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Neutron Scattering analysis of the bacterial holotranslocon

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In bacteria, up to 30% of all proteins are translocated into or through the bacterial membrane. This mechanism relies on the trimeric SecYEG (translocon) complex, which forms a pore through the membrane and can open laterally in order to integrate trans-membrane protein into the lipid bilayer1. The energy required to perform the translocation is provided either by the ribosome (co-translational pathway) or the secA ATPase (post-translational pathway)2.
Four additional subunits can join the core translocon :
• Sec D and Sec F favor the translocation by using the proton-motive force3
• YidC, a conserved membrane protein insertase
• YajC, a small protein whose function remains unknown.
This seven-subunit membrane complex is called the holotranslocon (HTL). It is thought to interact with the ribosome and secA and is more efficient for membrane protein integration.
A flexible lipid cavity has been described at the center of the holotranslocon (Botte et al., in revision). We are now investigating its function and dynamic.

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