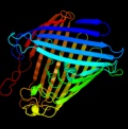
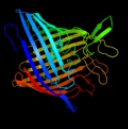
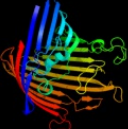
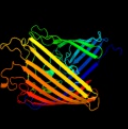
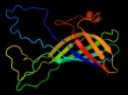
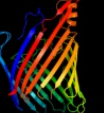
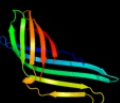
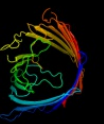
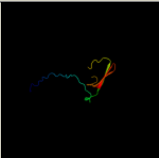


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1osma_	 Alignment		100.0	71	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
2	d1phoa_	 Alignment		100.0	66	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
3	c3nsgA_	 Alignment		100.0	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
4	d2zfqa1	 Alignment		100.0	62	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	16	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
9	c2o4vA_	 Alignment		99.9	12	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		98.7	14	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	d1p4ta_	 Alignment		98.5	14	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein

12	c2k0lA_	Alignment		98.5	13	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.
13	d1qj8a_	Alignment		98.4	16	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
14	c2y0kA_	Alignment		98.3	13	PDB header: transport protein Chain: A: PDB Molecule: pyroglutamate porin opdo; PDBTitle: crystal structure of pseudomonas aeruginosa opdo
15	c2f1tB_	Alignment		98.3	12	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
16	d1g90a_	Alignment		98.3	16	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
17	c3jtyB_	Alignment		98.1	10	PDB header: transport protein Chain: B: PDB Molecule: benf-like porin; PDBTitle: crystal structure of a benf-like porin from pseudomonas fluorescens2 pf-5
18	d1qjpa_	Alignment		98.1	18	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
19	c2y0lA_	Alignment		98.0	14	PDB header: transport protein Chain: A: PDB Molecule: cis-aconitate porin opdh; PDBTitle: crystal structure of pseudomonas aeruginosa opdo
20	d1t16a_	Alignment		98.0	16	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
21	c3nb3C_	Alignment	not modelled	97.9	18	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	c2x27X_	Alignment	not modelled	97.8	13	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein oprg; PDBTitle: crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
23	c2odjA_	Alignment	not modelled	97.8	11	PDB header: membrane protein Chain: A: PDB Molecule: porin d; PDBTitle: crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa
24	c2lhfA_	Alignment	not modelled	97.7	15	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
25	c2qtkB_	Alignment	not modelled	97.6	12	PDB header: membrane protein Chain: B: PDB Molecule: probable porin; PDBTitle: crystal structure of the outer membrane protein opdk from2 pseudomonas aeruginosa
26	c2y0hA_	Alignment	not modelled	97.3	12	PDB header: transport protein Chain: A: PDB Molecule: probable porin; PDBTitle: crystal structure of pseudomonas aeruginosa opdl
27	c2jmmA_	Alignment	not modelled	97.0	14	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
28	c3brzA_	Alignment	not modelled	97.0	15	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx

29	c3sljA_	Alignment	not modelled	96.7	14	PDB header: protein transport Chain: A: PDB Molecule: serine protease espp; PDBTitle: pre-cleavage structure of the autotransporter espp - n1023a mutant
30	c3dwoX_	Alignment	not modelled	96.5	14	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadl homologue
31	c2qomB_	Alignment	not modelled	95.7	15	PDB header: hydrolase Chain: B: PDB Molecule: serine protease espp; PDBTitle: the crystal structure of the e.coli espp autotransporter beta-domain.
32	c2x4mD_	Alignment	not modelled	93.8	15	PDB header: hydrolase Chain: D: PDB Molecule: coagulase/fibrinolysin; PDBTitle: yersinia pestis plasminogen activator pla
33	d1i78a_	Alignment	not modelled	93.6	17	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane protease OMPT
34	c3aehB_	Alignment	not modelled	91.9	17	PDB header: hydrolase Chain: B: PDB Molecule: hemoglobin-binding protease hbp autotransporter; PDBTitle: integral membrane domain of autotransporter hbp
35	c2iahA_	Alignment	not modelled	90.6	10	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.
36	c3bryB_	Alignment	not modelled	90.6	16	PDB header: transport protein Chain: B: PDB Molecule: tbux; PDBTitle: crystal structure of the ralstonia pickettii toluene2 transporter tbux
37	d1uynx_	Alignment	not modelled	89.0	11	Fold: Transmembrane beta-barrels Superfamily: Autotransporter Family: Autotransporter
38	c2wjgA_	Alignment	not modelled	88.9	12	PDB header: transport protein Chain: A: PDB Molecule: probable n-acetylneuraminic acid outer membrane channel PDBTitle: nanc porin structure in hexagonal crystal form.
39	c3qq2C_	Alignment	not modelled	87.2	14	PDB header: membrane protein/protein transport Chain: C: PDB Molecule: brka autotransporter; PDBTitle: crystal structure of the beta domain of the bordetella autotransporter2 brka
40	d1a0tp_	Alignment	not modelled	79.0	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
41	c2iwvD_	Alignment	not modelled	67.9	13	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
42	d2jnaa1	Alignment		65.1	18	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
43	d2gufa1	Alignment	not modelled	55.3	10	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
44	c3rbhC_	Alignment	not modelled	44.9	12	PDB header: transport protein Chain: C: PDB Molecule: alginate production protein alge; PDBTitle: structure of alginate export protein alge from pseudomonas aeruginosa
45	c2hdiA_	Alignment	not modelled	26.3	12	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.
46	c3fhha_	Alignment	not modelled	24.8	15	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
47	d1af6a_	Alignment	not modelled	19.9	11	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
48	c1xkwA_	Alignment	not modelled	19.8	9	PDB header: membrane protein Chain: A: PDB Molecule: fe(iii)-pyochelin receptor; PDBTitle: pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
49	c3kvnA_	Alignment	not modelled	16.2	17	PDB header: hydrolase Chain: A: PDB Molecule: esterase esta; PDBTitle: crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
50	d1fepa_	Alignment	not modelled	15.5	11	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
51	c2k4ta_	Alignment	not modelled	12.8	15	PDB header: membrane protein,apoptosis Chain: A: PDB Molecule: voltage-dependent anion-selective channel PDBTitle: solution structure of human vdac-1 in ldao micelles
52	c2vdaB_	Alignment	not modelled	11.2	25	PDB header: protein transport Chain: B: PDB Molecule: maltoporin; PDBTitle: solution structure of the seca-signal peptide complex
53	c2k3aA_	Alignment	not modelled	7.9	30	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
54	c3cslB_	Alignment	not modelled	7.4	16 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
55	c2grxB_	Alignment	not modelled	7.3	11 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
56	c1xkhC_	Alignment	not modelled	6.4	16 PDB header: membrane protein Chain: C: PDB Molecule: ferripyoverdine receptor; PDBTitle: pyoverdine outer membrane receptor fpva from pseudomonas aeruginosa2 pao1 bound to pyoverdine
57	c2kjoA_	Alignment	not modelled	6.0	44 PDB header: de novo protein Chain: A: PDB Molecule: lah4; PDBTitle: ph dependent structures of lah4 in micellar environment: mode of2 acting
58	d1by5a_	Alignment	not modelled	5.5	11 Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel