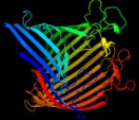
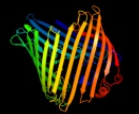
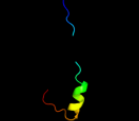
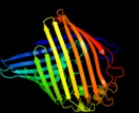
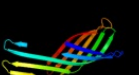
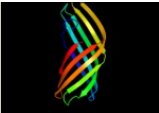


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1af6a_	 Alignment		100.0	100	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
2	d2mpa_	 Alignment		100.0	80	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
3	d1a0tp_	 Alignment		100.0	29	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Maltoporin-like
4	c3qraA_	 Alignment		96.9	11	PDB header: cell invasion Chain: A: PDB Molecule: attachment invasion locus protein; PDBTitle: the crystal structure of ail, the attachment invasion locus protein of <i>Yersinia pestis</i>
5	c2vdaB_	 Alignment		95.8	100	PDB header: protein transport Chain: B: PDB Molecule: maltoporin; PDBTitle: solution structure of the secA-signal peptide complex
6	c3nsgA_	 Alignment		93.7	12	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein f; PDBTitle: crystal structure of ompf, an outer membrane protein from <i>Salmonella typhi</i>
7	d2zfga1	 Alignment		93.1	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
8	d1qj8a_	 Alignment		92.7	13	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
9	d1phoa_	 Alignment		91.9	9	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
10	d1osma_	 Alignment		88.8	12	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
11	c2wjqa_	 Alignment		82.8	14	PDB header: transport protein Chain: A: PDB Molecule: probable n-acetylneuraminic acid outer membrane channel PDBTitle: nanc porin structure in hexagonal crystal form.

12	c3nb3C_	Alignment		79.4	10	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
13	dlqjpa_	Alignment		79.1	10	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
14	dlg90a_	Alignment		73.7	12	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
15	c2x4mD_	Alignment		60.4	21	PDB header: hydrolase Chain: D: PDB Molecule: coagulase/fibrinolysin; PDBTitle: yersinia pestis plasminogen activator pla
16	dli78a_	Alignment		59.4	17	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane protease OMPT
17	c2f1tB_	Alignment		59.1	8	PDB header: membrane protein Chain: B: PDB Molecule: outer membrane protein w; PDBTitle: outer membrane protein ompw
18	c2k0lA_	Alignment		57.5	11	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	c2jmmA_	Alignment		38.2	13	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
20	d2vdfa1	Alignment		37.3	14	Fold: Transmembrane beta-barrels Superfamily: OMPT-like Family: Outer membrane adhesin/invasin OpcA
21	c3dzmb_	Alignment	not modelled	35.6	19	PDB header: unknown function Chain: B: PDB Molecule: hypothetical conserved protein; PDBTitle: crystal structure of a major outer membrane protein from thermus2 thermophilus hb27
22	c2iwvD_	Alignment	not modelled	25.0	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
23	c2o4vA_	Alignment	not modelled	25.0	17	PDB header: membrane protein Chain: A: PDB Molecule: porin p; PDBTitle: an arginine ladder in oprp mediates phosphate specific transfer across2 the outer membrane
24	d2fgqx1	Alignment	not modelled	23.6	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
25	c2l8aA_	Alignment	not modelled	20.7	14	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: structure of a novel cbm3 lacking the calcium-binding site
26	d2jnaa1	Alignment	not modelled	18.6	33	Fold: Dodecin subunit-like Superfamily: YdgH-like Family: YdgH-like
27	c2bs5A_	Alignment	not modelled	12.7	35	PDB header: sugar binding protein Chain: A: PDB Molecule: fucose-binding lectin protein; PDBTitle: lectin from ralstonia solanacearum complexed with 2-2 fucosyllactose
28	dlcz5a2	Alignment	not modelled	9.3	50	Fold: Cdc48 domain 2-like Superfamily: Cdc48 domain 2-like Family: Cdc48 domain 2-like
29	c2wo4A_	Alignment	not modelled	9.3	16	PDB header: hydrolase Chain: A: PDB Molecule: glycoside hydrolase, family 9; PDBTitle: 3b' carbohydrate-binding module from the cel9v

						glycoside2 hydrolase from clostridium thermocellum, in-house data
30	c3aehB_	Alignment	not modelled	8.8	9	PDB header: hydrolase Chain: B: PDB Molecule: hemoglobin-binding protease hbp autotransporter; PDBTitle: integral membrane domain of autotransporter hbp
31	c2rfyB_	Alignment	not modelled	8.1	20	PDB header: hydrolase Chain: B: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: crystal structure of cellobiohydrolase from melanocarpus2 albomyces complexed with cellobiose
32	d2jb0b1	Alignment	not modelled	8.0	29	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: HNH-motif
33	c3sf5D_	Alignment	not modelled	7.7	9	PDB header: chaperone Chain: D: PDB Molecule: urease accessory protein ureh; PDBTitle: crystal structure of helicobacter pylori urease accessory protein2 uref/h complex
34	d1p4ta_	Alignment	not modelled	7.4	8	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
35	c2x27X_	Alignment	not modelled	7.0	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
36	d3prna_	Alignment	not modelled	6.7	13	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Porin
37	c3lywA_	Alignment	not modelled	6.3	39	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ybbr family protein; PDBTitle: crystal structure of ybbr family protein dhaf_0833 from2 desulfitobacterium hafniense dcb-2. northeast structural3 genomics consortium target id dhr29b
38	d2q07a3	Alignment	not modelled	6.2	14	Fold: Cystatin-like Superfamily: Pre-PUA domain Family: AF0587 pre C-terminal domain-like
39	d2v3la1	Alignment	not modelled	6.0	24	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
40	c3dwoX_	Alignment	not modelled	5.8	15	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadl homologue
41	c3qq2C_	Alignment	not modelled	5.8	11	PDB header: membrane protein/protein transport Chain: C: PDB Molecule: brka autotransporter; PDBTitle: crystal structure of the beta domain of the bordetella autotransporter2 brka
42	c2outA_	Alignment	not modelled	5.7	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: mu-like prophage flumu protein gp35, protein PDBTitle: solution structure of hi1506, a novel two domain protein2 from haemophilus influenzae
43	c3a2rX_	Alignment	not modelled	5.7	11	PDB header: membrane protein Chain: X: PDB Molecule: outer membrane protein ii; PDBTitle: crystal structure of outer membrane protein porb from neisseria2 meningitidis
44	c3kvnA_	Alignment	not modelled	5.7	12	PDB header: hydrolase Chain: A: PDB Molecule: esterase esta; PDBTitle: crystal structure of the full-length autotransporter esta from2 pseudomonas aeruginosa
45	d1g43a_	Alignment	not modelled	5.6	12	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family III
46	d1tpna_	Alignment	not modelled	5.6	57	Fold: Fnl-like domain Superfamily: Fnl-like domain Family: Fibronectin type I module
47	d1nbca_	Alignment	not modelled	5.4	14	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family III
48	c3kihC_	Alignment	not modelled	5.3	21	PDB header: sugar binding protein Chain: C: PDB Molecule: 5-bladed -propeller lectin; PDBTitle: the crystal structures of two fragments truncated from 5-bladed -2 propeller lectin, tachylectin-2 (lib2-d2-15)
49	d1ojja_	Alignment	not modelled	5.1	22	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
50	c2ei5B_	Alignment	not modelled	5.1	29	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein ttha0061; PDBTitle: crystal structure of hypothetical protein(ttha0061) from thermus2 thermophilus
51	d2outa2	Alignment	not modelled	5.1	31	Fold: GIN5/PriA/YqbF domain Superfamily: PriA/YqbF domain Family: YqbF N-terminal domain-like
52	d3ovva_	Alignment	not modelled	5.1	13	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core