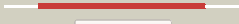



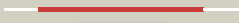






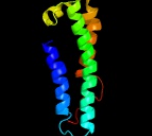












Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3152_(nuoH)_3519279_3520511
Date	Thu Aug 8 16:20:34 BST 2019
Unique Job ID	f15c7442c1220daf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6gcs1_	 Alignment		100.0	36	PDB header: oxidoreductase Chain: 1: PDB Molecule: nd1 subunit (nu1m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
2	c6humA_	 Alignment		100.0	37	PDB header: proton transport Chain: A: PDB Molecule: nad(p)h-quinone oxidoreductase subunit 1; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
3	c5lc5H_	 Alignment		100.0	40	PDB header: oxidoreductase Chain: H: PDB Molecule: nadh-ubiquinone oxidoreductase chain 1; PDBTitle: structure of mammalian respiratory complex i, class2
4	c6cfwM_	 Alignment		100.0	25	PDB header: membrane protein Chain: M: PDB Molecule: mbh13 nadh dehydrogenase subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
5	c4he8H_	 Alignment		100.0	38	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
6	c6g2jL_	 Alignment		91.3	20	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-ubiquinone oxidoreductase chain 5; PDBTitle: mouse mitochondrial complex i in the active state
7	c6gcs5_	 Alignment		91.1	15	PDB header: oxidoreductase Chain: 5: PDB Molecule: nd5 subunit (nu5m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
8	c4heaT_	 Alignment		90.4	18	PDB header: oxidoreductase Chain: T: PDB Molecule: nadh-quinone oxidoreductase subunit 12; PDBTitle: crystal structure of the entire respiratory complex i from thermus2 thermophilus
9	c5ldwM_	 Alignment		89.4	14	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4; PDBTitle: structure of mammalian respiratory complex i, class1
10	c6gcs4_	 Alignment		88.7	17	PDB header: oxidoreductase Chain: 4: PDB Molecule: nd4 subunit (nu4m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
11	c6gcs2_	 Alignment		88.3	7	PDB header: oxidoreductase Chain: 2: PDB Molecule: nd2 subunit (nu2m); PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica

12	c6cfwH_	Alignment		88.1	11	PDB header: membrane protein Chain: H: PDB Molecule: monovalent cation/h+ antiporter subunit d; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
13	c5ldwL_	Alignment		87.7	15	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-ubiquinone oxidoreductase chain 5; PDBTitle: structure of mammalian respiratory complex i, class1
14	c4he8M_	Alignment		87.2	11	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
15	c6humF_	Alignment		86.4	15	PDB header: proton transport Chain: F: PDB Molecule: nadh dehydrogenase subunit 5; PDBTitle: structure of the photosynthetic complex i from thermosynechococcus2 elongatus
16	c3rkoL_	Alignment		79.0	13	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-quinone oxidoreductase subunit I; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
17	c6humB_	Alignment		72.0	12	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
18	c5xtdi_	Alignment		50.2	9	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
19	c2jpkA_	Alignment		33.7	23	PDB header: antimicrobial protein Chain: A: PDB Molecule: bacteriocin lactococcin-g subunit beta; PDBTitle: lactococcin g-b in dpc
20	c4p6vE_	Alignment		33.4	12	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
21	d2a65a1	Alignment	not modelled	25.3	10	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
22	c2jpmA_	Alignment	not modelled	21.1	23	PDB header: antimicrobial protein Chain: A: PDB Molecule: bacteriocin lactococcin-g subunit beta; PDBTitle: lactococcin g-b in tfe
23	c5ldwN_	Alignment	not modelled	20.0	8	PDB header: oxidoreductase Chain: N: PDB Molecule: nadh-ubiquinone oxidoreductase chain 2; PDBTitle: structure of mammalian respiratory complex i, class1
24	c2kncA_	Alignment	not modelled	19.7	22	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib; PDBTitle: platelet integrin alfa-iib-beta3 transmembrane-cytoplasmic2 heterocomplex
25	d1xn8a_	Alignment	not modelled	18.8	19	Fold: Hypothetical protein YqbG Superfamily: Hypothetical protein YqbG Family: Hypothetical protein YqbG
26	d1jb0L_	Alignment	not modelled	16.8	20	Fold: Photosystem I reaction center subunit XI, PsaL Superfamily: Photosystem I reaction center subunit XI, PsaL Family: Photosystem I reaction center subunit XI, PsaL
27	c1wa7B_	Alignment	not modelled	14.5	60	PDB header: sh3 domain Chain: B: PDB Molecule: hypothetical 28.7 kda protein in dhfr 3'region PDBTitle: sh3 domain of human lyn tyrosine kinase in complex with a2 herpesviral ligand
28	c4djiA_	Alignment	not modelled	11.9	9	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
29	c2k1aA_	Alignment	not modelled	10.2	22	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iib;

29	c3k1aA	Alignment	not modelled	10.2	44	PDBTitle: bicelle-embedded integrin alpha(iib) transmembrane segment PDB header: structural genomics, unknown function
30	c3pesA	Alignment	not modelled	9.7	38	Chain: A; PDB Molecule: uncharacterized protein gp49; PDBTitle: crystal structure of uncharacterized protein from pseudomonas phage2 yua
31	c5cwwC	Alignment	not modelled	9.0	61	PDB header: transport protein Chain: C; PDB Molecule: nucleoporin nup159; PDBTitle: crystal structure of the chaetomium thermophilum heterotrimeric nup822 ntd-nup159 tail-nup145n apd complex
32	c2vxsB	Alignment	not modelled	8.5	36	PDB header: cytokine Chain: B; PDB Molecule: interleukin-17a; PDBTitle: structure of il-17a in complex with a potent, fully human2 neutralising antibody
33	c4q2uM	Alignment	not modelled	8.2	24	PDB header: toxin/toxin repressor Chain: M; PDB Molecule: antitoxin dinj; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
34	d1ufra	Alignment	not modelled	7.8	20	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
35	c4he8I	Alignment	not modelled	7.5	12	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
36	c5aexJ	Alignment	not modelled	7.2	17	PDB header: membrane protein Chain: J; PDB Molecule: ammonium transporter mep2; PDBTitle: crystal structure of saccharomyces cerevisiae mep2
37	c6ahzA	Alignment	not modelled	7.1	28	PDB header: sugar binding protein Chain: A; PDB Molecule: cmp-n-acetylneuraminate-poly-alpha-2,8-sialyltransferase; PDBTitle: the nmr structure of the polysialyltransferase domain (pstd) in2 polysialyltransferase st8siaiv
38	c2l8sA	Alignment	not modelled	6.9	30	PDB header: cell adhesion Chain: A; PDB Molecule: integrin alpha-1; PDBTitle: solution nmr structure of transmembrane and cytosolic regions of2 integrin alpha1 in detergent micelles
39	d1e6va1	Alignment	not modelled	6.8	30	Fold: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Superfamily: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain Family: Methyl-coenzyme M reductase alpha and beta chain C-terminal domain
40	c4h25C	Alignment	not modelled	6.8	57	PDB header: immune system Chain: C; PDB Molecule: peptide; PDBTitle: tcr interaction with peptide mimics of nickel offers structure2 insights to nickel contact allergy
41	c4h25F	Alignment	not modelled	6.8	57	PDB header: immune system Chain: F; PDB Molecule: peptide; PDBTitle: tcr interaction with peptide mimics of nickel offers structure2 insights to nickel contact allergy
42	c3llbA	Alignment	not modelled	6.6	16	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of the protein pa3983 with unknown2 function from pseudomonas aeruginosa pao1
43	d2f05a1	Alignment	not modelled	6.4	21	Fold: PAH2 domain Superfamily: PAH2 domain Family: PAH2 domain
44	c2a2bA	Alignment	not modelled	6.4	60	PDB header: antibiotic Chain: A; PDB Molecule: bacteriocin curvacin a; PDBTitle: curvacin a
45	d1tcaa	Alignment	not modelled	6.4	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
46	d1un8a4	Alignment	not modelled	6.3	26	Fold: DAK1/DegV-like Superfamily: DAK1/DegV-like Family: DAK1
47	d1s5qb	Alignment	not modelled	6.3	22	Fold: PAH2 domain Superfamily: PAH2 domain Family: PAH2 domain
48	c3qilM	Alignment	not modelled	6.2	26	PDB header: structural protein Chain: M; PDB Molecule: clathrin heavy chain 1; PDBTitle: crystal structure analysis of the clathrin trimerization domain
49	d1jpya	Alignment	not modelled	6.1	36	Fold: Cystine-knot cytokines Superfamily: Cystine-knot cytokines Family: Interleukin 17F, IL-17F
50	c3etoB	Alignment	not modelled	6.1	15	PDB header: signaling protein Chain: B; PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: 2 angstrom xray structure of the notch1 negative regulatory region2 (nrr)
51	c3m3nW	Alignment	not modelled	6.0	41	PDB header: structural protein Chain: W; PDB Molecule: neural wiskott-aldrich syndrome protein; PDBTitle: structure of a longitudinal actin dimer assembled by tandem w domains
52	c1q69B	Alignment	not modelled	5.9	36	PDB header: membrane protein/transferase Chain: B; PDB Molecule: proto-oncogene tyrosine-protein kinase lck; PDBTitle: solution structure of t-cell surface glycoprotein cd8 alpha2 chain and proto-oncogene tyrosine-protein kinase lck3 fragments
53	c1q68B	Alignment	not modelled	5.9	36	PDB header: membrane protein/transferase Chain: B; PDB Molecule: proto-oncogene tyrosine-protein kinase lck; PDBTitle: solution structure of t-cell surface glycoprotein cd4 and2 proto-oncogene tyrosine-protein kinase lck fragments
						PDB header: toxin

54	c2n07X_	Alignment	not modelled	5.7	67	Chain: X: PDB Molecule: alpha-conotoxin vc1a; PDBTitle: design of a highly stable disulfide-deleted mutant of analgesic cyclic2 alpha-conotoxin vc1.1
55	c3dyuB_	Alignment	not modelled	5.7	40	PDB header: transport protein Chain: B: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of snx9px-bar (230-595), h32
56	c2dbhA_	Alignment	not modelled	5.7	36	PDB header: signaling protein Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily PDBTitle: solution structure of the carboxyl-terminal card-like2 domain in human tnfr-related death receptor-6
57	d2r2za1	Alignment	not modelled	5.6	20	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: CorC/HlyC domain-like
58	c2ncyA_	Alignment	not modelled	5.6	33	PDB header: antimicrobial protein Chain: A: PDB Molecule: pseudin-2; PDBTitle: solution structure of pseudin-2 analog (ps-p)
59	c2jz8A_	Alignment	not modelled	5.5	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bh09830; PDBTitle: solution nmr structure of bh09830 from bartonella henselae2 modeled with one zn+2 bound. northeast structural genomics3 consortium target bnr55
60	c4qhuC_	Alignment	not modelled	5.4	36	PDB header: immune system Chain: C: PDB Molecule: interleukin-17a; PDBTitle: crystal structure of il-17a/fab6785 complex
61	c1q2iA_	Alignment	not modelled	5.3	40	PDB header: antitumor protein Chain: A: PDB Molecule: pnc27; PDBTitle: nmr solution structure of a peptide from the mdm-2 binding2 domain of the p53 protein that is selectively cytotoxic to3 cancer cells
62	c3lygA_	Alignment	not modelled	5.1	50	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntf2-like protein of unknown function; PDBTitle: crystal structure of ntf2-like protein of unknown function2 (yp_270605.1) from colwellia psychrerythraea 34h at 1.61 a resolution
63	d1iyka2	Alignment	not modelled	5.1	25	Fold: Acyl-CoA N-acyltransferases (Nat) Superfamily: Acyl-CoA N-acyltransferases (Nat) Family: N-myristoyl transferase, NMT
64	c2rajA_	Alignment	not modelled	5.0	40	PDB header: structural protein Chain: A: PDB Molecule: sorting nexin-9; PDBTitle: so4 bound px-bar membrane remodeling unit of sorting nexin 9
65	d2e9xa1	Alignment	not modelled	5.0	24	Fold: GINS helical bundle-like Superfamily: GINS helical bundle-like Family: PSF1 N-terminal domain-like