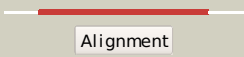
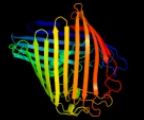
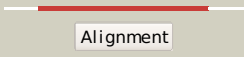
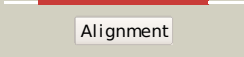
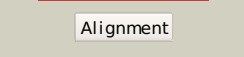
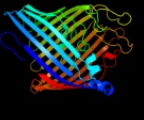
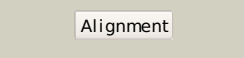
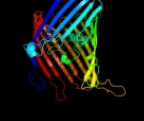
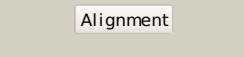
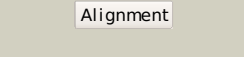
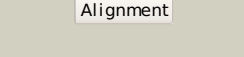
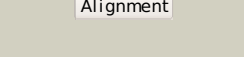
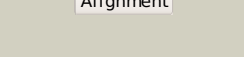
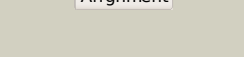
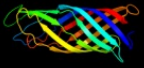
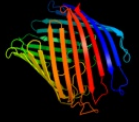
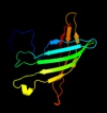
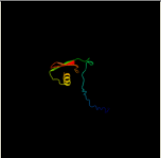


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2zfga1	 Alignment		100.0	99	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
2	d1phoa_	 Alignment		100.0	63	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
3	d1osma_	 Alignment		100.0	62	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
4	c3nsgA_	 Alignment		100.0	56	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein f; PDBTitle: crystal structure of ompf, an outer membrane protein from salmonella2 typhi
5	d2fgqx1	 Alignment		100.0	20	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	15	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	14	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		99.0	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		99.0	19	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein

12	d1qj8a_	Alignment		98.9	14	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
13	d1g90a_	Alignment		98.6	11	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
14	c2x27X_	Alignment		98.6	17	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein oprg; PDBTitle: crystal structure of the outer membrane protein oprg from2 pseudomonas aeruginosa
15	c3jtyB_	Alignment		98.5	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
16	c2f1tB_	Alignment		98.5	16	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
17	c2k0lA_	Alignment		98.4	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.
18	c2odjA_	Alignment		98.3	13	PDB header: membrane protein Chain: A: PDB Molecule: porin d; PDBTitle: crystal structure of the outer membrane protein oprd from pseudomonas2 aeruginosa
19	d1qjpa_	Alignment		98.2	13	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
20	c2lhfa_	Alignment		98.2	18	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
21	c2y0lA_	Alignment	not modelled	98.2	13	PDB header: transport protein Chain: A: PDB Molecule: cis-aconitate porin opdh; PDBTitle: crystal structure of pseudomonas aeruginosa opdo
22	c2y0kA_	Alignment	not modelled	98.1	12	PDB header: transport protein Chain: A: PDB Molecule: pyroglutamate porin opdo; PDBTitle: crystal structure of pseudomonas aeruginosa opdo
23	c3nb3C_	Alignment	not modelled	98.1	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
24	c2y0hA_	Alignment	not modelled	98.0	12	PDB header: transport protein Chain: A: PDB Molecule: probable porin; PDBTitle: crystal structure of pseudomonas aeruginosa opdl
25	c2qtKB_	Alignment	not modelled	98.0	12	PDB header: membrane protein Chain: B: PDB Molecule: probable porin; PDBTitle: crystal structure of the outer membrane protein opdk from2 pseudomonas aeruginosa
26	c3brzA_	Alignment	not modelled	97.9	10	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx
27	c3bryB_	Alignment	not modelled	97.6	16	PDB header: transport protein Chain: B: PDB Molecule: tbux; PDBTitle: crystal structure of the ralstonia pickettii toluene2 transporter tbux
28	d1a0tp_	Alignment	not modelled	97.2	11	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like

29	c3aehB	Alignment	not modelled	96.8	13	PDB header: hydrolase Chain: B: PDB Molecule: hemoglobin-binding protease hbp autotransporter; PDBTitle: integral membrane domain of autotransporter hbp
30	c2jmmA	Alignment	not modelled	96.8	10	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
31	d2mpa	Alignment	not modelled	96.7	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
32	d1af6a	Alignment	not modelled	96.3	14	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
33	d1uynx	Alignment	not modelled	95.6	9	Fold: Transmembrane beta-barrels Superfamily: Autotransporter Family: Autotransporter
34	c2wjgA	Alignment	not modelled	95.6	12	PDB header: transport protein Chain: A: PDB Molecule: probable n-acetylneuraminic acid outer membrane channel PDBTitle: nanc porin structure in hexagonal crystal form.
35	c3dwoX	Alignment	not modelled	95.0	15	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadl homologue
36	c2x4mD	Alignment	not modelled	94.8	15	PDB header: hydrolase Chain: D: PDB Molecule: coagulase/fibrinolysin; PDBTitle: yersinia pestis plasminogen activator pla
37	d1t16a	Alignment	not modelled	94.7	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
38	c2iwdD	Alignment	not modelled	94.5	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
39	c2qomB	Alignment	not modelled	94.4	13	PDB header: hydrolase Chain: B: PDB Molecule: serine protease espp; PDBTitle: the crystal structure of the e.coli espp autotransporter beta-domain.
40	c3kvnA	Alignment	not modelled	90.2	16	PDB header: hydrolase Chain: A: PDB Molecule: esterase esta; PDBTitle: crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
41	c3sljA	Alignment	not modelled	90.0	15	PDB header: protein transport Chain: A: PDB Molecule: serine protease espp; PDBTitle: pre-cleavage structure of the autotransporter espp - n1023a mutant
42	c3qq2C	Alignment	not modelled	86.2	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
43	d1i78a	Alignment	not modelled	84.5	16	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane protease OMPT
44	c3rbhC	Alignment	not modelled	80.2	9	PDB header: transport protein Chain: C: PDB Molecule: alginate production protein alge; PDBTitle: structure of alginate export protein alge from pseudomonas aeruginosa
45	d2jnaa1	Alignment		74.7	13	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
46	c1xkwA	Alignment	not modelled	55.7	14	PDB header: membrane protein Chain: A: PDB Molecule: fe(iii)-pyochelin receptor; PDBTitle: pyochelin outer membrane receptor fpta from pseudomonas2 aeruginosa
47	c3ay3C	Alignment	not modelled	21.9	29	PDB header: oxidoreductase Chain: C: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
48	c2iahA	Alignment	not modelled	20.2	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.
49	c2hdiA	Alignment	not modelled	18.0	20	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.
50	d1fepa	Alignment	not modelled	16.4	15	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
51	d1by5a	Alignment	not modelled	15.3	17	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
52	d2gufa1	Alignment	not modelled	14.8	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Ligand-gated protein channel
53	c2vdaB	Alignment	not modelled	11.8	35	PDB header: protein transport Chain: B: PDB Molecule: maltoporin; PDBTitle: solution structure of the seca-signal peptide complex
						PDB header: hydrolase

54	c2k3aA_	 Alignment	not modelled	7.5	26	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
55	c3g8cB_	 Alignment	not modelled	6.8	25	PDB header: ligase Chain: B: PDB Molecule: biotin carboxylase; PDBTitle: crystal stucture of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
56	c1ulzA_	 Alignment	not modelled	5.8	25	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
57	c2grxB_	 Alignment	not modelled	5.8	14	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
58	c3kipU_	 Alignment	not modelled	5.6	29	PDB header: lyase Chain: U: PDB Molecule: 3-dehydroquinase, type ii; PDBTitle: crystal structure of type-ii 3-dehydroquinase from c. albicans