

# Neutron Scattering analysis of the bacterial holotranslocon

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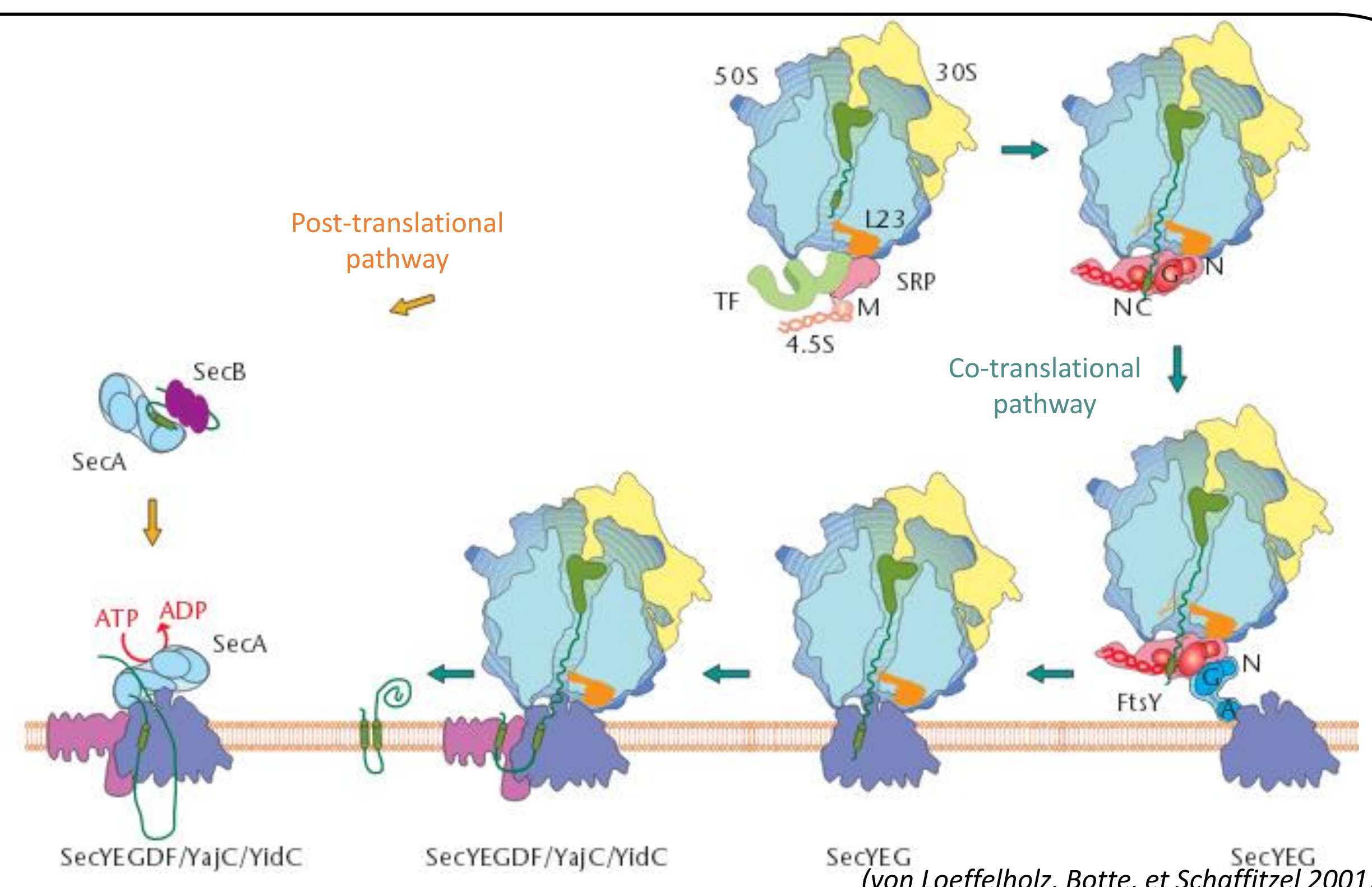
## Background

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 bilayer<sup>1</sup>. The energy required to perform the translocation is provided either by the ribosome (co-translational pathway) or the secA ATPase (post-translational pathway)<sup>2</sup>.

Four additional subunits can join the core translocon :

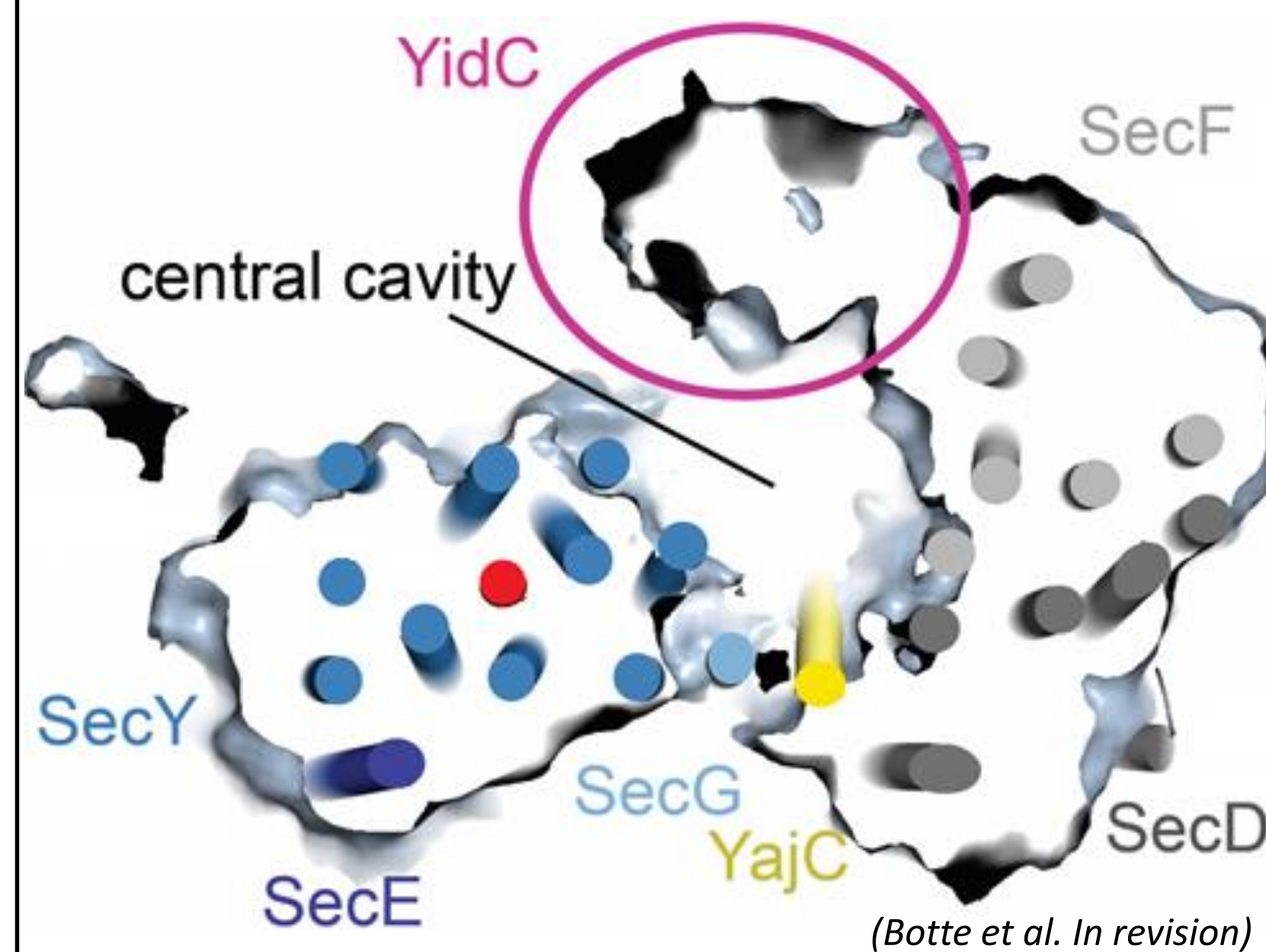
- Sec D and Sec F favor the translocation by using the proton-motive force<sup>3</sup>
- YidC, a conserved membrane protein insertase
- YajC, a small protein whose function remains unknown.

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<sup>3</sup>.



## PROJECT

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.

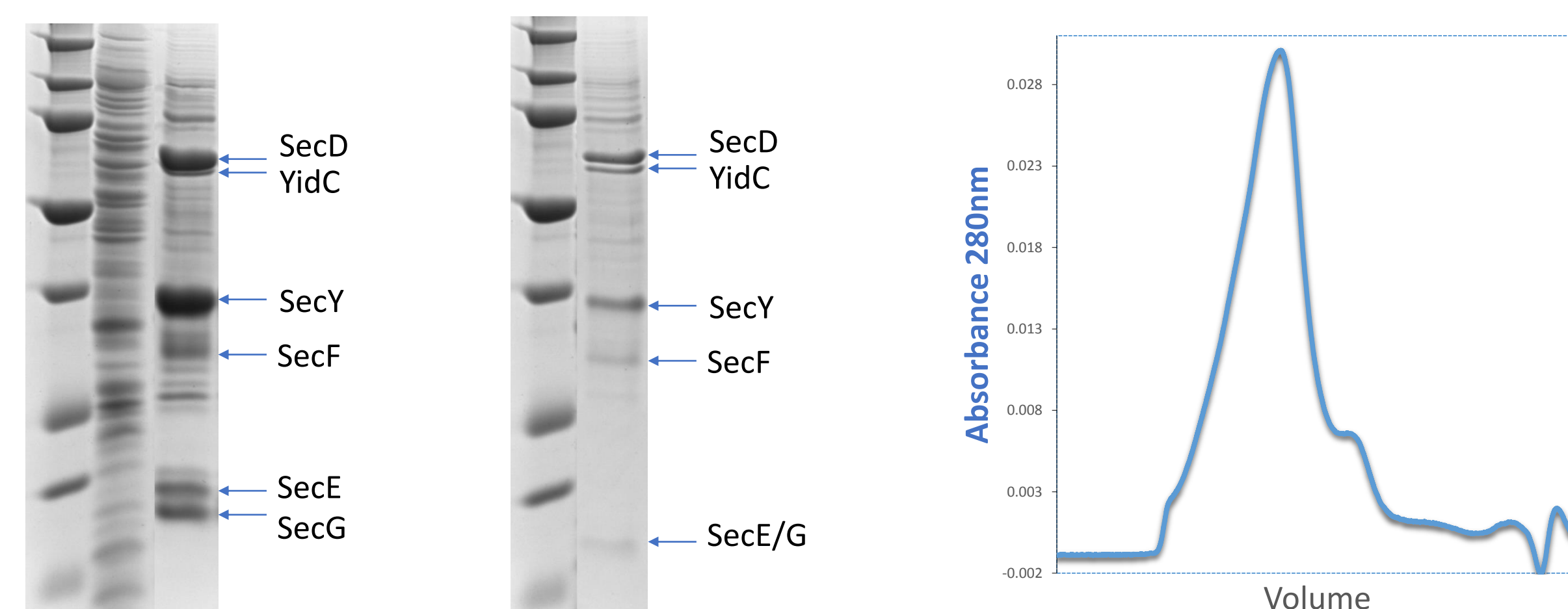
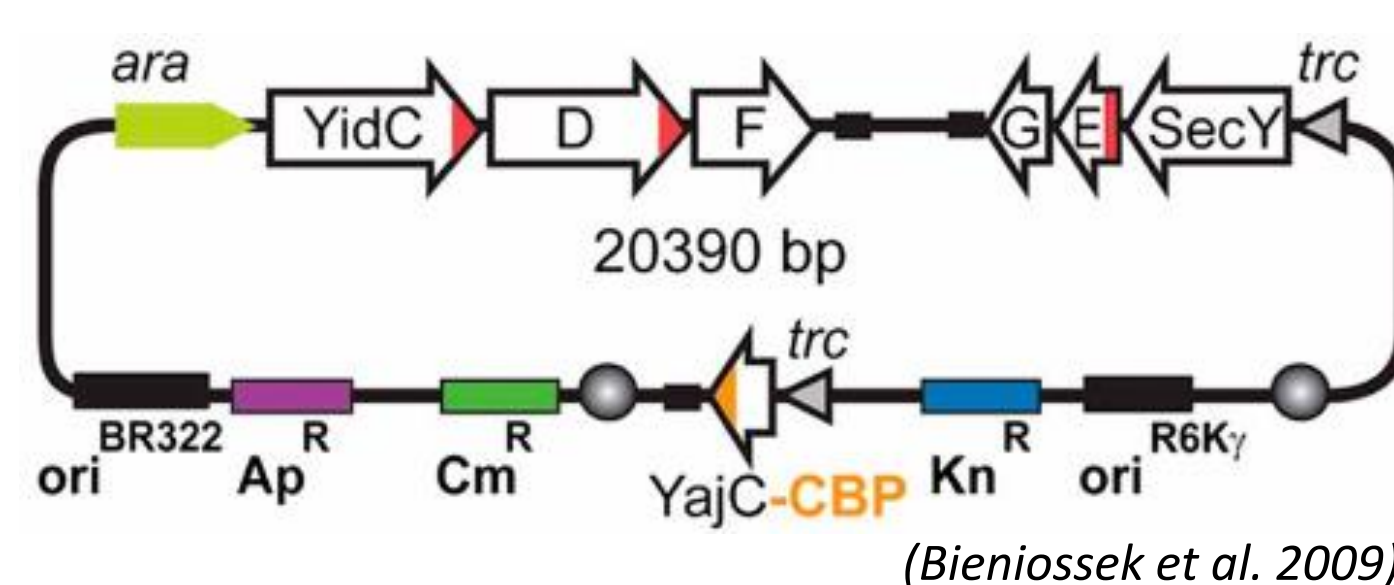


- Interactions with cytoplasmic partners
- Post-translational model
- Co-translational model
- Membrane protein integration

## METHODS

### Biochemical preparation

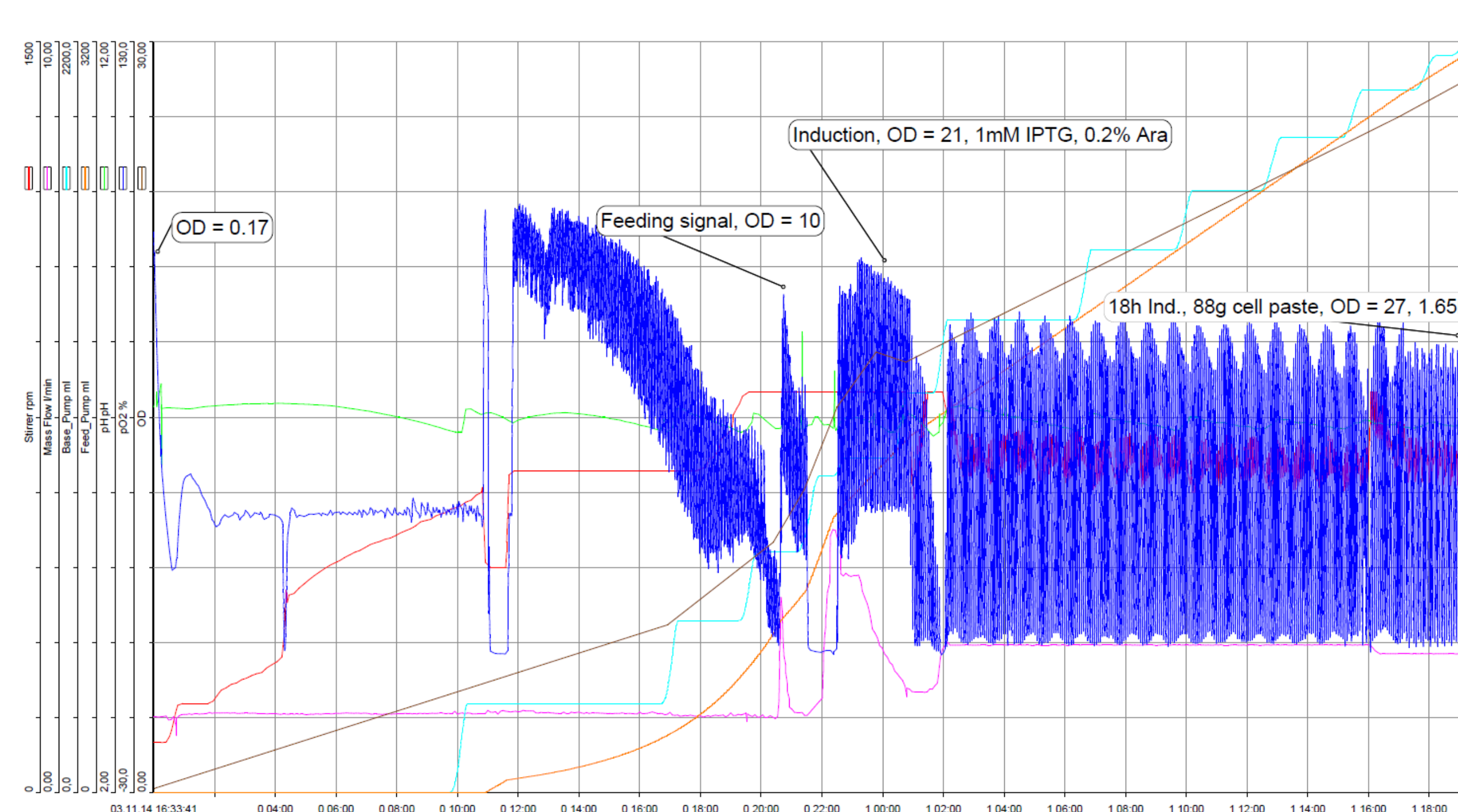
- Complex extracted from the membrane with a mild detergent : DoDecyl Maltoside (DDM)
- Two successive purification steps
- Detergent exchanged with synthetic amphiphatic polymers (Amphipol A8-35)
- Size exclusion chromatography



### Small angle Neutron scattering

- Contrast match analysis uses the natural scattering length density contrast to distinguish protein, lipids and detergent/polymers.

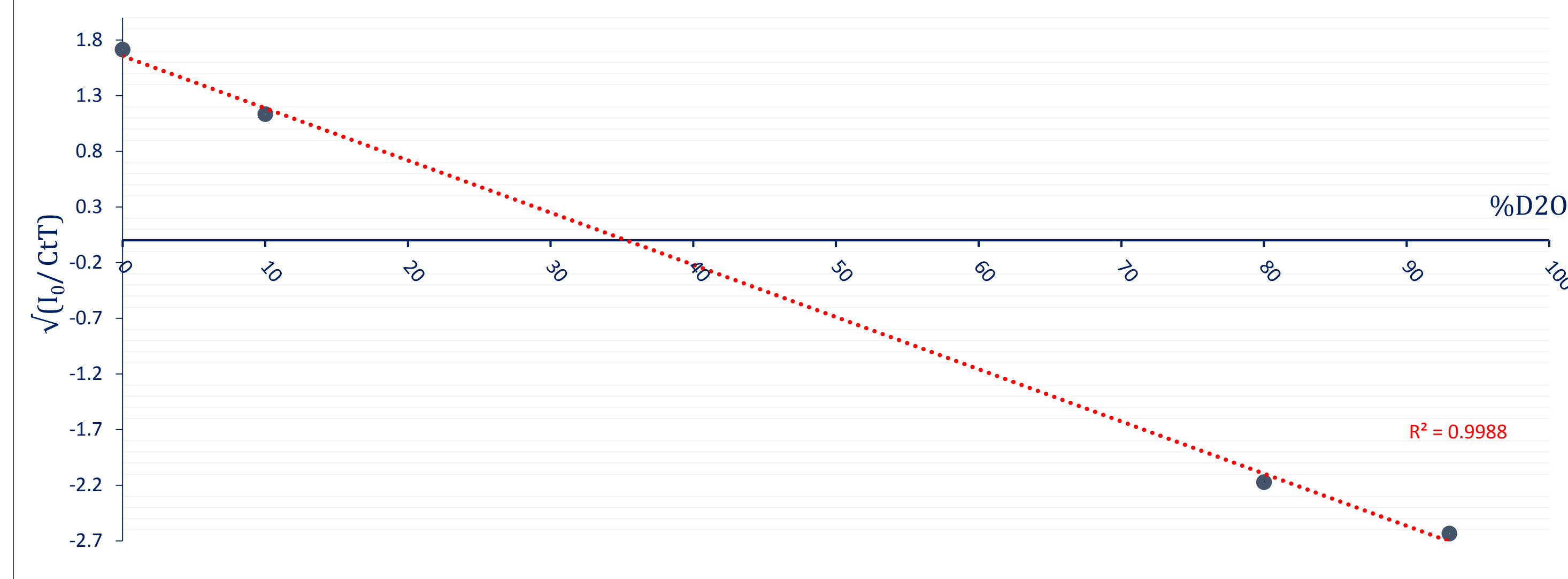
## PRELIMINARY WORK



Bacteria are cultivated in fermenters under controlled conditions :

- pH, temperature, pO<sub>2</sub>, carbon source
- Optimization of the yield for deuteration

### Contrast Match analysis



### Theoretical scattering length density :

- Protein : 40.7%
- Lipid : 7%
- Amphipol : 23.5%

### Estimated composition of the particle

- Protein : 82%
- Lipid : 14.1%
- Amphipol : 3.9%

### References:

1. Berg, B. van den *et al.* *Nature* **427**, 36–44 (2003).
2. Von Loeffelholz, O., Botte, M. & Schaffitzel, C. in *eLS* (John Wiley & Sons, Ltd, 2001).
3. Schulze, R. J. *et al.* *PNAS* **111**, 4844–4849 (2014).