













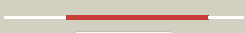










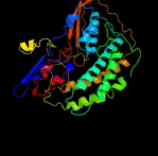

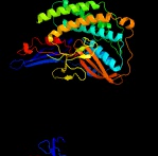
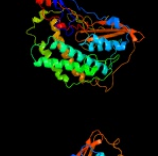
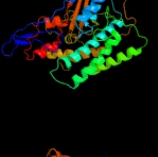
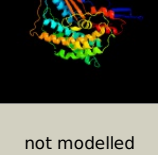


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0087_(hycE)_95411_96889
 Date Tue Jul 23 14:50:12 BST 2019
 Unique Job ID 35aa56c9d9f7d323

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5lc5D_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: D: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 2, PDBTitle: structure of mammalian respiratory complex i, class2
2	c6gcsC_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: C: PDB Molecule: 49-kda protein (nucm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
3	c6cfwL_	 Alignment		100.0	29	PDB header: membrane protein Chain: L: PDB Molecule: membrane-bound hydrogenase subunit alpha; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
4	c6humH_	 Alignment		100.0	24	PDB header: proton transport Chain: H: PDB Molecule: nad(p)h-quinone oxidoreductase subunit h; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
5	c2fug4_	 Alignment		100.0	27	PDB header: oxidoreductase Chain: 4: PDB Molecule: nadh-quinone oxidoreductase chain 4; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
6	d2fug41	 Alignment		100.0	27	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nqo4-like
7	d1e3db_	 Alignment		100.0	25	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
8	d1yq9h1	 Alignment		100.0	25	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
9	c1h2aL_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: L: PDB Molecule: hydrogenase; PDBTitle: single crystals of hydrogenase from desulfovibrio vulgaris
10	d1frfl_	 Alignment		100.0	25	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
11	c2wpmB_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: B: PDB Molecule: periplasmic [nifese] hydrogenase, large subunit, PDBTitle: structure of the oxidised, as-isolated nifese hydrogenase from d.2 vulgaris hildenborough

12	c6ehqM_	Alignment		100.0	24	PDB header: oxidoreductase Chain: M: PDB Molecule: hydrogenase-2 large chain; PDBTitle: e. coli hydrogenase-2 (as isolated form).
13	d1cc1_	Alignment		100.0	21	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
14	d1wui1	Alignment		100.0	26	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
15	c3zfsA_	Alignment		100.0	21	PDB header: oxidoreductase Chain: A: PDB Molecule: f420-reducing hydrogenase, subunit alpha; PDBTitle: cryo-em structure of the f420-reducing nife-hydrogenase from a2 methanogenic archaeon with bound substrate
16	c5aa5C_	Alignment		100.0	22	PDB header: oxidoreductase Chain: C: PDB Molecule: nife-hydrogenase large subunit, hofg; PDBTitle: actinobacterial-type nife-hydrogenase from ralstonia eutropha h16 at2 2.85 angstrom resolution
17	c5odqF_	Alignment		100.0	21	PDB header: oxidoreductase Chain: F: PDB Molecule: methyl-viologen reducing hydrogenase, subunit a; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus soaked with3 bromoethanesulfonate.
18	c5xf9H_	Alignment		100.0	19	PDB header: oxidoreductase Chain: H: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
19	c3myrB_	Alignment		100.0	27	PDB header: oxidoreductase Chain: B: PDB Molecule: nickel-dependent hydrogenase large subunit; PDBTitle: crystal structure of [nife] hydrogenase from allochromatium vinosum in2 its ni-a state
20	c5yy0A_	Alignment		100.0	15	PDB header: metal binding protein Chain: A: PDB Molecule: cytosolic nife-hydrogenase, alpha subunit; PDBTitle: crystal structure of the hylh-hypa complex (form ii)
21	c3useL_	Alignment	not modelled	100.0	22	PDB header: oxidoreductase Chain: L: PDB Molecule: hydrogenase-1 large chain; PDBTitle: crystal structure of e. coli hydrogenase-1 in its as-isolated form
22	c4c3oC_	Alignment	not modelled	100.0	21	PDB header: oxidoreductase Chain: C: PDB Molecule: hydrogenase-1 large subunit; PDBTitle: structure and function of an oxygen tolerant nife hydrogenase from2 salmonella
23	c6cfwK_	Alignment	not modelled	100.0	26	PDB header: membrane protein Chain: K: PDB Molecule: membrane-bound hydrogenase subunit beta; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
24	c6humJ_	Alignment	not modelled	100.0	30	PDB header: proton transport Chain: J: PDB Molecule: nad(p)h-quinone oxidoreductase subunit j; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
25	c6gcsG_	Alignment	not modelled	100.0	27	PDB header: oxidoreductase Chain: G: PDB Molecule: 30-kda protein (nugm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
26	c5ldwC_	Alignment	not modelled	100.0	25	PDB header: oxidoreductase Chain: C: PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 3, PDBTitle: structure of mammalian respiratory complex i, class1
27	d2fug51	Alignment	not modelled	100.0	25	Fold: Nqo5-like Superfamily: Nqo5-like Family: Nqo5-like
28	c3mcrA_	Alignment	not modelled	99.9	27	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh dehydrogenase, subunit c; PDBTitle: crystal structure of nadh dehydrogenase subunit c (tfu_2693) from2 thermobifida fusca yx-er1 at 2.65 a resolution

29	d1v97a4	Alignment	not modelled	50.5	6	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
30	c3r07C	Alignment	not modelled	43.1	13	PDB header: transferase Chain: C: PDB Molecule: putative lipocate-protein ligase a subunit 2; PDBTitle: structural analysis of an archaeal lipoylation system. a bi-partite2 lipocate protein ligase and its e2 lipoyl domain from thermoplasma3 acidophilum
31	d1ffvc1	Alignment	not modelled	42.4	15	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
32	c4mnoA	Alignment	not modelled	39.6	27	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 1a; PDBTitle: crystal structure of aif1a from pyrococcus abyssii
33	c4lqzA	Alignment	not modelled	37.3	37	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4909 family protein (sav1798) from2 staphylococcus aureus subsp. aureus mu50 at 1.92 a resolution
34	c5dkoA	Alignment	not modelled	33.3	10	PDB header: replication Chain: A: PDB Molecule: cell division protein zapd; PDBTitle: the structure of escherichia coli zapd
35	d1u07a	Alignment	not modelled	29.8	18	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
36	c2dgyA	Alignment	not modelled	27.3	20	PDB header: translation Chain: A: PDB Molecule: mgc11102 protein; PDBTitle: solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
37	c2grxC	Alignment	not modelled	26.5	17	PDB header: metal transport Chain: C: PDB Molecule: protein tonb; PDBTitle: crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
38	c5nz7A	Alignment	not modelled	25.1	18	PDB header: hydrolase Chain: A: PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase ligand free form
39	d1ni2a3	Alignment	not modelled	24.1	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: First domain of FERM
40	d1ef1a3	Alignment	not modelled	23.6	5	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: First domain of FERM
41	d2zpya3	Alignment	not modelled	22.1	10	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: First domain of FERM
42	d2ntka1	Alignment	not modelled	21.7	32	Fold: Ntn hydrolase-like Superfamily: Archaeal IMP cyclohydrolase PurO Family: Archaeal IMP cyclohydrolase PurO
43	c1xx3A	Alignment	not modelled	21.4	17	PDB header: transport protein Chain: A: PDB Molecule: tonb protein; PDBTitle: solution structure of escherichia coli tonb-ctd
44	c5uz9B	Alignment	not modelled	20.9	14	PDB header: immune system/rna Chain: B: PDB Molecule: crispr-associated protein csy2; PDBTitle: cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crRNA-guided crispr surveillance complex
45	d2gskb1	Alignment	not modelled	20.1	17	Fold: TolA/TonB C-terminal domain Superfamily: TolA/TonB C-terminal domain Family: TonB
46	d1gg3a3	Alignment	not modelled	19.7	15	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: First domain of FERM
47	c3kwIA	Alignment	not modelled	18.8	20	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a hypothetical protein from helicobacter pylori
48	c5j84A	Alignment	not modelled	18.6	24	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of l-arabinonate dehydratase in holo-form
49	d1iowa1	Alignment	not modelled	18.4	21	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
50	d1t3qc1	Alignment	not modelled	18.2	12	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
51	c4k59A	Alignment	not modelled	17.2	11	PDB header: rna binding protein Chain: A: PDB Molecule: rna binding protein rsmf; PDBTitle: crystal structure of pseudomonas aeruginosa rsmf
52	c6r4pA	Alignment	not modelled	16.9	28	PDB header: membrane protein Chain: A: PDB Molecule: adenylate cyclase 9; PDBTitle: structure of a soluble domain of adenylyl cyclase bound to an2 activated stimulatory g protein
53	c5fayA	Alignment	not modelled	16.8	17	PDB header: lyase Chain: A: PDB Molecule: choline trimethylamine-lyase; PDBTitle: y208f mutant of choline tma-lyase
54	d2oeza1	Alignment	not modelled	16.7	14	Fold: YacF-like Superfamily: YacF-like Family: YacF-like
						PDB header: oxidoreductase

55	c3hrdC_	Alignment	not modelled	16.1	12	Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
56	d1n62c1	Alignment	not modelled	16.1	16	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
57	d1v8ca2	Alignment	not modelled	15.6	43	Fold: TBP-like Superfamily: MoaD-related protein, C-terminal domain Family: MoaD-related protein, C-terminal domain
58	c2ibpB_	Alignment	not modelled	15.4	19	PDB header: transferase Chain: B: PDB Molecule: citrate synthase; PDBTitle: crystal structure of citrate synthase from pyrobaculum aerophilum
59	c6fipA_	Alignment	not modelled	15.1	28	PDB header: transport protein Chain: A: PDB Molecule: protein tonb; PDBTitle: solution nmr structure of pseudomonas aeruginosa tonb ctd
60	c5lw8A_	Alignment	not modelled	14.9	33	PDB header: metal transport Chain: A: PDB Molecule: protein tonb; PDBTitle: nmr solution structure of helicobacter pylori tonb-ctd (residues 194-2 285)
61	c2g40A_	Alignment	not modelled	14.8	29	PDB header: unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of a duf162 family protein (dr_1909) from2 deinococcus radiodurans at 1.70 a resolution
62	d2g40a1	Alignment	not modelled	14.8	29	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: YkgG-like
63	c1ufiD_	Alignment	not modelled	14.6	30	PDB header: dna binding protein Chain: D: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of the dimerization domain of human cenp-b
64	d1ufia_	Alignment	not modelled	14.4	30	Fold: ROP-like Superfamily: Dimerisation domain of CENP-B Family: Dimerisation domain of CENP-B
65	d1vqza1	Alignment	not modelled	14.2	14	Fold: SufE/NifU Superfamily: SufE/NifU Family: SP1160 C-terminal domain-like
66	c2oqkA_	Alignment	not modelled	14.2	14	PDB header: translation Chain: A: PDB Molecule: putative translation initiation factor eif-1a; PDBTitle: crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
67	d1l1aa3	Alignment	not modelled	14.0	9	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arthropod hemocyanin, C-terminal domain
68	d1gxma_	Alignment	not modelled	13.5	15	Fold: alpha/alpha toroid Superfamily: Family 10 polysaccharide lyase Family: Family 10 polysaccharide lyase
69	c3j81j_	Alignment	not modelled	12.5	11	PDB header: ribosome Chain: I: PDB Molecule: es8; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
70	d1r9da_	Alignment	not modelled	11.9	17	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: PFL-like
71	c5kpeA_	Alignment	not modelled	11.5	47	PDB header: de novo protein Chain: A: PDB Molecule: de novo beta sheet design protein or664; PDBTitle: solution nmr structure of denovo beta sheet design protein, northeast2 structural genomics consortium (nesg) target or664
72	d2qlvb1	Alignment	not modelled	11.5	15	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: AMPK-beta glycogen binding domain-like
73	c5hxaA_	Alignment	not modelled	11.3	20	PDB header: protein binding Chain: A: PDB Molecule: alpha,alpha-trehalose-phosphate synthase (udp-forming); PDBTitle: crystal structure of an udp-forming alpha, alpha-terhalose-phosphate2 synthase from burkholderia xenovorans
74	c2m2kA_	Alignment	not modelled	10.9	20	PDB header: transport protein Chain: A: PDB Molecule: hasb protein; PDBTitle: the structure of hasb ctd
75	d1ihra_	Alignment	not modelled	10.7	17	Fold: ToIA/TonB C-terminal domain Superfamily: ToIA/TonB C-terminal domain Family: TonB
76	d1d7qa_	Alignment	not modelled	10.7	11	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
77	c2k9kA_	Alignment	not modelled	10.7	29	PDB header: metal transport Chain: A: PDB Molecule: tonb2; PDBTitle: molecular characterization of the tonb2 protein from vibrio2 anguillarum
78	c5h42A_	Alignment	not modelled	10.7	18	PDB header: transferase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of 1,2-beta-oligoglucan phosphorylase from2 lachnoclostridium phytofermentans in complex with alpha-d-glucose-1-3 phosphate
79	c3ep3A_	Alignment	not modelled	10.6	17	PDB header: lyase Chain: A: PDB Molecule: s-adenosylmethionine decarboxylase alpha chain; PDBTitle: human adometdc d174n mutant with no putrescine bound
80	c2jisA_	Alignment	not modelled	10.6	18	PDB header: lyase Chain: A: PDB Molecule: cysteine sulfinic acid decarboxylase; PDBTitle: human cysteine sulfinic acid decarboxylase (csad) in2 complex with plp.

81	c5nz8A_	Alignment	not modelled	10.3	18	PDB header: hydrolase Chain: A; PDB Molecule: cellodextrin phosphorylase; PDBTitle: clostridium thermocellum cellodextrin phosphorylase with cellotetraose2 and phosphate bound
82	d1es6a2	Alignment	not modelled	10.2	36	Fold: EV matrix protein Superfamily: EV matrix protein Family: EV matrix protein
83	c3tcqA_	Alignment	not modelled	10.1	36	PDB header: viral protein Chain: A; PDB Molecule: matrix protein vp40; PDBTitle: crystal structure of matrix protein vp40 from ebola virus sudan
84	d1hc1a3	Alignment	not modelled	10.0	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Arthropod hemocyanin, C-terminal domain
85	d1qvia_	Alignment	not modelled	9.9	12	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
86	d1jroa3	Alignment	not modelled	9.7	9	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
87	c3u5cf_	Alignment	not modelled	9.7	16	PDB header: ribosome Chain: F; PDB Molecule: 40s ribosomal protein s5; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
88	c4byl5_	Alignment	not modelled	9.7	16	PDB header: ribosome Chain: 5; PDB Molecule: ubiquitin-40s ribosomal protein s31; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnamet2 eukaryotic translation initiation complex
89	c4uer9_	Alignment	not modelled	9.7	16	PDB header: translation Chain: 9; PDB Molecule: es31; PDBTitle: 40s-eif1-eif1a-eif3-eif3j translation initiation complex from2 lachancea kluyveri
90	c4byt5_	Alignment	not modelled	9.7	16	PDB header: ribosome Chain: 5; PDB Molecule: ubiquitin-40s ribosomal protein s31; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnamet2 eukaryotic translation initiation complex
91	c6bugA_	Alignment	not modelled	9.7	17	PDB header: membrane protein Chain: A; PDB Molecule: d-alanyl carrier protein; PDBTitle: crystal structure of a membrane protein, crystal form i
92	c2kboA_	Alignment	not modelled	9.6	10	PDB header: hydrolase Chain: A; PDB Molecule: dna dc->du-editing enzyme apobec-3g; PDBTitle: structure, interaction, and real-time monitoring of the2 enzymatic reaction of wild type apobec3g
93	c1bl1A_	Alignment	not modelled	9.6	56	PDB header: hormone receptor Chain: A; PDB Molecule: parathyroid hormone receptor; PDBTitle: pth receptor n-terminus fragment, nmr, 1 structure
94	c4bpp0_	Alignment	not modelled	9.5	14	PDB header: ribosome Chain: 0; PDB Molecule: translation initiation factor eif-1a family protein; PDBTitle: the crystal structure of the eukaryotic 40s ribosomal subunit in2 complex with eif1 and eif1a - complex 4
95	c3ut2B_	Alignment	not modelled	9.2	20	PDB header: oxidoreductase Chain: B; PDB Molecule: catalase-peroxidase 2; PDBTitle: crystal structure of fungal magkatg2
96	c5ibyA_	Alignment	not modelled	9.0	13	PDB header: ligase,transferase Chain: A; PDB Molecule: lipoate--protein ligase; PDBTitle: crystal structure of enterococcus faecalis lipoate-protein ligase a2 (lpla-2) in complex with lipoic acid
97	d1h4ra3	Alignment	not modelled	8.8	5	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: First domain of FERM
98	c5i2gB_	Alignment	not modelled	8.7	20	PDB header: lyase Chain: B; PDB Molecule: diol dehydratase; PDBTitle: 1,2-propanediol dehydration in roseburia inulinivorans; structural2 basis for substrate and enantiomer selectivity
99	c2nytB_	Alignment	not modelled	8.7	30	PDB header: hydrolase Chain: B; PDB Molecule: probable c->u-editing enzyme apobec-2; PDBTitle: the apobec2 crystal structure and functional implications2 for aid