		100.0	54	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	44	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	14	PDB header: unknown function Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeg_3380 f420 reductase
7	c2iabB_	 Alignment		98.9	16	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	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
9	c3tgvD_	 Alignment		98.6	20	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	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
11	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

12	d1w9aa_	Alignment		98.4	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
13	d1vl7a_	Alignment		98.3	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
14	c3db0B_	Alignment		98.3	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
15	c2htiA_	Alignment		98.2	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	d2htia1	Alignment		98.2	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
17	d2i02a1	Alignment		98.2	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
18	c3dnhB_	Alignment		98.2	19	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
19	d2fg9a1	Alignment		98.1	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
20	c3gasA_	Alignment		98.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
21	c5bncB_	Alignment	not modelled	98.0	22	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	16	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related2; PDBTitle: crystal structure of a pyridoxamine 5'-phosphate oxidase-related2 protein (ssuidraft_2804) from streptococcus suis 89/1591 at 2.00 a3 resolution
23	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
24	d2arza1	Alignment	not modelled	98.0	24	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
25	d2hq9a1	Alignment	not modelled	98.0	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
26	c3ec6A_	Alignment	not modelled	97.9	17	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
27	c2re7A_	Alignment	not modelled	97.9	17	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
						Fold: Split barrel-like

28	d2hq7a1	Alignment	not modelled	97.8	12	Superfamily: FMN-binding split barrel Family: PNP-oxidase like
29	d2fura1	Alignment	not modelled	97.7	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
30	c6eciQ_	Alignment	not modelled	97.7	21	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
31	c5escD	Alignment	not modelled	97.7	14	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
32	c3u0iA_	Alignment	not modelled	97.7	20	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
33	d1t9ma_	Alignment	not modelled	97.7	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
34	d2fhqa1	Alignment	not modelled	97.6	23	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
35	c3fkhB_	Alignment	not modelled	97.6	21	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
36	c4ybnB_	Alignment	not modelled	97.5	18	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
37	d1ty9a_	Alignment	not modelled	97.5	10	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
38	c1nrgA_	Alignment	not modelled	97.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
39	d1nrga_	Alignment	not modelled	97.4	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
40	c2q9kA_	Alignment	not modelled	97.4	12	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	c2a2jA_	Alignment	not modelled	97.4	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
42	d2a2ja1	Alignment	not modelled	97.3	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
43	c4hmwB_	Alignment	not modelled	97.3	11	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phzq from burkholderia lata 383
44	c3cp3A_	Alignment	not modelled	97.3	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
45	c2htdB_	Alignment	not modelled	97.2	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
46	d1xhna1	Alignment	not modelled	97.2	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
47	c3u34D_	Alignment	not modelled	97.2	18	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
48	d1ci0a_	Alignment	not modelled	97.1	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
49	d1dnla_	Alignment	not modelled	97.0	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
50	c3dmbA_	Alignment	not modelled	96.9	17	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
51	c2qeaB_	Alignment	not modelled	96.9	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
52	c6rk0A_	Alignment	not modelled	96.0	17	PDB header: flavoprotein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the flavocytochrome anf3 from azotobacter vinelandii

53	d2vpaa1	Alignment	not modelled	95.5	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
54	d1flma_	Alignment	not modelled	95.4	22	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
55	c2i51B_	Alignment	not modelled	92.5	14	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
56	d2ptfa1	Alignment	not modelled	86.4	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
57	c4n7rD_	Alignment	not modelled	85.6	13	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
58	c2ou5B_	Alignment	not modelled	84.8	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
59	c2ptfB_	Alignment	not modelled	84.5	11	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
60	c2ol5B_	Alignment	not modelled	83.2	14	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
61	d2imla1	Alignment	not modelled	33.9	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
62	c4wt5A_	Alignment	not modelled	11.7	17	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
63	d2nr4a1	Alignment	not modelled	10.7	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
64	c4a2nB_	Alignment	not modelled	10.2	27	PDB header: transferase Chain: B: PDB Molecule: isoprenylcysteine carboxyl methyltransferase; PDBTitle: crystal structure of ma-icmt
65	c5v7pA_	Alignment	not modelled	9.3	20	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
66	c5jfzB_	Alignment	not modelled	8.5	15	PDB header: transferase Chain: B: PDB Molecule: uncharacterized protein yhfq; PDBTitle: e. coli ecfct in complex with ecfica mutant e28g
67	c5knwA_	Alignment	not modelled	8.3	20	PDB header: rna binding protein Chain: A: PDB Molecule: la-related protein 7; PDBTitle: solution nmr structure of human larp7 xrrm2
68	d1kb0a2	Alignment	not modelled	8.2	33	Fold: 8-bladed beta-propeller Superfamily: Quinoprotein alcohol dehydrogenase-like Family: Quinoprotein alcohol dehydrogenase-like
69	c5jfzF_	Alignment	not modelled	7.9	15	PDB header: transferase Chain: F: PDB Molecule: uncharacterized protein yhfq; PDBTitle: e. coli ecfct in complex with ecfica mutant e28g
70	d1k3ra1	Alignment	not modelled	7.7	11	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Hypothetical protein MTH1 (MT0001), insert domain
71	d1v54m_	Alignment	not modelled	7.6	40	Fold: Single transmembrane helix Superfamily: Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX) Family: Mitochondrial cytochrome c oxidase subunit VIIIb (aka IX)
72	d1owxa_	Alignment	not modelled	7.6	5	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
73	c4mqdB_	Alignment	not modelled	7.5	20	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: dna-entry nuclease inhibitor; PDBTitle: crystal structure of comj, inhibitor of the dna degrading activity of2 nuca, from bacillus subtilis
74	c1ztnA_	Alignment	not modelled	7.3	43	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
75	c3qrqA_	Alignment	not modelled	7.0	18	PDB header: rna binding protein/rna Chain: A: PDB Molecule: putative uncharacterized protein ttb192; PDBTitle: structure of thermus thermophilus cse3 bound to an rna representing a2 pre-cleavage complex
76	c3b5mD_	Alignment	not modelled	6.8	16	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved uncharacterized protein from2 rhodospirillum rubrum
77	c6mk1V_	Alianment	not modelled	6.6	67	PDB header: protein fibril Chain: V: PDB Molecule:

						PDBTitle: cryo-em of self-assembly peptide filament heat_r1
78	c2levA	Alignment	not modelled	6.2	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	c2dhyA	Alignment	not modelled	6.0	20	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)
80	c3jqoC	Alignment	not modelled	6.0	50	PDB header: transport protein Chain: C: PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
81	d1zq1c1	Alignment	not modelled	6.0	21	Fold: GatB/YqeY motif Superfamily: GatB/YqeY motif Family: GatB/GatE C-terminal domain-like
82	c4u65A	Alignment	not modelled	5.9	18	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
83	d1c9ka	Alignment	not modelled	5.7	50	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RecA protein-like (ATPase-domain)
84	c3jqoU	Alignment	not modelled	5.7	50	PDB header: transport protein Chain: U: PDB Molecule: tran protein; PDBTitle: crystal structure of the outer membrane complex of a type iv secretion2 system
85	c3zbiX	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: X: PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
86	c3zbiR	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: R: PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
87	c3zbig	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: G: PDB Molecule: traf protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
88	c3zbiF	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: F: PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
89	c3zbiI	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: I: PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
90	c3zbiC	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: C: PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
91	c3zbia	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: A: PDB Molecule: traf protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
92	c3zbiL	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: L: PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
93	c3zbiU	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: U: PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
94	c3zbij	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: J: PDB Molecule: traf protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
95	c3zbim	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: M: PDB Molecule: traf protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
96	c3zbiO	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: O: PDB Molecule: tran protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
97	c3zbid	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: D: PDB Molecule: traf protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
98	c3zbip	Alignment	not modelled	5.7	50	PDB header: cell adhesion Chain: P: PDB Molecule: traf protein; PDBTitle: fitting result in the o-layer of the subnanometer structure of the2 bacterial pkm101 type iv secretion system core complex digested with3 elastase
99	c3jqoL	Alignment	not modelled	5.6	50	PDB header: transport protein Chain: L: PDB Molecule: tran protein;

