


















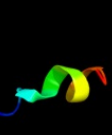


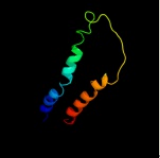
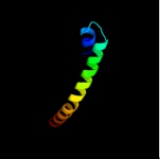
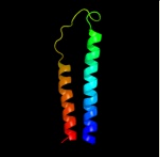

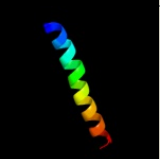
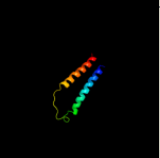
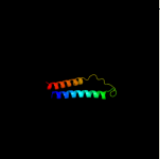

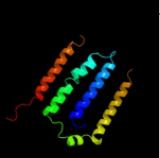


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3giaA_	 Alignment		100.0	15	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
2	c3lrcC_	 Alignment		100.0	21	PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
3	c2jlnA_	 Alignment		100.0	9	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
4	c2xq2A_	 Alignment		99.6	10	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vsgl
5	c3dh4A_	 Alignment		99.5	10	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
6	d2a65a1	 Alignment		98.6	14	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
7	c2w8aC_	 Alignment		98.1	12	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
8	c3hfxA_	 Alignment		96.1	8	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
9	d1fftb2	 Alignment		56.0	12	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
10	c2l1nA_	 Alignment		17.7	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of the protein yp_399305.1
11	c2kncA_	 Alignment		17.2	9	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiib; PDBTitle: platelet integrin alfa-iiib-beta3 transmembrane-cytoplasmic2 heterocomplex

12	c1fftG_	Alignment		14.9	12	PDB header: oxidoreductase Chain: G: PDB Molecule: ubiquinol oxidase; PDBTitle: the structure of ubiquinol oxidase from escherichia coli
13	c3qnqD_	Alignment		13.2	11	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the 2 n,n'-diacetylchitobiose-specific phosphotransferase system
14	c1m57H_	Alignment		12.0	14	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c oxidase; PDBTitle: structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant)
15	c1zxaB_	Alignment		8.7	40	PDB header: transferase Chain: B: PDB Molecule: cgmp-dependent protein kinase 1, alpha isozyme; PDBTitle: solution structure of the coiled-coil domain of cgmp-2 dependent protein kinase ia
16	c2rddB_	Alignment		7.7	4	PDB header: membrane protein/transport protein Chain: B: PDB Molecule: upf0092 membrane protein yajc; PDBTitle: x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
17	c1qlqB_	Alignment		7.6	15	PDB header: oxidoreductase/immune system Chain: B: PDB Molecule: cytochrome c oxidase polypeptide ii; PDBTitle: cryo-structure of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
18	c1ar1B_	Alignment		7.6	15	PDB header: complex (oxidoreductase/antibody) Chain: B: PDB Molecule: cytochrome c oxidase; PDBTitle: structure at 2.7 angstrom resolution of the paracoccus2 denitrificans two-subunit cytochrome c oxidase complexed3 with an antibody fv fragment
19	c2bbjB_	Alignment		7.5	10	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
20	c3rkoF_	Alignment		7.3	10	PDB header: oxidoreductase Chain: F: PDB Molecule: nadh-quinone oxidoreductase subunit j; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
21	c3b8eC_	Alignment	not modelled	7.0	11	PDB header: hydrolase/transport protein Chain: C: PDB Molecule: sodium/potassium-transporting atpase subunit PDBTitle: crystal structure of the sodium-potassium pump
22	d1iwga8	Alignment	not modelled	6.9	12	Fold: Multidrug efflux transporter AcrB transmembrane domain Superfamily: Multidrug efflux transporter AcrB transmembrane domain Family: Multidrug efflux transporter AcrB transmembrane domain
23	c3ixzA_	Alignment	not modelled	6.5	11	PDB header: hydrolase Chain: A: PDB Molecule: potassium-transporting atpase alpha; PDBTitle: pig gastric h+/k+-atpase complexed with aluminium fluoride
24	d3ehbb2	Alignment	not modelled	6.0	15	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
25	d3dtub2	Alignment	not modelled	5.2	14	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region