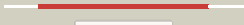
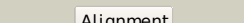
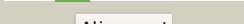
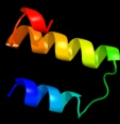
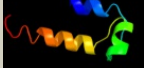
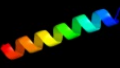
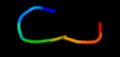


| #  | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                                                      |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c3k07A_</a> |  Alignment   |    | 100.0      | 10     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> cation efflux system protein cusa;<br><b>PDBTitle:</b> crystal structure of cusa                                                                                                                            |
| 2  | <a href="#">cloy8A_</a> |  Alignment   |    | 100.0      | 13     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> acriflavine resistance protein b;<br><b>PDBTitle:</b> structural basis of multiple drug binding capacity of the acrb2 multidrug efflux pump                                                                  |
| 3  | <a href="#">c3aqpB_</a> |  Alignment   |    | 100.0      | 36     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable secdf protein-export membrane protein;<br><b>PDBTitle:</b> crystal structure of secdf, a translocon-associated membrane protein,2 from thermus thrmophilus                                          |
| 4  | <a href="#">dliwga8</a> |  Alignment   |   | 100.0      | 17     | <b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain<br><b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain<br><b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain                                                                |
| 5  | <a href="#">dliwga7</a> |  Alignment |  | 99.9       | 15     | <b>Fold:</b> Multidrug efflux transporter AcrB transmembrane domain<br><b>Superfamily:</b> Multidrug efflux transporter AcrB transmembrane domain<br><b>Family:</b> Multidrug efflux transporter AcrB transmembrane domain                                                                |
| 6  | <a href="#">c3aqpD_</a> |  Alignment |  | 99.7       | 34     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> probable secdf protein-export membrane protein;<br><b>PDBTitle:</b> structure and function of a membrane component secdf that enhances2 protein export                                                       |
| 7  | <a href="#">dliwga6</a> |  Alignment |  | 98.7       | 6      | <b>Fold:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains<br><b>Superfamily:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains<br><b>Family:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains |
| 8  | <a href="#">dliwga5</a> |  Alignment |  | 95.8       | 8      | <b>Fold:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains<br><b>Superfamily:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains<br><b>Family:</b> Multidrug efflux transporter AcrB TolC docking domain; DN and DC subdomains |
| 9  | <a href="#">dliwga4</a> |  Alignment |  | 95.2       | 10     | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains<br><b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains                                                     |
| 10 | <a href="#">dliwga2</a> |  Alignment |  | 94.5       | 6      | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains<br><b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains                                                     |
| 11 | <a href="#">dliwga1</a> |  Alignment |  | 59.5       | 7      | <b>Fold:</b> Ferredoxin-like<br><b>Superfamily:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains<br><b>Family:</b> Multidrug efflux transporter AcrB pore domain; PN1, PN2, PC1 and PC2 subdomains                                                     |

|    |                         |           |                                                                                     |      |    |                                                                                                                                                                                                                                                                                                  |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|------|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c1ciiA_</a> | Alignment |     | 41.1 | 19 | <b>PDB header:</b> transmembrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> colicin ia;<br><b>PDBTitle:</b> colicin ia                                                                                                                                                                     |
| 13 | <a href="#">c2bbjB_</a> | Alignment |    | 34.8 | 8  | <b>PDB header:</b> metal transport/membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein;<br><b>PDBTitle:</b> crystal structure of the cora mg2+ transporter                                                                                       |
| 14 | <a href="#">d2r6gf1</a> | Alignment |    | 15.4 | 19 | <b>Fold:</b> MalF N-terminal region-like<br><b>Superfamily:</b> MalF N-terminal region-like<br><b>Family:</b> MalF N-terminal region-like                                                                                                                                                        |
| 15 | <a href="#">c2yvxD_</a> | Alignment |    | 14.7 | 13 | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> mg2+ transporter mgte;<br><b>PDBTitle:</b> crystal structure of magnesium transporter mgte                                                                                                                         |
| 16 | <a href="#">c2qtsA_</a> | Alignment |    | 10.9 | 30 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> acid-sensing ion channel;<br><b>PDBTitle:</b> structure of an acid-sensing ion channel 1 at 1.9 a resolution and low2 ph                                                                                            |
| 17 | <a href="#">d2iuba2</a> | Alignment |    | 8.3  | 11 | <b>Fold:</b> Transmembrane helix hairpin<br><b>Superfamily:</b> Magnesium transport protein CorA, transmembrane region<br><b>Family:</b> Magnesium transport protein CorA, transmembrane region                                                                                                  |
| 18 | <a href="#">d1pbyc_</a> | Alignment |  | 7.0  | 63 | <b>Fold:</b> Non-globular all-alpha subunits of globular proteins<br><b>Superfamily:</b> Quinohemoprotein amine dehydrogenase C chain<br><b>Family:</b> Quinohemoprotein amine dehydrogenase C chain                                                                                             |
| 19 | <a href="#">d1xmeb2</a> | Alignment |  | 6.8  | 22 | <b>Fold:</b> Transmembrane helix hairpin<br><b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region<br><b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region                                                                                          |
| 20 | <a href="#">d1jmxg_</a> | Alignment |  | 6.3  | 38 | <b>Fold:</b> Non-globular all-alpha subunits of globular proteins<br><b>Superfamily:</b> Quinohemoprotein amine dehydrogenase C chain<br><b>Family:</b> Quinohemoprotein amine dehydrogenase C chain                                                                                             |
| 21 | <a href="#">c2xznC_</a> | Alignment | not modelled                                                                        | 6.2  | 13 | <b>PDB header:</b> ribosome<br><b>Chain:</b> C: <b>PDB Molecule:</b> kh domain containing protein;<br><b>PDBTitle:</b> 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 |
| 22 | <a href="#">d2axte1</a> | Alignment | not modelled                                                                        | 6.2  | 12 | <b>Fold:</b> Single transmembrane helix<br><b>Superfamily:</b> Cytochrome b559 subunits<br><b>Family:</b> Cytochrome b559 subunits                                                                                                                                                               |