



Outer membrane porin OmpC from Escherichia coli (PDB ID: 2J1N)



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Summary

A 3D-printed molecular model of the Escherichia coli porin OmpC (PDB ID: 2J1N).

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Outer membrane porin OmpC from Escherichia coli (PDB ID: 2J1N*). The model shows how antiparallel β -sheets fold into a barrel (β -barrel) that spans the outer membrane and encloses a central channel. Three such monomers associate into a stable trimer. One loop folds back into the channel and forms a constriction roughly halfway through the pore. There, residues with opposite charges create a transverse electric field, and this field influences which molecules can pass through the channel.

- Orange and yellow – two of the three monomers of the porin;
- The third monomer highlights the antiparallel β -sheet regions in blue, the α -helical regions in red and the loops in white;
- Yellow – hydrogen bonds stabilising the interactions between adjacent β -strands.

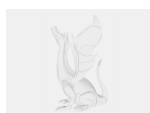
Together, these elements illustrate the fundamental principle that a protein's three-dimensional shape determines its function. For OmpC, that function is the selective diffusion of nutrients and of some antibiotics, such

as β -lactams, across the outer membrane of Gram-negative bacteria. Mutations in the constriction zone, for example D18E, change the pore's size and electrostatics. Loss of porins likewise reduces antibiotic entry into the cell. Both are ways in which bacteria become resistant to antibiotics.

Model generated from the PDB iD: 2J1n using **3DP-Jmol**, a Jmol/JSmol script that automatically generates 3D printable molecular models from structural data.

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Model files



untitled.blend



2j1n_fixed.obj



2j1n_fixed_core1_mmu3.3mf

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