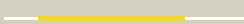
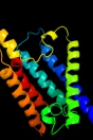
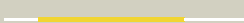
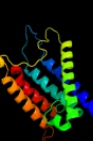
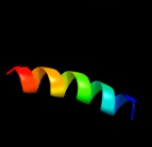


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3klzE_	 Alignment		100.0	43	PDB header: membrane protein Chain: E: PDB Molecule: putative formate transporter 1; PDBTitle: pentameric formate channel with formate bound
2	c3kcvG_	 Alignment		100.0	53	PDB header: transport protein Chain: G: PDB Molecule: probable formate transporter 1; PDBTitle: structure of formate channel
3	d1rc2a_	 Alignment		92.4	9	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
4	c3llqB_	 Alignment		90.7	10	PDB header: membrane protein Chain: B: PDB Molecule: aquaporin z 2; PDBTitle: aquaporin structure from plant pathogen agrobacterium tumefaciens
5	d1fx8a_	 Alignment		88.8	18	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
6	c1ldaA_	 Alignment		88.8	18	PDB header: transport protein Chain: A: PDB Molecule: glycerol uptake facilitator protein; PDBTitle: crystal structure of the e. coli glycerol facilitator (glpf) without2 substrate glycerol
7	c2d57A_	 Alignment		77.7	10	PDB header: transport protein Chain: A: PDB Molecule: aquaporin-4; PDBTitle: double layered 2d crystal structure of aquaporin-4 (aqp4m23) at 3.2 a2 resolution by electron crystallography
8	c3gd8A_	 Alignment		76.0	11	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin-4; PDBTitle: crystal structure of human aquaporin 4 at 1.8 and its mechanism of2 conductance
9	d1j4na_	 Alignment		73.4	15	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
10	c2w2eA_	 Alignment		71.1	16	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin; PDBTitle: 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqy1, in a closed conformation at ph 3.5
11	c3iyzA_	 Alignment		67.9	13	PDB header: transport protein Chain: A: PDB Molecule: aquaporin-4; PDBTitle: structure of aquaporin-4 s180d mutant at 10.0 a resolution from2 electron micrograph

12	d1ymga1	Alignment		57.2	14	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
13	c1ymgA_	Alignment		57.2	14	PDB header: membrane protein Chain: A: PDB Molecule: lens fiber major intrinsic protein; PDBTitle: the channel architecture of aquaporin o at 2.2 angstrom resolution
14	c2b5fD_	Alignment		49.4	9	PDB header: transport protein,membrane protein Chain: D: PDB Molecule: aquaporin; PDBTitle: crystal structure of the spinach aquaporin sopip2;1 in an2 open conformation to 3.9 resolution
15	d1h6ia_	Alignment		38.2	13	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
16	c3d9sB_	Alignment		35.6	15	PDB header: membrane protein Chain: B: PDB Molecule: aquaporin-5; PDBTitle: human aquaporin 5 (aqp5) - high resolution x-ray structure
17	c2f2bA_	Alignment		32.0	11	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin aqpm; PDBTitle: crystal structure of integral membrane protein aquaporin aqpm at 1.68a2 resolution
18	d1c17m_	Alignment		21.4	17	Fold: F1F0 ATP synthase subunit A Superfamily: F1F0 ATP synthase subunit A Family: F1F0 ATP synthase subunit A
19	c3c02A_	Alignment		17.5	9	PDB header: membrane protein Chain: A: PDB Molecule: aquaglyceroporin; PDBTitle: x-ray structure of the aquaglyceroporin from plasmodium falciparum
20	c2jy0A_	Alignment		11.4	50	PDB header: membrane protein, viral protein Chain: A: PDB Molecule: protease ns2-3; PDBTitle: solution nmr structure of hcv ns2 protein, membrane segment2 (1-27)
21	d2c1wa1	Alignment	not modelled	10.6	67	Fold: EndoU-like Superfamily: EndoU-like Family: Eukaryotic EndoU ribonuclease
22	d2foka2	Alignment	not modelled	8.7	10	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Restriction endonuclease FokI, N-terminal (recognition) domain
23	c2kncA_	Alignment	not modelled	6.9	21	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
24	c3if8B_	Alignment	not modelled	6.3	11	PDB header: cell cycle Chain: B: PDB Molecule: protein zwilch homolog; PDBTitle: crystal structure of zwilch, a member of the rzz kinetochore complex
25	c2h3oA_	Alignment	not modelled	5.9	19	PDB header: membrane protein Chain: A: PDB Molecule: merf; PDBTitle: structure of merft, a membrane protein with two trans-2 membrane helices
26	c2voyG_	Alignment	not modelled	5.8	39	PDB header: hydrolase Chain: G: PDB Molecule: sarcoplasmic/endoplasmic reticulum calcium PDBTitle: cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
27	c2kncB_	Alignment	not modelled	5.8	21	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
28	d1o5wa1	Alignment	not modelled	5.7	25	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain