
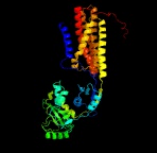
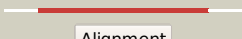

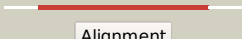



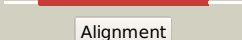
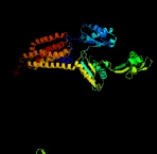


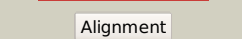

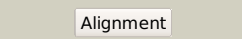

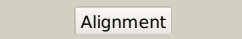

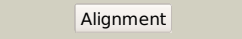
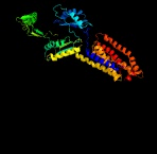
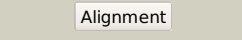



Phyre2

| | |
|---------------|----------------------------------|
| Email | mdejesus@rockefeller.edu |
| Description | RVBD2587c_(secD)_2914025_2915746 |
| Date | Wed Aug 7 12:50:22 BST 2019 |
| Unique Job ID | 9df7a617771e712b |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|--|---|------------|--------|---|
| 1 | c3aqpB_ |  Alignment |  | 100.0 | 28 | PDB header: membrane protein Chain: B: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: crystal structure of secdf, a translocon-associated membrane protein,2 from thermus throphilus |
| 2 | c5xamA_ |  Alignment |  | 100.0 | 30 | PDB header: membrane protein Chain: A: PDB Molecule: protein translocase subunit secdf; PDBTitle: crystal structure of secdf in i form at 4 a resolution |
| 3 | c5lq3F_ |  Alignment |  | 100.0 | 13 | PDB header: transport protein Chain: F: PDB Molecule: cmeb; PDBTitle: structures and transport dynamics of the campylobacter jejuni2 multidrug efflux pump cmeb |
| 4 | c2v50A_ |  Alignment |  | 100.0 | 14 | PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein mexb; PDBTitle: the missing part of the bacterial mexab-oprm system: structural2 determination of the multidrug exporter mexb |
| 5 | c6owsB_ |  Alignment |  | 100.0 | 13 | PDB header: membrane protein Chain: B: PDB Molecule: efflux pump membrane transporter; PDBTitle: cryo-em structure of an acinetobacter baumannii multidrug efflux pump |
| 6 | c3k07A_ |  Alignment |  | 100.0 | 10 | PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusa; PDBTitle: crystal structure of cusa |
| 7 | c4mt1A_ |  Alignment |  | 100.0 | 13 | PDB header: membrane protein, tranport protein Chain: A: PDB Molecule: drug efflux protein; PDBTitle: crystal structure of the neisseria gonorrhoeae mtrd inner membrane2 multidrug efflux pump |
| 8 | c1oy8A_ |  Alignment |  | 100.0 | 15 | PDB header: membrane protein Chain: A: PDB Molecule: acriflavine resistance protein b; PDBTitle: structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump |
| 9 | c6csxA_ |  Alignment |  | 100.0 | 16 | PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux pump subunit acrb; PDBTitle: single particles cryo-em structure of acrb d407a associated with lipid2 bilayer at 3.0 angstrom |
| 10 | c4k0eA_ |  Alignment |  | 100.0 | 14 | PDB header: transport protein Chain: A: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii |
| 11 | c4k0eC_ |  Alignment |  | 100.0 | 15 | PDB header: transport protein Chain: C: PDB Molecule: heavy metal cation tricomponent efflux pump znea(czca- PDBTitle: x-ray crystal structure of a heavy metal efflux pump, crystal form ii |

| | | | | | | |
|----|-------------------------|-----------|--------------|-------|----|--|
| 12 | c5mg3D_ | Alignment | | 100.0 | 24 | PDB header: chaperone Chain: D: PDB Molecule: protein translocase subunit secD; PDBTitle: em fitted model of bacterial holo-translocon |
| 13 | c5mg3F_ | Alignment | | 100.0 | 18 | PDB header: chaperone Chain: F: PDB Molecule: protein translocase subunit secF; PDBTitle: em fitted model of bacterial holo-translocon |
| 14 | c6ajjA_ | Alignment | | 100.0 | 15 | PDB header: membrane protein, hydrolase Chain: A: PDB Molecule: drug exporters of the rnd superfamily-like protein, PDBTitle: crystal structure of mycolic acid transporter mmp13 from mycobacterium2 smegmatis complexed with ica38 |
| 15 | c6dmoA_ | Alignment | | 100.0 | 11 | PDB header: protein binding Chain: A: PDB Molecule: protein patched homolog 1; PDBTitle: cryo-em structure of human ptch1 with three mutations2 I282q/t500f/p504l |
| 16 | c5khnB_ | Alignment | | 100.0 | 15 | PDB header: membrane protein Chain: B: PDB Molecule: rnd transporter; PDBTitle: crystal structures of the burkholderia multivorans hopanoid2 transporter hpnn |
| 17 | d1iwga8 | Alignment | | 100.0 | 12 | Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain |
| 18 | d1iwga7 | Alignment | | 99.9 | 17 | Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain |
| 19 | c3jd8A_ | Alignment | | 99.9 | 12 | PDB header: membrane protein Chain: A: PDB Molecule: niemann-pick c1 protein; PDBTitle: cryo-em structure of the full-length human npc1 at 4.4 angstrom |
| 20 | c3aqaD_ | Alignment | | 99.9 | 31 | PDB header: membrane protein Chain: D: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: structure and function of a membrane component secdf that enhances2 protein export |
| 21 | c5ensA_ | Alignment | not modelled | 99.7 | 15 | PDB header: transport protein Chain: A: PDB Molecule: multidrug efflux pump subunit acrb,multidrug efflux pump PDBTitle: rhodamine bound structure of bacterial efflux pump. |
| 22 | c4r86B_ | Alignment | not modelled | 99.1 | 11 | PDB header: protein transport Chain: B: PDB Molecule: rnd family aminoglycoside/multidrug efflux pump; PDBTitle: crystal structure of aminoglycoside/multidrug efflux system acrd from2 salmonella typhimurium |
| 23 | d1iwga1 | Alignment | not modelled | 98.1 | 18 | Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains |
| 24 | c1ciiA_ | Alignment | not modelled | 51.8 | 13 | PDB header: transmembrane protein Chain: A: PDB Molecule: colicin ia; PDBTitle: colicin ia |
| 25 | c2yvxD_ | Alignment | not modelled | 40.7 | 14 | PDB header: transport protein Chain: D: PDB Molecule: mg2+ transporter mgte; PDBTitle: crystal structure of magnesium transporter mgte |
| 26 | c2rrnA_ | Alignment | not modelled | 33.6 | 18 | PDB header: protein transport Chain: A: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: solution structure of secdf periplasmic domain p4 |
| 27 | d1iwga3 | Alignment | not modelled | 29.4 | 9 | Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains |
| | | | | | | Fold: PurS-like |

| | | | | | | |
|----|-------------------------|-----------|--------------|------|----|---|
| 28 | d1vq3a_ | Alignment | not modelled | 26.8 | 11 | Superfamily: PurS-like Family: PurS subunit of FGAM synthetase |
| 29 | d1iwga5 | Alignment | not modelled | 26.3 | 9 | Fold: Multidrug efflux transporter AcrB ToIC docking domain; DN and DC subdomains Superfamily: Multidrug efflux transporter AcrB ToIC docking domain; DN and DC subdomains Family: Multidrug efflux transporter AcrB ToIC docking domain; DN and DC subdomains |
| 30 | d1iwga2 | Alignment | not modelled | 24.6 | 19 | Fold: Ferredoxin-like Superfamily: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains Family: Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains |
| 31 | c2xznC_ | Alignment | not modelled | 23.4 | 9 | PDB header: ribosome Chain: C: PDB Molecule: kh domain 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 2 |
| 32 | c2zw2B_ | Alignment | not modelled | 18.7 | 19 | PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein sts178; PDBTitle: crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs) |
| 33 | c5udtD_ | Alignment | not modelled | 14.3 | 16 | PDB header: transferase Chain: D: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with amp |
| 34 | c3zeyX_ | Alignment | not modelled | 14.1 | 12 | PDB header: ribosome Chain: X: PDB Molecule: 40s ribosomal protein s3, putative; PDBTitle: high-resolution cryo-electron microscopy structure of the trypanosoma2 brucei ribosome |
| 35 | c5xyiD_ | Alignment | not modelled | 12.9 | 12 | PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein s3, putative; PDBTitle: small subunit of trichomonas vaginalis ribosome |
| 36 | c5oonA_ | Alignment | not modelled | 10.5 | 21 | PDB header: membrane protein Chain: A: PDB Molecule: undecaprenyl-diphosphatase; PDBTitle: structure of undecaprenyl-pyrophosphate phosphatase, baca |
| 37 | c4p6vE_ | Alignment | not modelled | 10.4 | 17 | 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 |
| 38 | c4ky0B_ | Alignment | not modelled | 10.1 | 18 | PDB header: transport protein, membrane protein Chain: B: PDB Molecule: proton/glutamate symporter, sdf family; PDBTitle: crystal structure of a substrate-free glutamate transporter homologue2 from thermococcus kodakarensis |
| 39 | c3izbB_ | Alignment | not modelled | 9.8 | 21 | PDB header: ribosome Chain: B: PDB Molecule: 40s ribosomal protein rps3 (s3p); PDBTitle: localization of the small subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome |
| 40 | c5lj7B_ | Alignment | not modelled | 9.7 | 17 | PDB header: transport protein Chain: B: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of aggregatibacter actinomycetemcomitans macb bound to atp2 (p21) |
| 41 | c3fewX_ | Alignment | not modelled | 9.2 | 15 | PDB header: immune system Chain: X: PDB Molecule: colicin s4; PDBTitle: structure and function of colicin s4, a colicin with a duplicated2 receptor binding domain |
| 42 | c1s1hC_ | Alignment | not modelled | 9.1 | 22 | PDB header: ribosome Chain: C: PDB Molecule: 40s ribosomal protein s3; 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. |
| 43 | c2jvfA_ | Alignment | not modelled | 9.0 | 27 | PDB header: de novo protein Chain: A: PDB Molecule: de novo protein m7; PDBTitle: solution structure of m7, a computationally-designed2 artificial protein |
| 44 | d1gtda_ | Alignment | not modelled | 8.6 | 13 | Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase |
| 45 | c5n9yB_ | Alignment | not modelled | 8.4 | 9 | PDB header: membrane protein Chain: B: PDB Molecule: zinc transport protein zntb; PDBTitle: the full-length structure of zntb |
| 46 | c3j20C_ | Alignment | not modelled | 8.3 | 18 | PDB header: ribosome Chain: C: PDB Molecule: 30s ribosomal protein s3p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit) |
| 47 | c4a01B_ | Alignment | not modelled | 7.9 | 11 | PDB header: hydrolase Chain: B: PDB Molecule: proton pyrophosphatase; PDBTitle: crystal structure of the h-translocating pyrophosphatase |
| 48 | c4o9uB_ | Alignment | not modelled | 7.9 | 17 | PDB header: membrane protein Chain: B: PDB Molecule: nad(p) transhydrogenase subunit beta; PDBTitle: mechanism of transhydrogenase coupling proton translocation and2 hydride transfer |
| 49 | c2bbjB_ | Alignment | not modelled | 7.3 | 11 | PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter |
| 50 | c1rh1A_ | Alignment | not modelled | 7.2 | 12 | PDB header: antibiotic Chain: A: PDB Molecule: colicin b; PDBTitle: crystal structure of the cytotoxic bacterial protein2 colicin b at 2.5 a resolution |
| 51 | c5nikK_ | Alignment | not modelled | 7.1 | 16 | PDB header: transport protein Chain: K: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: structure of the macab-tolc abc-type tripartite multidrug |

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|----|-------------------------|-----------|--------------|-----|----|--|
| | | | | | | efflux pump |
| 52 | c2zkqc_ | Alignment | not modelled | 7.0 | 13 | PDB header: ribosomal protein/rna Chain: C: PDB Molecule: rna expansion segment es4; 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 |
| 53 | d1cola_ | Alignment | not modelled | 6.7 | 18 | Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin |
| 54 | c2yx5A_ | Alignment | not modelled | 6.7 | 13 | PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0062 protein mj1593; PDBTitle: crystal structure of methanocaldococcus jannaschii purs, one of the2 subunits of formylglycinamide ribonucleotide amidotransferase in the3 purine biosynthetic pathway |
| 55 | d1t4aa_ | Alignment | not modelled | 6.6 | 11 | Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase |
| 56 | c4od5C_ | Alignment | not modelled | 6.6 | 15 | PDB header: transferase Chain: C: PDB Molecule: 4-hydroxybenzoate octaprenyltransferase; PDBTitle: substrate-bound structure of a ubia homolog from aeropyrum pernix k1 |
| 57 | d1c1ia1 | Alignment | not modelled | 6.5 | 13 | Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin |
| 58 | c2kyzA_ | Alignment | not modelled | 6.3 | 21 | PDB header: metal binding protein Chain: A: PDB Molecule: heavy metal binding protein; PDBTitle: nmr structure of heavy metal binding protein tm0320 from thermotoga2 maritima |
| 59 | c4ev6E_ | Alignment | not modelled | 6.1 | 12 | PDB header: metal transport Chain: E: PDB Molecule: magnesium transport protein cora; PDBTitle: the complete structure of cora magnesium transporter from2 methanocaldococcus jannaschii |
| 60 | c2i88A_ | Alignment | not modelled | 6.0 | 18 | PDB header: membrane protein Chain: A: PDB Molecule: colicin-e1; PDBTitle: crystal structure of the channel-forming domain of colicin e1 |
| 61 | c4kppA_ | Alignment | not modelled | 6.0 | 10 | PDB header: membrane protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of h+/ca2+ exchanger cax |
| 62 | c4djiA_ | Alignment | not modelled | 5.6 | 12 | PDB header: transport protein Chain: A: PDB Molecule: probable glutamate/gamma-aminobutyrate antiporter; PDBTitle: structure of glutamate-gaba antiporter gadc |
| 63 | c1qysA_ | Alignment | not modelled | 5.4 | 27 | PDB header: de novo protein Chain: A: PDB Molecule: top7; PDBTitle: crystal structure of top7: a computationally designed2 protein with a novel fold |
| 64 | c6fvqE_ | Alignment | not modelled | 5.4 | 10 | PDB header: membrane protein Chain: E: PDB Molecule: cys-loop ligand-gated ion channel; PDBTitle: the active form of a pentameric ion channel (stelic) gated by alkaline2 ph - r86a |
| 65 | c5vwxD_ | Alignment | not modelled | 5.3 | 42 | PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-h0-h3glt |
| 66 | c5vwxB_ | Alignment | not modelled | 5.3 | 42 | PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-h0-h3glt |
| 67 | d1a87a_ | Alignment | not modelled | 5.3 | 12 | Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin |
| 68 | c1a87A_ | Alignment | not modelled | 5.3 | 12 | PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n |
| 69 | d2uubc2 | Alignment | not modelled | 5.1 | 20 | Fold: Ribosomal protein S3 C-terminal domain Superfamily: Ribosomal protein S3 C-terminal domain Family: Ribosomal protein S3 C-terminal domain |