
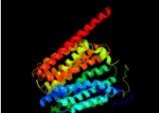
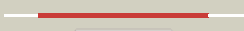








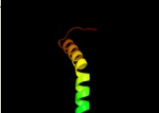

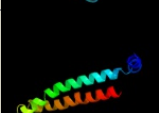



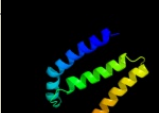

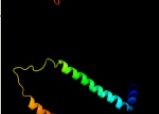


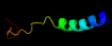





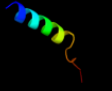
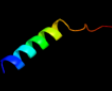



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1pw4a_</a>	 Alignment		100.0	18	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> Glycerol-3-phosphate transporter
2	<a href="#">d1pv7a_</a>	 Alignment		100.0	12	<b>Fold:</b> MFS general substrate transporter <b>Superfamily:</b> MFS general substrate transporter <b>Family:</b> LacY-like proton/sugar symporter
3	<a href="#">c2gfpA_</a>	 Alignment		100.0	16	<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		100.0	14	<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		100.0	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="#">c3qngD_</a>	 Alignment		34.6	13	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> pts system, cellobiose-specific iic component; <b>PDBTitle:</b> crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
7	<a href="#">d3b60a2</a>	 Alignment		22.7	9	<b>Fold:</b> ABC transporter transmembrane region <b>Superfamily:</b> ABC transporter transmembrane region <b>Family:</b> ABC transporter transmembrane region
8	<a href="#">d2pkgc1</a>	 Alignment		18.5	33	<b>Fold:</b> T-antigen specific domain-like <b>Superfamily:</b> T-antigen specific domain-like <b>Family:</b> T-antigen specific domain-like
9	<a href="#">c3hd6A_</a>	 Alignment		14.8	15	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter rh type c; <b>PDBTitle:</b> crystal structure of the human rhesus glycoprotein rhcg
10	<a href="#">d1pf4a2</a>	 Alignment		10.7	9	<b>Fold:</b> ABC transporter transmembrane region <b>Superfamily:</b> ABC transporter transmembrane region <b>Family:</b> ABC transporter transmembrane region
11	<a href="#">c3b9yA_</a>	 Alignment		10.4	17	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> ammonium transporter family rh-like protein; <b>PDBTitle:</b> crystal structure of the nitrosomonas europaea rh protein

12	<a href="#">c2kncA_</a>	Alignment		10.1	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alfaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex
13	<a href="#">c2g9pA_</a>	Alignment		9.6	21	<b>PDB header:</b> antimicrobial protein <b>Chain:</b> A: <b>PDB Molecule:</b> antimicrobial peptide laticin 2a; <b>PDBTitle:</b> nmr structure of a novel antimicrobial peptide, laticin 2a,2 from spider (lachesana tarabaevi) venom
14	<a href="#">d3proc1</a>	Alignment		9.4	12	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Alpha-lytic protease prodomain <b>Family:</b> Alpha-lytic protease prodomain
15	<a href="#">d1fc3a_</a>	Alignment		7.6	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> Spo0A
16	<a href="#">d1lqla_</a>	Alignment		7.1	16	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> C-terminal effector domain of the bipartite response regulators <b>Family:</b> Spo0A
17	<a href="#">c2aj2A_</a>	Alignment		6.5	25	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical upf0301 protein vc0467; <b>PDBTitle:</b> x-ray crystal structure of protein vc0467 from vibrio2 cholerae. northeast structural genomics consortium target3 vcr8.
18	<a href="#">c3arct_</a>	Alignment		6.0	12	<b>PDB header:</b> electron transport, photosynthesis <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
19	<a href="#">c3a0bT_</a>	Alignment		6.0	12	<b>PDB header:</b> electron transport <b>Chain:</b> T: <b>PDB Molecule:</b> photosystem ii reaction center protein t; <b>PDBTitle:</b> crystal structure of br-substituted photosystem ii complex
20	<a href="#">d2oara1</a>	Alignment		5.6	16	<b>Fold:</b> Gated mechanosensitive channel <b>Superfamily:</b> Gated mechanosensitive channel <b>Family:</b> Gated mechanosensitive channel
21	<a href="#">c3shpA_</a>	Alignment	not modelled	5.5	36	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative acetyltransferase sthe_0691; <b>PDBTitle:</b> crystal structure of putative acetyltransferase from sphaerobacter2 thermophilus dsm 20745 <b>Fold:</b> Transmembrane helix hairpin <b>Superfamily:</b> Cytochrome c oxidase subunit II-like, transmembrane region <b>Family:</b> Cytochrome c oxidase subunit II-like, transmembrane region
22	<a href="#">d1fftb2</a>	Alignment	not modelled	5.2	10	