



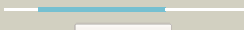

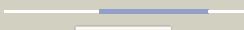










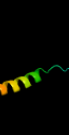






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2272_(-)_2545747_2546115
Date	Mon Aug 5 13:25:41 BST 2019
Unique Job ID	df1204fec672b713

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3jbrE_	 Alignment		55.2	7	PDB header: membrane protein Chain: E: PDB Molecule: voltage-dependent calcium channel gamma-1 subunit; PDBTitle: cryo-em structure of the rabbit voltage-gated calcium channel cav1.12 complex at 4.2 angstrom
2	c4hr1A_	 Alignment		39.9	45	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure of pav1-137, a protein from the virus pav1 that infects2 pyrococcus abyssi.
3	c4ymkA_	 Alignment		34.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: acyl-coa desaturase 1; PDBTitle: crystal structure of stearyl-coenzyme a desaturase 1
4	c2yevB_	 Alignment		29.6	3	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c oxidase subunit 2; PDBTitle: structure of caa3-type cytochrome oxidase
5	c6c4vA_	 Alignment		29.5	58	PDB header: transport protein Chain: A: PDB Molecule: polyketide synthase pks13; PDBTitle: 1.9 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1350-1461) of polyketide synthase pks13 from3 mycobacterium tuberculosis
6	c5ldxZ_	 Alignment		18.6	21	PDB header: oxidoreductase Chain: Z: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: structure of mammalian respiratory complex i, class3.
7	c5lc5Z_	 Alignment		18.6	21	PDB header: oxidoreductase Chain: Z: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: structure of mammalian respiratory complex i, class2
8	c5ldwZ_	 Alignment		18.6	21	PDB header: oxidoreductase Chain: Z: PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: structure of mammalian respiratory complex i, class1
9	d1rh5b_	 Alignment		18.3	8	Fold: Single transmembrane helix Superfamily: Preprotein translocase SecE subunit Family: Preprotein translocase SecE subunit
10	d1o4ua2	 Alignment		16.0	35	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
11	c6qj4E_	 Alignment		15.8	80	PDB header: cell cycle Chain: E: PDB Molecule: condensin complex subunit 2; PDBTitle: crystal structure of the c. thermophilum condensin ycs4-brn12 subcomplex bound to the smc4 atpase head in complex with the c-3 terminal domain of brn1

12	c2l0gA_			14.1	36	PDB header: protein binding Chain: A; PDB Molecule: dna polymerase iota; PDBTitle: solution nmr structure of ubiquitin-binding motif (ubm2) of human2 polymerase iota
13	c2khuA_			12.0	36	PDB header: transferase/protein binding Chain: A; PDB Molecule: immunoglobulin g-binding protein g, dna PDBTitle: solution structure of the ubiquitin-binding motif of human2 polymerase iota
14	d1p4ea1			11.9	50	Fold: SAM domain-like Superfamily: lambda integrase-like, N-terminal domain Family: lambda integrase-like, N-terminal domain
15	c3mk7F_			11.0	12	PDB header: oxidoreductase Chain: F; PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase
16	c6an7D_			10.3	4	PDB header: transport protein Chain: D; PDB Molecule: transport permease protein; PDBTitle: crystal structure of o-antigen polysaccharide abc-transporter
17	c2mc7A_			9.7	10	PDB header: membrane protein Chain: A; PDB Molecule: regulatory peptide; PDBTitle: structure of salmonella mgtr
18	d2ipqx1			9.5	40	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: STY4665 C-terminal domain-like
19	d1v97a2			9.4	33	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
20	c3g43F_			9.2	50	PDB header: metal binding protein Chain: F; PDB Molecule: voltage-dependent l-type calcium channel subunit alpha-1c; PDBTitle: crystal structure of the calmodulin-bound cav1.2 c-terminal regulatory2 domain dimer
21	c6gcsW_		not modelled	8.9	18	PDB header: oxidoreductase Chain: W; PDB Molecule: nb6m subunit; PDBTitle: cryo-em structure of respiratory complex i from yarrowia lipolytica
22	c2mkvA_		not modelled	8.8	11	PDB header: transport protein Chain: A; PDB Molecule: sodium/potassium-transporting atpase subunit gamma; PDBTitle: structure of the na,k-atpase regulatory protein fxyd2b in micelles
23	c2vziB_		not modelled	8.4	28	PDB header: cell adhesion Chain: B; PDB Molecule: alpha-parvin; PDBTitle: crystal structure of the c-terminal calponin homology domain of alpha-2 parvin in complex with paxillin ld4 motif
24	c2kwuA_		not modelled	8.2	23	PDB header: protein binding/signaling protein Chain: A; PDB Molecule: dna polymerase iota; PDBTitle: solution structure of ubm2 of murine polymerase iota in complex with2 ubiquitin
25	d1s7ba_		not modelled	8.0	14	Fold: Multidrug resistance efflux transporter EmrE Superfamily: Multidrug resistance efflux transporter EmrE Family: Multidrug resistance efflux transporter EmrE
26	c1fftG_		not modelled	7.8	12	PDB header: oxidoreductase Chain: G; PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from escherichia coli
27	c5o31Z_		not modelled	7.5	21	PDB header: oxidoreductase Chain: Z; PDB Molecule: nadh dehydrogenase [ubiquinone] 1 alpha subcomplex subunit PDBTitle: mitochondrial complex i in the deactive state
28	c3oxqF_		not modelled	7.5	50	PDB header: metal binding protein/transport protein Chain: F; PDB Molecule: voltage-dependent l-type calcium channel subunit alpha-1c; PDBTitle: crystal structure of ca2+/cam-cav1.2 pre-ic/iq domain

						complex
29	c2jo1A_	Alignment	not modelled	7.2	25	PDB header: hydrolase regulator Chain: A: PDB Molecule: phospholemman; PDBTitle: structure of the na,k-atpase regulatory protein fxyd1 in2 micelles
30	c6cfwl_	Alignment	not modelled	7.1	8	PDB header: membrane protein Chain: I: PDB Molecule: mbh subunit; PDBTitle: cryoem structure of a respiratory membrane-bound hydrogenase
31	c5xyiY_	Alignment	not modelled	6.8	43	PDB header: ribosome Chain: Y: PDB Molecule: ribosomal protein s24e, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome
32	c3shgB_	Alignment	not modelled	6.5	33	PDB header: transferase/protein binding Chain: B: PDB Molecule: vbha; PDBTitle: vbht fic protein from bartonella schoenbuchensis in complex with vbha2 antitoxin
33	c1a10B_	Alignment	not modelled	6.5	39	PDB header: virus Chain: B: PDB Molecule: scaffolding protein gpb; PDBTitle: procapsid of bacteriophage phix174
34	c2retE_	Alignment	not modelled	6.4	25	PDB header: protein transport Chain: E: PDB Molecule: pseudopilin epsi; PDBTitle: the crystal structure of a binary complex of two pseudopilins: epsi2 and epsj from the type 2 secretion system of vibrio vulnificus
35	c5lnkq_	Alignment	not modelled	6.4	21	PDB header: oxidoreductase Chain: Q: PDB Molecule: PDBTitle: entire ovine respiratory complex i
36	d1pdaa2	Alignment	not modelled	6.3	13	Fold: dsRBD-like Superfamily: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain Family: Porphobilinogen deaminase (hydroxymethylbilane synthase), C-terminal domain
37	d1jroa2	Alignment	not modelled	6.1	25	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
38	d1dxxa1	Alignment	not modelled	6.1	23	Fold: CH domain-like Superfamily: Calponin-homology domain, CH-domain Family: Calponin-homology domain, CH-domain
39	d2reta1	Alignment	not modelled	5.9	25	Fold: Pili subunits Superfamily: Pili subunits Family: GSP11 I/J protein-like
40	d1qlec_	Alignment	not modelled	5.8	13	Fold: Cytochrome c oxidase subunit III-like Superfamily: Cytochrome c oxidase subunit III-like Family: Cytochrome c oxidase subunit III-like
41	c6nd1A_	Alignment	not modelled	5.7	14	PDB header: protein transport Chain: A: PDB Molecule: protein translocation protein sec63; PDBTitle: cryoem structure of the sec complex from yeast
42	c3wwtB_	Alignment	not modelled	5.6	44	PDB header: transcription/viral protein Chain: B: PDB Molecule: protein c'; PDBTitle: crystal structure of the y3:stat1nd complex
43	c2k48A_	Alignment	not modelled	5.2	40	PDB header: viral protein Chain: A: PDB Molecule: nucleoprotein; PDBTitle: nmr structure of the n-terminal coiled coil domain of the2 andes hantavirus nucleocapsid protein
44	c3m7kA_	Alignment	not modelled	5.2	100	PDB header: hydrolase/dna Chain: A: PDB Molecule: restriction endonuclease paci; PDBTitle: crystal structure of paci-dna enzyme product complex
45	d1qcrd2	Alignment	not modelled	5.2	80	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain