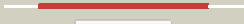
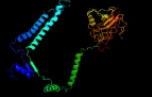

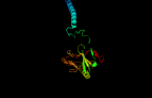

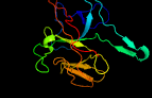

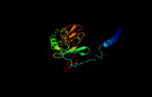



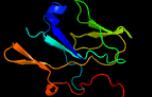
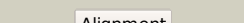








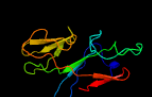


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2195_(qcrA)_2458400_2459689
Date	Mon Aug 5 13:25:32 BST 2019
Unique Job ID	0e03e826dcc7c175

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6hwhB_	 Alignment		100.0	81	PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
2	c2fyuE_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit, PDBTitle: crystal structure of bovine heart mitochondrial bc1 with jg1442 inhibitor
3	d1nyka_	 Alignment		100.0	32	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
4	c2fynO_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: O: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur PDBTitle: crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex
5	c2e76D_	 Alignment		99.9	27	PDB header: photosynthesis Chain: D: PDB Molecule: cytochrome b6-f complex iron-sulfur subunit; PDBTitle: crystal structure of the cytochrome b6f complex with tridecyl-2 stigmatellin (tds) from m.laminosus
6	d1jm1a_	 Alignment		99.9	26	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
7	c1p84E_	 Alignment		99.9	18	PDB header: oxidoreductase Chain: E: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: hdbt inhibited yeast cytochrome bc1 complex
8	d3cx5e1	 Alignment		99.9	21	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
9	d1riea_	 Alignment		99.9	20	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
10	c4aayH_	 Alignment		99.9	24	PDB header: oxidoreductase Chain: H: PDB Molecule: arob; PDBTitle: crystal structure of the arsenite oxidase protein complex2 from rhizobium species strain nt-26
11	d1g8kb_	 Alignment		99.8	29	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)

12	c2nvgA_	Alignment		99.8	25	PDB header: oxidoreductase Chain: A: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: soluble domain of rieske iron sulfur protein.
13	c6fo2R_	Alignment		99.8	25	PDB header: membrane protein Chain: R: PDB Molecule: cytochrome b-c1 complex subunit rieske, mitochondrial; PDBTitle: cryoem structure of bovine cytochrome bc1 with no ligand bound
14	d1rfsa_	Alignment		99.7	30	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
15	d2e74d1	Alignment		99.7	34	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
16	d1q90c_	Alignment		99.6	33	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
17	c2qpzA_	Alignment		99.5	23	PDB header: metal binding protein Chain: A: PDB Molecule: naphthalene 1,2-dioxygenase system ferredoxin PDBTitle: naphthalene 1,2-dioxygenase rieske ferredoxin
18	d1fqta_	Alignment		99.4	26	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
19	c2i7fB_	Alignment		99.4	23	PDB header: oxidoreductase Chain: B: PDB Molecule: ferredoxin component of dioxygenase; PDBTitle: sphingomonas yanoikuyae b1 ferredoxin
20	c3gceA_	Alignment		99.4	31	PDB header: oxidoreductase Chain: A: PDB Molecule: ferredoxin component of carbazole 1,9a- PDBTitle: ferredoxin of carbazole 1,9a-dioxygenase from nocardiooides2 aromaticivorans ic177
21	c5cxmC_	Alignment	not modelled	99.4	31	PDB header: metal binding protein Chain: C: PDB Molecule: cytochrome b6/f complex iron-sulfur subunit; PDBTitle: crystal structure of the cyanobacterial plasma membrane rieske protein2 petc3 from synechocystis pcc 6803
22	d1vm9a_	Alignment	not modelled	99.3	23	Fold: ISP domain Superfamily: ISP domain Family: Rieske iron-sulfur protein (ISP)
23	c2de7E_	Alignment	not modelled	99.3	24	PDB header: oxidoreductase Chain: E: PDB Molecule: ferredoxin component of carbazole; PDBTitle: the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
24	c3dqyA_	Alignment	not modelled	99.3	29	PDB header: oxidoreductase Chain: A: PDB Molecule: toluene 1,2-dioxygenase system ferredoxin PDBTitle: crystal structure of toluene 2,3-dioxygenase ferredoxin
25	d3c0da1	Alignment	not modelled	99.1	19	Fold: ISP domain Superfamily: ISP domain Family: NirD-like
26	d2jzaa1	Alignment	not modelled	99.0	13	Fold: ISP domain Superfamily: ISP domain Family: NirD-like
27	c4aivA_	Alignment	not modelled	99.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: probable nitrite reductase [nad(p)h] small subunit nird; PDBTitle: crystal structure of putative nadh-dependent nitrite reductase small2 subunit from mycobacterium tuberculosis
28	d2jo6a1	Alignment	not modelled	98.9	15	Fold: ISP domain Superfamily: ISP domain Family: NirD-like

29	d2de6a1	Alignment	not modelled	98.9	21	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
30	c3d89A	Alignment	not modelled	98.8	17	PDB header: electron transport Chain: A: PDB Molecule: rieske domain-containing protein; PDBTitle: crystal structure of a soluble rieske ferredoxin from mus musculus
31	d1ulia1	Alignment	not modelled	98.8	25	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
32	d1z01a1	Alignment	not modelled	98.6	22	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
33	d1wqla1	Alignment	not modelled	98.5	22	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
34	d1o7na1	Alignment	not modelled	98.5	20	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
35	d2bmoa1	Alignment	not modelled	98.4	22	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
36	d2b1xa1	Alignment	not modelled	98.3	16	Fold: ISP domain Superfamily: ISP domain Family: Ring hydroxylating alpha subunit ISP domain
37	c4qdfA	Alignment	not modelled	97.6	24	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: 3-ketosteroid 9alpha-hydroxylase oxygenase; PDBTitle: crystal structure of apo ksha5 and ksha1 in complex with 1,4-30q-coa2 from r. rhodochrous
38	c4qdfB	Alignment	not modelled	97.3	20	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: B: PDB Molecule: 3-ketosteroid 9alpha-hydroxylase oxygenase; PDBTitle: crystal structure of apo ksha5 and ksha1 in complex with 1,4-30q-coa2 from r. rhodochrous
39	c3gcfC	Alignment	not modelled	96.9	21	PDB header: oxidoreductase Chain: C: PDB Molecule: terminal oxygenase component of carbazole 1,9a- PDBTitle: terminal oxygenase of carbazole 1,9a-dioxygenase from2 nocardioides aromaticivorans ic177
40	c3gteB	Alignment	not modelled	96.6	23	PDB header: electron transport, oxidoreductase Chain: B: PDB Molecule: ddmc; PDBTitle: crystal structure of dicamba monooxygenase with non-heme iron
41	c2zylA	Alignment	not modelled	96.5	20	PDB header: oxidoreductase Chain: A: PDB Molecule: possible oxidoreductase; PDBTitle: crystal structure of 3-ketosteroid-9-alpha-hydroxylase2 (ksha) from m. tuberculosis
42	c2b1xE	Alignment	not modelled	96.5	15	PDB header: oxidoreductase Chain: E: PDB Molecule: naphthalene dioxygenase large subunit; PDBTitle: crystal structure of naphthalene 1,2-dioxygenase from rhodococcus sp.
43	c3gkqB	Alignment	not modelled	96.4	21	PDB header: oxidoreductase Chain: B: PDB Molecule: terminal oxygenase component of carbazole 1,9a-dioxygenase; PDBTitle: terminal oxygenase of carbazole 1,9a-dioxygenase from novosphingobium2 sp. ka1
44	c1z01D	Alignment	not modelled	96.4	23	PDB header: oxidoreductase Chain: D: PDB Molecule: 2-oxo-1,2-dihydroquinoline 8-monooxygenase, oxygenase PDBTitle: 2-oxoquinoline 8-monooxygenase component: active site modulation by2 rieske-[2fe-2s] center oxidation/reduction
45	c3n0qA	Alignment	not modelled	96.4	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative aromatic-ring hydroxylating dioxygenase; PDBTitle: crystal structure of a putative aromatic-ring hydroxylating2 dioxygenase (tm1040_3219) from silicibacter sp. tm1040 at 1.80 a3 resolution
46	c2de7B	Alignment	not modelled	96.1	20	PDB header: oxidoreductase Chain: B: PDB Molecule: terminal oxygenase component of carbazole; PDBTitle: the substrate-bound complex between oxygenase and2 ferredoxin in carbazole 1,9a-dioxygenase
47	c3vcaA	Alignment	not modelled	96.1	26	PDB header: oxidoreductase Chain: A: PDB Molecule: ring-hydroxylating dioxygenase; PDBTitle: quaternary ammonium oxidative demethylation: x-ray crystallographic,2 resonance raman and uv-visible spectroscopic analysis of a rieske-3 type demethylase
48	c1uljA	Alignment	not modelled	96.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: biphenyl dioxygenase large subunit; PDBTitle: biphenyl dioxygenase (bpha1a2) in complex with the substrate
49	c2gbxE	Alignment	not modelled	95.9	21	PDB header: oxidoreductase Chain: E: PDB Molecule: biphenyl 2,3-dioxygenase alpha subunit; PDBTitle: crystal structure of biphenyl 2,3-dioxygenase from sphingomonas2 yanoikuyae b1 bound to biphenyl
50	c1wqlA	Alignment	not modelled	95.5	19	PDB header: oxidoreductase Chain: A: PDB Molecule: iron-sulfur protein large subunit of cumene dioxygenase; PDBTitle: cumene dioxygenase (cuma1a2) from pseudomonas fluorescens ip01
51	c2hmnA	Alignment	not modelled	95.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: naphthalene 1,2-dioxygenase alpha subunit; PDBTitle: crystal structure of the naphthalene 1,2-dioxygenase f352v2 mutant bound to anthracene.
52	c2pny	Alignment	not modelled	49.0	21	PDB header: transferase Chain: X: PDB Molecule: thymidylate synthase;

52	c0egyA	Alignment	not modelled	48.0	31	PDBTitle: crystal structure of human thymidylate synthase a191k with loop 181-2 197 stabilized in the inactive conformation PDB header: transferase
53	c1hw3A	Alignment	not modelled	38.7	31	Chain: A; PDB Molecule: thymidylate synthase; PDBTitle: structure of human thymidylate synthase suggests advantages of 2 chemotherapy with noncompetitive inhibitors
54	d1t12a	Alignment	not modelled	29.7	21	Fold: 5-bladed beta-propeller Superfamily: Tachylectin-2 Family: Tachylectin-2
55	c3a44D	Alignment	not modelled	29.6	14	PDB header: metal binding protein Chain: D; PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
56	d2nvp1	Alignment	not modelled	27.9	33	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: CPF0428-like
57	c6d80A	Alignment	not modelled	26.1	12	PDB header: transport protein Chain: A; PDB Molecule: mitochondrial calcium uniporter; PDBTitle: cryo-em structure of the mitochondrial calcium uniporter from n.2 fischeri bound to saposin
58	d1seja2	Alignment	not modelled	26.1	38	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
59	c5yq72	Alignment	not modelled	25.8	21	PDB header: photosynthesis Chain: 2; PDB Molecule: beta subunit of light-harvesting 1; PDBTitle: cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
60	d1sfea1	Alignment	not modelled	25.6	27	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
61	c2oipE	Alignment	not modelled	23.8	38	PDB header: transferase, oxidoreductase Chain: E; PDB Molecule: chain a, crystal structure of dhfr; PDBTitle: crystal structure of the s290g active site mutant of ts-dhfr from 2 cryptosporidium hominis
62	c2aydA	Alignment	not modelled	23.0	19	PDB header: transcription Chain: A; PDB Molecule: wrky transcription factor 1; PDBTitle: crystal structure of the c-terminal wrky domain of atwrky1, an sa-2 induced and partially npr1-dependent transcription factor
63	c3k2hA	Alignment	not modelled	21.8	43	PDB header: transferase Chain: A; PDB Molecule: dihydrofolate reductase/thymidylate synthase; PDBTitle: co-crystal structure of dihydrofolate reductase/thymidylate synthase2 from babesia bovis with dump, pemetrexed and nadp
64	d1qnta1	Alignment	not modelled	21.4	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Methylated DNA-protein cysteine methyltransferase, C-terminal domain Family: Methylated DNA-protein cysteine methyltransferase, C-terminal domain
65	c5b6dB	Alignment	not modelled	21.3	21	PDB header: transferase Chain: B; PDB Molecule: cmp 5-hydroxymethylase; PDBTitle: crystal structure of cytidine monophosphate hydroxymethylase mila with 2 cmp
66	c2k8sA	Alignment	not modelled	20.7	36	PDB header: oxidoreductase Chain: A; PDB Molecule: thioredoxin; PDBTitle: solution nmr structure of dimeric thioredoxin-like protein2 ne0084 from nitrosomonas europea: northeast structural3 genomics target net6
67	c5zkaA	Alignment	not modelled	20.5	26	PDB header: viral protein Chain: A; PDB Molecule: envelope glycoprotein; PDBTitle: the postfusion structure of human-infecting bourbon virus envelope2 glycoprotein
68	c2a2vA	Alignment	not modelled	20.4	37	PDB header: toxin Chain: A; PDB Molecule: jingzhaotoxin-xi; PDBTitle: the solution structure of jingzhaotoxin-xi
69	c6hu9u	Alignment	not modelled	20.0	20	PDB header: oxidoreductase/electron transport Chain: U; PDB Molecule: cytochrome b-c1 complex subunit 10; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
70	d1j3kc	Alignment	not modelled	20.0	43	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
71	c4iu8A	Alignment	not modelled	19.5	12	PDB header: transport protein Chain: A; PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter (selenomethionine2 derivative)
72	d1qzfa2	Alignment	not modelled	19.3	38	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
73	c3v8hB	Alignment	not modelled	19.0	36	PDB header: transferase Chain: B; PDB Molecule: thymidylate synthase; PDBTitle: crystal structure of thymidylate synthase from burkholderia2 thailandensis
74	d1hvya	Alignment	not modelled	18.6	43	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
75	c3qj7D	Alignment	not modelled	18.1	43	PDB header: transferase Chain: D; PDB Molecule: thymidylate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis thymidylate2 synthase (thya) bound to dump
76	d2g8oa1	Alignment	not modelled	18.1	43	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
						Fold: Thymidylate synthase/dCMP hydroxymethylase

77	d1bkpa_	Alignment	not modelled	17.9	36	Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
78	d1rnfa_	Alignment	not modelled	17.6	21	Fold: RNase A-like Superfamily: RNase A-like Family: Ribonuclease A-like
79	c1yx3A_	Alignment	not modelled	17.3	37	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein dsrc; PDBTitle: nmr structure of allochromatium vinosum dsrc: northeast2 structural genomics consortium target op4
80	c5mb9C_	Alignment	not modelled	17.1	75	PDB header: chaperone Chain: C: PDB Molecule: putative ribosome associated protein; PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair
81	c6rlxA_	Alignment	not modelled	16.9	57	PDB header: hormone(muscle relaxant) Chain: A: PDB Molecule: relaxin, a-chain; PDBTitle: x-ray structure of human relaxin at 1.5 angstroms. comparison to2 insulin and implications for receptor binding determinants
82	c2mv1A_	Alignment	not modelled	16.9	57	PDB header: signaling protein Chain: A: PDB Molecule: relaxin a chain; PDBTitle: solution nmr structure of human relaxin-2
83	c6rlxC_	Alignment	not modelled	16.9	57	PDB header: hormone(muscle relaxant) Chain: C: PDB Molecule: relaxin, a-chain; PDBTitle: x-ray structure of human relaxin at 1.5 angstroms. comparison to2 insulin and implications for receptor binding determinants
84	d1b5ea_	Alignment	not modelled	16.7	14	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
85	c4fo9A_	Alignment	not modelled	16.5	32	PDB header: ligase Chain: A: PDB Molecule: e3 sumo-protein ligase pias2; PDBTitle: crystal structure of the e3 sumo ligase pias2
86	d2tsra_	Alignment	not modelled	16.3	43	Fold: Thymidylate synthase/dCMP hydroxymethylase Superfamily: Thymidylate synthase/dCMP hydroxymethylase Family: Thymidylate synthase/dCMP hydroxymethylase
87	c4eckB_	Alignment	not modelled	16.2	43	PDB header: transferase, oxidoreductase Chain: B: PDB Molecule: bifunctional dihydrofolate reductase-thymidylate synthase; PDBTitle: crystal structure of the toxoplasma gondii ts-dhfr
88	d1wj2a_	Alignment	not modelled	16.2	38	Fold: WRKY DNA-binding domain Superfamily: WRKY DNA-binding domain Family: WRKY DNA-binding domain
89	c4iu9A_	Alignment	not modelled	16.1	12	PDB header: transport protein Chain: A: PDB Molecule: nitrite extrusion protein 2; PDBTitle: crystal structure of a membrane transporter
90	c4hg6B_	Alignment	not modelled	15.9	16	PDB header: transferase Chain: B: PDB Molecule: cellulose synthase subunit b; PDBTitle: structure of a cellulose synthase - cellulose translocation2 intermediate
91	c5mb9D_	Alignment	not modelled	15.5	75	PDB header: chaperone Chain: D: PDB Molecule: putative ribosome associated protein; PDBTitle: crystal structure of the eukaryotic ribosome associated complex (rac),2 a unique hsp70/hsp40 pair
92	c6et5u_	Alignment	not modelled	15.0	20	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
93	c4wvmA_	Alignment	not modelled	14.6	21	PDB header: toxin Chain: A: PDB Molecule: stonustoxin subunit alpha; PDBTitle: stonustoxin structure
94	c5zjih_	Alignment	not modelled	14.1	14	PDB header: membrane protein Chain: H: PDB Molecule: photosystem i reaction center subunit vi, chloroplastic; PDBTitle: structure of photosystem i supercomplex with light-harvesting2 complexes i and ii
95	c5yq7C_	Alignment	not modelled	13.9	43	PDB header: photosynthesis Chain: C: PDB Molecule: cytochrome subunit of photosynthetic reaction center; PDBTitle: cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii
96	d2ewla1	Alignment	not modelled	13.6	46	Fold: E7 C-terminal domain-like Superfamily: E7 C-terminal domain-like Family: E7 C-terminal domain-like
97	c2narA_	Alignment	not modelled	13.6	11	PDB header: protein binding Chain: A: PDB Molecule: effector protein avr3a; PDBTitle: solution structure of avr3a_60-147 from phytophthora infestans
98	c5zktA_	Alignment	not modelled	13.5	38	PDB header: transcription Chain: A: PDB Molecule: putative transcription factor pcf6; PDBTitle: crystal structure of tcp domain of pcf6 in oryza sativa
99	c3wmmP_	Alignment	not modelled	13.4	22	PDB header: photosynthesis Chain: P: PDB Molecule: lh1 beta polypeptide; PDBTitle: crystal structure of the lh1-rc complex from thermochromatium tepidum2 in c2 form