

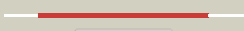




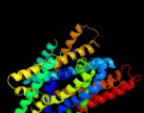











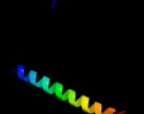




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3giaA_	 Alignment		100.0	12	PDB header: transport protein Chain: A: PDB Molecule: uncharacterized protein mj0609; PDBTitle: crystal structure of apct transporter
2	c3lrcC_	 Alignment		100.0	17	PDB header: transport protein Chain: C: PDB Molecule: arginine/agmatine antiporter; PDBTitle: structure of e. coli adic (p1)
3	c2jlnA_	 Alignment		100.0	10	PDB header: membrane protein Chain: A: PDB Molecule: mhp1; PDBTitle: structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
4	c3dh4A_	 Alignment		99.6	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
5	c2xq2A_	 Alignment		99.6	10	PDB header: transport protein Chain: A: PDB Molecule: sodium/glucose cotransporter; PDBTitle: structure of the k294a mutant of vs9lt
6	d2a65a1	 Alignment		98.0	14	Fold: SNF-like Superfamily: SNF-like Family: SNF-like
7	c2w8aC_	 Alignment		97.6	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	11	PDB header: transport protein Chain: A: PDB Molecule: l-carnitine/gamma-butyrobetaine antiporter; PDBTitle: crystal structure of carnitine transporter
9	c2l2tA_	 Alignment		32.1	7	PDB header: membrane protein Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-4; PDBTitle: solution nmr structure of the erbb4 dimeric membrane domain
10	c2jwaA_	 Alignment		29.3	23	PDB header: transferase Chain: A: PDB Molecule: receptor tyrosine-protein kinase erbb-2; PDBTitle: erbb2 transmembrane segment dimer spatial structure
11	d1fftb2	 Alignment		27.5	5	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region

12	c1m57H_	Alignment		18.6	17	PDB header: oxidoreductase Chain: H: PDB Molecule: cytochrome c oxidase; PDBTitle: structure of cytochrome c oxidase from rhodobacter2 sphaeroides (eq(i-286) mutant)
13	c2bbjB_	Alignment		12.6	13	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
14	c1ar1B_	Alignment		9.8	10	PDB header: complex (oxidoreductase/antibody) Chain: B: PDB Molecule: cytochrome c oxidase; PDBTitle: structure at 2.7 angstrom resolution of the paracoccus denitrificans four-subunit2 cytochrome c oxidase in the completely oxidized state3 complexed with an antibody fv fragment
15	c1qleB_	Alignment		9.8	10	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
16	c2w2eA_	Alignment		8.5	11	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin; PDBTitle: 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqyl, in a closed conformation at ph 3.5
17	c2rm9A_	Alignment		8.1	17	PDB header: neuropeptide Chain: A: PDB Molecule: stressin2b; PDBTitle: stressin2b
18	c4a19X_	Alignment		7.9	24	PDB header: ribosome Chain: X: PDB Molecule: rpl18a; PDBTitle: t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 26s rna and3 proteins of molecule 2.
19	d3ehbb2	Alignment		6.4	9	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
20	c3rkoA_	Alignment		6.4	9	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-quinone oxidoreductase subunit a; PDBTitle: crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
21	c3rkoF_	Alignment	not modelled	5.7	13	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
22	d3dtub2	Alignment	not modelled	5.5	17	Fold: Transmembrane helix hairpin Superfamily: Cytochrome c oxidase subunit II-like, transmembrane region Family: Cytochrome c oxidase subunit II-like, transmembrane region
23	c2rddb_	Alignment	not modelled	5.2	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.