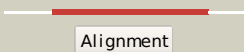

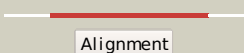


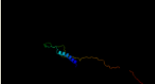
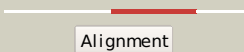
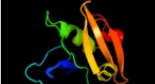
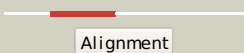


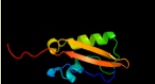




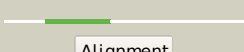

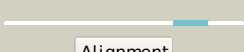
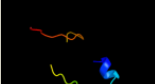
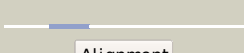







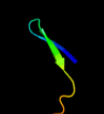
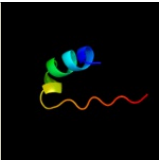


| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information   |
|----|-------------------------|---|---|------------|--------|--|
| 1  | <a href="#">c2vh1A_</a> |  Alignment   |    | 100.0      | 100    | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsq;<br><b>PDBTitle:</b> crystal structure of bacterial cell division protein ftsq2 from e.coli  |
| 2  | <a href="#">c2vh2A_</a> |  Alignment   |    | 100.0      | 72     | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A: <b>PDB Molecule:</b> cell division protein ftsq;<br><b>PDBTitle:</b> crystal structure of cell division protein ftsq from 2 yersinia enterocolitica  |
| 3  | <a href="#">c3j00Z_</a> |  Alignment   |    | 99.8       | 89     | <b>PDB header:</b> ribosome/ribosomal protein<br><b>Chain:</b> Z: <b>PDB Molecule:</b> cell division protein ftsq;<br><b>PDBTitle:</b> structure of the ribosome-secE complex in the membrane environment  |
| 4  | <a href="#">c2aljA_</a> |  Alignment   |    | 98.6       | 12     | <b>PDB header:</b> cell cycle<br><b>Chain:</b> A: <b>PDB Molecule:</b> cell-division initiation protein;<br><b>PDBTitle:</b> structure of the cis conformer of the major extracytoplasmic domain of the bacterial cell division protein DivB from Geobacillus stearothermophilus |
| 5  | <a href="#">c2qcZA_</a> |  Alignment |  | 94.0       | 14     | <b>PDB header:</b> membrane protein, protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein assembly factor YaeT;<br><b>PDBTitle:</b> structure of N-terminal domain of E. coli YaeT  |
| 6  | <a href="#">c3efcA_</a> |  Alignment |  | 92.6       | 14     | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein assembly factor YaeT;<br><b>PDBTitle:</b> crystal structure of YaeT periplasmic domain   |
| 7  | <a href="#">c2x8xX_</a> |  Alignment |  | 79.3       | 12     | <b>PDB header:</b> chaperone<br><b>Chain:</b> X: <b>PDB Molecule:</b> tir1789 protein;<br><b>PDBTitle:</b> structure of the N-terminal domain of Omp85 from the thermophilic cyanobacterium Thermosynechococcus elongatus  |
| 8  | <a href="#">c2v9hA_</a> |  Alignment |  | 61.4       | 14     | <b>PDB header:</b> protein-binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein assembly factor YaeT;<br><b>PDBTitle:</b> solution structure of an Escherichia coli YaeT tandem POTRA2 domain   |
| 9  | <a href="#">c3og5A_</a> |  Alignment |  | 52.2       | 16     | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane protein assembly complex, YaeT protein;<br><b>PDBTitle:</b> crystal structure of Bama POTRA45 tandem  |
| 10 | <a href="#">c3f41B_</a> |  Alignment |  | 39.2       | 27     | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> phytase;<br><b>PDBTitle:</b> structure of the tandemly repeated protein tyrosine 2 phosphatase-like phytase from Mitsuokella multitacida   |
| 11 | <a href="#">c2qdzA_</a> |  Alignment |  | 20.4       | 4      | <b>PDB header:</b> protein transport<br><b>Chain:</b> A: <b>PDB Molecule:</b> tpsb transporter FhaC;<br><b>PDBTitle:</b> structure of the membrane protein FhaC: a member of the Omp85/tpsb transporter family   |

|    |                         |           |   |      |    |   |
|----|-------------------------|-----------|---|------|----|---|
| 12 | <a href="#">c2cw5B_</a> | Alignment |     | 13.4 | 17 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> bacterial fluorinating enzyme homolog;<br><b>PDBTitle:</b> crystal structure of a conserved hypothetical protein from2 thermus thermophilus hb8 |
| 13 | <a href="#">c3mc8A_</a> | Alignment |    | 12.7 | 11 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> alr2269 protein;<br><b>PDBTitle:</b> potra1-3 of the periplasmic domain of omp85 from anabaena   |
| 14 | <a href="#">d1q1va_</a> | Alignment |    | 12.5 | 11 | <b>Fold:</b> Another 3-helical bundle<br><b>Superfamily:</b> DEK C-terminal domain<br><b>Family:</b> DEK C-terminal domain  |
| 15 | <a href="#">c3lnoA_</a> | Alignment |    | 10.6 | 17 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> putative uncharacterized protein;<br><b>PDBTitle:</b> crystal structure of domain of unknown function duf59 from2 bacillus anthracis                                 |
| 16 | <a href="#">c3jruB_</a> | Alignment |    | 8.5  | 11 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> probable cytosol aminopeptidase;<br><b>PDBTitle:</b> crystal structure of leucyl aminopeptidase (pepa) from xoo0834,2 xanthomonas oryzae pv. oryzae kacc10331               |
| 17 | <a href="#">d1qyta2</a> | Alignment |    | 7.6  | 15 | <b>Fold:</b> Phosphorylase/hydrolase-like<br><b>Superfamily:</b> Zn-dependent exopeptidases<br><b>Family:</b> Leucine aminopeptidase, C-terminal domain   |
| 18 | <a href="#">c3m92B_</a> | Alignment |  | 6.6  | 10 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> B: <b>PDB Molecule:</b> protein ycin;<br><b>PDBTitle:</b> the structure of ycin, an unchracterized protein from shigella2 flexneri.                                     |

19 [d1uwda\\_](#)

Alignment



5.4

13

**Fold:**Alpha-lytic protease prodomain-like  
**Superfamily:**Fe-S cluster assembly (FSCA) domain-like  
**Family:**PaaD-like