

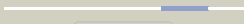
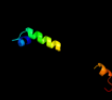

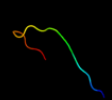



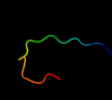


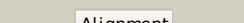











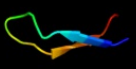





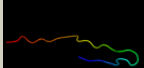


| #  | Template                | Alignment Coverage  | 3D Model  | Confidence | % i.d. | Template Information  |
|----|-------------------------|---|---|------------|--------|---|
| 1  | <a href="#">c3bjqA_</a> |  Alignment   |    | 25.0       | 23     | <b>PDB header:</b> viral protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> phage-related protein;<br><b>PDBTitle:</b> crystal structure of a phage-related protein (bb3626) from bordetella2 bronchiseptica rb50 at 2.05 a resolution                      |
| 2  | <a href="#">c2e52A_</a> |  Alignment   |    | 20.4       | 26     | <b>PDB header:</b> hydrolase/dna<br><b>Chain:</b> A: <b>PDB Molecule:</b> type ii restriction enzyme hindiii;<br><b>PDBTitle:</b> crystal structural analysis of hindiii restriction endonuclease in2 complex with cognate dna at 2.0 angstrom resolution |
| 3  | <a href="#">d1m9za_</a> |  Alignment   |    | 18.2       | 12     | <b>Fold:</b> Snake toxin-like<br><b>Superfamily:</b> Snake toxin-like<br><b>Family:</b> Extracellular domain of cell surface receptors  |
| 4  | <a href="#">d1ks6a_</a> |  Alignment   |    | 18.0       | 29     | <b>Fold:</b> Snake toxin-like<br><b>Superfamily:</b> Snake toxin-like<br><b>Family:</b> Extracellular domain of cell surface receptors  |
| 5  | <a href="#">d2pjyb1</a> |  Alignment |  | 17.7       | 12     | <b>Fold:</b> Snake toxin-like<br><b>Superfamily:</b> Snake toxin-like<br><b>Family:</b> Extracellular domain of cell surface receptors  |
| 6  | <a href="#">d1ploa_</a> |  Alignment |  | 16.7       | 12     | <b>Fold:</b> Snake toxin-like<br><b>Superfamily:</b> Snake toxin-like<br><b>Family:</b> Extracellular domain of cell surface receptors  |
| 7  | <a href="#">c2kgmA_</a> |  Alignment |  | 14.9       | 41     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein ste5;<br><b>PDBTitle:</b> solution structure of ste5pm24 in sds micelle   |
| 8  | <a href="#">c2l4uA_</a> |  Alignment |  | 11.8       | 41     | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> 24mer peptide from protein ste5;<br><b>PDBTitle:</b> solution structure of ste5pm24 in the presence of sds micelle  |
| 9  | <a href="#">c1xk5A_</a> |  Alignment |  | 9.3        | 38     | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> snurportin-1;<br><b>PDBTitle:</b> crystal structure of the m3g-cap-binding domain of2 snurportin1 in complex with a m3gpppg-cap dinucleotide                                |
| 10 | <a href="#">d1ukfa_</a> |  Alignment |  | 9.0        | 19     | <b>Fold:</b> Cysteine proteinases<br><b>Superfamily:</b> Cysteine proteinases<br><b>Family:</b> Avirulence protein Avrpph3  |
| 11 | <a href="#">d2fcwa1</a> |  Alignment |  | 8.9        | 32     | <b>Fold:</b> RAP domain-like<br><b>Superfamily:</b> RAP domain-like<br><b>Family:</b> RAP domain  |

|    |                         |           |   |     |    |   |
|----|-------------------------|-----------|---|-----|----|---|
| 12 | <a href="#">c3gb8B_</a> | Alignment |     | 8.0 | 38 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> snurportin-1;<br><b>PDBTitle:</b> crystal structure of crm1/snurportin-1 complex  |
| 13 | <a href="#">c3gjeE_</a> | Alignment |    | 7.6 | 38 | <b>PDB header:</b> protein transport<br><b>Chain:</b> E: <b>PDB Molecule:</b> snurportin-1;<br><b>PDBTitle:</b> crystal structure of the nuclear export complex crm1-2 snurportin1-rangtp                                       |
| 14 | <a href="#">c3h7hA_</a> | Alignment |    | 7.3 | 41 | <b>PDB header:</b> transcription<br><b>Chain:</b> A: <b>PDB Molecule:</b> transcription elongation factor spt4;<br><b>PDBTitle:</b> crystal structure of the human transcription elongation factor dsif,2 hspt4/hspt5 (176-273) |
| 15 | <a href="#">c2zxrA_</a> | Alignment |    | 6.3 | 44 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> A: <b>PDB Molecule:</b> single-stranded dna specific exonuclease recj;<br><b>PDBTitle:</b> crystal structure of recj in complex with mg2+ from thermus2 thermophilus hb8          |
| 16 | <a href="#">d2foka1</a> | Alignment |    | 6.2 | 16 | <b>Fold:</b> DNA/RNA-binding 3-helical bundle<br><b>Superfamily:</b> "Winged helix" DNA-binding domain<br><b>Family:</b> Restriction endonuclease FokI, N-terminal (recognition) domain   |
| 17 | <a href="#">c1txkA_</a> | Alignment |   | 6.2 | 28 | <b>PDB header:</b> biosynthetic protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> glucans biosynthesis protein g;<br><b>PDBTitle:</b> crystal structure of escherichia coli opgg   |
| 18 | <a href="#">d1f44a1</a> | Alignment |  | 6.1 | 21 | <b>Fold:</b> SAM domain-like<br><b>Superfamily:</b> lambda integrase-like, N-terminal domain<br><b>Family:</b> lambda integrase-like, N-terminal domain   |
| 19 | <a href="#">d1j0sa_</a> | Alignment |  | 6.1 | 12 | <b>Fold:</b> beta-Trefoil<br><b>Superfamily:</b> Cytokine<br><b>Family:</b> Interleukin-1 (IL-1)  |
| 20 | <a href="#">d1txka2</a> | Alignment |  | 6.1 | 28 | <b>Fold:</b> Supersandwich<br><b>Superfamily:</b> Galactose mutarotase-like<br><b>Family:</b> MdoG-like   |
| 21 | <a href="#">d2ftua1</a> | Alignment | not modelled  | 6.0 | 32 | <b>Fold:</b> RAP domain-like<br><b>Superfamily:</b> RAP domain-like<br><b>Family:</b> RAP domain  |
| 22 | <a href="#">c2kgnA_</a> | Alignment | not modelled  | 6.0 | 41 | <b>PDB header:</b> signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein ste5;<br><b>PDBTitle:</b> solution structure of ste5pm24 in the zwitterionic dpc2 micelle   |
| 23 | <a href="#">c2hyij_</a> | Alignment | not modelled  | 5.7 | 29 | <b>PDB header:</b> hydrolase/rna binding protein/rna<br><b>Chain:</b> J: <b>PDB Molecule:</b> protein casc3;<br><b>PDBTitle:</b> structure of the human exon junction complex with a trapped2 dead-box helicase bound to rna    |