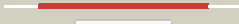



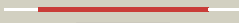



















Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0086_(hycQ)_93948_95414
 Date Tue Jul 23 14:50:12 BST 2019
 Unique Job ID 42420079602b05db

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4heaT_	 Alignment		100.0	23	PDB header: oxidoreductase Chain: T; PDB Molecule: nadh-quinone oxidoreductase subunit 12; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
2	c3rkoM_	 Alignment		100.0	22	PDB header: oxidoreductase Chain: M; PDB Molecule: nadh-quinone oxidoreductase subunit m; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
3	c3rkoL_	 Alignment		100.0	24	PDB header: oxidoreductase Chain: L; PDB Molecule: nadh-quinone oxidoreductase subunit l; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
4	c6humB_	 Alignment		100.0	21	PDB header: proton transport Chain: B; PDB Molecule: nad(p)h-quinone oxidoreductase subunit 2; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
5	c6humF_	 Alignment		100.0	22	PDB header: proton transport Chain: F; PDB Molecule: nadh dehydrogenase subunit 5; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
6	c6humD_	 Alignment		100.0	21	PDB header: proton transport Chain: D; PDB Molecule: nad(p)h-quinone oxidoreductase chain 4 1; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
7	c4he8M_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: M; PDB Molecule: nadh-quinone oxidoreductase subunit 13; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
8	c3rkoN_	 Alignment		100.0	21	PDB header: oxidoreductase Chain: N; PDB Molecule: nadh-quinone oxidoreductase subunit n; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
9	c6gcs5_	 Alignment		100.0	20	PDB header: oxidoreductase Chain: 5; PDB Molecule: nd5 subunit (nu5m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
10	c6gcs4_	 Alignment		100.0	18	PDB header: oxidoreductase Chain: 4; PDB Molecule: nd4 subunit (nu4m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
11	c5ldwL_	 Alignment		100.0	19	PDB header: oxidoreductase Chain: L; PDB Molecule: nadh-ubiquinone oxidoreductase chain 5; PDBTitle: structure of mammalian respiratory complex i, class1

12	c6cfwH_	Alignment		100.0	24	PDB header: membrane protein Chain: H: PDB Molecule: monovalent cation/h+ antiporter subunit d; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
13	c6g2jL_	Alignment		100.0	18	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-ubiquinone oxidoreductase chain 5; PDBTitle: mouse mitochondrial complex i in the active state
14	c4he8L_	Alignment		100.0	25	PDB header: oxidoreductase Chain: I: PDB Molecule: nadh-quinone oxidoreductase subunit 14; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
15	c5ldwM_	Alignment		100.0	15	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4; PDBTitle: structure of mammalian respiratory complex i, class1
16	c6gcs2_	Alignment		100.0	16	PDB header: oxidoreductase Chain: 2: PDB Molecule: nd2 subunit (nu2m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
17	c5xtdj_	Alignment		100.0	15	PDB header: oxidoreductase/electron transport Chain: I: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: cryo-em structure of human respiratory complex i
18	c6g2jN_	Alignment		100.0	18	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-ubiquinone oxidoreductase chain 2; PDBTitle: mouse mitochondrial complex i in the active state
19	c5ldwN_	Alignment		100.0	17	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-ubiquinone oxidoreductase chain 2; PDBTitle: structure of mammalian respiratory complex i, class1
20	c5lc5H_	Alignment		71.6	12	PDB header: oxidoreductase Chain: H: PDB Molecule: nadh-ubiquinone oxidoreductase chain 1; PDBTitle: structure of mammalian respiratory complex i, class2
21	c6cfwM_	Alignment	not modelled	70.3	11	PDB header: membrane protein Chain: M: PDB Molecule: mbh13 nadh dehydrogenase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
22	c6gcs1_	Alignment	not modelled	69.9	14	PDB header: oxidoreductase Chain: 1: PDB Molecule: nd1 subunit (nu1m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
23	d1a6qa1	Alignment	not modelled	45.9	23	Fold: Another 3-helical bundle Superfamily: Protein serine/threonine phosphatase 2C, C-terminal domain Family: Protein serine/threonine phosphatase 2C, C-terminal domain PDB header: proton transport
24	c6humA_	Alignment	not modelled	42.1	14	Chain: A: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 1; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
25	c2l3iA_	Alignment	not modelled	37.8	33	PDB header: antimicrobial protein Chain: A: PDB Molecule: aoxki4a, antimicrobial peptide in spider venom; PDBTitle: oaxki4a, spider derived antimicrobial peptide
26	c6cfwG_	Alignment	not modelled	37.0	18	PDB header: membrane protein Chain: G: PDB Molecule: monovalent cation/h+ antiporter subunit c; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
27	c6gcsL_	Alignment	not modelled	36.4	15	PDB header: oxidoreductase Chain: L: PDB Molecule: nd4l subunit (nulm); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
28	c6g2jK_	Alignment	not modelled	35.7	10	PDB header: oxidoreductase Chain: K: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4l; PDBTitle: mouse mitochondrial complex i in the active state
						PDB header: oxidoreductase

29	c4heaK_	Alignment	not modelled	33.1	9	Chain: K; PDB Molecule: nadh-quinone oxidoreductase subunit 11; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
30	c4x84C_	Alignment	not modelled	31.8	15	PDB header: isomerase Chain: C; PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
31	c5lnkm_	Alignment	not modelled	31.5	13	PDB header: oxidoreductase Chain: M; PDB Molecule: mitochondrial complex i, nd4 subunit; PDBTitle: entire ovine respiratory complex i
32	d1o8bb1	Alignment	not modelled	30.5	14	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
33	c6humE_	Alignment	not modelled	30.4	10	PDB header: proton transport Chain: E; PDB Molecule: nad(p)h-quinone oxidoreductase subunit 4i; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
34	c3rkoK_	Alignment	not modelled	28.6	7	PDB header: oxidoreductase Chain: K; PDB Molecule: nadh-quinone oxidoreductase subunit k; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
35	c4kppA_	Alignment	not modelled	23.8	11	PDB header: membrane protein Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of h+/ca2+ exchanger cax
36	c3u7jA_	Alignment	not modelled	20.2	16	PDB header: isomerase Chain: A; PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
37	c5lc5b_	Alignment	not modelled	18.2	16	PDB header: oxidoreductase Chain: B; PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class2
38	c5ldwb_	Alignment	not modelled	18.2	16	PDB header: oxidoreductase Chain: B; PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class1
39	c5o31b_	Alignment	not modelled	18.2	16	PDB header: oxidoreductase Chain: B; PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: mitochondrial complex i in the deactive state
40	c5ldxb_	Alignment	not modelled	18.2	16	PDB header: oxidoreductase Chain: B; PDB Molecule: nadh dehydrogenase [ubiquinone] iron-sulfur protein 7, PDBTitle: structure of mammalian respiratory complex i, class3.
41	d1r6ea_	Alignment	not modelled	16.7	43	Fold: SopE-like GEF domain Superfamily: SopE-like GEF domain Family: SopE-like GEF domain
42	c3vrbG_	Alignment	not modelled	16.3	15	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: G; PDB Molecule: cytochrome b-large subunit; PDBTitle: mitochondrial rodoquinol-fumarate reductase from the parasitic2 nematode ascaris suum with the specific inhibitor flutolanil and3 substrate fumarate
43	c2kncA_	Alignment	not modelled	16.2	9	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
44	c5ldwK_	Alignment	not modelled	16.0	11	PDB header: oxidoreductase Chain: K; PDB Molecule: nadh-ubiquinone oxidoreductase chain 4i; PDBTitle: structure of mammalian respiratory complex i, class1
45	c5lc5K_	Alignment	not modelled	16.0	11	PDB header: oxidoreductase Chain: K; PDB Molecule: nadh-ubiquinone oxidoreductase chain 4i; PDBTitle: structure of mammalian respiratory complex i, class2
46	c4ddpA_	Alignment	not modelled	15.5	36	PDB header: membrane protein Chain: A; PDB Molecule: beclin-1; PDBTitle: crystal structure of beclin 1 evolutionarily conserved domain(ecd)
47	c6odmK_	Alignment	not modelled	15.3	50	PDB header: viral protein Chain: K; PDB Molecule: capsid vertex component 2; PDBTitle: herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
48	c3vp7A_	Alignment	not modelled	15.0	55	PDB header: protein transport Chain: A; PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: crystal structure of the beta-alpha repeated, autophagy-specific2 (bara) domain of vps30/atg6
49	c3c25A_	Alignment	not modelled	14.0	67	PDB header: hydrolase/dna Chain: A; PDB Molecule: noti restriction endonuclease; PDBTitle: crystal structure of noti restriction endonuclease bound to cognate2 dna
50	c3r24A_	Alignment	not modelled	13.4	44	PDB header: transferase, viral protein Chain: A; PDB Molecule: 2'-o-methyl transferase; PDBTitle: crystal structure of nsp10/nsp16 complex of sars coronavirus" if2 possible
51	c2jwaA_	Alignment	not modelled	13.0	29	PDB header: transferase Chain: A; PDB Molecule: receptor tyrosine-protein kinase erb2; PDBTitle: erb2 transmembrane segment dimer spatial structure
52	c2ks1A_	Alignment	not modelled	13.0	29	PDB header: transferase Chain: A; PDB Molecule: receptor tyrosine-protein kinase erb2; PDBTitle: heterodimeric association of transmembrane domains of erb1 and erb22 receptors enabling kinase activation
53	d1s1qa_	Alignment	not modelled	12.9	31	Fold: UBC-like Superfamily: UBC-like Family: UEV domain
54	c4lnsA_	Alignment	not modelled	12.7	13	PDB header: ligase Chain: A; PDB Molecule: asparagine synthetase a; PDBTitle: crystal structure of asparagine synthetase a (asna) from

						trypanosoma2 brucei
55	c3na2C_	Alignment	not modelled	12.7	33	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function from mine drainage2 metagenome leptospirillum rubarum
56	c5ynpA_	Alignment	not modelled	12.6	22	PDB header: transferase Chain: A: PDB Molecule: nsp16 protein; PDBTitle: crystal structure of mers-cov nsp16/nsp10 complex bound to sinefungin2 and m7gpppa
57	c3mesB_	Alignment	not modelled	12.2	31	PDB header: transferase Chain: B: PDB Molecule: choline kinase; PDBTitle: crystal structure of choline kinase from cryptosporidium2 parvum iowa ii, cgd3_2030
58	c5o60M_	Alignment	not modelled	12.0	40	PDB header: ribosome Chain: M: PDB Molecule: 50s ribosomal protein l15; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
59	c2ks1B_	Alignment	not modelled	11.8	24	PDB header: transferase Chain: B: PDB Molecule: epidermal growth factor receptor; PDBTitle: heterodimeric association of transmembrane domains of erbb1 and erbb2 receptors enabling kinase activation
60	c3qngD_	Alignment	not modelled	11.7	9	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
61	d1n9wa2	Alignment	not modelled	11.6	50	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
62	d3dtub2	Alignment	not modelled	11.6	16	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
63	c4j15A_	Alignment	not modelled	11.6	50	PDB header: ligase Chain: A: PDB Molecule: aspartate--trna ligase, cytoplasmic; PDBTitle: crystal structure of human cytosolic aspartyl-trna synthetase, a2 component of multi-trna synthetase complex
64	c1n9wA_	Alignment	not modelled	11.4	50	PDB header: biosynthetic protein Chain: A: PDB Molecule: aspartyl-trna synthetase 2; PDBTitle: crystal structure of the non-discriminating and archaeal-2 type aspartyl-trna synthetase from thermus thermophilus
65	c1r6rA_	Alignment	not modelled	11.3	22	PDB header: viral protein Chain: A: PDB Molecule: genome polyprotein; PDBTitle: solution structure of dengue virus capsid protein reveals a2 new fold
66	d1r6ra_	Alignment	not modelled	11.3	22	Fold: Flavivirus capsid protein C Superfamily: Flavivirus capsid protein C Family: Flavivirus capsid protein C
67	d1j4na_	Alignment	not modelled	11.0	14	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
68	c6humG_	Alignment	not modelled	10.8	9	PDB header: proton transport Chain: G: PDB Molecule: nadh dehydrogenase subunit 6; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
69	c2kwtA_	Alignment	not modelled	10.8	17	PDB header: viral protein Chain: A: PDB Molecule: protease ns2-3; PDBTitle: solution structure of ns2 [27-59]
70	c3bjuB_	Alignment	not modelled	10.8	63	PDB header: ligase Chain: B: PDB Molecule: lysyl-trna synthetase; PDBTitle: crystal structure of tetrameric form of human lysyl-trna synthetase
71	c1vw48_	Alignment	not modelled	10.7	31	PDB header: ribosome Chain: 8: PDB Molecule: 54s ribosomal protein l13, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
72	c4he8H_	Alignment	not modelled	10.7	12	PDB header: oxidoreductase Chain: H: PDB Molecule: nadh-quinone oxidoreductase subunit 8; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 thermus thermophilus
73	c5elnC_	Alignment	not modelled	10.6	50	PDB header: ligase Chain: C: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from cryptosporidium parvum2 complexed with l-lysine
74	c4o2dB_	Alignment	not modelled	10.4	38	PDB header: ligase Chain: B: PDB Molecule: aspartate--trna ligase; PDBTitle: crystal structure of aspartyl-trna synthetase from mycobacterium2 smegmatis with bound aspartic acid
75	c5v11D_	Alignment	not modelled	10.3	38	PDB header: ligase Chain: D: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase from mycobacterium ulcerans2 complexed with l-lysine
76	c4ex5A_	Alignment	not modelled	10.3	38	PDB header: transferase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of lysyl-trna synthetase lysrs from burkholderia2 thailandensis bound to lysine
77	c4k8nF_	Alignment	not modelled	10.3	25	PDB header: lipid transport Chain: F: PDB Molecule: glycolipid transfer protein domain-containing protein 1; PDBTitle: crystal structure of human ceramide-1-phosphate transfer protein2 (cptp) in complex with 18:1 ceramide-1-phosphate (18:1-c1p)
78	c5dfzD_	Alignment	not modelled	10.3	35	PDB header: transferase Chain: D: PDB Molecule: vacuolar protein sorting-associated protein 30; PDBTitle: structure of vps34 complex ii from s. cerevisiae.
79	d1swxa_	Alignment	not modelled	10.3	25	Fold: Glycolipid transfer protein, GLTP Superfamily: Glycolipid transfer protein, GLTP

						Family: Glycolipid transfer protein, GLTP
80	d1unca_	Alignment	not modelled	10.3	11	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
81	c5hgqD_	Alignment	not modelled	10.2	63	PDB header: ligase/ligase inhibitor Chain: D: PDB Molecule: lysine--trna ligase; PDBTitle: loa loa lysyl-trna synthetase in complex with cladosporin.
82	c1b8aB_	Alignment	not modelled	10.2	50	PDB header: ligase Chain: B: PDB Molecule: protein (aspartyl-trna synthetase); PDBTitle: aspartyl-trna synthetase
83	c4upaA_	Alignment	not modelled	10.2	25	PDB header: ligase Chain: A: PDB Molecule: lysine--trna ligase; PDBTitle: crystal structure of entamoeba histolytica lysyl-trna synthetase in2 complex with amppnp
84	d1gzsb_	Alignment	not modelled	10.1	48	Fold: SopE-like GEF domain Superfamily: SopE-like GEF domain Family: SopE-like GEF domain
85	c5oqtC_	Alignment	not modelled	10.1	24	PDB header: transport protein Chain: C: PDB Molecule: uncharacterized protein ynem; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue
86	c6f34C_	Alignment	not modelled	10.1	24	PDB header: membrane protein Chain: C: PDB Molecule: smgts; PDBTitle: crystal structure of a bacterial cationic amino acid transporter (cat)2 homologue bound to arginine.
87	c2pjmA_	Alignment	not modelled	10.1	19	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
88	d1yu8x1_	Alignment	not modelled	10.1	22	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
89	c1ceuA_	Alignment	not modelled	10.0	17	PDB header: viral protein Chain: A: PDB Molecule: protein (hiv-1 regulatory protein n-terminal PDBTitle: nmr structure of the (1-51) n-terminal domain of the hiv-12 regulatory protein
90	d1unda_	Alignment	not modelled	10.0	11	Fold: VHP, Villin headpiece domain Superfamily: VHP, Villin headpiece domain Family: VHP, Villin headpiece domain
91	c1wydB_	Alignment	not modelled	9.9	63	PDB header: ligase Chain: B: PDB Molecule: hypothetical aspartyl-trna synthetase; PDBTitle: crystal structure of aspartyl-trna synthetase from sulfobolobus tokodaii
92	c3arcl_	Alignment	not modelled	9.9	13	PDB header: electron transport, photosynthesis Chain: L: PDB Molecule: photosystem ii reaction center protein i; PDBTitle: crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
93	c4doyE_	Alignment	not modelled	9.9	18	PDB header: oxidoreductase Chain: E: PDB Molecule: dibenzothiophene desulfurization enzyme c; PDBTitle: crystal structure of dibenzothiophene desulfurization enzyme c
94	c2xgtB_	Alignment	not modelled	9.8	25	PDB header: ligase Chain: B: PDB Molecule: asparaginyl-trna synthetase, cytoplasmic; PDBTitle: asparaginyl-trna synthetase from brugia malayi complexed2 with the sulphamoyl analogue of asparaginyl-adenylate
95	c2i3fA_	Alignment	not modelled	9.8	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: glycolipid transfer-like protein; PDBTitle: crystal structure of a glycolipid transfer-like protein from galdieria2 sulphuraria
96	c2re3A_	Alignment	not modelled	9.7	36	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a duf1285 family protein (spo_0140) from2 silicibacter pomeroyi dss-3 at 2.50 a resolution
97	c5tszA_	Alignment	not modelled	9.7	31	PDB header: cell invasion Chain: A: PDB Molecule: pv cell-traversal protein; PDBTitle: crystal structure of plasmodium vivax celts
98	c4p6vE_	Alignment	not modelled	9.7	10	PDB header: oxidoreductase Chain: E: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit e; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
99	c5kdiA_	Alignment	not modelled	9.7	25	PDB header: lipid transport Chain: A: PDB Molecule: pleckstrin homology domain-containing family a member 8; PDBTitle: how fapp2 selects simple glycosphingolipids using the gntp-fold