






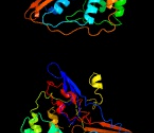
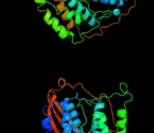


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3148_(nuoD)_3513335_3514657
 Date Thu Aug 8 16:20:33 BST 2019
 Unique Job ID a2e937c1d7335efd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5lc5D_	Alignment		100.0	44	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	40	PDB header: oxidoreductase Chain: C: PDB Molecule: 49-kda protein (nucm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
3	c6humH_	Alignment		100.0	39	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
4	c6cfwL_	Alignment		100.0	32	PDB header: membrane protein Chain: L: PDB Molecule: membrane-bound hydrogenase subunit alpha; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
5	d2fug41	Alignment		100.0	49	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nqo4-like
6	c2fug4_	Alignment		100.0	49	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
7	d1e3db_	Alignment		100.0	22	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
8	d1frfl_	Alignment		100.0	18	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
9	d1yq9h1	Alignment		100.0	21	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
10	c1h2aL_	Alignment		100.0	23	PDB header: oxidoreductase Chain: L: PDB Molecule: hydrogenase; PDBTitle: single crystals of hydrogenase from desulfovibrio vulgaris
11	c5aa5C_	Alignment		100.0	20	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

12	c2wpnB_	Alignment		100.0	18	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
13	c6ehqM_	Alignment		100.0	20	PDB header: oxidoreductase Chain: M: PDB Molecule: hydrogenase-2 large chain; PDBTitle: e. coli hydrogenase-2 (as isolated form).
14	d1cc1_	Alignment		100.0	18	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
15	c3myrB_	Alignment		100.0	21	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
16	c5odqF_	Alignment		100.0	13	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.
17	c5xf9H_	Alignment		100.0	15	PDB header: oxidoreductase Chain: H: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
18	d1wuil1	Alignment		100.0	19	Fold: HydB/Nqo4-like Superfamily: HydB/Nqo4-like Family: Nickel-iron hydrogenase, large subunit
19	c3zfsA_	Alignment		100.0	20	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
20	c3useL_	Alignment		100.0	18	PDB header: oxidoreductase Chain: L: PDB Molecule: hydrogenase-1 large chain; PDBTitle: crystal structure of e. coli hydrogenase-1 in its as-isolated form
21	c4c3oC_	Alignment	not modelled	100.0	19	PDB header: oxidoreductase Chain: C: PDB Molecule: hydrogenase-1 large subunit; PDBTitle: structure and function of an oxygen tolerant nife hydrogenase from2 salmonella
22	c5yy0A_	Alignment	not modelled	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)
23	c3r07C_	Alignment	not modelled	63.6	19	PDB header: transferase Chain: C: PDB Molecule: putative lipoate-protein ligase a subunit 2; PDBTitle: structural analysis of an archaeal lipoylation system. a bi-partite2 lipoate protein ligase and its e2 lipoyl domain from thermoplasma3 acidophilum
24	d2g40a1	Alignment	not modelled	59.5	25	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: YkgG-like
25	c2g40A_	Alignment	not modelled	59.5	25	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
26	d1v97a4	Alignment	not modelled	46.4	8	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
27	c5ymrB_	Alignment	not modelled	33.3	18	PDB header: lyase Chain: B: PDB Molecule: formate acetyltransferase; PDBTitle: the crystal structure of iseg
28	d1yeya2	Alignment	not modelled	32.4	4	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
						Fold: Ntn hydrolase-like

29	d2ntka1	Alignment	not modelled	32.1	9	Superfamily: Archaeal IMP cyclohydrolase PurO Family: Archaeal IMP cyclohydrolase PurO
30	d1ffvc1	Alignment	not modelled	31.0	21	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
31	d1r9da_	Alignment	not modelled	28.5	15	Fold: PFL-like glycy radical enzymes Superfamily: PFL-like glycy radical enzymes Family: PFL-like
32	c4k59A_	Alignment	not modelled	26.6	55	PDB header: rna binding protein Chain: A: PDB Molecule: rna binding protein rsmf; PDBTitle: crystal structure of pseudomonas aeruginosa rsmf
33	c1ufiD_	Alignment	not modelled	25.7	40	PDB header: dna binding protein Chain: D: PDB Molecule: major centromere autoantigen b; PDBTitle: crystal structure of the dimerization domain of human cenp-b
34	d1ufia_	Alignment	not modelled	25.5	40	Fold: ROP-like Superfamily: Dimerisation domain of CENP-B Family: Dimerisation domain of CENP-B
35	c2w3zA_	Alignment	not modelled	23.6	11	PDB header: hydrolase Chain: A: PDB Molecule: putative deacetylase; PDBTitle: structure of a streptococcus mutans ce4 esterase
36	d1jroa3	Alignment	not modelled	22.4	26	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
37	d1vqza1	Alignment	not modelled	21.5	17	Fold: SufE/NifU Superfamily: SufE/NifU Family: SP1160 C-terminal domain-like
38	c4lqzA_	Alignment	not modelled	19.8	33	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf4909 family protein (sav1798) from staphylococcus aureus subsp. aureus mu50 at 1.92 a resolution
39	c5ze4A_	Alignment	not modelled	19.0	15	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the structure of holo- structure of dhad complex with [2fe-2s] cluster
40	c4mnoA_	Alignment	not modelled	18.0	15	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 1a; PDBTitle: crystal structure of aif1a from pyrococcus abyssi
41	c2f3oB_	Alignment	not modelled	17.8	17	PDB header: unknown function Chain: B: PDB Molecule: pyruvate formate-lyase 2; PDBTitle: crystal structure of a glycy radical enzyme from archaeoglobus2 fulgidus
42	c5j84A_	Alignment	not modelled	17.5	18	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of l-arabinonate dehydratase in holo-form
43	c5dkaA_	Alignment	not modelled	16.8	18	PDB header: replication Chain: A: PDB Molecule: cell division protein zapd; PDBTitle: the structure of escherichia coli zapd
44	d1rm6b1	Alignment	not modelled	15.8	18	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
45	c3hrdC_	Alignment	not modelled	15.5	12	PDB header: oxidoreductase Chain: C: PDB Molecule: nicotinate dehydrogenase fad-subunit; PDBTitle: crystal structure of nicotinate dehydrogenase
46	c2w3rG_	Alignment	not modelled	15.5	26	PDB header: oxidoreductase Chain: G: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of xanthine dehydrogenase (desulfo form)2 from rhodobacter capsulatus in complex with hypoxanthine
47	d1jdfa2	Alignment	not modelled	14.7	9	Fold: Enolase N-terminal domain-like Superfamily: Enolase N-terminal domain-like Family: Enolase N-terminal domain-like
48	d1u07a_	Alignment	not modelled	13.8	17	Fold: ToIA/TonB C-terminal domain Superfamily: ToIA/TonB C-terminal domain Family: TonB
49	c2dd9C_	Alignment	not modelled	13.2	15	PDB header: luminescent protein Chain: C: PDB Molecule: green fluorescent protein; PDBTitle: a mutant of gfp-like protein from chironomus tentans
50	d1t3qc1	Alignment	not modelled	11.7	18	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
51	d1n62c1	Alignment	not modelled	11.6	15	Fold: CO dehydrogenase flavoprotein C-domain-like Superfamily: CO dehydrogenase flavoprotein C-terminal domain-like Family: CO dehydrogenase flavoprotein C-terminal domain-like
52	c2dgyA_	Alignment	not modelled	11.5	16	PDB header: translation Chain: A: PDB Molecule: mgc11102 protein; PDBTitle: solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
53	d1x2ga1	Alignment	not modelled	11.3	17	Fold: SufE/NifU Superfamily: SufE/NifU Family: SP1160 C-terminal domain-like
54	c4af3D_	Alignment	not modelled	11.0	13	PDB header: transferase/inhibitor Chain: D: PDB Molecule: inner centromere protein; PDBTitle: human aurora b kinase in complex with incenp and vx-680
55	c3o6uB_	Alignment	not modelled	11.0	10	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein cpe2226; PDBTitle: crystal structure of cpe2226 protein from clostridium

						perfringens.2 northeast structural genomics consortium target cpr195
56	c2vgpD_	Alignment	not modelled	10.9	13	PDB header: transferase Chain: D: PDB Molecule: inner centromere protein a; PDBTitle: crystal structure of aurora b kinase in complex with a2 aminothiazole inhibitor
57	c2grxC_	Alignment	not modelled	10.9	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
58	c5ibyA_	Alignment	not modelled	10.8	21	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
59	c3km3B_	Alignment	not modelled	10.5	28	PDB header: hydrolase Chain: B: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: crystal structure of eoxycytidine triphosphate deaminase from2 anaplasma phagocytophilum at 2.1a resolution
60	c1wvtA_	Alignment	not modelled	10.4	5	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st2180; PDBTitle: crystal structure of uncharacterized protein st2180 from sulfobolus2 tokodaii
61	c5i2gB_	Alignment	not modelled	10.4	14	PDB header: lyase Chain: B: PDB Molecule: diol dehydratase; PDBTitle: 1,2-propanediol dehydration in roseburia inulinivorans; structural2 basis for substrate and enantiomer selectivity
62	d2p7ja1	Alignment	not modelled	10.4	17	Fold: Profilin-like Superfamily: Sensory domain-like Family: Ykul C-terminal domain-like
63	c6gr8B_	Alignment	not modelled	10.2	13	PDB header: transferase Chain: B: PDB Molecule: inner centromere protein; PDBTitle: human aurk incenp complex bound to brd-7880
64	c3fa4D_	Alignment	not modelled	9.5	21	PDB header: lyase Chain: D: PDB Molecule: 2,3-dimethylmalate lyase; PDBTitle: crystal structure of 2,3-dimethylmalate lyase, a pep mutase/isocitrate2 lyase superfamily member, triclinic crystal form
65	c4qamB_	Alignment	not modelled	9.5	27	PDB header: signaling protein Chain: B: PDB Molecule: x-linked retinitis pigmentosa gtpase regulator-interacting PDBTitle: crystal structure of the rpgr rcc1-like domain in complex with the2 rpgr-interacting domain of rpgr1p
66	c4dmbA_	Alignment	not modelled	9.2	13	PDB header: immune system Chain: A: PDB Molecule: hd domain-containing protein 2; PDBTitle: x-ray structure of human hepatitis c virus ns5a-transactivated protein2 2 at the resolution 1.9a, northeast structural genomics consortium3 (nesg) target hr6723
67	c2dnwA_	Alignment	not modelled	9.0	17	PDB header: transport protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of rsgi ruh-059, an acp domain of acyl2 carrier protein, mitochondrial [precursor] from human cdna
68	c2mw4D_	Alignment	not modelled	8.9	24	PDB header: transcription Chain: D: PDB Molecule: transcription factor protein; PDBTitle: tetramerization domain of the ciona intestinalis p53/p73-b2 transcription factor protein
69	d2gskb1	Alignment	not modelled	8.9	17	Fold: ToIA/TonB C-terminal domain Superfamily: ToIA/TonB C-terminal domain Family: TonB
70	c3va8A_	Alignment	not modelled	8.6	5	PDB header: lyase Chain: A: PDB Molecule: probable dehydratase; PDBTitle: crystal structure of enolase fg03645.1 (target efi-502278) from2 gibberella zeae ph-1 complexed with magnesium, formate and sulfate
71	c2m1mA_	Alignment	not modelled	8.6	14	PDB header: transcription Chain: A: PDB Molecule: auxin-induced protein iaa4; PDBTitle: solution structure of the psia4 oligomerization domain reveals2 interaction modes for transcription factors in early auxin response
72	c2l9fA_	Alignment	not modelled	8.5	3	PDB header: transferase Chain: A: PDB Molecule: cale8; PDBTitle: nmr solution structure of meacp
73	c2p4vA_	Alignment	not modelled	8.4	12	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor greb; PDBTitle: crystal structure of the transcript cleavage factor, greb2 at 2.6a resolution
74	d1ik0a_	Alignment	not modelled	8.4	14	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Short-chain cytokines
75	c5ij6A_	Alignment	not modelled	8.1	11	PDB header: ligase,transferase Chain: A: PDB Molecule: lipoate--protein ligase; PDBTitle: crystal structure of enterococcus faecalis lipoate-protein ligase a2 (lpla-1) in complex with lipoic acid
76	c2oqkA_	Alignment	not modelled	8.0	19	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
77	c5fayA_	Alignment	not modelled	7.9	19	PDB header: lyase Chain: A: PDB Molecule: choline trimethylamine-lyase; PDBTitle: y208f mutant of choline tma-lyase
78	c4byl5_	Alignment	not modelled	7.9	5	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
79	c4uer9_	Alignment	not modelled	7.9	5	PDB header: translation Chain: 9: PDB Molecule: es31; PDBTitle: 40s-eif1-eif1a-eif3j translation initiation complex from2 lachancea kluyveri
80	c3u5cf_	Alignment	not modelled	7.9	5	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
81	c4byt5	Alignment	not modelled	7.9	5	PDB header: ribosome Chain: 5: PDB Molecule: ubiquitin-40s ribosomal protein s31; PDBTitle: cryo-em reconstruction of the 80s-eif5b-met-itnmet2 eukaryotic translation initiation complex
82	c5fmtB	Alignment	not modelled	7.8	17	PDB header: protein transport Chain: B: PDB Molecule: flagellar associated protein; PDBTitle: crift54 ch-domain
83	d1o98a1	Alignment	not modelled	7.7	12	Fold: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Superfamily: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
84	c5ikfA	Alignment	not modelled	7.6	11	PDB header: transcription Chain: A: PDB Molecule: chromatin remodeling factor mit1; PDBTitle: crystal structure of the c-terminal domain of the mit1 nucleosome2 remodeler in complex with clr1
85	d2up1a2	Alignment	not modelled	7.6	21	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
86	d1qxha	Alignment	not modelled	7.5	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
87	c6eacC	Alignment	not modelled	7.5	13	PDB header: transferase Chain: C: PDB Molecule: selo; PDBTitle: pseudomonas syringae selo
88	c4tr3A	Alignment	not modelled	7.3	9	PDB header: oxidoreductase Chain: A: PDB Molecule: type iii iodothyronine deiodinase; PDBTitle: mouse iodothyronine deiodinase 3 catalytic core, semet-labeled active2 site mutant secys->cys
89	d1rtya	Alignment	not modelled	7.3	9	Fold: Ferritin-like Superfamily: Cobalamin adenosyltransferase-like Family: Cobalamin adenosyltransferase
90	c1xx3A	Alignment	not modelled	7.1	12	PDB header: transport protein Chain: A: PDB Molecule: tonb protein; PDBTitle: solution structure of escherichia coli tonb-ctd
91	d2oeza1	Alignment	not modelled	6.9	18	Fold: YacF-like Superfamily: YacF-like Family: YacF-like
92	c1rm6E	Alignment	not modelled	6.7	16	PDB header: oxidoreductase Chain: E: PDB Molecule: 4-hydroxybenzoyl-coa reductase beta subunit; PDBTitle: structure of 4-hydroxybenzoyl-coa reductase from thauera2 aromatica
93	c4cuyf	Alignment	not modelled	6.7	4	PDB header: ribosome Chain: F: PDB Molecule: us7; PDBTitle: kluveromyces lactis 80s ribosome in complex with crpv-ires
94	c4f4fB	Alignment	not modelled	6.7	11	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: x-ray crystal structure of plp bound threonine synthase from brucella2 melitensis
95	c3j81i	Alignment	not modelled	6.7	20	PDB header: ribosome Chain: I: PDB Molecule: es8; PDBTitle: cryoem structure of a partial yeast 48s preinitiation complex
96	c5djnA	Alignment	not modelled	6.7	30	PDB header: transport protein Chain: A: PDB Molecule: kinesin-like protein; PDBTitle: crystal structure of the kinesin-3 kif13a nc-cc1 mutant - deletion of2 p390
97	c3sc0A	Alignment	not modelled	6.5	13	PDB header: oxidoreductase Chain: A: PDB Molecule: methylmalonic aciduria and homocystinuria type c protein; PDBTitle: crystal structure of mmachc (1-238), a human b12 processing enzyme,2 complexed with methylcobalamin
98	d1rtyb	Alignment	not modelled	6.5	10	Fold: Ferritin-like Superfamily: Cobalamin adenosyltransferase-like Family: Cobalamin adenosyltransferase
99	c5ehbA	Alignment	not modelled	6.5	35	PDB header: de novo protein Chain: A: PDB Molecule: phiosyi; PDBTitle: a de novo designed hexameric coiled-coil peptide with iodotyrosine