

Nanopore single-molecule analysis towards peptide and protein sequencing

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Nanopore-based protein sequencing is of crucial importance for the development of proteomics analysis applications in order to develop highly performant devices for tomorrow's medicine. Up to now, either wild-type biological nanopores or artificial nanopores did not provide a sufficient resolution to screen or to read peptides with a single amino acid resolution. In the first part of my talk, I will present our latest results showing the detection and discrimination of short peptides with a single amino acid resolution [1]. In the second part of my talk, I will discuss our strategy leading to provide the first sequence library of all the 20 different amino acids. Our work opens new perspectives towards biomarkers analysis, peptide sample purity analysis, and *de novo* protein sequencing.

[1] Piguet, F., Ouldali, H., Pastoriza-Gallego, M., Manivet, P., Pelta, J., & Oukhaled, A. (2018). Identification of single amino acid differences in uniformly charged homopolymeric peptides with aerolysin nanopore. *Nature Communications*, 9(1), 966.