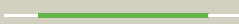


| #  | Template                | Alignment Coverage                                                                            | 3D Model                                                                            | Confidence | % i.d. | Template Information                                                                                                                                                                                                                                             |
|----|-------------------------|-----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|------------|--------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1  | <a href="#">c2vpzG_</a> |  Alignment   |    | 100.0      | 22     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G: <b>PDB Molecule:</b> hypothetical membrane spanning protein;<br><b>PDBTitle:</b> polysulfide reductase native structure                                                                                    |
| 2  | <a href="#">c2w8aC_</a> |  Alignment   |    | 53.3       | 11     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> glycine betaine transporter betp;<br><b>PDBTitle:</b> crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate |
| 3  | <a href="#">c3hfxA_</a> |  Alignment   |    | 24.9       | 11     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> l-carnitine/gamma-butyrobetaine antiporter;<br><b>PDBTitle:</b> crystal structure of carnitine transporter                                                                         |
| 4  | <a href="#">d1xmea1</a> |  Alignment   |    | 22.4       | 10     | <b>Fold:</b> Cytochrome c oxidase subunit I-like<br><b>Superfamily:</b> Cytochrome c oxidase subunit I-like<br><b>Family:</b> Cytochrome c oxidase subunit I-like                                                                                                |
| 5  | <a href="#">c3eh4A_</a> |  Alignment |  | 18.3       | 10     | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c oxidase subunit 1;<br><b>PDBTitle:</b> structure of the reduced form of cytochrome ba3 oxidase from thermus2 thermophilus                                                |
| 6  | <a href="#">d1ejxb_</a> |  Alignment |  | 7.7        | 38     | <b>Fold:</b> beta-clip<br><b>Superfamily:</b> Urease, beta-subunit<br><b>Family:</b> Urease, beta-subunit                                                                                                                                                        |
| 7  | <a href="#">c2a5yA_</a> |  Alignment |  | 7.4        | 15     | <b>PDB header:</b> apoptosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> apoptosis regulator ced-9;<br><b>PDBTitle:</b> structure of a ced-4/ced-9 complex                                                                                                          |
| 8  | <a href="#">d1zy3a1</a> |  Alignment |  | 7.3        | 20     | <b>Fold:</b> Toxins' membrane translocation domains<br><b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death<br><b>Family:</b> Bcl-2 inhibitors of programmed cell death                                                                                 |
| 9  | <a href="#">d1ysga1</a> |  Alignment |  | 7.2        | 15     | <b>Fold:</b> Toxins' membrane translocation domains<br><b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death<br><b>Family:</b> Bcl-2 inhibitors of programmed cell death                                                                                 |
| 10 | <a href="#">c2yv6A_</a> |  Alignment |  | 6.8        | 15     | <b>PDB header:</b> apoptosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> bcl-2 homologous antagonist/killer;<br><b>PDBTitle:</b> crystal structure of human bcl-2 family protein bak                                                                                |
| 11 | <a href="#">d1bxa_</a>  |  Alignment |  | 6.8        | 15     | <b>Fold:</b> Toxins' membrane translocation domains<br><b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death<br><b>Family:</b> Bcl-2 inhibitors of programmed cell death                                                                                 |

|    |                         |           |                                                                                     |     |    |                                                                                                                                                                                                                                                  |
|----|-------------------------|-----------|-------------------------------------------------------------------------------------|-----|----|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 12 | <a href="#">c2zt9E_</a> | Alignment |    | 6.6 | 35 | <b>PDB header:</b> photosynthesis<br><b>Chain:</b> E: <b>PDB Molecule:</b> cytochrome b6-f complex subunit 6;<br><b>PDBTitle:</b> crystal structure of the cytochrome b6f complex from nostoc sp. pcc2 7120                                      |
| 13 | <a href="#">dle9ya1</a> | Alignment |    | 6.6 | 50 | <b>Fold:</b> beta-clip<br><b>Superfamily:</b> Urease, beta-subunit<br><b>Family:</b> Urease, beta-subunit                                                                                                                                        |
| 14 | <a href="#">d4ubpb_</a> | Alignment |    | 6.5 | 38 | <b>Fold:</b> beta-clip<br><b>Superfamily:</b> Urease, beta-subunit<br><b>Family:</b> Urease, beta-subunit                                                                                                                                        |
| 15 | <a href="#">c2o2fA_</a> | Alignment |    | 6.5 | 15 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> apoptosis regulator bcl-2;<br><b>PDBTitle:</b> solution structure of the anti-apoptotic protein bcl-2 in2 complex with an acyl-sulfonamide-based ligand                    |
| 16 | <a href="#">c3rkoA_</a> | Alignment |    | 6.3 | 11 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> A: <b>PDB Molecule:</b> nadh-quinone oxidoreductase subunit a;<br><b>PDBTitle:</b> crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution |
| 17 | <a href="#">c3chxF_</a> | Alignment |    | 6.2 | 17 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> pmox;<br><b>PDBTitle:</b> crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo)                                            |
| 18 | <a href="#">c2xa0A_</a> | Alignment |  | 6.1 | 15 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> apoptosis regulator bcl-2;<br><b>PDBTitle:</b> crystal structure of bcl-2 in complex with a bax bh32 peptide                                                               |
| 19 | <a href="#">dlg5ma_</a> | Alignment |  | 6.1 | 15 | <b>Fold:</b> Toxins' membrane translocation domains<br><b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death<br><b>Family:</b> Bcl-2 inhibitors of programmed cell death                                                                 |
| 20 | <a href="#">dlpq1a_</a> | Alignment |  | 6.1 | 15 | <b>Fold:</b> Toxins' membrane translocation domains<br><b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death<br><b>Family:</b> Bcl-2 inhibitors of programmed cell death                                                                 |
| 21 | <a href="#">dl00la_</a> | Alignment | not modelled                                                                        | 6.0 | 20 | <b>Fold:</b> Toxins' membrane translocation domains<br><b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death<br><b>Family:</b> Bcl-2 inhibitors of programmed cell death                                                                 |
| 22 | <a href="#">c3qbrA_</a> | Alignment | not modelled                                                                        | 6.0 | 33 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> sjchgc06286 protein;<br><b>PDBTitle:</b> bakbh3 in complex with sjc                                                                                                        |
| 23 | <a href="#">dl0hua_</a> | Alignment | not modelled                                                                        | 5.7 | 14 | <b>Fold:</b> Toxins' membrane translocation domains<br><b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death<br><b>Family:</b> Bcl-2 inhibitors of programmed cell death                                                                 |
| 24 | <a href="#">dlak0a_</a> | Alignment | not modelled                                                                        | 5.6 | 16 | <b>Fold:</b> Phospholipase C/P1 nuclease<br><b>Superfamily:</b> Phospholipase C/P1 nuclease<br><b>Family:</b> P1 nuclease                                                                                                                        |
| 25 | <a href="#">d2ponb1</a> | Alignment | not modelled                                                                        | 5.5 | 15 | <b>Fold:</b> Toxins' membrane translocation domains<br><b>Superfamily:</b> Bcl-2 inhibitors of programmed cell death<br><b>Family:</b> Bcl-2 inhibitors of programmed cell death                                                                 |
| 26 | <a href="#">c1m56G_</a> | Alignment | not modelled                                                                        | 5.4 | 10 | <b>PDB header:</b> oxidoreductase<br><b>Chain:</b> G: <b>PDB Molecule:</b> cytochrome c oxidase;<br><b>PDBTitle:</b> structure of cytochrome c oxidase from rhodobactor2 sphaeroides (wild type)                                                 |