

MS07 Membrane Proteins

MS7-04

Toward the comprehension of the assembly and opening of the MexAB-OprM efflux pump involved in the antibiotic resistance of *Pseudomonas aeruginosa*

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Abstract

Bacterial infections remain a major public concern due to the accelerated increase in the appearance of antibiotic resistance. Among the different mechanisms used by bacteria to resist to antibiotics, the active efflux plays a major role. In Gram-negative bacteria, this is achieved by tripartite efflux pumps that form a macromolecular assembly spanning both membranes of the cellular wall. In *Pseudomonas aeruginosa*, an opportunistic pathogen highly involved in nosocomial diseases, the constitutive pump is MexAB-OprM.

Along with functional studies, many crystal structures were solved for the individual components of this pump and homologous ones [1-6]. Nevertheless, a lot of questions concerning the assembly recognition and specificity, the mechanism of efflux, and the opening of the whole pump are still a matter of active research, as the blockage of these pumps could restore the utility of the actual therapeutic arsenal. By a combined approach involving crystallography and cryo-EM together with biophysical analysis and in cellulo complementation experiments, we were able to bring new insides into the comprehension of these mechanisms.

References

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Cryo-EM structure of the MexAB-OprM efflux pump

