




















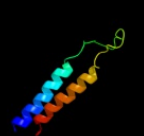
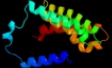





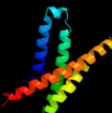
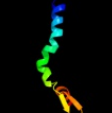
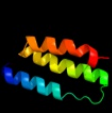


| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|----|-------------------------|---|---|------------|--------|--|
| 1 | c2xq2A_ |  Alignment |  | 100.0 | 16 | PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsplt |
| 2 | c3dh4A_ |  Alignment |  | 100.0 | 15 | PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus |
| 3 | c2jlnA_ |  Alignment |  | 99.7 | 11 | PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter |
| 4 | c3giaA_ |  Alignment |  | 99.7 | 10 | PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter |
| 5 | c3lrcC_ |  Alignment |  | 99.3 | 12 | PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1) |
| 6 | c2w8aC_ |  Alignment |  | 98.2 | 10 | PDB header: membrane protein Chain: C: PDB Molecule: glycine betaine transporter betp; PDBTitle: crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate |
| 7 | c3hfxA_ |  Alignment |  | 97.6 | 13 | PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter |
| 8 | d2a65a1 |  Alignment |  | 96.8 | 12 | Fold: SNF-like Superfamily: SNF-like Family: SNF-like |
| 9 | c3b9yA_ |  Alignment |  | 29.7 | 17 | PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein |
| 10 | c3rlbA_ |  Alignment |  | 22.4 | 20 | PDB header: thiamine-binding protein Chain: A: PDB Molecule: thit; PDBTitle: crystal structure at 2.0 a of the s-component for thiamin from an ecf-2 type abc transporter |
| 11 | c3mk7F_ |  Alignment |  | 14.1 | 19 | PDB header: oxidoreductase Chain: F: PDB Molecule: cytochrome c oxidase, cbb3-type, subunit p; PDBTitle: the structure of cbb3 cytochrome oxidase |

| | | | | | | |
|----|-------------------------|-----------|---|-----|----|---|
| 12 | c3hd6A_ | Alignment |  | 8.7 | 10 | PDB header: membrane protein, transport protein Chain: A: PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg |
| 13 | c2k9yB_ | Alignment |  | 7.7 | 26 | PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0 |
| 14 | c2k9yA_ | Alignment |  | 7.7 | 26 | PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0 |
| 15 | d1u7ga_ | Alignment |  | 7.7 | 16 | Fold: Ammonium transporter Superfamily: Ammonium transporter Family: Ammonium transporter |
| 16 | c4a2nB_ | Alignment |  | 6.4 | 9 | PDB header: transferase Chain: B: PDB Molecule: isoprenylcysteine carboxyl methyltransferase; PDBTitle: crystal structure of ma-icmt |
| 17 | c3chxF_ | Alignment |  | 5.3 | 22 | PDB header: membrane protein Chain: F: PDB Molecule: pmoa; PDBTitle: crystal structure of methylosinus trichosporium ob3b2 particulate methane monooxygenase (pmmo) |
| 18 | c3p5nA_ | Alignment |  | 5.3 | 21 | PDB header: transport protein Chain: A: PDB Molecule: riboflavin uptake protein; PDBTitle: structure and mechanism of the s component of a bacterial ecf2 transporter |
| 19 | c1yewF_ | Alignment |  | 5.2 | 20 | PDB header: oxidoreductase, membrane protein Chain: F: PDB Molecule: particulate methane monooxygenase, a subunit; PDBTitle: crystal structure of particulate methane monooxygenase |
| 20 | c1a87A_ | Alignment |  | 5.2 | 13 | PDB header: bacteriocin Chain: A: PDB Molecule: colicin n; PDBTitle: colicin n |
| 21 | d1a87a_ | Alignment | not modelled | 5.2 | 13 | Fold: Toxins' membrane translocation domains Superfamily: Colicin Family: Colicin |
| 22 | c3o7xC_ | Alignment | not modelled | 5.1 | 12 | PDB header: rna binding protein Chain: C: PDB Molecule: piwi-like protein 2; PDBTitle: crystal structure of human hili paz domain |