
















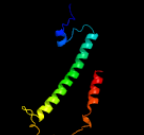

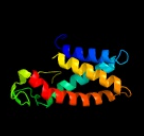


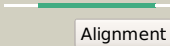

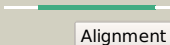

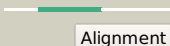

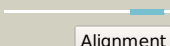
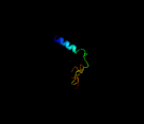
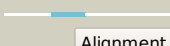

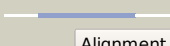

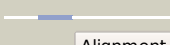
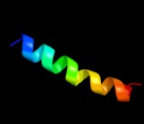
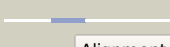
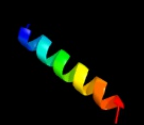
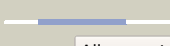

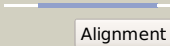
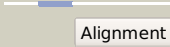
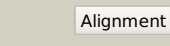
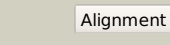
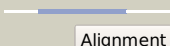
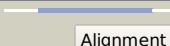
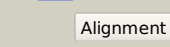


# Phyre2

|               |                                |
|---------------|--------------------------------|
| Email         | mdejesus@rockefeller.edu       |
| Description   | RVBD1614_(lgt)_1813178_1814584 |
| Date          | Fri Aug 2 13:30:20 BST 2019    |
| Unique Job ID | 437c426af8e6264f               |

Detailed template information

| #  | Template                 | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|--------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c5azcA_</a>  |  Alignment   |    | 100.0      | 22     | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> prolipoprotein diacylglyceryl transferase;<br><b>PDBTitle:</b> crystal structure of escherichia coli lgt in complex with 2 phosphatidylglycerol  |
| 2  | <a href="#">c6m97A_</a>  |  Alignment   |    | 81.4       | 11     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> chimera protein of high affinity copper uptake protein 1<br><b>PDBTitle:</b> crystal structure of the high-affinity copper transporter ctr1  |
| 3  | <a href="#">c4kppA_</a>  |  Alignment   |    | 80.1       | 10     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of h+/ca2+ exchanger cax  |
| 4  | <a href="#">c5voxb_</a>  |  Alignment   |   | 62.8       | 11     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B; <b>PDB Molecule:</b> v-type proton atpase subunit b;<br><b>PDBTitle:</b> yeast v-atpase in complex with legionella pneumophila effector sidk2 (rotational state 1)  |
| 5  | <a href="#">c6dlnB_</a>  |  Alignment |  | 62.4       | 20     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B; <b>PDB Molecule:</b> transmembrane protein gp41;<br><b>PDBTitle:</b> oligomeric structure of the hiv gp41 mper-tmd in phospholipid bilayers  |
| 6  | <a href="#">c6o7xa_</a>  |  Alignment |  | 60.7       | 15     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A; <b>PDB Molecule:</b> vacuolar atp synthase catalytic subunit a;<br><b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-v1vo state 3  |
| 7  | <a href="#">c6qkcJ_</a>  |  Alignment |  | 58.1       | 17     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> J; <b>PDB Molecule:</b> voltage-dependent calcium channel gamma-8 subunit;<br><b>PDBTitle:</b> glua1/2 in complex with auxiliary subunit gamma-8  |
| 8  | <a href="#">c6ccciA_</a> |  Alignment |  | 55.6       | 22     | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> protein eskimo 1;<br><b>PDBTitle:</b> the crystal structure of xoat1   |
| 9  | <a href="#">c1m57H_</a>  |  Alignment |  | 50.9       | 20     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> H; <b>PDB Molecule:</b> cytochrome c oxidase;<br><b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant)  |
| 10 | <a href="#">c5iwsA_</a>  |  Alignment |  | 48.5       | 19     | <b>PDB header:</b> transferase<br><b>Chain:</b> A; <b>PDB Molecule:</b> protein-n(pi)-phosphohistidine-sugar phosphotransferase<br><b>PDBTitle:</b> crystal structure of the transporter malt, the eic domain from the2 maltose-specific phosphotransferase system |
| 11 | <a href="#">c5kzoA_</a>  |  Alignment |  | 47.4       | 20     | <b>PDB header:</b> transcription<br><b>Chain:</b> A; <b>PDB Molecule:</b> neurogenic locus notch homolog protein 1;<br><b>PDBTitle:</b> notch1 transmembrane and associated jxtamembrane segment   |

|    |                         |   |   |      |    |  |
|----|-------------------------|---|---|------|----|--|
| 12 | <a href="#">c3m7eA_</a> |  Alignment   |    | 46.4 | 11 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein teha homolog;<br><b>PDBTitle:</b> crystal structure of plant slac1 homolog teha   |
| 13 | <a href="#">c3m7bA_</a> |  Alignment   |    | 46.4 | 11 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> tellurite resistance protein teha homolog;<br><b>PDBTitle:</b> crystal structure of plant slac1 homolog teha   |
| 14 | <a href="#">c5a1sB_</a> |  Alignment   |    | 44.4 | 15 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> citrate-sodium symporter;<br><b>PDBTitle:</b> crystal structure of the sodium-dependent citrate symporter secits2 form salmonella enterica.  |
| 15 | <a href="#">c6nbxG_</a> |  Alignment   |    | 35.6 | 18 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit j;<br><b>PDBTitle:</b> t.elongatus ndh (data-set 2)   |
| 16 | <a href="#">c2k21A_</a> |  Alignment   |    | 31.3 | 38 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e<br><b>PDBTitle:</b> nmr structure of human kcne1 in Impg micelles at ph 6.0 and2 40 degree c  |
| 17 | <a href="#">c3nd0A_</a> |  Alignment   |   | 29.8 | 14 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sl10855 protein;<br><b>PDBTitle:</b> x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter  |
| 18 | <a href="#">c6e8wC_</a> |  Alignment |  | 28.2 | 20 | <b>PDB header:</b> viral protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> envelope glycoprotein gp160;<br><b>PDBTitle:</b> mper-tm domain of hiv-1 envelope glycoprotein (env)   |
| 19 | <a href="#">c2m0qA_</a> |  Alignment |  | 27.4 | 10 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e member 2;<br><b>PDBTitle:</b> solution nmr analysis of intact kcne2 in detergent micelles2 demonstrate a straight transmembrane helix       |
| 20 | <a href="#">c6btmC_</a> |  Alignment |  | 27.1 | 16 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> alternative complex iii subunit c;<br><b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)   |
| 21 | <a href="#">c3wajA_</a> |  Alignment | not modelled  | 25.7 | 12 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane oligosaccharyl transferase;<br><b>PDBTitle:</b> crystal structure of the archaeoglobus fulgidus2 oligosaccharyltransferase (o29867_arcfu) complex with zn and sulfate          |
| 22 | <a href="#">c2mg1A_</a> |  Alignment | not modelled  | 25.0 | 22 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> transmembrane protein gp41;<br><b>PDBTitle:</b> nmr assignment and structure of a peptide derived from the trans-2 membrane region of hiv-1 gp41 in the presence of3 hexafluoroisopropanol |
| 23 | <a href="#">c2ndjA_</a> |  Alignment | not modelled  | 24.4 | 5  | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> potassium voltage-gated channel subfamily e member 3;<br><b>PDBTitle:</b> structural basis for kcne3 and estrogen modulation of the kcnq12 channel                                      |
| 24 | <a href="#">c5t4oj_</a> |  Alignment | not modelled  | 23.5 | 9  | <b>PDB header:</b> hydrolase<br><b>Chain:</b> J: <b>PDB Molecule:</b> atp synthase subunit b;<br><b>PDBTitle:</b> autoinhibited e. coli atp synthase state 1   |
| 25 | <a href="#">c5yq7L_</a> |  Alignment | not modelled  | 22.9 | 13 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> L: <b>PDB Molecule:</b> precursor for l subunits of photosynthetic reaction center;<br><b>PDBTitle:</b> cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii                                |
| 26 | <a href="#">c6f0kF_</a> |  Alignment | not modelled  | 22.8 | 10 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> actf;<br><b>PDBTitle:</b> alternative complex iii   |
| 27 | <a href="#">d2i5nl1</a> |  Alignment | not modelled  | 22.6 | 20 | <b>Fold:</b> Bacterial photosystem II reaction centre, L and M subunits<br><b>Superfamily:</b> Bacterial photosystem II reaction centre, L and M subunits<br><b>Family:</b> Bacterial photosystem II reaction centre, L and M subunits                               |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 28 | <a href="#">c2miiA</a>  | Alignment | not modelled | 22.4 | 13 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> penicillin-binding protein activator lpob;<br><b>PDBTitle:</b> nmr structure of e. coli lpob  |
| 29 | <a href="#">c2b6pA</a>  | Alignment | not modelled | 21.5 | 13 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> lens fiber major intrinsic protein;<br><b>PDBTitle:</b> x-ray structure of lens aquaporin-0 (aqp0) (lens mip) in an open pore2 state   |
| 30 | <a href="#">c3kzfE</a>  | Alignment | not modelled | 21.3 | 10 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> E: <b>PDB Molecule:</b> putative formate transporter 1;<br><b>PDBTitle:</b> pentameric formate channel with formate bound  |
| 31 | <a href="#">c5ir6A</a>  | Alignment | not modelled | 21.1 | 13 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> bd-type quinol oxidase subunit i;<br><b>PDBTitle:</b> the structure of bd oxidase from geobacillus thermodenitrificans   |
| 32 | <a href="#">c4dveA</a>  | Alignment | not modelled | 20.9 | 9  | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> biotin transporter bioj;<br><b>PDBTitle:</b> crystal structure at 2.1 a of the s-component for biotin from an ecf-2 type abc transporter  |
| 33 | <a href="#">c2ls4A</a>  | Alignment | not modelled | 20.8 | 11 | <b>PDB header:</b> metal transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> high affinity copper uptake protein 1;<br><b>PDBTitle:</b> 1h chemical shift assignments for the third transmembrane domain from2 the human copper transport 1                      |
| 34 | <a href="#">c4o9uB</a>  | Alignment | not modelled | 20.4 | 9  | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> nad(p) transhydrogenase subunit beta;<br><b>PDBTitle:</b> mechanism of transhydrogenase coupling proton translocation and2 hydride transfer  |
| 35 | <a href="#">d2j8c1</a>  | Alignment | not modelled | 20.1 | 15 | <b>Fold:</b> Bacterial photosystem II reaction centre, L and M subunits<br><b>Superfamily:</b> Bacterial photosystem II reaction centre, L and M subunits<br><b>Family:</b> Bacterial photosystem II reaction centre, L and M subunits                          |
| 36 | <a href="#">c5wsnC</a>  | Alignment | not modelled | 19.5 | 19 | <b>PDB header:</b> virus<br><b>Chain:</b> C: <b>PDB Molecule:</b> e protein;<br><b>PDBTitle:</b> structure of japanese encephalitis virus   |
| 37 | <a href="#">c2ht2B</a>  | Alignment | not modelled | 18.9 | 11 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> h(+)/cl(-) exchange transporter clca;<br><b>PDBTitle:</b> structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex                                     |
| 38 | <a href="#">c6fkip</a>  | Alignment | not modelled | 18.5 | 14 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> P: <b>PDB Molecule:</b> atp synthase subunit c, chloroplastic;<br><b>PDBTitle:</b> chloroplast f1fo conformation 3   |
| 39 | <a href="#">c1m06j</a>  | Alignment | not modelled | 18.4 | 43 | <b>PDB header:</b> virus/dna<br><b>Chain:</b> J: <b>PDB Molecule:</b> small core protein;<br><b>PDBTitle:</b> structural studies of bacteriophage alpha3 assembly, x-ray2 crystallography   |
| 40 | <a href="#">c1rb8j</a>  | Alignment | not modelled | 18.3 | 43 | <b>PDB header:</b> virus/dna<br><b>Chain:</b> J: <b>PDB Molecule:</b> small core protein;<br><b>PDBTitle:</b> the phix174 dna binding protein j in two different capsid2 environments.  |
| 41 | <a href="#">c5xu1M</a>  | Alignment | not modelled | 17.8 | 17 | <b>PDB header:</b> transport protein<br><b>Chain:</b> M: <b>PDB Molecule:</b> abc transporter permeae;<br><b>PDBTitle:</b> structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6   |
| 42 | <a href="#">c2m59B</a>  | Alignment | not modelled | 17.1 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> vascular endothelial growth factor receptor 2;<br><b>PDBTitle:</b> spatial structure of dimeric vegfr2 membrane domain in dpc micelles  |
| 43 | <a href="#">c2m59A</a>  | Alignment | not modelled | 17.1 | 17 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> vascular endothelial growth factor receptor 2;<br><b>PDBTitle:</b> spatial structure of dimeric vegfr2 membrane domain in dpc micelles  |
| 44 | <a href="#">c4hzuS</a>  | Alignment | not modelled | 16.9 | 15 | <b>PDB header:</b> hydrolase, transport protein<br><b>Chain:</b> S: <b>PDB Molecule:</b> predicted membrane protein;<br><b>PDBTitle:</b> structure of a bacterial energy-coupling factor transporter  |
| 45 | <a href="#">c4hydA</a>  | Alignment | not modelled | 16.9 | 18 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> structure of a presenilin family intramembrane aspartate protease in2 c2221 space group                                      |
| 46 | <a href="#">d1kpla</a>  | Alignment | not modelled | 16.9 | 14 | <b>Fold:</b> Clc chloride channel<br><b>Superfamily:</b> Clc chloride channel<br><b>Family:</b> Clc chloride channel  |
| 47 | <a href="#">c6bbjC</a>  | Alignment | not modelled | 16.8 | 11 | <b>PDB header:</b> metal transport<br><b>Chain:</b> C: <b>PDB Molecule:</b> transient receptor potential cation channel, subfamily v,<br><b>PDBTitle:</b> xenopus tropicalis trpv4  |
| 48 | <a href="#">c2yiuE</a>  | Alignment | not modelled | 16.5 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome c1, heme protein;<br><b>PDBTitle:</b> x-ray structure of the dimeric cytochrome bc1 complex from2 the soil bacterium paracoccus denitrificans at 2.73 angstrom resolution |
| 49 | <a href="#">c3kcvG</a>  | Alignment | not modelled | 16.2 | 12 | <b>PDB header:</b> transport protein<br><b>Chain:</b> G: <b>PDB Molecule:</b> probable formate transporter 1;<br><b>PDBTitle:</b> structure of formate channel  |
| 50 | <a href="#">d1czan3</a> | Alignment | not modelled | 16.1 | 43 | <b>Fold:</b> Ribonuclease H-like motif<br><b>Superfamily:</b> Actin-like ATPase domain<br><b>Family:</b> Hexokinase   |
| 51 | <a href="#">c5nikK</a>  | Alignment | not modelled | 16.0 | 19 | <b>PDB header:</b> transport protein<br><b>Chain:</b> K: <b>PDB Molecule:</b> macrolide export atp-binding/permease protein macb;<br><b>PDBTitle:</b> structure of the macab-tolc abc-type tripartite multidrug efflux pump                                     |
| 52 | <a href="#">d1j4na</a>  | Alignment | not modelled | 15.8 | 14 | <b>Fold:</b> Aquaporin-like<br><b>Superfamily:</b> Aquaporin-like<br><b>Family:</b> Aquaporin-like  |
| 53 | <a href="#">c6rfuE</a>  | Alignment | not modelled | 15.7 | 10 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> monovalent cation/h+ antiporter subunit b;   |

|    |                         |           |              |      |    |   |
|----|-------------------------|-----------|--------------|------|----|---|
| 53 | <a href="#">c0c1w1_</a> | Alignment | not modelled | 13.7 | 10 | <b>PDBTitle:</b> cryoem structure of a respiratory membrane-bound hydrogenase   |
| 54 | <a href="#">c5aexB_</a> | Alignment | not modelled | 15.5 | 15 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> ammonium transporter mep2;<br><b>PDBTitle:</b> crystal structure of saccharomyces cerevisiae mep2  |
| 55 | <a href="#">c2bpa3_</a> | Alignment | not modelled | 15.5 | 43 | <b>PDB header:</b> virus/dna<br><b>Chain:</b> 3: <b>PDB Molecule:</b> protein (subunit of bacteriophage phix174);<br><b>PDBTitle:</b> atomic structure of single-stranded dna bacteriophage2 phix174 and its functional implications  |
| 56 | <a href="#">d1eysl_</a> | Alignment | not modelled | 14.8 | 17 | <b>Fold:</b> Bacterial photosystem II reaction centre, L and M subunits<br><b>Superfamily:</b> Bacterial photosystem II reaction centre, L and M subunits<br><b>Family:</b> Bacterial photosystem II reaction centre, L and M subunits  |
| 57 | <a href="#">c1w9nA_</a> | Alignment | not modelled | 14.6 | 11 | <b>PDB header:</b> antibiotic<br><b>Chain:</b> A: <b>PDB Molecule:</b> epilancin 15x;<br><b>PDBTitle:</b> isolation and characterization of epilancin 15x, a novel antibiotic2 from a clinical strain of staphylococcus epidermidis   |
| 58 | <a href="#">c6o7ua_</a> | Alignment | not modelled | 14.6 | 11 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b><br><b>PDBTitle:</b> saccharomyces cerevisiae v-atpase stv1-vo  |
| 59 | <a href="#">c5levA_</a> | Alignment | not modelled | 14.4 | 15 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> udp-n-acetylglucosamine--dolichyl-phosphate n-<br><b>PDBTitle:</b> crystal structure of human udp-n-acetylglucosamine-dolichyl-phosphate2 n-acetylglucosaminephosphotransferase (dpagt1) (v264g mutant)                                   |
| 60 | <a href="#">d1k8ke_</a> | Alignment | not modelled | 14.3 | 9  | <b>Fold:</b> Arp2/3 complex 21 kDa subunit ARPC3<br><b>Superfamily:</b> Arp2/3 complex 21 kDa subunit ARPC3<br><b>Family:</b> Arp2/3 complex 21 kDa subunit ARPC3   |
| 61 | <a href="#">d1bg3a1</a> | Alignment | not modelled | 14.1 | 43 | <b>Fold:</b> Ribonuclease H-like motif<br><b>Superfamily:</b> Actin-like ATPase domain<br><b>Family:</b> Hexokinase   |
| 62 | <a href="#">d1czan1</a> | Alignment | not modelled | 14.1 | 43 | <b>Fold:</b> Ribonuclease H-like motif<br><b>Superfamily:</b> Actin-like ATPase domain<br><b>Family:</b> Hexokinase   |
| 63 | <a href="#">c5d7tC_</a> | Alignment | not modelled | 14.1 | 10 | <b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> s-component for folate;<br><b>PDBTitle:</b> folate ecf transporter: apo state   |
| 64 | <a href="#">c1p58C_</a> | Alignment | not modelled | 13.6 | 18 | <b>PDB header:</b> virus<br><b>Chain:</b> C: <b>PDB Molecule:</b> major envelope protein e;<br><b>PDBTitle:</b> complex organization of dengue virus membrane proteins as revealed by2 9.5 angstrom cryo-em reconstruction  |
| 65 | <a href="#">d1bg3a3</a> | Alignment | not modelled | 13.5 | 50 | <b>Fold:</b> Ribonuclease H-like motif<br><b>Superfamily:</b> Actin-like ATPase domain<br><b>Family:</b> Hexokinase   |
| 66 | <a href="#">d1v4sa1</a> | Alignment | not modelled | 13.5 | 50 | <b>Fold:</b> Ribonuclease H-like motif<br><b>Superfamily:</b> Actin-like ATPase domain<br><b>Family:</b> Hexokinase   |
| 67 | <a href="#">c2fynH_</a> | Alignment | not modelled | 13.5 | 14 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> H: <b>PDB Molecule:</b> cytochrome c1;<br><b>PDBTitle:</b> crystal structure analysis of the double mutant rhodobacter2 sphaeroides bc1 complex  |
| 68 | <a href="#">c2j3tB_</a> | Alignment | not modelled | 13.4 | 8  | <b>PDB header:</b> transport<br><b>Chain:</b> B: <b>PDB Molecule:</b> trafficking protein particle complex subunit 6a;<br><b>PDBTitle:</b> the crystal structure of the bet3-trs33-bet5-trs23 complex.  |
| 69 | <a href="#">c5aexA_</a> | Alignment | not modelled | 13.1 | 13 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> mep2;<br><b>PDBTitle:</b> crystal structure of candida albicans mep2   |
| 70 | <a href="#">c5nf8A_</a> | Alignment | not modelled | 12.9 | 5  | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> respiratory supercomplex factor 1, mitochondrial;<br><b>PDBTitle:</b> solution structure of detergent-solubilized rcf1, a yeast2 mitochondrial inner membrane protein involved in respiratory complex3 iii/iv supercomplex formation |
| 71 | <a href="#">c6nr3A_</a> | Alignment | not modelled | 12.8 | 18 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m<br><b>PDBTitle:</b> cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium   |
| 72 | <a href="#">c6nr3D_</a> | Alignment | not modelled | 12.8 | 18 | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m<br><b>PDBTitle:</b> cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium   |
| 73 | <a href="#">c6nr3B_</a> | Alignment | not modelled | 12.8 | 18 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m<br><b>PDBTitle:</b> cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium   |
| 74 | <a href="#">c6nr3C_</a> | Alignment | not modelled | 12.8 | 18 | <b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> transient receptor potential cation channel subfamily m<br><b>PDBTitle:</b> cryo-em structure of the trpm8 ion channel in complex with high2 occupancy icilin, pi(4,5)p2, and calcium   |
| 75 | <a href="#">c4djiA_</a> | Alignment | not modelled | 12.6 | 7  | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> probable glutamate/gamma-aminobutyrate antiporter;<br><b>PDBTitle:</b> structure of glutamate-gaba antiporter gadc  |
| 76 | <a href="#">c6c5wA_</a> | Alignment | not modelled | 12.3 | 15 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> calcium uniporter;<br><b>PDBTitle:</b> crystal structure of the mitochondrial calcium uniporter  |
| 77 | <a href="#">c3tdsC_</a> | Alignment | not modelled | 12.3 | 14 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> formate/nitrite transporter;   |

|    |                         |           |              |      |    |  |
|----|-------------------------|-----------|--------------|------|----|--|
|    |                         |           |              |      |    | <b>PDBTitle:</b> crystal structure of hsc f194i  |
| 78 | <a href="#">c6btmD_</a> | Alignment | not modelled | 12.2 | 13 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> alternative complex iii subunit d;<br><b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)                       |
| 79 | <a href="#">c1zrtD_</a> | Alignment | not modelled | 12.2 | 4  | <b>PDB header:</b> oxidoreductase/metal transport<br><b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome c1;<br><b>PDBTitle:</b> rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound                                       |
| 80 | <a href="#">d1eysm_</a> | Alignment | not modelled | 12.1 | 17 | <b>Fold:</b> Bacterial photosystem II reaction centre, L and M subunits<br><b>Superfamily:</b> Bacterial photosystem II reaction centre, L and M subunits<br><b>Family:</b> Bacterial photosystem II reaction centre, L and M subunits     |
| 81 | <a href="#">c6dnfA_</a> | Alignment | not modelled | 12.1 | 18 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> mitochondrial calcium uniporter mcu;<br><b>PDBTitle:</b> cryo-em structure of the mitochondrial calcium uniporter mcu from the2 fungus cyphellophora europaea |
| 82 | <a href="#">c6gcsj_</a> | Alignment | not modelled | 12.0 | 10 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> J: <b>PDB Molecule:</b> nujm subunit;<br><b>PDBTitle:</b> cryo-em structure of respiratory complex i from yarrowia lipolytica   |
| 83 | <a href="#">c4b03A_</a> | Alignment | not modelled | 11.8 | 13 | <b>PDB header:</b> virus<br><b>Chain:</b> A: <b>PDB Molecule:</b> dengue virus 1 e protein;<br><b>PDBTitle:</b> 6a electron cryomicroscopy structure of immature dengue virus serotype2 1  |
| 84 | <a href="#">c6agfB_</a> | Alignment | not modelled | 11.8 | 13 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> sodium channel subunit beta-1;<br><b>PDBTitle:</b> structure of the human voltage-gated sodium channel nav1.4 in complex2 with beta1                          |
| 85 | <a href="#">c5yq72_</a> | Alignment | not modelled | 11.7 | 20 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> 2: <b>PDB Molecule:</b> beta subunit of light-harvesting 1;<br><b>PDBTitle:</b> cryo-em structure of the rc-lh core complex from roseiflexus2 castenholzii                              |
| 86 | <a href="#">c2jpiA_</a> | Alignment | not modelled | 11.6 | 33 | <b>PDB header:</b> antimicrobial protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> bacteriocin lactococcin-g subunit alpha;<br><b>PDBTitle:</b> lactococcin g-a in dpc  |
| 87 | <a href="#">c2mj2A_</a> | Alignment | not modelled | 11.6 | 6  | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> agnoprotein;<br><b>PDBTitle:</b> structure of the dimerization domain of the human polyoma, jc virus2 agnoprotein is an amphipathic alpha-helix.                 |
| 88 | <a href="#">c3tijA_</a> | Alignment | not modelled | 11.5 | 17 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> nupc family protein;<br><b>PDBTitle:</b> crystal structure of a concentrative nucleoside transporter from2 vibrio cholerae                                    |
| 89 | <a href="#">c5zbgC_</a> | Alignment | not modelled | 11.5 | 17 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> short transient receptor potential channel 3;<br><b>PDBTitle:</b> cryo-em structure of human trpc3 at 4.36a resolution  |
| 90 | <a href="#">c6j5ib_</a> | Alignment | not modelled | 11.4 | 10 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> atp synthase subunit alpha, mitochondrial;<br><b>PDBTitle:</b> cryo-em structure of the mammalian dp-state atp synthase                                       |
| 91 | <a href="#">c6btmF_</a> | Alignment | not modelled | 11.4 | 9  | <b>PDB header:</b> membrane protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> alternative complex iii subunit f;<br><b>PDBTitle:</b> structure of alternative complex iii from flavobacterium johnsoniae2 (wild type)                       |
| 92 | <a href="#">c3orgB_</a> | Alignment | not modelled | 11.1 | 12 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> cmclc;<br><b>PDBTitle:</b> crystal structure of a eukaryotic clc transporter   |
| 93 | <a href="#">c1p84D_</a> | Alignment | not modelled | 11.0 | 10 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> D: <b>PDB Molecule:</b> cytochrome c1, heme protein;<br><b>PDBTitle:</b> hdbt inhibited yeast cytochrome bc1 complex  |
| 94 | <a href="#">c3iyzA_</a> | Alignment | not modelled | 10.9 | 18 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> aquaporin-4;<br><b>PDBTitle:</b> structure of aquaporin-4 s180d mutant at 10.0 a resolution from2 electron micrograph  |
| 95 | <a href="#">c5lnko_</a> | Alignment | not modelled | 10.9 | 17 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> O: <b>PDB Molecule:</b><br><b>PDBTitle:</b> entire ovine respiratory complex i  |
| 96 | <a href="#">c5dirD_</a> | Alignment | not modelled | 10.8 | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> D: <b>PDB Molecule:</b> lipoprotein signal peptidase;<br><b>PDBTitle:</b> membrane protein at 2.8 angstroms  |
| 97 | <a href="#">c5l2bc_</a> | Alignment | not modelled | 10.8 | 16 | <b>PDB header:</b> transport protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> nucleoside permease;<br><b>PDBTitle:</b> structure of cntnw n149s, e332a in an outward-facing state  |
| 98 | <a href="#">c3llqB_</a> | Alignment | not modelled | 10.7 | 11 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> aquaporin z 2;<br><b>PDBTitle:</b> aquaporin structure from plant pathogen agrobacterium tumefaciens  |
| 99 | <a href="#">c3j8eG_</a> | Alignment | not modelled | 10.7 | 9  | <b>PDB header:</b> transport protein/isomerase<br><b>Chain:</b> G: <b>PDB Molecule:</b> ryanodine receptor 1;<br><b>PDBTitle:</b> cryo-em structure of ryanodine receptor/calstabin-2 complex  |