LUXEMBOURG INSTITUTE OF HEALTH
RESEARCH DEDICATED TO LIFE

UNIVERSITÉ DU LUXEMBOURG

LECTURE SERIES & WORKSHOPS

TRANSLATIONAL BIOINFORMATICS AND SYSTEMS BIOMEDICINE

07
FEB. 2019
Thursday

LECTURE
Maison des Sciences Humaines
"Blackbox" room
(11, Porte des Sciences
L-4366 Esch-sur-Alzette)
3.00 - 4.00 pm

MEET THE SPEAKER*
Light snacks provided
Biotech 2 building (BT2)
(6 Avenue de Swing, Belvaux)
Riken conference room
ground floor
5.00 - 6.00 pm

1 2 3 4 5 6 7 8

*Please register by sending a mail to florence.henry@lih.lu

SPEAKER
Prof Vera VAN NOORT
Centre of Microbial and Plant Genetics, Leuven, Belgium

HOSTS:
LIH/University of Luxembourg
RESPONSIBLE SCIENTIST:
Roland Krause
(roland.krause@uni.lu)

MODELING THE EFFECT OF POST-TRANSLATIONAL MODIFICATIONS ON INTERACTIONS IN LARGE EUKARYOTIC PROTEIN COMPLEXES

ABSTRACT

Protein post-translational modifications (PTMs) have an indispensable role in living cells as they expand chemical diversity of the proteome, providing a fine regulatory layer that can govern protein-protein interactions in changing environmental conditions. We have investigated the effects of acetylation and phosphorylation on the stability of subunit interactions in purified *Saccharomyces cerevisiae* complexes, namely exosome, RNA polymerase II and proteasome. I will present a computational framework that consists of conformational sampling of the complexes by molecular dynamics simulations, followed by Gibbs energy calculation by MM/GBSA. After benchmarking against published tools such as FoldX and Mechismo, we could apply the framework for the first time on large protein assemblies with the aim of predicting the effects of PTMs located on interfaces of subunits on binding stability.

We discovered that acetylation predominantly contributes to subunits' interactions in a locally stabilizing manner, while phosphorylation shows the opposite effect. Even though the local binding contributions of PTMs may be predictable to an extent, the long range effects and overall impact on subunits' binding were only captured because of our dynamical approach. Employing the developed, widely applicable workflow on other large systems will shed more light on the roles of PTMs in protein complex formation.

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