


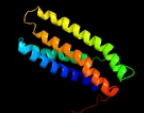
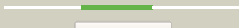
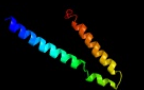
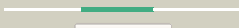
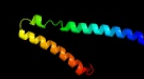







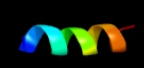






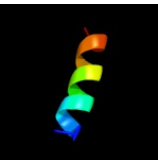
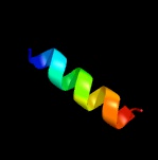




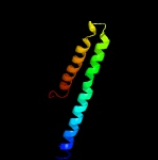

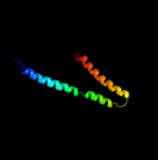


Phyre2

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|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2536 (-) _2860462_2861154 |
| Date | Wed Aug 7 12:50:17 BST 2019 |
| Unique Job ID | 4108c18227a0d62f |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c6hwhb_ |  Alignment |  | 79.9 | 16 | PDB header: electron transport Chain: B: PDB Molecule: ubiquinol-cytochrome c reductase iron-sulfur subunit; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis |
| 2 | c6ajjA_ |  Alignment |  | 66.5 | 10 | PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: drug exporters of the rnd superfamily-like protein, PDBTitle: crystal structure of mycolic acid transporter mmpI3 from mycobacterium2 smegmatis complexed with ica38 |
| 3 | c3nd0A_ |  Alignment |  | 51.9 | 19 | PDB header: transport protein Chain: A: PDB Molecule: slI0855 protein; PDBTitle: x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter |
| 4 | d1otsa_ |  Alignment |  | 47.2 | 20 | Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel |
| 5 | c4tkrB_ |  Alignment |  | 46.3 | 22 | PDB header: membrane protein Chain: B: PDB Molecule: thiamine transporter thia; PDBTitle: native-sad phasing for thit from listeria monocytogenes serovar. |
| 6 | d1iqva_ |  Alignment |  | 41.7 | 40 | Fold: Ribosomal protein S7 Superfamily: Ribosomal protein S7 Family: Ribosomal protein S7 |
| 7 | c2zkgg_ |  Alignment |  | 41.6 | 35 | PDB header: ribosomal protein/rna Chain: G: PDB Molecule: rna helix; PDBTitle: structure of a mammalian ribosomal 40s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map |
| 8 | c5xyiF_ |  Alignment |  | 36.1 | 40 | PDB header: ribosome Chain: F: PDB Molecule: 40s ribosomal protein s5-b, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome |
| 9 | c3izbF_ |  Alignment |  | 35.6 | 40 | PDB header: ribosome Chain: F: PDB Molecule: 40s ribosomal protein rps5 (s7p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 10 | c5khnB_ |  Alignment |  | 35.4 | 11 | PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn |
| 11 | c2xzmG_ |  Alignment |  | 34.0 | 40 | PDB header: ribosome Chain: G: PDB Molecule: ribosomal protein s7 containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1 |

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|----|-------------------------|-----------|---|------|----|---|
| 12 | c3zey2_ | Alignment |  | 33.1 | 33 | PDB header: ribosome Chain: 2: PDB Molecule: 40s ribosomal protein s5, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 13 | c1s1hG_ | Alignment |  | 30.1 | 40 | PDB header: ribosome Chain: G: PDB Molecule: 40s ribosomal protein s5; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from yeast2 obtained by docking atomic models for rna and protein components into3 a 11.7 a cryo-em map. this file, 1s1h, contains 40s subunit. the 60s4 ribosomal subunit is in file 1s1i. |
| 14 | c1p58E_ | Alignment |  | 30.0 | 22 | PDB header: virus Chain: E: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction |
| 15 | d1husa_ | Alignment |  | 29.6 | 47 | Fold: Ribosomal protein S7 Superfamily: Ribosomal protein S7 Family: Ribosomal protein S7 |
| 16 | d1rssa_ | Alignment |  | 29.6 | 47 | Fold: Ribosomal protein S7 Superfamily: Ribosomal protein S7 Family: Ribosomal protein S7 |
| 17 | d2qalg1 | Alignment |  | 28.5 | 47 | Fold: Ribosomal protein S7 Superfamily: Ribosomal protein S7 Family: Ribosomal protein S7 |
| 18 | c6coyB_ | Alignment |  | 28.2 | 10 | PDB header: transport protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: human clc-1 chloride ion channel, transmembrane domain |
| 19 | c3gtyS_ | Alignment |  | 27.2 | 33 | PDB header: chaperone/ribosomal protein Chain: S: PDB Molecule: 30s ribosomal protein s7; PDBTitle: promiscuous substrate recognition in folding and assembly activities2 of the trigger factor chaperone |
| 20 | c2ht2B_ | Alignment |  | 26.6 | 20 | PDB header: membrane protein Chain: B: PDB Molecule: h(+)/cl(-) exchange transporter clca; PDBTitle: structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex |
| 21 | c3j6vG_ | Alignment | not modelled | 26.4 | 40 | PDB header: ribosome Chain: G: PDB Molecule: 28s ribosomal protein s7, mitochondrial; PDBTitle: cryo-em structure of the small subunit of the mammalian mitochondrial2 ribosome |
| 22 | c2lowA_ | Alignment | not modelled | 25.7 | 39 | PDB header: membrane protein Chain: A: PDB Molecule: apelin receptor; PDBTitle: solution structure of ar55 in 50% hfp |
| 23 | c5wsnD_ | Alignment | not modelled | 24.7 | 24 | PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: structure of japanese encephalitis virus |
| 24 | c5o5jG_ | Alignment | not modelled | 24.6 | 47 | PDB header: ribosome Chain: G: PDB Molecule: 30s ribosomal protein s7; PDBTitle: structure of the 30s small ribosomal subunit from mycobacterium2 smegmatis |
| 25 | c3bbnG_ | Alignment | not modelled | 23.4 | 33 | PDB header: ribosome Chain: G: PDB Molecule: ribosomal protein s7; PDBTitle: homology model for the spinach chloroplast 30s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome. |
| 26 | c6rdr8_ | Alignment | not modelled | 23.3 | 30 | PDB header: proton transport Chain: 8: PDB Molecule: mitochondrial atp synthase subunit asa8; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substase 1d,2 monomer-masked refinement |
| 27 | c6rdi8_ | Alignment | not modelled | 23.3 | 30 | PDB header: proton transport Chain: 8: PDB Molecule: mitochondrial atp synthase subunit asa8; PDBTitle: cryo-em structure of polytomella f-atp synthase, rotary substase 1a,2 monomer-masked refinement |
| 28 | c3j0xl_ | Alignment | not modelled | 22.7 | 47 | PDB header: ribosome Chain: J: PDB Molecule: 30s ribosomal protein s7; PDBTitle: structural characterization of mrna-trna translocation intermediates2 (30s ribosome of class 4b of the six classes) |
| | | | | | | PDB header: viral protein |

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|----|-------------------------|-----------|--------------|------|----|--|
| 29 | c6hhkB_ | Alignment | not modelled | 22.6 | 14 | Chain: B: PDB Molecule: gp105; PDBTitle: structure of gp105 of listeria bacteriophage a511 |
| 30 | c1vs5G_ | Alignment | not modelled | 21.8 | 47 | PDB header: ribosome Chain: G: PDB Molecule: 30s ribosomal protein s7; PDBTitle: crystal structure of the bacterial ribosome from escherichia coli in2 complex with the antibiotic kasugamycin at 3.5a resolution. this file3 contains the 30s subunit of one 70s ribosome. the entire crystal4 structure contains two 70s ribosomes and is described in remark 400. |
| 31 | c5tr1A_ | Alignment | not modelled | 20.8 | 10 | PDB header: transport protein Chain: A: PDB Molecule: chloride channel protein; PDBTitle: cryo-electron microscopy structure of a bovine clc-k chloride channel,2 alternate (class 2) conformation |
| 32 | c3j2pD_ | Alignment | not modelled | 19.5 | 22 | PDB header: viral protein Chain: D: PDB Molecule: small envelope protein m; PDBTitle: cryoem structure of dengue virus envelope protein heterotetramer |
| 33 | c6hwhX_ | Alignment | not modelled | 19.5 | 11 | PDB header: electron transport Chain: X: PDB Molecule: cytochrome c oxidase polypeptide 4; PDBTitle: structure of a functional obligate respiratory supercomplex from2 mycobacterium smegmatis |
| 34 | d1kpla_ | Alignment | not modelled | 19.0 | 20 | Fold: Clc chloride channel Superfamily: Clc chloride channel Family: Clc chloride channel |
| 35 | c2k9pA_ | Alignment | not modelled | 17.5 | 33 | PDB header: membrane protein Chain: A: PDB Molecule: pheromone alpha factor receptor; PDBTitle: structure of tm1_tm2 in lppg micelles |
| 36 | c6qvcB_ | Alignment | not modelled | 17.5 | 10 | PDB header: membrane protein Chain: B: PDB Molecule: chloride channel protein 1; PDBTitle: cryoem structure of the human clc-1 chloride channel, cbs state 1 |
| 37 | c2losA_ | Alignment | not modelled | 15.6 | 24 | PDB header: membrane protein Chain: A: PDB Molecule: transmembrane protein 14c; PDBTitle: backbone structure of human membrane protein tmem14c |
| 38 | c2k9yB_ | Alignment | not modelled | 14.7 | 15 | PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0 |
| 39 | c6eyuA_ | Alignment | not modelled | 14.3 | 20 | PDB header: membrane protein Chain: A: PDB Molecule: bacteriorhodopsin; PDBTitle: crystal structure of the inward h(+)- pump xenorhodopsin |
| 40 | c2mpnA_ | Alignment | not modelled | 14.2 | 23 | PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli |
| 41 | c2mpnB_ | Alignment | not modelled | 14.2 | 23 | PDB header: membrane protein Chain: B: PDB Molecule: inner membrane protein ygap; PDBTitle: 3d nmr structure of the transmembrane domain of the full-length inner2 membrane protein ygap from escherichia coli |
| 42 | c3e37B_ | Alignment | not modelled | 13.7 | 16 | PDB header: transferase Chain: B: PDB Molecule: protein farnesyltransferase subunit beta; PDBTitle: protein farnesyltransferase complexed with bisubstrate2 ethylenediamine scaffold inhibitor 5 |
| 43 | c5ireD_ | Alignment | not modelled | 13.5 | 22 | PDB header: virus Chain: D: PDB Molecule: m protein; PDBTitle: the cryo-em structure of zika virus |
| 44 | c1p58F_ | Alignment | not modelled | 13.3 | 22 | PDB header: virus Chain: F: PDB Molecule: envelope protein m; PDBTitle: complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction |
| 45 | c3dinD_ | Alignment | not modelled | 13.3 | 18 | PDB header: membrane protein, protein transport Chain: D: PDB Molecule: preprotein translocase subunit sece; PDBTitle: crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase |
| 46 | c6dmoA_ | Alignment | not modelled | 13.1 | 11 | PDB header: protein binding Chain: A: PDB Molecule: protein patched homolog 1; PDBTitle: cryo-em structure of human ptch1 with three mutations2 l282q/t500f/p504l |
| 47 | c6fosK_ | Alignment | not modelled | 12.3 | 47 | PDB header: photosynthesis Chain: K: PDB Molecule: photosystem i reaction center subunit x; PDBTitle: cyanidioschyzon merolae photosystem i |
| 48 | c5z62N_ | Alignment | not modelled | 11.8 | 28 | PDB header: electron transport Chain: N: PDB Molecule: cytochrome c oxidase subunit ndufa4; PDBTitle: structure of human cytochrome c oxidase |
| 49 | c2k9yA_ | Alignment | not modelled | 11.3 | 16 | PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0 |
| 50 | c5zghK_ | Alignment | not modelled | 11.3 | 47 | PDB header: photosynthesis Chain: K: PDB Molecule: psak; PDBTitle: cryo-em structure of the red algal psi-lhcr |
| 51 | c3q7aB_ | Alignment | not modelled | 10.6 | 19 | PDB header: transferase/transferase inhibitor Chain: B: PDB Molecule: farnesyltransferase beta subunit; PDBTitle: cryptococcus neoformans protein farnesyltransferase in complex with2 fpp and l-778,123 |
| 52 | c4ydeB_ | Alignment | not modelled | 10.2 | 22 | PDB header: transferase Chain: B: PDB Molecule: protein farnesyltransferase/geranylgeranyltransferase type- PDBTitle: crystal structure of candida albicans protein farnesyltransferase2 binary complex with the isoprenoid farnesylidiphosphate |
| 53 | c4px7A_ | Alignment | not modelled | 9.7 | 18 | PDB header: hydrolase Chain: A: PDB Molecule: phosphatidylglycerophosphatase; PDBTitle: crystal structure of lipid phosphatase e. coli pgpb |
| 54 | c6f46A_ | Alignment | not modelled | 9.1 | 22 | PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-like protein 1; |

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|----|-------------------------|-----------|--------------|-----|----|---|
| 54 | c0r4vA_ | Alignment | not modelled | 8.1 | 32 | PDBTitle: structure of the transmembrane helix of bclxl in phospholipid2 nanodiscs PDB header: dna binding protein Chain: A; PDB Molecule: probable transcriptional regulatory protein; |
| 55 | c5n1cA_ | Alignment | not modelled | 8.8 | 26 | PDBTitle: iodinated form of the mycobacterium tuberculosis repressor ethr2 PDB header: oxidoreductase |
| 56 | c3aygA_ | Alignment | not modelled | 8.7 | 14 | Chain: A; PDB Molecule: nitric oxide reductase; PDBTitle: crystal structure of nitric oxide reductase complex with hqno |
| 57 | c4cdiC_ | Alignment | not modelled | 8.5 | 43 | PDB header: membrane protein Chain: C; PDB Molecule: predicted protein; PDBTitle: crystal structure of acrb-acrz complex |
| 58 | c6igzL_ | Alignment | not modelled | 8.5 | 36 | PDB header: plant protein Chain: L; PDB Molecule: psal; PDBTitle: structure of psi-lhci |
| 59 | d2soba_ | Alignment | not modelled | 8.4 | 20 | Fold: OB-fold Superfamily: Staphylococcal nuclease Family: Staphylococcal nuclease |
| 60 | c4nj7P_ | Alignment | not modelled | 8.2 | 19 | PDB header: protein binding Chain: P; PDB Molecule: auxin response factor 7; PDBTitle: pb1 domain of atarf7 - semet derivative |
| 61 | c4mbgB_ | Alignment | not modelled | 8.0 | 27 | PDB header: transferase Chain: B; PDB Molecule: caax farnesyltransferase beta subunit ram1; PDBTitle: crystal structure of aspergillus fumigatus protein farnesyltransferase2 binary complex with farnesyldiphosphate |
| 62 | c6f0kD_ | Alignment | not modelled | 7.8 | 19 | PDB header: membrane protein Chain: D; PDB Molecule: actd; PDBTitle: alternative complex iii |
| 63 | d2h6fb1 | Alignment | not modelled | 7.7 | 15 | Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Protein prenyltransferases |
| 64 | c4y7jE_ | Alignment | not modelled | 6.9 | 16 | PDB header: membrane protein,transport protein Chain: E; PDB Molecule: large conductance mechanosensitive channel protein, PDBTitle: structure of an archaeal mechanosensitive channel in expanded state |
| 65 | c4cbfB_ | Alignment | not modelled | 6.7 | 25 | PDB header: virus Chain: B; PDB Molecule: m protein; PDBTitle: near-atomic resolution cryo-em structure of dengue serotype 4 virus |
| 66 | c5fruB_ | Alignment | not modelled | 6.5 | 27 | PDB header: transcription Chain: B; PDB Molecule: positive phenol-degradative gene regulator; PDBTitle: crystal structure of the phenol-responsive sensory domain2 of the transcription activator poxr |
| 67 | d2osoa1 | Alignment | not modelled | 6.4 | 33 | Fold: Ligand-binding domain in the NO signalling and Golgi transport Superfamily: Ligand-binding domain in the NO signalling and Golgi transport Family: MJ1460-like |
| 68 | c2v5iA_ | Alignment | not modelled | 6.0 | 43 | PDB header: viral protein Chain: A; PDB Molecule: salmonella typhimurium db7155 bacteriophage det7 tailspike; PDBTitle: structure of the receptor-binding protein of bacteriophage det7: a2 podoviral tailspike in a myovirus |
| 69 | c5kbhB_ | Alignment | not modelled | 5.9 | 36 | PDB header: transcription Chain: B; PDB Molecule: mopr; PDBTitle: crystal structure of the aromatic sensor domain of mopr in complex2 with 3-chloro-phenol |
| 70 | c2j5dA_ | Alignment | not modelled | 5.9 | 47 | PDB header: membrane protein Chain: A; PDB Molecule: bcl2/adenovirus e1b 19 kda protein-interacting protein 3; PDBTitle: nmr structure of bnip3 transmembrane domain in lipid bicelles |
| 71 | d1kf6c_ | Alignment | not modelled | 5.4 | 16 | Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Succinate dehydrogenase/Fumarate reductase transmembrane subunits (SdhC/FrdC and SdhD/FrdD) |
| 72 | c3ofgA_ | Alignment | not modelled | 5.1 | 11 | PDB header: chaperone Chain: A; PDB Molecule: boca/mesd chaperone for ywtd beta-propeller-egf protein 1; PDBTitle: structured domain of caenorhabditis elegans bmy-1 |
| 73 | c4m0qB_ | Alignment | not modelled | 5.1 | 26 | PDB header: viral protein Chain: B; PDB Molecule: membrane-associated protein vp24; PDBTitle: ebola virus vp24 structure |
| 74 | c1mowG_ | Alignment | not modelled | 5.1 | 36 | PDB header: hydrolase/dna Chain: G; PDB Molecule: chimera of homing endonuclease i-dmoi and dna endonuclease PDBTitle: e-drei |