
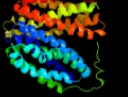

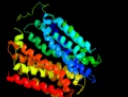
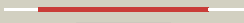
















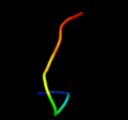


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1pv7a_</a>	 Alignment		100.0	11	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> LacY-like proton/sugar symporter
2	<a href="#">d1pw4a_</a>	 Alignment		100.0	10	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> Glycerol-3-phosphate transporter
3	<a href="#">c2gfpA_</a>	 Alignment		100.0	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance protein d; <b>PDBTitle:</b> structure of the multidrug transporter emrd from2 escherichia coli
4	<a href="#">c3o7pA_</a>	 Alignment		99.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-fucose-proton symporter; <b>PDBTitle:</b> crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
5	<a href="#">c2xutC_</a>	 Alignment		99.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> proton/peptide symporter family protein; <b>PDBTitle:</b> crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
6	<a href="#">c2w8aC_</a>	 Alignment		11.8	13	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
7	<a href="#">c2q9pA_</a>	 Alignment		11.8	14	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> antimicrobial peptide latarcin 2a; <b>PDBTitle:</b> nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
8	<a href="#">c2xq2A_</a>	 Alignment		8.7	7	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> structure of the k294a mutant of vsplt
9	<a href="#">c2ks1B_</a>	 Alignment		8.4	20	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> epidermal growth factor receptor; <b>PDBTitle:</b> heterodimeric association of transmembrane domains of erbb1 and erbb22 receptors enabling kinase activation
10	<a href="#">c2bbjB_</a>	 Alignment		8.0	9	<b>PDB header:</b> metal transport/membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> divalent cation transport-related protein; <b>PDBTitle:</b> crystal structure of the cora mg2+ transporter
11	<a href="#">d2vuti1</a>	 Alignment		7.2	30	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Erythroid transcription factor GATA-1

12	<a href="#">dly0ja1</a>	Alignment		5.9	40	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> Erythroid transcription factor GATA-1
----	-------------------------	-----------	--	-----	----	---