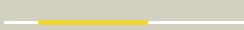
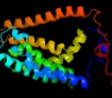
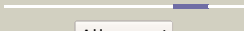


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	 Alignment		100.0	14	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: Glycerol-3-phosphate transporter
2	c3o7pA_	 Alignment		100.0	10	PDB header: transport protein Chain: A: PDB Molecule: l-fucose-proton symporter; PDBTitle: crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
3	d1pv7a_	 Alignment		100.0	11	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter
4	c2gfpA_	 Alignment		100.0	8	PDB header: membrane protein Chain: A: PDB Molecule: multidrug resistance protein d; PDBTitle: structure of the multidrug transporter emrd from2 escherichia coli
5	c2xutC_	 Alignment		100.0	10	PDB header: transport protein Chain: C: PDB Molecule: proton/peptide symporter family protein; PDBTitle: crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
6	c3b9yA_	 Alignment		70.0	10	PDB header: transport protein Chain: A: PDB Molecule: ammonium transporter family rh-like protein; PDBTitle: crystal structure of the nitrosomonas europaea rh protein
7	c3hd6A_	 Alignment		52.1	13	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: ammonium transporter rh type c; PDBTitle: crystal structure of the human rhesus glycoprotein rhcg
8	c2e8pA_	 Alignment		18.5	33	PDB header: signaling protein Chain: A: PDB Molecule: elf3 protein; PDBTitle: solution structure of the n-terminal sam-domain of e74-like2 factor 3
9	c2rddB_	 Alignment		10.5	13	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.
10	c2l92A_	 Alignment		9.4	29	PDB header: dna binding protein Chain: A: PDB Molecule: histone family protein nucleoid-structuring protein h-ns; PDBTitle: solution structure of the c-terminal domain of h-ns like protein bv3f
11	c2g9pA_	 Alignment		7.9	14	PDB header: antimicrobial protein Chain: A: PDB Molecule: antimicrobial peptide laticin 2a; PDBTitle: nmr structure of a novel antimicrobial peptide, laticin 2a,2 from spider (lachesana tarabaei) venom

12	c2bbjB_	Alignment		7.0	12	PDB header: metal transport/membrane protein Chain: B: PDB Molecule: divalent cation transport-related protein; PDBTitle: crystal structure of the cora mg2+ transporter
13	c3jyvT_	Alignment		5.9	19	PDB header: ribosome Chain: T: PDB Molecule: s19e protein; PDBTitle: structure of the 40s rrna and proteins and p/e trna for eukaryotic2 ribosome based on cryo-em map of thermomyces lanuginosus ribosome at3 8.9a resolution
14	c3lgeG_	Alignment		5.8	16	PDB header: lyase/protein binding Chain: G: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of rabbit muscle aldolase-snx9 lc4 complex
15	c3lgeF_	Alignment		5.8	16	PDB header: lyase/protein binding Chain: F: PDB Molecule: sorting nexin-9; PDBTitle: crystal structure of rabbit muscle aldolase-snx9 lc4 complex
16	c2inpD_	Alignment		5.5	25	PDB header: oxidoreductase Chain: D: PDB Molecule: phenol hydroxylase component phl; PDBTitle: structure of the phenol hydroxylase-regulatory protein2 complex
17	d2imha1	Alignment		5.4	29	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: SPO2555-like

18 c3hftA_ Alignment		5.2	35 PDB header:hydrolase Chain: A: PDB Molecule:wbms, polysaccharide deacetylase involved in o-antigen PDBTitle: crystal structure of a putative polysaccharide deacetylase involved in2 o-antigen biosynthesis (wbms, bb0128) from bordetella bronchiseptica3 at 1.90 a resolution
---	--	-----	---