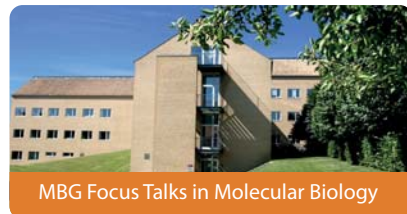


MBG FOCUS TALK

hosted by Poul Nissen & Magnus Kjærgaard



Tuesday 4 July from 11:30-12:15

Venue: Twin auditorium, 1324-025, building 1324, Aarhus University

By Nikos Hatzakis

Dept. Chemistry, University of Copenhagen

Novonordisk center for Protein Research, University of Copenhagen

Dept. Pediatrics, Boston Children hospital Harvard Medical school



A quantum leap of understanding protein structure dynamics to function correlation by Single molecule studies and machine learning analysis

Single molecule studies have revolutionized our understanding of biomolecular recognition and have provided direct evidence of the intricate correlation of conformational dynamics, spatial localization and functional output. smFRET and single particle tracking have become a mainstream technique for studying biomolecular structural dynamics and spatial localization. The inherently complex behavior of biological systems can vary drastically both in time and across systems, consequently imposing considerable analytical challenges.

We have developed tools based on machine learning for the rapid and automated analysis, processing and data classification of smFRET and single particle tracking data. Implementation of machine learning analysis allows for acceleration of data treatment by a few orders of magnitude without a priori knowledge of the systems while at the same time is free of potential cognitive biases. Based on this sophisticated analysis we have introduced the concept of Biased metabolism of metabolic enzymes, the mechanism of CRISPR-Cas12a and deciphered cell entry pathway of proteins and viruses.

Relevant publications of my group

- 1 Stella, S. *et al.* Conformational Activation Promotes CRISPR-Cas12a Catalysis and Resetting of the Endonuclease Activity. *Cell* **2018**, 175, 1856-1871.e1821.
- 2 Jensen, S. B. *et al.* Biased cytochrome P450-mediated metabolism via small-molecule ligands binding P450 oxidoreductase. *Nat. Commun.* **2021**, 12, 2260.
- 3 Pinholt, H. D. *et al.* Single-particle diffusional fingerprinting: A machine-learning framework for quantitative analysis of heterogeneous diffusion. *Proceedings of the National Academy of Sciences* **2021**, 118, e2104624118.
- 4 Malle, M. G. *et al.* Single-particle combinatorial multiplexed liposome fusion mediated by DNA. *Nat. Chem.* **2022**.
- 5 Schmidt, S. G. *et al.* The dopamine transporter antiports potassium to increase the uptake of dopamine. *Nat. Commun.* **2022**, 13, 2446.

Everyone interested is very welcome to attend.