
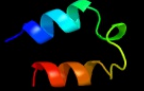







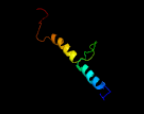







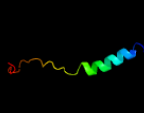



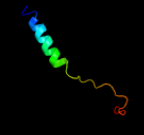





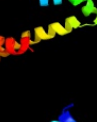





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0205 (-) _243384_244487
Date	Tue Jul 23 14:50:26 BST 2019
Unique Job ID	46d05e8c1434932b

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3x0uB_	 Alignment		42.6	19	PDB header: toxin Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of pirb
2	c3zljC_	 Alignment		36.1	35	PDB header: dna binding protein/dna Chain: C: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of full-length e.coli dna mismatch repair protein2 muts d835r mutant in complex with gt mismatched dna
3	c3zljD_	 Alignment		35.5	35	PDB header: dna binding protein/dna Chain: D: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of full-length e.coli dna mismatch repair protein2 muts d835r mutant in complex with gt mismatched dna
4	d1ppjc2	 Alignment		14.6	15	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
5	c2kncA_	 Alignment		11.8	14	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: platelet integrin alfaIib-beta3 transmembrane-cytoplasmic2 heterocomplex
6	d1kkxa_	 Alignment		11.5	12	Fold: DNA/RNA-binding 3-helical bundle Superfamily: ARID-like Family: ARID domain
7	c6caaA_	 Alignment		11.5	19	PDB header: transport protein Chain: A: PDB Molecule: electrogenic sodium bicarbonate cotransporter 1; PDBTitle: cryoem structure of human slc4a4 sodium-coupled acid-base transporter2 nbce1
8	c6cb6A_	 Alignment		10.8	18	PDB header: viral protein Chain: A: PDB Molecule: protein a6; PDBTitle: crystal structure of vaccinia virus a6 n-terminus (space group c2)
9	c6hwhR_	 Alignment		10.2	26	PDB header: electron transport Chain: R: PDB Molecule: msmeg_4693; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis
10	d1bccc3	 Alignment		9.1	14	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
11	c6adql_	 Alignment		8.6	26	PDB header: electron transport Chain: I: PDB Molecule: cytochrome c oxidase subunit ctaj; PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis

12	c3cwbC_	Alignment		8.1	13	PDB header: oxidoreductase Chain: C; PDB Molecule: cytochrome b; PDBTitle: chicken cytochrome bc1 complex inhibited by an iodinated analogue of2 the polyketide crocacin-d
13	c3j8bF_	Alignment		7.9	42	PDB header: translation Chain: F; PDB Molecule: eukaryotic translation initiation factor 3 subunit f; PDBTitle: model of the human eif3 pci-mpn octamer docked into the 43s-hcv ires2 em map
14	c3j8cF_	Alignment		7.9	42	PDB header: translation Chain: F; PDB Molecule: eukaryotic translation initiation factor 3 subunit f; PDBTitle: model of the human eif3 pci-mpn octamer docked into the 43s em map
15	c3j7kF_	Alignment		7.9	42	PDB header: translation Chain: F; PDB Molecule: eukaryotic translation initiation factor 3 subunit f; PDBTitle: model of the human eif3 pci-mpn octamer docked into the 43s em map
16	c3j7jF_	Alignment		7.9	42	PDB header: translation Chain: F; PDB Molecule: eukaryotic translation initiation factor 3 subunit f; PDBTitle: model of the human eif3 pci-mpn octamer docked into the 43s-hcv ires2 em map
17	c5sv9B_	Alignment		7.3	9	PDB header: transport protein Chain: B; PDB Molecule: bor1p boron transporter; PDBTitle: structure of the slc4 transporter bor1p in an inward-facing2 conformation
18	c6hu9t_	Alignment		7.3	32	PDB header: oxidoreductase/electron transport Chain: T; PDB Molecule: cytochrome b-c1 complex subunit 9; PDBTitle: iii2-iv2 mitochondrial respiratory supercomplex from s. cerevisiae
19	c4j72B_	Alignment		7.1	18	PDB header: transferase Chain: B; PDB Molecule: phospho-n-acetylmuramoyl-pentapeptide-transferase; PDBTitle: crystal structure of polyprenyl-phosphate n-acetyl hexosamine 1-2 phosphate transferase
20	c2l8sA_	Alignment		6.5	23	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
21	d3cx5c2	Alignment	not modelled	6.1	17	Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
22	c4p6vB_	Alignment	not modelled	6.1	14	PDB header: oxidoreductase Chain: B; PDB Molecule: na(+)-translocating nadh-quinone reductase subunit b; PDBTitle: crystal structure of the na+-translocating nadh: ubiquinone2 oxidoreductase from vibrio cholerae
23	c2ww9B_	Alignment	not modelled	5.8	26	PDB header: ribosome Chain: B; PDB Molecule: protein transport protein sss1; PDBTitle: cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
24	c2qjkM_	Alignment	not modelled	5.7	13	PDB header: electron transport Chain: M; PDB Molecule: cytochrome b; PDBTitle: crystal structure analysis of mutant rhodobacter2 sphaeroides bc1 with stigmatellin and antimycin
25	c6o7xa_	Alignment	not modelled	5.5	13	PDB header: membrane protein Chain: A; PDB Molecule: vacuolar atp synthase catalytic subunit a; PDBTitle: saccharomyces cerevisiae v-atpase stv1-v1vo state 3
26	c2lcyA_	Alignment	not modelled	5.5	44	PDB header: viral protein Chain: A; PDB Molecule: virion spike glycoprotein; PDBTitle: nmr structure of the complete internal fusion loop from ebolavirus gp22 at ph 5.5
27	c5d92B_	Alignment	not modelled	5.5	8	PDB header: membrane protein Chain: B; PDB Molecule: af2299 protein,phosphatidylinositol synthase; PDBTitle: structure of a phosphatidylinositolphosphate (pip) synthase from2 renibacterium salmoninarum
28	c2oarA_	Alignment	not modelled	5.4	11	PDB header: membrane protein Chain: A; PDB Molecule: large-conductance mechanosensitive channel;

29	d2e74a1	Alignment	not modelled	5.2	15	PDBTitle: mechanosensitive channel of large conductance (mscl) Fold: Heme-binding four-helical bundle Superfamily: Transmembrane di-heme cytochromes Family: Cytochrome b of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
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