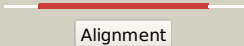

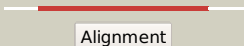

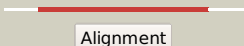







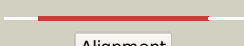


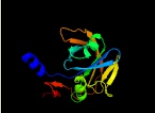








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3567c_(-)_4008898_4009461
Date	Fri Aug 9 18:20:25 BST 2019
Unique Job ID	cd618d9a51ff7361

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3nfwB_	 Alignment		100.0	82	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
2	c5zc2B_	 Alignment		100.0	32	PDB header: flavoprotein Chain: B: PDB Molecule: p-hydroxyphenylacetate 3-hydroxylase, reductase component; PDBTitle: acinetobacter baumannii p-hydroxyphenylacetate 3-hydroxylase (hpah),2 reductase component (c1)
3	c3rh7A_	 Alignment		100.0	36	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
4	c4hx6D_	 Alignment		100.0	35	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: streptomyces globisporus c-1027 nadh:fad oxidoreductase sgce6
5	c3k87B_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: chlorophenol-4-monooxygenase component 1; PDBTitle: crystal structure of nadh:fad oxidoreductase (tftc) - fad2 complex
6	c3pftA_	 Alignment		100.0	27	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
7	c4xhyA_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin reductase domain protein, fmn-binding protein; PDBTitle: nadh:fmn oxidoreductase from paracoccus denitrificans
8	c2qckA_	 Alignment		100.0	24	PDB header: oxidoreductase 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
9	c4l82D_	 Alignment		100.0	33	PDB header: oxidoreductase Chain: D: PDB Molecule: rifea.00250.a; PDBTitle: structure of a putative oxidoreductase from rickettsia felis
10	c2r0xA_	 Alignment		100.0	21	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
11	c3cb0B_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxyphenylacetate 3-monooxygenase; PDBTitle: cobr

12	c2d38A_	Alignment		100.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: hypothetical nadh-dependent fmn oxidoreductase; PDBTitle: the crystal structure of flavin reductase hpac complexed with nadp+
13	c4f07A_	Alignment		100.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: styrene monooxygenase component 2; PDBTitle: structure of the styrene monooxygenase flavin reductase (smob) from2 pseudomonas putida s12
14	c2ecrA_	Alignment		100.0	30	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-monooxygenase
15	d1rz0a_	Alignment		100.0	32	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
16	d1wgba_	Alignment		100.0	24	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
17	d1i0ra_	Alignment		100.0	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
18	c3bnkB_	Alignment		100.0	15	PDB header: electron transport Chain: B: PDB Molecule: flavodoxin; PDBTitle: x-ray crystal structure of flavodoxin from methanosarcina2 acetivorans
19	d1usca_	Alignment		100.0	23	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
20	c2r6vA_	Alignment		100.0	19	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
21	d1ejea_	Alignment	not modelled	100.0	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
22	c3hmzA_	Alignment	not modelled	100.0	17	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 (sbal_0626) from shewanella baltica os155 at 1.50 a resolution
23	c3bpkB_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: B: PDB Molecule: nitritotriacetate monooxygenase component b; PDBTitle: crystal structure of nitritotriacetate monooxygenase component b from2 bacillus cereus
24	c3e4vA_	Alignment	not modelled	100.0	19	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
25	c4z85A_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-nitrobenzoate nitroreductase; PDBTitle: crystal structur of pseudomonas fluorescens 2-nitrobenzoate 2-2 nitroreductase nbaa
26	c3fgeA_	Alignment	not modelled	100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative flavin reductase with split barrel domain; PDBTitle: crystal structure of putative flavin reductase with split barre12 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution
27	c2d5mA_	Alignment	not modelled	100.0	16	PDB header: electron transport Chain: A: PDB Molecule: flavodoxin; PDBTitle: flavodoxin of desulfovibrio vulgaris (miyazaki f)

28	c3b5mD_	Alignment	not modelled	99.9	13	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of conserved uncharacterized protein from2 rhodopirellula baltica
29	d2imla1	Alignment	not modelled	99.4	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
30	d2nr4a1	Alignment	not modelled	98.8	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
31	c2ptfB_	Alignment	not modelled	98.7	20	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
32	d2ptfa1	Alignment	not modelled	98.7	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
33	c2q9kA_	Alignment	not modelled	95.8	13	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	c5escD_	Alignment	not modelled	95.3	11	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
35	c2htdB_	Alignment	not modelled	95.0	9	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
36	d1flma_	Alignment	not modelled	94.8	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
37	d1vl7a_	Alignment	not modelled	89.8	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
38	c3tqvD_	Alignment	not modelled	81.4	6	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
39	d2hq7a1	Alignment	not modelled	77.3	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
40	c3f7eB_	Alignment	not modelled	77.1	20	PDB header: unknown function Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeg_3380 f420 reductase
41	d2asfa1	Alignment	not modelled	74.1	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
42	c3u0iA_	Alignment	not modelled	72.0	12	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
43	c2htiA_	Alignment	not modelled	71.4	17	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
44	d2htia1	Alignment	not modelled	71.4	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
45	d1rfea_	Alignment	not modelled	69.2	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
46	c3u34D_	Alignment	not modelled	62.7	9	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
47	d2hq9a1	Alignment	not modelled	58.6	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
48	d2fhqa1	Alignment	not modelled	57.1	6	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
49	d1w9aa_	Alignment	not modelled	55.0	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
50	c2ig6B_	Alignment	not modelled	53.2	9	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
51	c2re7A_	Alignment	not modelled	51.8	16	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
52	c3db0B_	Alignment	not modelled	43.3	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
53	c3ec6A_	Alignment	not modelled	43.1	19	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
54	d2i02a1	Alignment	not modelled	38.7	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
55	c3dmbA_	Alignment	not modelled	38.2	9	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
56	d1ty9a_	Alignment	not modelled	23.9	9	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
57	c2hhzA_	Alignment	not modelled	21.2	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
58	d1t9ma_	Alignment	not modelled	19.9	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
59	d2a2ja1	Alignment	not modelled	18.8	22	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
60	d1dnla_	Alignment	not modelled	18.7	19	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
61	c2a2jA_	Alignment	not modelled	18.7	22	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of a putative pyridoxamine 5'-phosphate oxidase2 (rv2607) from mycobacterium tuberculosis
62	d1nrqa_	Alignment	not modelled	18.4	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
63	c1nrqA_	Alignment	not modelled	18.4	11	PDB header: oxidoreductase Chain: A: PDB Molecule: pyridoxine 5'-phosphate oxidase; PDBTitle: structure and properties of recombinant human pyridoxine-5'-phosphate2 oxidase
64	d1p3qq_	Alignment	not modelled	17.8	22	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain
65	d2fura1	Alignment	not modelled	15.3	12	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
66	c3cp3A_	Alignment	not modelled	14.9	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
67	d2fg9a1	Alignment	not modelled	13.3	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
68	d2arza1	Alignment	not modelled	12.7	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
69	c4hmwB_	Alignment	not modelled	10.2	17	PDB header: oxidoreductase Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase; PDBTitle: crystal structure of phzg from burkholderia lata 383
70	c3fkhB_	Alignment	not modelled	9.6	5	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
71	c5cnlA_	Alignment	not modelled	9.2	17	PDB header: protein transport Chain: A: PDB Molecule: icml-like; PDBTitle: crystal structure of an icml-like type iv secretion system protein2 (lpg0120) from legionella pneumophila subsp. pneumophila str.3 philadelphia 1 at 2.65 a resolution
72	d1qasa3	Alignment	not modelled	9.1	12	Fold: TIM beta/alpha-barrel Superfamily: PLC-like phosphodiesterases Family: Mammalian PLC
73	d1hywa_	Alignment	not modelled	8.5	30	Fold: gpW/XkdW-like Superfamily: Head-to-tail joining protein W, gpW Family: Head-to-tail joining protein W, gpW
74	d1p3qr_	Alignment	not modelled	8.4	23	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: CUE domain
75	c2iabB_	Alignment	not modelled	7.9	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
76	d1dmla2	Alignment	not modelled	6.8	30	Fold: DNA clamp Superfamily: DNA clamp Family: DNA polymerase processivity factor
77	d1kl9a2	Alignment	not modelled	6.3	27	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
78	c5m30B_	Alignment	not modelled	6.2	15	PDB header: secretion system Chain: B: PDB Molecule: type vi secretion protein; PDBTitle: structure of tssk from t6ss eaec in complex with

					nanobody nb18
79	c6eciQ_	Alignment	not modelled	5.9	13 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
80	c3dnhB_	Alignment	not modelled	5.7	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
81	c4bluB_	Alignment	not modelled	5.7	24 PDB header: transferase Chain: B: PDB Molecule: ribosomal rna large subunit methyltransferase j; PDBTitle: crystal structure of escherichia coli 23s rrna (a2030-n6)-2 methyltransferase rimj
82	c2ou5B_	Alignment	not modelled	5.5	15 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