











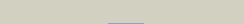









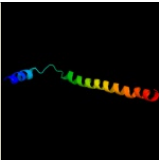
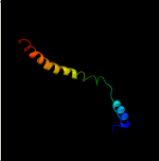
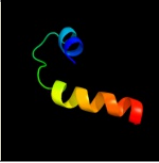


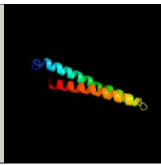
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1otsa_</a>	 Alignment		100.0	100	<b>Fold:</b> Clc chloride channel <b>Superfamily:</b> Clc chloride channel <b>Family:</b> Clc chloride channel
2	<a href="#">c2ht2B_</a>	 Alignment		100.0	100	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> h(+)/cl(-) exchange transporter clca; <b>PDBTitle:</b> structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
3	<a href="#">d1kpla_</a>	 Alignment		100.0	81	<b>Fold:</b> Clc chloride channel <b>Superfamily:</b> Clc chloride channel <b>Family:</b> Clc chloride channel
4	<a href="#">c3nd0A_</a>	 Alignment		100.0	40	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sl10855 protein; <b>PDBTitle:</b> x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
5	<a href="#">c3orgB_</a>	 Alignment		100.0	23	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> cmclc; <b>PDBTitle:</b> crystal structure of a eukaryotic clc transporter
6	<a href="#">c3p5nA_</a>	 Alignment		26.9	21	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> riboflavin uptake protein; <b>PDBTitle:</b> structure and mechanism of the s component of a bacterial ecf2 transporter
7	<a href="#">c2ksfA_</a>	 Alignment		21.4	12	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> sensor protein kdpc; <b>PDBTitle:</b> backbone structure of the membrane domain of e. coli2 histidine kinase receptor kdpc, center for structures of3 membrane proteins (csm) target 4312c
8	<a href="#">d1v54a_</a>	 Alignment		12.9	13	<b>Fold:</b> Cytochrome c oxidase subunit I-like <b>Superfamily:</b> Cytochrome c oxidase subunit I-like <b>Family:</b> Cytochrome c oxidase subunit I-like
9	<a href="#">c3c4rC_</a>	 Alignment		10.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein encoded by2 cryptic prophage
10	<a href="#">c2dw3A_</a>	 Alignment		7.7	40	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> intrinsic membrane protein pufx; <b>PDBTitle:</b> solution structure of the rhodobacter sphaeroides pufx2 membrane protein
11	<a href="#">c3mk7F_</a>	 Alignment		7.5	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> F: <b>PDB Molecule:</b> cytochrome c oxidase, cbb3-type, subunit p; <b>PDBTitle:</b> the structure of cbb3 cytochrome oxidase

12	<a href="#">c3dinD_</a>	Alignment		5.9	11	<b>PDB header:</b> membrane protein, protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> preprotein translocase subunit sece; <b>PDBTitle:</b> crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
13	<a href="#">c2akhZ_</a>	Alignment		5.6	12	<b>PDB header:</b> protein transport <b>Chain:</b> Z: <b>PDB Molecule:</b> preprotein translocase sece subunit; <b>PDBTitle:</b> normal mode-based flexible fitted coordinates of a non-2 translocating secyeg protein-conducting channel into the3 cryo-em map of a secyeg-nascent chain-70s ribosome complex4 from e. coli
14	<a href="#">c2kjfA_</a>	Alignment		5.3	21	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> carnocyclin-a; <b>PDBTitle:</b> the solution structure of the circular bacteriocin2 carnocyclin a (ccla)

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[c2yl4A\\_](#)

Alignment



5.1

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**PDB header:**membrane protein  
**Chain:** A: **PDB Molecule:**atp-binding cassette sub-family b member 10,  
**PDBTitle:** structure of the human mitochondrial abc transporter, abcb10