

Two OMPs: Autotranslocation and LPS-Deacylation

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The outer membrane proteins (OMPs) of Gram-negative bacteria are often involved in pathogenesis. Their exposure to the extracellular environment make them potential targets for antimicrobial treatments. We present recent crystal structures of two outer membrane proteins, NalP [1] and PagL.

NalP belongs to the autotransporter family. Autotransporters secrete their own N-terminal passenger domain with their C-terminal translocator domain. The crystal structure of the translocator domain of NalP from *Neisseria meningitidis* reveals an N-terminal helix inside the pore of the β -barrel. This structure supports the model of passenger domain transport through the narrow β -barrel pore and is inconsistent with a model for transport through a central channel formed by an oligomer of translocator domains.

PagL is an enzyme that removes the 3-*O*-acyl chain of LPS, resulting in less toxic LPS. The crystal structure of PagL from *Pseudomonas aeruginosa* reveals a Ser-His-Glu catalytic triad. The surface hydrophobicity and the positions of aromatic residues, strongly suggest an unusual tilt of the β -barrel axis with respect to the membrane. We have modeled a substrate to the active site of PagL, providing insight into the specificity of PagL towards its substrate.

[1] Oomen C.J., Van Ulsen P., Van Gelder P., Feijen M., Tommassen J., Gros P., *EMBO J.*, 2004, **23**(6).

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