
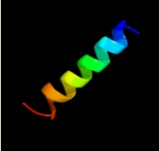

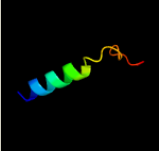



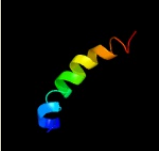

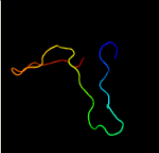

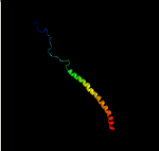

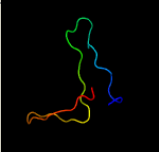

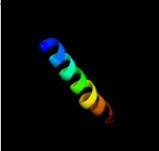



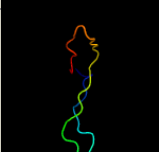


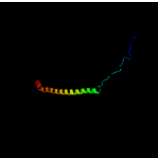
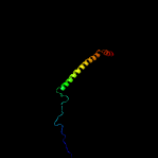
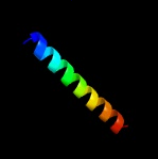
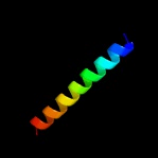
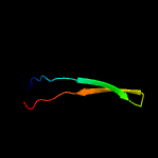
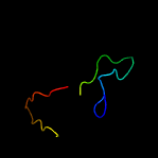

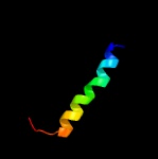
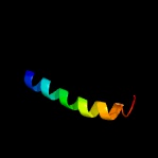


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2235 (-)_2507645_2508460
Date	Mon Aug 5 13:25:36 BST 2019
Unique Job ID	8648ff69cefbe0fa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2mc7A_	 Alignment		50.8	33	PDB header: membrane protein Chain: A: PDB Molecule: regulatory peptide; PDBTitle: structure of salmonella mgtr
2	c1zzaA_	 Alignment		33.4	12	PDB header: membrane protein Chain: A: PDB Molecule: stannin; PDBTitle: solution nmr structure of the membrane protein stannin
3	c5n9yB_	 Alignment		29.2	14	PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb
4	c2lx0A_	 Alignment		28.6	14	PDB header: membrane protein Chain: A: PDB Molecule: membrane fusion protein p14; PDBTitle: arced helix (arch) nmr structure of the reovirus p14 fusion-associated2 small transmembrane (fast) protein transmembrane domain (tmd) in3 dodecyl phosphocholine (dpc) micelles
5	c3tqzA_	 Alignment		28.0	17	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: structure of a deoxyuridine 5'-triphosphate nucleotidohydrolase (dut)2 from coxiella burnetii
6	c6gcsW_	 Alignment		26.3	12	PDB header: oxidoreductase Chain: W: PDB Molecule: nb6m subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
7	d1sixa_	 Alignment		26.1	22	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
8	c2i5nH_	 Alignment		25.0	12	PDB header: photosynthesis Chain: H: PDB Molecule: reaction center protein h chain; PDBTitle: 1.96 a x-ray structure of photosynthetic reaction center from2 rhodospseudomonas viridis:crystals grown by microfluidic technique
9	c2bbjB_	 Alignment		23.4	24	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
10	c3ca9A_	 Alignment		20.2	19	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine triphosphatase; PDBTitle: evolution of chlorella virus dutpase
11	d2r6ia1	 Alignment		18.3	15	Fold: ATP12-like Superfamily: ATP12-like Family: ATP12-like

12	c5lnkq_	Alignment		18.2	17	PDB header: oxidoreductase Chain: Q: PDB Molecule: PDBTitle: entire ovine respiratory complex i
13	c5o31Z_	Alignment		16.7	17	PDB header: oxidoreductase Chain: Z: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: mitochondrial complex i in the deactive state
14	c6rdr8_	Alignment		16.4	21	PDB header: proton transport Chain: 8: PDB Molecule: mitochondrial atp synthase subunit asa8; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1d,2 monomer-masked refinement
15	c6rdi8_	Alignment		16.4	21	PDB header: proton transport Chain: 8: PDB Molecule: mitochondrial atp synthase subunit asa8; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substate 1a,2 monomer-masked refinement
16	d1thqa_	Alignment		15.4	33	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane enzyme PagP
17	c6maiA_	Alignment		15.3	19	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of deoxyuridine 5'-triphosphate nucleotidohydrolase2 from legionella pneumophila philadelphia 1
18	c6mplA_	Alignment		14.4	35	PDB header: membrane protein Chain: A: PDB Molecule: matrix protein 2; PDBTitle: racemic m2-tm i39a crystallized from racemic detergent
19	c2na6A_	Alignment		14.2	26	PDB header: apoptosis Chain: A: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
20	c2na6B_	Alignment		14.2	26	PDB header: apoptosis Chain: B: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
21	c2na6C_	Alignment	not modelled	14.2	26	PDB header: apoptosis Chain: C: PDB Molecule: tumor necrosis factor receptor superfamily member 6; PDBTitle: transmembrane domain of mouse fas/cd95 death receptor
22	c4xtnj_	Alignment	not modelled	14.1	6	PDB header: membrane protein Chain: J: PDB Molecule: sodium pumping rhodopsin; PDBTitle: crystal structure of the light-driven sodium pump kr2 in the2 pentameric red form, ph 4.9
23	d1xmeb2	Alignment	not modelled	13.1	18	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
24	c6roiC_	Alignment	not modelled	12.8	17	PDB header: lipid transport Chain: C: PDB Molecule: cell division control protein 50; PDBTitle: cryo-em structure of the partially activated drs2p-cdc50p
25	c3so2A_	Alignment	not modelled	12.7	17	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: chlorella dutpase
26	c2vovE_	Alignment	not modelled	12.7	18	PDB header: hydrolase Chain: E: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium atpase 1; PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
27	c2p9oB_	Alignment	not modelled	12.4	8	PDB header: hydrolase Chain: B: PDB Molecule: dutp pyrophosphatase-like protein; PDBTitle: structure of dutpase from arabidopsis thaliana
28	d2vvpA1	Alignment	not modelled	12.0	17	Fold: Ribose/Galactose isomerase RpiB/AlsB Superfamily: Ribose/Galactose isomerase RpiB/AlsB Family: Ribose/Galactose isomerase RpiB/AlsB

29	c3ddIB_	Alignment	not modelled	11.6	15	PDB header: transport protein Chain: B: PDB Molecule: xanthorhodopsin; PDBTitle: crystallographic structure of xanthorhodopsin, a light-driven ion pump2 with dual chromophore
30	d1sjna_	Alignment	not modelled	11.2	22	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
31	c5xywD_	Alignment	not modelled	9.9	67	PDB header: protein binding Chain: D: PDB Molecule: gd21652; PDBTitle: crystal structure of drosophila simulans rhino chromoshadow domain in2 complex with n-terminal domain
32	c4ev6E_	Alignment	not modelled	9.8	7	PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii
33	d2iuba2	Alignment	not modelled	9.7	25	Fold: Transmembrane helix hairpin Superfamily: Magnesium transport protein CorA, transmembrane region Family: Magnesium transport protein CorA, transmembrane region
34	c3h6xA_	Alignment	not modelled	9.7	19	PDB header: hydrolase Chain: A: PDB Molecule: dutpase; PDBTitle: crystal structure of dutpase from streptococcus mutans
35	c2kncA_	Alignment	not modelled	9.5	38	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
36	c3c3iA_	Alignment	not modelled	9.5	19	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine triphosphatase; PDBTitle: evolution of chlorella virus dutpase
37	c6elhA_	Alignment	not modelled	9.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide reductase; PDBTitle: low resolution structure of neisseria meningitidis qnor
38	c6mpnB_	Alignment	not modelled	9.4	30	PDB header: membrane protein Chain: B: PDB Molecule: matrix protein 2; PDBTitle: racemic m2-tm i42e crystallized from racemic detergent
39	c6mpnA_	Alignment	not modelled	9.4	30	PDB header: membrane protein Chain: A: PDB Molecule: matrix protein 2; PDBTitle: racemic m2-tm i42e crystallized from racemic detergent
40	c5kk2E_	Alignment	not modelled	9.1	21	PDB header: membrane protein, transport protein, sig Chain: E: PDB Molecule: voltage-dependent calcium channel gamma-2 subunit; PDBTitle: architecture of fully occupied glua2 ampa receptor - tarp complex2 elucidated by single particle cryo-electron microscopy
41	c3krbB_	Alignment	not modelled	9.0	13	PDB header: oxidoreductase Chain: B: PDB Molecule: aldose reductase; PDBTitle: structure of aldose reductase from giardia lamblia at 1.75a resolution
42	c6adqP_	Alignment	not modelled	9.0	20	PDB header: electron transport Chain: P: PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
43	c2axtc_	Alignment	not modelled	8.7	14	PDB header: electron transport Chain: C: PDB Molecule: photosystem ii cp43 protein; PDBTitle: crystal structure of photosystem ii from thermosynechococcus elongatus
44	d2axtc1	Alignment	not modelled	8.7	14	Fold: Photosystem II antenna protein-like Superfamily: Photosystem II antenna protein-like Family: Photosystem II antenna protein-like
45	d1ehkb2	Alignment	not modelled	8.6	18	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
46	c3sokB_	Alignment	not modelled	8.3	11	PDB header: cell adhesion Chain: B: PDB Molecule: fimbrial protein; PDBTitle: dichelobacter nodosus pilin fima
47	c4g0hA_	Alignment	not modelled	7.9	20	PDB header: toxin Chain: A: PDB Molecule: cytotoxicity-associated immunodominant antigen; PDBTitle: crystal structure of the n-terminal domain of helicobacter pylori caga2 protein
48	d1vmha_	Alignment	not modelled	7.0	60	Fold: YjbQ-like Superfamily: YjbQ-like Family: YjbQ-like
49	d1vpha_	Alignment	not modelled	7.0	40	Fold: YjbQ-like Superfamily: YjbQ-like Family: YjbQ-like
50	c5xyvC_	Alignment	not modelled	7.0	50	PDB header: protein binding Chain: C: PDB Molecule: protein deadlock; PDBTitle: crystal structure of drosophila melanogaster rhino chromoshadow domain2 in complex with deadlock n-terminal domain
51	d1vmfa_	Alignment	not modelled	6.9	60	Fold: YjbQ-like Superfamily: YjbQ-like Family: YjbQ-like
52	c3lqwA_	Alignment	not modelled	6.8	14	PDB header: hydrolase Chain: A: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: crystal structure of deoxyuridine 5-triphosphate2 nucleotidohydrolase from entamoeba histolytica
53	c1fooA_	Alignment	not modelled	6.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase; PDBTitle: bovine endothelial nitric oxide synthase heme domain complexed with l-2 arg and no(h4b-free)
						Fold: Nitric oxide (NO) synthase oxygenase domain

54	d1nosa_	Alignment	not modelled	6.6	15	Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
55	c1ve0A_	Alignment	not modelled	6.6	60	PDB header: metal binding protein Chain: A: PDB Molecule: hypothetical protein (st2072); PDBTitle: crystal structure of uncharacterized protein st2072 from sulfolobus2 tokodaii
56	c2cu5C_	Alignment	not modelled	6.6	60	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: conserved hypothetical protein tt1486; PDBTitle: crystal structure of the conserved hypothetical protein tt1486 from2 thermus thermophilus hb8
57	d1vmja_	Alignment	not modelled	6.5	60	Fold: YjbQ-like Superfamily: YjbQ-like Family: YjbQ-like
58	c2n1pA_	Alignment	not modelled	6.5	21	PDB header: viral protein Chain: A: PDB Molecule: non-structural protein 5b, ns5b; PDBTitle: structure of the c-terminal membrane domain of hcv ns5b protein
59	c4xtrG_	Alignment	not modelled	6.5	32	PDB header: hydrolase/transport protein Chain: G: PDB Molecule: pep12p; PDBTitle: structure of get3 bound to the transmembrane domain of pep12
60	c3zf6A_	Alignment	not modelled	6.4	9	PDB header: hydrolase Chain: A: PDB Molecule: dutpase; PDBTitle: phage dutpases control transfer of virulence genes by a proto-2 oncogenic g protein-like mechanism. (staphylococcus bacteriophage3 80alpha dutpase d81a d110c s168c mutant with dupnhpp).
61	c4rp9A_	Alignment	not modelled	6.3	22	PDB header: membrane protein Chain: A: PDB Molecule: ascorbate-specific permease iic component ulaa; PDBTitle: bacterial vitamin c transporter ulaa/sgat in c2 form
62	d1om4a_	Alignment	not modelled	6.2	20	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
63	c2p6hB_	Alignment	not modelled	6.1	60	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of hypothetical protein ape1520 from aeropyrum2 pernix k1
64	d1eysh2	Alignment	not modelled	6.1	28	Fold: Single transmembrane helix Superfamily: Photosystem II reaction centre subunit H, transmembrane region Family: Photosystem II reaction centre subunit H, transmembrane region
65	c4kkpA_	Alignment	not modelled	6.1	25	PDB header: structural protein Chain: A: PDB Molecule: rbma protein; PDBTitle: crystal structure of vibrio cholerae rbma (crystal form 2)
66	c4djiA_	Alignment	not modelled	6.1	14	PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc
67	c2p6cB_	Alignment	not modelled	6.0	80	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: aq_2013 protein; PDBTitle: crystal structure of hypothetical protein aq_2013 from aquifex2 aeolicus vf5.
68	c5azdA_	Alignment	not modelled	5.9	16	PDB header: transport protein Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: crystal structure of thermophilic rhodopsin.
69	d1euwa_	Alignment	not modelled	5.8	19	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
70	c2okdB_	Alignment	not modelled	5.7	11	PDB header: hydrolase Chain: B: PDB Molecule: deoxyuridine 5'-triphosphate nucleotidohydrolase; PDBTitle: high resolution crystal structures of vaccinia virus dutpase
71	c3ecyA_	Alignment	not modelled	5.6	14	PDB header: hydrolase Chain: A: PDB Molecule: cg4584-pa, isoform a (bcdna.ld08534); PDBTitle: crystal structural analysis of drosophila melanogaster dutpase
72	c5zdnA_	Alignment	not modelled	5.6	18	PDB header: hydrolase Chain: A: PDB Molecule: fomd; PDBTitle: the complex structure of fomd with cdp
73	c3am6C_	Alignment	not modelled	5.6	22	PDB header: transport protein Chain: C: PDB Molecule: rhodopsin-2; PDBTitle: crystal structure of the proton pumping rhodopsin ar2 from marine alga2 acetabularia acetabulum
74	d1c6va_	Alignment	not modelled	5.6	43	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Retroviral integrase, catalytic domain
75	c2an7A_	Alignment	not modelled	5.5	17	PDB header: dna binding protein Chain: A: PDB Molecule: protein pard; PDBTitle: solution structure of the bacterial antidote pard
76	d1m9ma_	Alignment	not modelled	5.2	17	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
77	c5lc5m_	Alignment	not modelled	5.2	13	PDB header: oxidoreductase Chain: M: PDB Molecule: nadh-ubiquinone oxidoreductase chain 4; PDBTitle: structure of mammalian respiratory complex i, class2
78	d1q5uz_	Alignment	not modelled	5.1	8	Fold: beta-clip Superfamily: dUTPase-like Family: dUTPase-like
79	c2rifA_	Alignment	not modelled	5.1	25	PDB header: proton transport Chain: A: PDB Molecule: matrix protein 2; PDBTitle: proton channel m2 from influenza a in complex with2 inhibitor rimantadine
						Fold: ATP12-like

