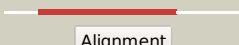



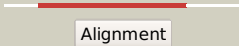



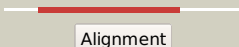
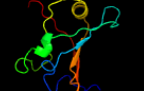


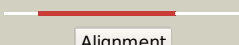
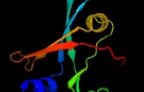


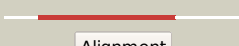




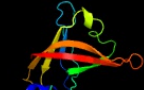


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0441c (-) _530299_530727
Date	Tue Jul 23 14:50:51 BST 2019
Unique Job ID	7f40abfd659b4563

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2re7A_	 Alignment		97.8	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
2	c5escD_	 Alignment		97.5	17	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
3	d1w9aa_	 Alignment		97.4	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
4	d2i02a1	 Alignment		97.3	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
5	c2htdB_	 Alignment		97.3	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
6	c2q9kA_	 Alignment		97.2	17	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
7	c2iabB_	 Alignment		97.0	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
8	c2hhzA_	 Alignment		97.0	14	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
9	d2fhqa1	 Alignment		96.9	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
10	d2hq7a1	 Alignment		96.9	9	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
11	c3dmbA_	 Alignment		96.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative general stress protein 26 with a prp-oxidase like PDBTitle: crystal structure of a putative general stress family protein2 (xcc2264) from xanthomonas campestris pv. campestris at 2.30 a3 resolution

12	c3f7eB_	Alignment		96.5	18	PDB header: unknown function Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeg_3380 f420 reductase
13	d1flma_	Alignment		96.4	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
14	d2asfa1	Alignment		96.3	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
15	c3db0B_	Alignment		96.3	17	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	c3tgvD_	Alignment		96.3	18	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
17	d1rfea_	Alignment		96.2	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
18	c2qeaB_	Alignment		96.0	19	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
19	c3ec6A_	Alignment		96.0	14	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
20	c3u34D_	Alignment		95.9	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
21	c2ig6B_	Alignment	not modelled	95.7	18	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
22	d1vl7a_	Alignment	not modelled	95.6	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
23	c4zkyB_	Alignment	not modelled	95.6	24	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5-phosphate oxidase; PDBTitle: structure of f420 binding protein, msmeg_6526, from mycobacterium2 smegmatis
24	c3u0iA_	Alignment	not modelled	95.5	16	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
25	d1ty9a_	Alignment	not modelled	94.7	22	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
26	c3cp3A_	Alignment	not modelled	94.4	19	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
27	d2hq9a1	Alignment	not modelled	94.1	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
28	d1t9ma_	Alignment	not modelled	93.9	26	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like

29	d2fg9a1	Alignment	not modelled	93.9	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
30	c3fkhB	Alignment	not modelled	92.8	9	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
31	d1dnla	Alignment	not modelled	92.6	23	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
32	c4hmwB	Alignment	not modelled	92.4	17	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phzg from burkholderia lata 383
33	c6eciQ	Alignment	not modelled	91.7	19	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
34	c2htiA	Alignment	not modelled	91.3	16	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
35	d2htia1	Alignment	not modelled	91.3	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
36	d1nrga	Alignment	not modelled	90.1	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
37	c1nrgA	Alignment	not modelled	90.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
38	c2ou5B	Alignment	not modelled	80.3	13	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
39	c2a2jA	Alignment	not modelled	78.0	17	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
40	d2a2ja1	Alignment	not modelled	78.0	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
41	d2fura1	Alignment	not modelled	62.2	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
42	c3h96B	Alignment	not modelled	61.7	12	PDB header: flavoprotein Chain: B: PDB Molecule: f420-h2 dependent reductase a; PDBTitle: msmeq_3358 f420 reductase
43	c3r5zB	Alignment	not modelled	60.7	18	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
44	c4l82D	Alignment	not modelled	58.1	7	PDB header: oxidoreductase Chain: D: PDB Molecule: rifea.00250.a; PDBTitle: structure of a putative oxidoreductase from rickettsia felis
45	c3r5yC	Alignment	not modelled	50.0	25	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
46	d2fug31	Alignment	not modelled	47.5	44	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
47	c3dnhB	Alignment	not modelled	45.3	23	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	c3r5wO	Alignment	not modelled	44.6	22	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
49	d1ci0a	Alignment	not modelled	43.6	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
50	c4y9iA	Alignment	not modelled	39.1	18	PDB header: oxidoreductase Chain: A: PDB Molecule: mycobacterium tuberculosis paralogous family 11; PDBTitle: structure of f420-h2 dependent reductase (fdr-a) msmeq_2027
51	c5yanE	Alignment	not modelled	36.0	78	PDB header: structural protein Chain: E: PDB Molecule: collagen; PDBTitle: deconstructing the salt-bridge network of a computationally designed2 collagen heterotrimer
52	c5yanC	Alignment	not modelled	35.7	78	PDB header: structural protein Chain: C: PDB Molecule: collagen; PDBTitle: deconstructing the salt-bridge network of a computationally designed2 collagen heterotrimer
53	c2bsjB	Alignment	not modelled	35.5	28	PDB header: chaperone Chain: B: PDB Molecule: chaperone protein syct; PDBTitle: native crystal structure of the type iii secretion chaperone

						sycT from2 yersinia enterocolitica
54	c5yanF_	Alignment	not modelled	35.3	78	PDB header: structural protein Chain: F: PDB Molecule: collagen; PDBTitle: deconstructing the salt-bridge network of a computationally designed2 collagen heterotrimer
55	c5yanB_	Alignment	not modelled	34.9	78	PDB header: structural protein Chain: B: PDB Molecule: collagen; PDBTitle: deconstructing the salt-bridge network of a computationally designed2 collagen heterotrimer
56	d1t62a_	Alignment	not modelled	34.2	19	Fold: PUA domain-like Superfamily: PUA domain-like Family: Hypothetical protein EF3133
57	c4ybnB_	Alignment	not modelled	32.8	22	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
58	c3s9xA_	Alignment	not modelled	30.1	0	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: asch domain; PDBTitle: high resolution crystal structure of asch domain from lactobacillus2 crispatus jv v101
59	c3nfwB_	Alignment	not modelled	29.8	19	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin reductase-like, fmn-binding protein; PDBTitle: crystal structure of nitrilotriacetate monooxygenase component b2 (a0r521 homolog) from mycobacterium thermoresistibile
60	c2r0xA_	Alignment	not modelled	29.3	12	PDB header: oxidoreductase Chain: A: PDB Molecule: possible flavin reductase; PDBTitle: crystal structure of a putative flavin reductase (ycdh_h5_1225) from2 haemophilus somnus 129pt at 1.06 a resolution
61	d2arza1	Alignment	not modelled	28.2	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
62	c2cjqA_	Alignment	not modelled	24.4	20	PDB header: transferase Chain: A: PDB Molecule: rna-directed rna polymerase; PDBTitle: bovine viral diarrhoea virus cp7-r12 rna-dependent rna2 polymerase
63	c3mfbA_	Alignment	not modelled	24.0	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the s-type pyocin domain of eca1669 protein from2 erwinia carotovora, northeast structural genomics consortium target3 ewr82c
64	c3isyA_	Alignment	not modelled	24.0	18	PDB header: protein binding Chain: A: PDB Molecule: intracellular proteinase inhibitor; PDBTitle: crystal structure of an intracellular proteinase inhibitor (ipi_2 bsu11130) from bacillus subtilis at 2.61 a resolution
65	c4z29B_	Alignment	not modelled	21.6	36	PDB header: signaling protein Chain: B: PDB Molecule: magnetotaxis protein mtxa; PDBTitle: crystal structure of the magnetobacterial protein mtxa c-terminal2 domain
66	c3pftA_	Alignment	not modelled	20.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase; PDBTitle: crystal structure of untagged c54a mutant flavin reductase (dszd) in2 complex with fmn from mycobacterium goodii
67	d1gx5a_	Alignment	not modelled	17.4	30	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
68	c4makA_	Alignment	not modelled	16.3	29	PDB header: hydrolase Chain: A: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: crystal structure of a putative ssrna endonuclease cas2, crispr2 adaptation protein from e.coli
69	c2kl6A_	Alignment	not modelled	16.1	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the cardb domain of pf1109 from2 pyrococcus furiosus. northeast structural genomics3 consortium target pfr193a
70	c3gasA_	Alignment	not modelled	15.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
71	d1nb4a_	Alignment	not modelled	15.0	30	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
72	c2o15B_	Alignment	not modelled	14.5	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
73	c3o44G_	Alignment	not modelled	13.2	38	PDB header: toxin Chain: G: PDB Molecule: hemolysin; PDBTitle: crystal structure of the vibrio cholerae cytolysin (hlyA) heptameric2 pore
74	c5mqrA_	Alignment	not modelled	12.3	19	PDB header: hydrolase Chain: A: PDB Molecule: beta-l-arabinobiosidase; PDBTitle: sialidase bt_1020
75	d2foka4	Alignment	not modelled	12.0	26	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease FokI, C-terminal (catalytic) domain
76	d1s48a_	Alignment	not modelled	11.5	20	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: RNA-dependent RNA-polymerase
77	c5y6rA_	Alignment	not modelled	11.3	20	PDB header: transferase Chain: A: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of csfv ns5b
78	c5bncB_	Alignment	not modelled	11.2	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
						PDB header: hydrolase/dna

79	c1fokA_	Alignment	not modelled	11.0	26	Chain: A: PDB Molecule: protein (foki restriction endonucleas); PDBTitle: structure of restriction endonuclease foki bound to dna
80	c3k87B_	Alignment	not modelled	10.8	10	PDB header: oxidoreductase Chain: B: PDB Molecule: chlorophenol-4-monoxygenase component 1; PDBTitle: crystal structure of nadh:fad oxidoreductase (ttfc) - fad2 complex
81	c4p6iB_	Alignment	not modelled	10.5	28	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: crystal structure of the cas1-cas2 complex from escherichia coli
82	c2kd2A_	Alignment	not modelled	10.3	56	PDB header: apoptosis Chain: A: PDB Molecule: fas apoptotic inhibitory molecule 1; PDBTitle: nmr structure of faim-ctd
83	c5jzrA_	Alignment	not modelled	9.4	30	PDB header: viral protein Chain: A: PDB Molecule: coat protein; PDBTitle: solid-state mas nmr structure of acinetobacter phage 205 (ap205) coat2 protein in assembled capsid particles
84	d1br2a1	Alignment	not modelled	8.7	45	Fold: SH3-like barrel Superfamily: Myosin S1 fragment, N-terminal domain Family: Myosin S1 fragment, N-terminal domain
85	c1xezA_	Alignment	not modelled	8.6	38	PDB header: toxin Chain: A: PDB Molecule: hemolysin; PDBTitle: crystal structure of the vibrio cholerae cytotoxin (hlyA)2 pro-toxin with octylglucoside bound
86	c2phcB_	Alignment	not modelled	7.8	27	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein ph0987; PDBTitle: crystal structure of conserved uncharacterized protein ph0987 from2 pyrococcus horikoshii
87	c5dudB_	Alignment	not modelled	7.6	40	PDB header: unknown function Chain: B: PDB Molecule: ybgj; PDBTitle: crystal structure of e. coli ybgjk
88	d1j5ya2	Alignment	not modelled	7.6	16	Fold: HPr-like Superfamily: Putative transcriptional regulator TM1602, C-terminal domain Family: Putative transcriptional regulator TM1602, C-terminal domain
89	c1ztgD_	Alignment	not modelled	6.9	8	PDB header: dna, rna binding protein/dna Chain: D: PDB Molecule: poly(rc)-binding protein 1; PDBTitle: human alpha polyc binding protein kh1
90	c5i07B_	Alignment	not modelled	6.6	29	PDB header: transcription Chain: B: PDB Molecule: quorum-sensing transcriptional activator; PDBTitle: crystal structure of quorum-sensing transcriptional activator from2 yersinia enterocolitica
91	c4zkcA_	Alignment	not modelled	6.3	36	PDB header: viral protein/cytokine Chain: A: PDB Molecule: chemokine binding protein; PDBTitle: the chemokine binding protein of orf virus complexed with ccl7
92	c5c2mA_	Alignment	not modelled	6.2	15	PDB header: structural protein Chain: A: PDB Molecule: predicted protein; PDBTitle: the de novo evolutionary emergence of a symmetrical protein is shaped2 by folding constraints
93	c5n06A_	Alignment	not modelled	6.1	21	PDB header: signaling protein Chain: A: PDB Molecule: tyrosine-protein kinase receptor tie-1; PDBTitle: crystal structure of tie1 fibronectin-like domain 3
94	c5bu6B_	Alignment	not modelled	6.0	24	PDB header: hydrolase Chain: B: PDB Molecule: bpsb (pgab), poly-beta-1,6-n-acetyl-d-glucosamine n- PDBTitle: structure of bpsb deaceylase domain from bordetella bronchiseptica
95	d1viga_	Alignment	not modelled	6.0	16	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
96	c5mhjA_	Alignment	not modelled	5.8	27	PDB header: transcription Chain: A: PDB Molecule: major viral transcription factor icp4; PDBTitle: icp4 dna-binding domain, lacking intrinsically disordered region, in2 complex with 12mer dna duplex from its own promoter
97	c3gl5A_	Alignment	not modelled	5.5	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative dsba oxidoreductase sco1869; PDBTitle: crystal structure of probable dsba oxidoreductase sco1869 from2 streptomyces coelicolor
98	c2zp2B_	Alignment	not modelled	5.4	47	PDB header: transferase inhibitor Chain: B: PDB Molecule: kinase a inhibitor; PDBTitle: c-terminal domain of kipi from bacillus subtilis
99	d2phcb1	Alignment	not modelled	5.3	27	Fold: Cyclophilin-like Superfamily: Cyclophilin-like Family: PH0987 C-terminal domain-like