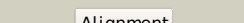
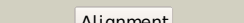
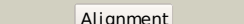
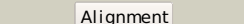
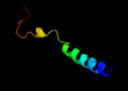
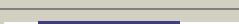
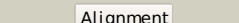
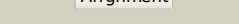
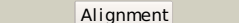


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3klzE_	 Alignment		100.0	27	PDB header: membrane protein Chain: E: PDB Molecule: putative formate transporter 1; PDBTitle: pentameric formate channel with formate bound
2	c3kcvG_	 Alignment		100.0	28	PDB header: transport protein Chain: G: PDB Molecule: probable formate transporter 1; PDBTitle: structure of formate channel
3	c3llqB_	 Alignment		95.5	9	PDB header: membrane protein Chain: B: PDB Molecule: aquaporin z 2; PDBTitle: aquaporin structure from plant pathogen agrobacterium tumefaciens
4	c1ldaA_	 Alignment		93.7	10	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
5	c3d9sB_	 Alignment		93.1	9	PDB header: membrane protein Chain: B: PDB Molecule: aquaporin-5; PDBTitle: human aquaporin 5 (aqp5) - high resolution x-ray structure
6	d1j4na_	 Alignment		91.2	11	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
7	d1fx8a_	 Alignment		88.9	10	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
8	d1rc2a_	 Alignment		87.5	12	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
9	c1ymgA_	 Alignment		78.5	12	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
10	d1ymga1	 Alignment		78.5	12	Fold: Aquaporin-like Superfamily: Aquaporin-like Family: Aquaporin-like
11	c2kncA_	 Alignment		73.0	21	PDB header: cell adhesion Chain: A: PDB Molecule: integrin alpha-iiB; PDBTitle: platelet integrin alfaIIb-beta3 transmembrane-cytoplasmic2 heterocomplex

12	c3c02A_	 Alignment		62.1	11	PDB header: membrane protein Chain: A: PDB Molecule: aquaglyceroporin; PDBTitle: x-ray structure of the aquaglyceroporin from plasmodium falciparum
13	c2b5fD_	 Alignment		36.3	10	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
14	c2w2eA_	 Alignment		35.9	9	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin; PDBTitle: 1.15 angstrom crystal structure of p.pastoris aquaporin,2 aqyl, in a closed conformation at ph 3.5
15	c3gd8A_	 Alignment		34.3	14	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
16	c3iyzA_	 Alignment		29.1	15	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
17	d1pv7a_	 Alignment		16.5	15	Fold: MFS general substrate transporter Superfamily: MFS general substrate transporter Family: LacY-like proton/sugar symporter
18	d1c17m_	 Alignment		15.9	22	Fold: F1F0 ATP synthase subunit A Superfamily: F1F0 ATP synthase subunit A Family: F1F0 ATP synthase subunit A
19	d2nr9a1	 Alignment		11.4	14	Fold: Rhomboid-like Superfamily: Rhomboid-like Family: Rhomboid-like
20	c2rddB_	 Alignment		9.8	14	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.
21	c2jy0A_	 Alignment	not modelled	9.7	39	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)
22	c2f2bA_	 Alignment	not modelled	7.5	13	PDB header: membrane protein Chain: A: PDB Molecule: aquaporin aqpm; PDBTitle: crystal structure of integral membrane protein aquaporin aqpm at 1.68a2 resolution
23	c3qngD_	 Alignment	not modelled	7.4	9	PDB header: membrane protein, transport protein Chain: D: PDB Molecule: pts system, cellobiose-specific iic component; PDBTitle: crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
24	d2foka2	 Alignment	not modelled	6.2	30	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Restriction endonuclease FokI, N-terminal (recognition) domain
25	d2c1wa1	 Alignment	not modelled	6.1	50	Fold: EndoU-like Superfamily: EndoU-like Family: Eukaryotic EndoU ribonuclease
26	c2jp3A_	 Alignment	not modelled	6.1	14	PDB header: transcription Chain: A: PDB Molecule: fyxd domain-containing ion transport regulator 4; PDBTitle: solution structure of the human fyxd4 (chif) protein in sds2 micelles
27	c2vv5D_	 Alignment	not modelled	5.9	12	PDB header: membrane protein Chain: D: PDB Molecule: small-conductance mechanosensitive channel; PDBTitle: the open structure of msccs
						PDB header: hydrolase Chain: G: PDB Molecule: sarcoplasmic/endoplasmic reticulum

28 [c2voyG_](#)

Alignment

not modelled

5.9

50

calcium
PDBTitle: cryoem model of copa, the copper transporting atpase
from2 archaeoglobus fulgidus