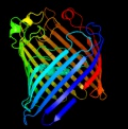
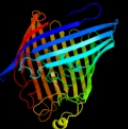
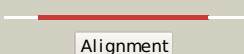
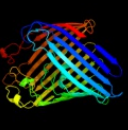
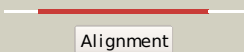
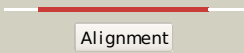
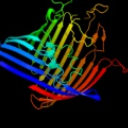
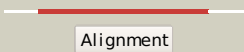
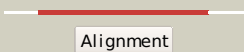
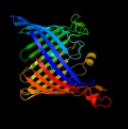
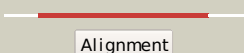
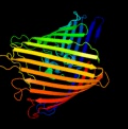
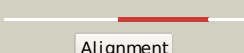
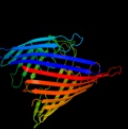
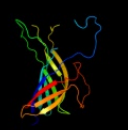
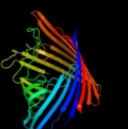
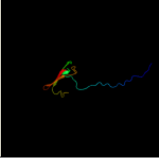


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1osma_	 Alignment		100.0	78	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
2	c3nsgA_	 Alignment		100.0	55	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein f; PDBTitle: crystal structure of ompf, an outer membrane protein from salmonella2 typhi
3	d1phoa_	 Alignment		100.0	59	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
4	d2zfga1	 Alignment		100.0	63	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
5	d2fgqx1	 Alignment		100.0	18	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
6	c3a2rX_	 Alignment		100.0	19	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein ii; PDBTitle: crystal structure of outer membrane protein porb from neisseria2 meningitidis
7	d2pora_	 Alignment		100.0	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
8	d3prna_	 Alignment		100.0	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
9	c2o4vA_	 Alignment		99.9	13	PDB header: membrane protein Chain: A: PDB Molecule: porin p; PDBTitle: an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
10	c3qraA_	 Alignment		99.1	16	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
11	d1g90a_	 Alignment		99.0	15	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein

12	d1p4ta_	Alignment		98.9	18	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
13	d1qj8a_	Alignment		98.8	16	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
14	c2odjA_	Alignment		98.8	11	PDB header: membrane protein Chain: A: PDB Molecule: porin d; PDBTitle: crystal structure of the outer membrane protein opod from pseudomonas2 aeruginosa
15	c2y0kA_	Alignment		98.7	12	PDB header: transport protein Chain: A: PDB Molecule: pyroglutamate porin opdo; PDBTitle: crystal structure of pseudomonas aeruginosa opdo
16	c3jtyB_	Alignment		98.7	9	PDB header: transport protein Chain: B: PDB Molecule: benf-like porin; PDBTitle: crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
17	c2y0hA_	Alignment		98.6	12	PDB header: transport protein Chain: A: PDB Molecule: probable porin; PDBTitle: crystal structure of pseudomonas aeruginosa opdl
18	c2k0lA_	Alignment		98.5	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.
19	c2y0lA_	Alignment		98.5	13	PDB header: transport protein Chain: A: PDB Molecule: cis-aconitate porin opdh; PDBTitle: crystal structure of pseudomonas aeruginosa opdo
20	d1qjpa_	Alignment		98.4	14	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
21	c3nb3C_	Alignment	not modelled	98.3	14	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
22	c2lhfA_	Alignment	not modelled	98.3	17	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
23	c2f1tB_	Alignment	not modelled	98.3	16	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
24	c2qtKB_	Alignment	not modelled	98.3	13	PDB header: membrane protein Chain: B: PDB Molecule: probable porin; PDBTitle: crystal structure of the outer membrane protein opdk from2 pseudomonas aeruginosa
25	d1t16a_	Alignment	not modelled	98.2	15	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
26	c3dwoX_	Alignment	not modelled	98.1	17	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadl homologue
27	c2x27X_	Alignment	not modelled	97.9	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
28	c3brzA_	Alignment	not modelled	97.9	16	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx

29	d1af6a_	Alignment	not modelled	97.6	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
30	d2mpa_	Alignment	not modelled	97.4	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
31	c3bryB_	Alignment	not modelled	97.0	16	PDB header: transport protein Chain: B: PDB Molecule: tbux; PDBTitle: crystal structure of the ralstonia pickettii toluene2 transporter tbux
32	c2wjgA_	Alignment	not modelled	96.9	15	PDB header: transport protein Chain: A: PDB Molecule: probable n-acetylneuraminic acid outer membrane channel PDBTitle: nanc porin structure in hexagonal crystal form.
33	c2jmmA_	Alignment	not modelled	96.7	11	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
34	d1a0tp_	Alignment	not modelled	96.7	10	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
35	c3sljA_	Alignment	not modelled	95.4	16	PDB header: protein transport Chain: A: PDB Molecule: serine protease espp; PDBTitle: pre-cleavage structure of the autotransporter espp - n1023a mutant
36	c3rbhC_	Alignment	not modelled	94.8	8	PDB header: transport protein Chain: C: PDB Molecule: alginate production protein alge; PDBTitle: structure of alginate export protein alge from pseudomonas aeruginosa
37	c3qq2C_	Alignment	not modelled	91.1	16	PDB header: membrane protein/protein transport Chain: C: PDB Molecule: brka autotransporter; PDBTitle: crystal structure of the beta domain of the bordetella autotransporter2 brka
38	c3aehB_	Alignment	not modelled	90.0	11	PDB header: hydrolase Chain: B: PDB Molecule: hemoglobin-binding protease hbp autotransporter; PDBTitle: integral membrane domain of autotransporter hbp
39	d1uynx_	Alignment	not modelled	89.0	5	Fold: Transmembrane beta-barrels Superfamily: Autotransporter Family: Autotransporter
40	c2qomB_	Alignment	not modelled	88.4	14	PDB header: hydrolase Chain: B: PDB Molecule: serine protease espp; PDBTitle: the crystal structure of the e.coli espp autotransporter beta-domain.
41	c2x4mD_	Alignment	not modelled	85.6	19	PDB header: hydrolase Chain: D: PDB Molecule: coagulase/fibrinolysin; PDBTitle: yersinia pestis plasminogen activator pla
42	c3fhhA_	Alignment	not modelled	84.5	13	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane heme receptor shua; PDBTitle: crystal structure of the heme/hemoglobin outer membrane2 transporter shua from shigella dysenteriae
43	c3kvnA_	Alignment	not modelled	84.2	22	PDB header: hydrolase Chain: A: PDB Molecule: esterase esta; PDBTitle: crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
44	d2jnaa1	Alignment		78.3	14	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
45	dli78a_	Alignment	not modelled	76.8	21	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane protease OMPT
46	c2iwwD_	Alignment	not modelled	76.2	12	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
47	c2hdiA_	Alignment	not modelled	66.7	15	PDB header: protein transport,antimicrobial protein Chain: A: PDB Molecule: colicin i receptor; PDBTitle: crystal structure of the colicin i receptor cir from e.coli in complex2 with receptor binding domain of colicin ia.
48	c2grxB_	Alignment	not modelled	61.8	12	PDB header: metal transport Chain: B: PDB Molecule: ferrichrome-iron receptor; PDBTitle: crystal structure of tonb in complex with fhua, e. coli2 outer membrane receptor for ferrichrome
49	d2gufa1	Alignment	not modelled	54.5	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
50	c2iahA_	Alignment	not modelled	53.3	13	PDB header: membrane protein Chain: A: PDB Molecule: ferripyoverdine receptor; PDBTitle: crystal structure of the ferripyoverdine receptor of the outer2 membrane of pseudomonas aeruginosa bound to ferripyoverdine.
51	d1by5a_	Alignment	not modelled	39.0	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
52	c1xkwA_	Alignment	not modelled	22.0	12	PDB header: membrane protein Chain: A: PDB Molecule: fe(iii)-pyochelin receptor; PDBTitle: pyochelin outer membrane receptor fpta from pseudomonas aeruginosa
53	c2vdaB_	Alignment	not modelled	19.9	25	PDB header: protein transport Chain: B: PDB Molecule: maltoporin; PDBTitle: solution structure of the seca-signal peptide complex
						PDB header: membrane protein,apoptosis

54	c2k4tA_	Alignment	not modelled	18.1	14	Chain: A: PDB Molecule: voltage-dependent anion-selective channel PDBTitle: solution structure of human vdac-1 in ldao micelles
55	c3csIB_	Alignment	not modelled	16.1	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
56	c2k3aA_	Alignment	not modelled	9.5	26	PDB header: hydrolase Chain: A: PDB Molecule: chap domain protein; PDBTitle: nmr solution structure of staphylococcus saprophyticus chap2 (cysteine, histidine-dependent amidohydrolases/peptidases)3 domain protein. northeast structural genomics consortium4 target syr11