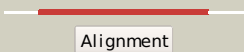

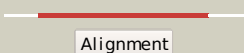

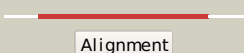

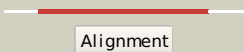

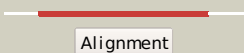

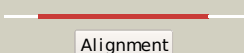

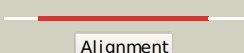

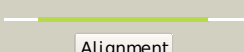

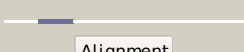
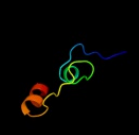
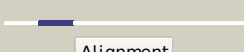
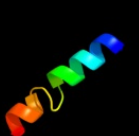
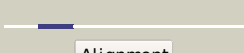



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3giaA_</a>	 Alignment		100.0	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj0609; <b>PDBTitle:</b> crystal structure of apct transporter
2	<a href="#">c3lrcC_</a>	 Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> arginine/agmatine antiporter; <b>PDBTitle:</b> structure of e. coli adic (p1)
3	<a href="#">c2jlnA_</a>	 Alignment		99.9	8	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mhp1; <b>PDBTitle:</b> structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
4	<a href="#">c2xq2A_</a>	 Alignment		98.8	11	<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 vsgl
5	<a href="#">c3dh4A_</a>	 Alignment		98.7	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
6	<a href="#">d2a65a1</a>	 Alignment		98.0	15	<b>Fold:</b> SNF-like <b>Superfamily:</b> SNF-like <b>Family:</b> SNF-like
7	<a href="#">c2w8aC_</a>	 Alignment		96.9	11	<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
8	<a href="#">c3hfxA_</a>	 Alignment		62.0	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-carnitine/gamma-butyrobetaine antiporter; <b>PDBTitle:</b> crystal structure of carnitine transporter
9	<a href="#">d1llca1</a>	 Alignment		10.7	25	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> LDH N-terminal domain-like
10	<a href="#">d1s0ya_</a>	 Alignment		9.7	29	<b>Fold:</b> Tautomerase/MIF <b>Superfamily:</b> Tautomerase/MIF <b>Family:</b> 4-oxalocrotonate tautomerase-like
11	<a href="#">c1byyA_</a>	 Alignment		7.7	43	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (sodium channel alpha-subunit); <b>PDBTitle:</b> sodium channel iia inactivation gate

12 [c3qe7A](#)

Alignment

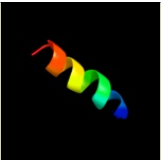


7.5

11 **PDB header:**transport protein  
**Chain:** A: **PDB Molecule:**uracil permease;  
**PDBTitle:** crystal structure of uracil transporter--uraa

13 [d1v92a\\_](#)

Alignment



5.7

20

**Fold:**RuvA C-terminal domain-like  
**Superfamily:**UBA-like  
**Family:**TAP-C domain-like