

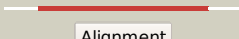

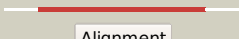




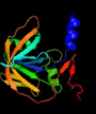

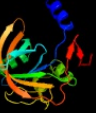


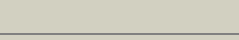



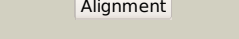





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3007c_(-)_3365846_3366460
Date	Thu Aug 8 16:20:17 BST 2019
Unique Job ID	1c633d05c962f214

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3rh7A_	 Alignment		100.0	26	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
2	c5zc2B_	 Alignment		100.0	19	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	c4hx6D_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: streptomyces globisporus c-1027 nadh:fad oxidoreductase sgce6
4	c3nfwB_	 Alignment		100.0	18	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
5	c2qckA_	 Alignment		100.0	27	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
6	c3k87B_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: B: PDB Molecule: chlorophenol-4-monooxygenase component 1; PDBTitle: crystal structure of nadh:fad oxidoreductase (tftc) - fad2 complex
7	c3pftA_	 Alignment		100.0	17	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
8	d1wgba_	 Alignment		100.0	23	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
9	c2r0xA_	 Alignment		100.0	22	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
10	c3cb0B_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-hydroxyphenylacetate 3-monooxygenase; PDBTitle: cobr
11	c4l82D_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: rifea.00250.a; PDBTitle: structure of a putative oxidoreductase from rickettsia felis

12	c2d38A_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: hypothetical nadh-dependent fmn oxidoreductase; PDBTitle: the crystal structure of flavin reductase hpac complexed with nadp+
13	c4xhyA_	Alignment		100.0	20	PDB header: oxidoreductase Chain: A; PDB Molecule: flavin reductase domain protein, fmn-binding protein; PDBTitle: nadh:fmn oxidoreductase from paracoccus denitrificans
14	c2ecrA_	Alignment		100.0	18	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	d1i0ra_	Alignment		100.0	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
16	c4f07A_	Alignment		100.0	21	PDB header: oxidoreductase Chain: A; PDB Molecule: styrene monooxygenase component 2; PDBTitle: structure of the styrene monooxygenase flavin reductase (smob) from2 pseudomonas putida s12
17	d1rz0a_	Alignment		100.0	25	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
18	c3bnkB_	Alignment		100.0	16	PDB header: electron transport Chain: B; PDB Molecule: flavodoxin; PDBTitle: x-ray crystal structure of flavodoxin from methanosarcina2 acetivorans
19	d1usca_	Alignment		100.0	21	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: NADH:FMN oxidoreductase-like
20	c2r6vA_	Alignment		100.0	14	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	c3e4vA_	Alignment	not modelled	100.0	17	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
23	c3hmzA_	Alignment	not modelled	100.0	19	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 (sba1_0626) from shewanella baltica os155 at 1.50 a resolution
24	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
25	c3fgeA_	Alignment	not modelled	100.0	10	PDB header: oxidoreductase Chain: A; PDB Molecule: putative flavin reductase with split barrel domain; PDBTitle: crystal structure of putative flavin reductase with split barrel2 domain (yp_750721.1) from shewanella frigidimarina ncimb 400 at 1.743 a resolution
26	c2d5mA_	Alignment	not modelled	100.0	19	PDB header: electron transport Chain: A; PDB Molecule: flavodoxin; PDBTitle: flavodoxin of desulfovibrio vulgaris (miyazaki f)
27	c4z85A_	Alignment	not modelled	100.0	16	PDB header: oxidoreductase Chain: A; PDB Molecule: 2-nitrobenzoate nitroreductase; PDBTitle: crystal structur of pseudomonas fluorescens 2-nitrobenzoate 2-2 nitroreductase nbaa

28	c3b5mD_	Alignment	not modelled	99.9	12	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	99.1	20	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
30	d2nr4a1	Alignment	not modelled	98.4	17	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
31	c2ptfB_	Alignment	not modelled	98.3	14	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	98.2	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: MTH863-like
33	c2kn9A_	Alignment	not modelled	97.5	5	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin; PDBTitle: solution structure of zinc-substituted rubredoxin b (rv3250c) from2 mycobacterium tuberculosis. seattle structural genomics center for3 infectious disease target mytud.01635.a
34	c2q9kA_	Alignment	not modelled	96.1	10	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	d1lkoa2	Alignment	not modelled	96.0	23	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
36	c5escD_	Alignment	not modelled	95.1	13	PDB header: oxidoreductase Chain: D: PDB Molecule: hupz; PDBTitle: crystal structure of group a streptococcus hupz
37	d1yuza2	Alignment	not modelled	95.0	5	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
38	d1nnqa2	Alignment	not modelled	94.8	15	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
39	d1flma_	Alignment	not modelled	94.7	18	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
40	c2htdB_	Alignment	not modelled	94.6	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	c2hr5B_	Alignment	not modelled	93.8	12	PDB header: metal binding protein Chain: B: PDB Molecule: rubrerythrin; PDBTitle: pf1283- rubrerythrin from pyrococcus furiosus iron bound form
42	c1dvbA_	Alignment	not modelled	92.5	23	PDB header: electron transport Chain: A: PDB Molecule: rubrerythrin; PDBTitle: rubrerythrin
43	c1yuzB_	Alignment	not modelled	91.7	5	PDB header: oxidoreductase Chain: B: PDB Molecule: nigerythrin; PDBTitle: partially reduced state of nigerythrin
44	c3tqvD_	Alignment	not modelled	91.4	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
45	c4tpuA_	Alignment	not modelled	91.2	11	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin; PDBTitle: crystal structure of ferredoxin-dependent disulfide reductase from2 methanosarcina acetivorans
46	d1vl7a_	Alignment	not modelled	89.0	9	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
47	d6rxna_	Alignment	not modelled	87.1	7	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
48	d1qcva_	Alignment	not modelled	86.3	7	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
49	d1iu5a_	Alignment	not modelled	85.7	9	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
50	d4rxna_	Alignment	not modelled	85.5	14	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
51	d2dsxa1	Alignment	not modelled	85.5	9	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
52	d1rb9a_	Alignment	not modelled	85.5	8	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
53	d2rdva_	Alignment	not modelled	85.4	7	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
						Fold: Rubredoxin-like

54	d1iroa_	Alignment	not modelled	85.4	14	Superfamily: Rubredoxin-like Family: Rubredoxin
55	c2ms3A_	Alignment	not modelled	85.3	0	PDB header: electron transport Chain: A: PDB Molecule: anaerobic nitric oxide reductase flavorubredoxin; PDBTitle: the nmr structure of the rubredoxin domain of the no reductase2 flavorubredoxin from escherichia coli
56	d1s24a_	Alignment	not modelled	85.3	7	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
57	c1s24A_	Alignment	not modelled	85.3	7	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin 2; PDBTitle: rubredoxin domain ii from pseudomonas oleovorans
58	d1brfa_	Alignment	not modelled	85.2	7	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
59	d1h7va_	Alignment	not modelled	84.8	20	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
60	c2v3bB_	Alignment	not modelled	84.3	7	PDB header: oxidoreductase Chain: B: PDB Molecule: rubredoxin 2; PDBTitle: crystal structure of the electron transfer complex rubredoxin -2 rubredoxin reductase from pseudomonas aeruginosa.
61	c2m4yA_	Alignment	not modelled	82.1	0	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin; PDBTitle: rubredoxin type protein from mycobacterium ulcerans
62	d1w9aa_	Alignment	not modelled	79.6	14	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
63	c3f7eB_	Alignment	not modelled	65.8	15	PDB header: unknown function Chain: B: PDB Molecule: pyridoxamine 5'-phosphate oxidase-related, fmn- PDBTitle: msmeg_3380 f420 reductase
64	c3dmbA_	Alignment	not modelled	63.3	4	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
65	c3u34D_	Alignment	not modelled	62.8	6	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
66	c3db0B_	Alignment	not modelled	54.3	14	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
67	d2fhqa1	Alignment	not modelled	52.2	9	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
68	c2re7A_	Alignment	not modelled	43.5	3	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
69	c3ec6A_	Alignment	not modelled	41.0	13	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
70	d2htia1	Alignment	not modelled	40.8	5	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
71	c2htiA_	Alignment	not modelled	40.8	5	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
72	c5z58w_	Alignment	not modelled	33.1	8	PDB header: splicing Chain: W: PDB Molecule: PDBTitle: cryo-em structure of a human activated spliceosome (early bact) at 4.92 angstrom.
73	d2i02a1	Alignment	not modelled	31.8	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
74	d2asfa1	Alignment	not modelled	30.6	16	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
75	d1rfea_	Alignment	not modelled	29.4	11	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
76	c3gasA_	Alignment	not modelled	28.0	12	PDB header: oxidoreductase Chain: A: PDB Molecule: heme oxygenase; PDBTitle: crystal structure of helicobacter pylori heme oxygenase hugz2 in complex with heme
77	c2ig6B_	Alignment	not modelled	26.7	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
78	c4a17Y_	Alignment	not modelled	25.7	0	PDB header: ribosome Chain: Y: PDB Molecule: rpl37a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 2.
79	c3izrM_	Alignment	not modelled	25.7	15	PDB header: ribosome Chain: M: PDB Molecule: 60s ribosomal protein l23 (l14p); PDBTitle: localization of the large subunit ribosomal proteins into a

						5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
80	d1pfva3	Alignment	not modelled	25.1	15	Fold: Rubredoxin-like Superfamily: Methionyl-tRNA synthetase (MetRS), Zn-domain Family: Methionyl-tRNA synthetase (MetRS), Zn-domain
81	d2hq7a1	Alignment	not modelled	24.7	15	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
82	c3j39p_	Alignment	not modelled	24.7	8	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17; PDBTitle: structure of the d. melanogaster 60s ribosomal proteins
83	c3cc4Z_	Alignment	not modelled	23.7	0	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: co-crystal structure of anisomycin bound to the 50s ribosomal subunit
84	c2hhzA_	Alignment	not modelled	23.5	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
85	d1ffkw_	Alignment	not modelled	23.4	8	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein l37ae
86	c1yshD_	Alignment	not modelled	23.4	15	PDB header: structural protein/rna Chain: D: PDB Molecule: ribosomal protein l37a; PDBTitle: localization and dynamic behavior of ribosomal protein l30e
87	d1vqoz1	Alignment	not modelled	23.3	0	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein l37ae
88	c2qa4Z_	Alignment	not modelled	23.3	0	PDB header: ribosome Chain: Z: PDB Molecule: 50s ribosomal protein l37ae; PDBTitle: a more complete structure of the the l7/l12 stalk of the2 haloarcula marismortui 50s large ribosomal subunit
89	c3zf7o_	Alignment	not modelled	23.2	0	PDB header: ribosome Chain: O: PDB Molecule: 60s ribosomal protein l13a, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome
90	c2zkrz_	Alignment	not modelled	22.5	0	PDB header: ribosomal protein/rna Chain: Z: PDB Molecule: e site t-rna; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
91	c4b6ap_	Alignment	not modelled	22.4	0	PDB header: ribosome Chain: P: PDB Molecule: 60s ribosomal protein l17-a; PDBTitle: cryo-em structure of the 60s ribosomal subunit in complex2 with arx1 and rei1
92	d1jj2y_	Alignment	not modelled	22.3	8	Fold: Rubredoxin-like Superfamily: Zn-binding ribosomal proteins Family: Ribosomal protein l37ae
93	c3j21i_	Alignment	not modelled	21.5	8	PDB header: ribosome Chain: l: PDB Molecule: 50s ribosomal protein l13p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
94	d2arza1	Alignment	not modelled	20.0	13	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
95	d1mkya3	Alignment	not modelled	19.8	15	Fold: Alpha-lytic protease prodomain-like Superfamily: Probable GTPase Der, C-terminal domain Family: Probable GTPase Der, C-terminal domain
96	c5m30B_	Alignment	not modelled	19.1	12	PDB header: secretion system Chain: B: PDB Molecule: type vi secretion protein; PDBTitle: structure of tssk from t6ss eaec in complex with nanobody nb18
97	c1s1i9_	Alignment	not modelled	18.7	0	PDB header: ribosome Chain: 9: PDB Molecule: 60s ribosomal protein l43; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1i, contains 60s subunit. the 40s4 ribosomal subunit is in file 1s1h.
98	c2m6oA_	Alignment	not modelled	18.6	29	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the actinobacterial transcription factor rbpa binds to the principal2 sigma subunit of rna polymerase
99	c2lv2A_	Alignment	not modelled	18.5	6	PDB header: transcription Chain: A: PDB Molecule: insulinoma-associated protein 1; PDBTitle: solution nmr structure of c2h2-type zinc-fingers 4 and 5 from human2 insulinoma-associated protein 1 (fragment 424-497), northeast3 structural genomics consortium target hr7614b