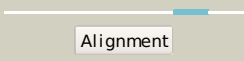

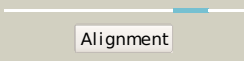
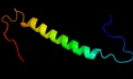
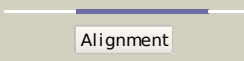

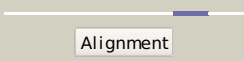
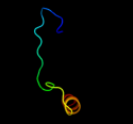
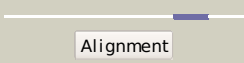
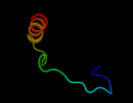
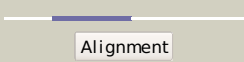

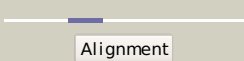

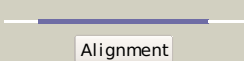

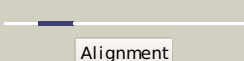

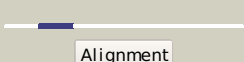
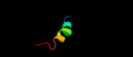
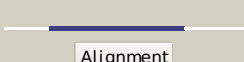

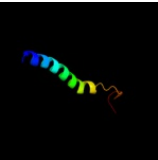
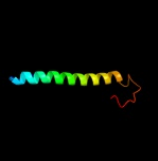
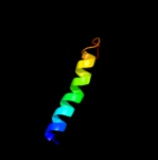



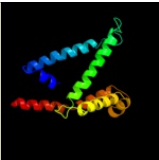
| #  | Template                | Alignment Coverage   | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|--|---|------------|--------|--|
| 1  | <a href="#">c1qleB_</a> | <br>Alignment   |    | 36.5       | 16     | <b>PDB header:</b> oxidoreductase/immune system<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase polypeptide ii;<br><b>PDBTitle:</b> cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment |
| 2  | <a href="#">c1ar1B_</a> | <br>Alignment   |    | 36.5       | 16     | <b>PDB header:</b> complex (oxidoreductase/antibody)<br><b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c oxidase;<br><b>PDBTitle:</b> structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment                       |
| 3  | <a href="#">c3m7bA_</a> | <br>Alignment   |    | 17.6       | 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   |
| 4  | <a href="#">d1ejxc2</a> | <br>Alignment   |    | 16.1       | 25     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Metallo-dependent hydrolases<br><b>Family:</b> alpha-subunit of urease, catalytic domain   |
| 5  | <a href="#">d1e9yb2</a> | <br>Alignment |  | 15.3       | 16     | <b>Fold:</b> TIM beta/alpha-barrel<br><b>Superfamily:</b> Metallo-dependent hydrolases<br><b>Family:</b> alpha-subunit of urease, catalytic domain   |
| 6  | <a href="#">d2r6gf2</a> | <br>Alignment |  | 12.6       | 10     | <b>Fold:</b> Metl-like<br><b>Superfamily:</b> Metl-like<br><b>Family:</b> Metl-like  |
| 7  | <a href="#">d2hkua2</a> | <br>Alignment |  | 11.7       | 25     | <b>Fold:</b> Tetracyclin repressor-like, C-terminal domain<br><b>Superfamily:</b> Tetracyclin repressor-like, C-terminal domain<br><b>Family:</b> Tetracyclin repressor-like, C-terminal domain  |
| 8  | <a href="#">c2xq2A_</a> | <br>Alignment |  | 10.7       | 13     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter;<br><b>PDBTitle:</b> structure of the k294a mutant of vsglt   |
| 9  | <a href="#">c2ktaA_</a> | <br>Alignment |  | 8.9        | 21     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative helicase;<br><b>PDBTitle:</b> solution nmr structure of a domain of protein a6ky75 from bacteroides2 vulgatus, northeast structural genomics target bvr106a   |
| 10 | <a href="#">c2f3oB_</a> | <br>Alignment |  | 8.0        | 5      | <b>PDB header:</b> unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> pyruvate formate-lyase 2;<br><b>PDBTitle:</b> crystal structure of a glycyl radical enzyme from archaeoglobus2 fulgidus   |
| 11 | <a href="#">c3fh6F_</a> | <br>Alignment |  | 7.9        | 9      | <b>PDB header:</b> transport protein<br><b>Chain:</b> F: <b>PDB Molecule:</b> maltose transport system permease protein malf;<br><b>PDBTitle:</b> crystal structure of the resting state maltose transporter from e.2 coli   |

|    |                         |           |   |     |    |  |
|----|-------------------------|-----------|---|-----|----|--|
| 12 | <a href="#">c2kncA_</a> | Alignment |   | 7.3 | 15 | <b>PDB header:</b> cell adhesion<br><b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB;<br><b>PDBTitle:</b> platelet integrin alphaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex  |
| 13 | <a href="#">d3dtub2</a> | Alignment |  | 6.7 | 20 | <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  |
| 14 | <a href="#">d2iuba2</a> | Alignment |  | 6.2 | 17 | <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  |
| 15 | <a href="#">c2v5iA_</a> | Alignment |  | 5.9 | 25 | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> salmonella typhimurium db7155 bacteriophage det7<br><b>PDBTitle:</b> structure of the receptor-binding protein of bacteriophage2 det7: a podoviral tailspike in a myovirus |

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[c3hfxA](#)

Alignment



5.6

13

**PDB header:**transport protein  
**Chain:** A: **PDB Molecule:**l-carnitine/gamma-butyrobetaine antiporter;  
**PDBTitle:** crystal structure of carnitine transporter