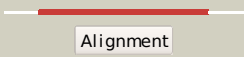
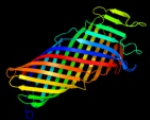
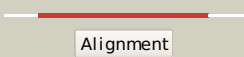
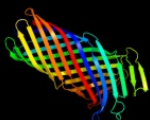
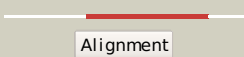

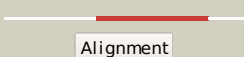



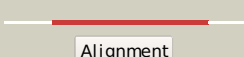

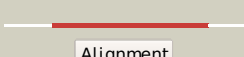

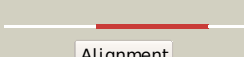

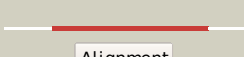
















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dli78a_	 Alignment		100.0	72	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane protease OMPT
2	c2x4mD_	 Alignment		100.0	49	PDB header: hydrolase Chain: D: PDB Molecule: coagulase/fibrinolysin; PDBTitle: yersinia pestis plasminogen activator pla
3	c2x27X_	 Alignment		98.3	12	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein oprg; PDBTitle: crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
4	d1p4ta_	 Alignment		98.2	17	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
5	c2f1tB_	 Alignment		97.9	10	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
6	c3sljA_	 Alignment		97.5	13	PDB header: protein transport Chain: A: PDB Molecule: serine protease esp; PDBTitle: pre-cleavage structure of the autotransporter esp - n1023a mutant
7	c2qomB_	 Alignment		97.5	11	PDB header: hydrolase Chain: B: PDB Molecule: serine protease esp; PDBTitle: the crystal structure of the e.coli esp autotransporter beta-domain.
8	c2k0lA_	 Alignment		97.4	18	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein a; PDBTitle: nmr structure of the transmembrane domain of the outer2 membrane protein a from klebsiella pneumoniae in dhpc3 micelles.
9	c3qq2C_	 Alignment		97.4	13	PDB header: membrane protein/protein transport Chain: C: PDB Molecule: brka autotransporter; PDBTitle: crystal structure of the beta domain of the bordetella autotransporter2 brka
10	c3nb3C_	 Alignment		97.3	21	PDB header: virus Chain: C: PDB Molecule: outer membrane protein a; PDBTitle: the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components
11	d1g90a_	 Alignment		97.2	18	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein

12	c3dwoX_	Alignment		97.2	16	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadI homologue
13	d1t16a_	Alignment		97.1	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
14	d1qj8a_	Alignment		96.9	15	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
15	c3qraA_	Alignment		96.8	15	PDB header: cell invasion Chain: A: PDB Molecule: attachment invasion locus protein; PDBTitle: the crystal structure of ail, the attachment invasion locus protein of2 yersinia pestis
16	d1qjpa_	Alignment		96.7	28	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
17	c3aehB_	Alignment		96.5	9	PDB header: hydrolase Chain: B: PDB Molecule: hemoglobin-binding protease hbp autotransporter; PDBTitle: integral membrane domain of autotransporter hbp
18	c3a2rX_	Alignment		95.2	24	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein ii; PDBTitle: crystal structure of outer membrane protein porb from neisseria2 meningitidis
19	c2lhfa_	Alignment		95.2	11	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein h1; PDBTitle: solution structure of outer membrane protein h (oprh) from p.2 aeruginosa in dhpc micelles
20	c2iwvD_	Alignment		95.0	14	PDB header: ion channel Chain: D: PDB Molecule: outer membrane protein g; PDBTitle: structure of the monomeric outer membrane porin ompg in the2 open and closed conformation
21	d1uynx_	Alignment	not modelled	94.4	11	Fold: Transmembrane beta-barrels Superfamily: Autotransporter Family: Autotransporter
22	c3kvnA_	Alignment	not modelled	94.1	18	PDB header: hydrolase Chain: A: PDB Molecule: esterase esta; PDBTitle: crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
23	c2jmmA_	Alignment	not modelled	93.9	17	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein a; PDBTitle: nmr solution structure of a minimal transmembrane beta-2 barrel platform protein
24	c3brzA_	Alignment	not modelled	93.5	9	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx
25	d2fgqx1	Alignment	not modelled	88.2	10	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
26	c3dzmb_	Alignment	not modelled	87.3	17	PDB header: unknown function Chain: B: PDB Molecule: hypothetical conserved protein; PDBTitle: crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
27	d2zfga1	Alignment	not modelled	75.3	11	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
28	d1phoa_	Alignment	not modelled	73.6	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
						PDB header: membrane protein

29	c3nsgA	Alignment	not modelled	72.7	14	Chain: A: PDB Molecule: outer membrane protein f; PDBTitle: crystal structure of ompf, an outer membrane protein from salmonella2 typhi
30	c3bryB	Alignment	not modelled	70.4	9	PDB header: transport protein Chain: B: PDB Molecule: tbux; PDBTitle: crystal structure of the ralstonia pickettii toluene2 transporter tbux
31	d1osma	Alignment	not modelled	59.9	19	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
32	d1af6a	Alignment	not modelled	58.5	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
33	d1a0tp	Alignment	not modelled	40.8	11	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
34	d3prna	Alignment	not modelled	26.6	27	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
35	d2mpa	Alignment	not modelled	18.1	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
36	d2pora	Alignment	not modelled	15.2	18	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
37	c3csIB	Alignment	not modelled	13.0	17	PDB header: membrane protein/heme binding protein Chain: B: PDB Molecule: hasr protein; PDBTitle: structure of the serratia marcescens hemophore receptor hasr in2 complex with its hemophore hasa and heme
38	c3ghnA	Alignment	not modelled	11.8	9	PDB header: hydrolase Chain: A: PDB Molecule: a disintegrin and metalloproteinase with thrombospondin PDBTitle: crystal structure of the exosite-containing fragment of human adamts132 (form-2)
39	d1fepa	Alignment	not modelled	9.9	9	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
40	c3uajA	Alignment	not modelled	9.8	12	PDB header: viral protein/immune system Chain: A: PDB Molecule: envelope protein; PDBTitle: crystal structure of the envelope glycoprotein ectodomain from dengue2 virus serotype 4 in complex with the fab fragment of the chimpanzee3 monoclonal antibody 5h2
41	d1i8ta2	Alignment	not modelled	7.9	8	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: UDP-galactopyranose mutase
42	d1na6a1	Alignment	not modelled	7.9	14	Fold: DNA-binding pseudobarrel domain Superfamily: DNA-binding pseudobarrel domain Family: Type II restriction endonuclease effector domain