LECTURE SERIES 2024

# INFECTION & IMMUNITY

LUXEMBOURG INSTITUTE OF HEALTH | UNIVERSITÉ DU LUXEMBOURG

**08 NOV 2024**
Friday

**LECTURE**
**11.00am - 12.00pm**

**MEET & EAT ***
Light lunch provided
**12.30pm - 2pm**


# The TOPAS project: exploiting the tumor proteome activity status for future cancer therapies

## ABSTRACT

It is important to realize that cancer is not primarily a genetic but a disease of malfunctioning signalling pathways that are regulated by the proteome. It is also important to know that the molecular "wiring" of these pathways is very heterogeneous, context-dependent and differs a lot between individual patients. It is therefore of paramount importance to understand the tumor biology of a particular patient to identify therapeutically actionable mechanisms.

It is sometimes forgotten that most therapeutic drugs act on proteins and that any of the drugs known today rarely only have one effect on an organism. Yet, it has been known since the days of Paracelsus that drugs exert their effects in a dose-dependent fashion. The molecular processes leading to a drug-induced change in cellular phenotype can be roughly divided into: i) target binding, ii) pathway engagement, and iii) cellular reprogramming to arrive at a new viable state or cell death, together forming the mechanism of action (MoA) of a drug.

Today, quantitative mass spectrometry is the most comprehensive approach for the proteome-wide characterization of patient tumors as well as drugs because of its unique ability to assay thousands of proteins and their post-translational modifications in complex cellular backgrounds in parallel.

In this presentation, I will introduce our approach to profiling the (phospho)proteomes of cancer patients and how we derive information regarding the likely molecular drivers of individual disease. I will also describe the decryptT, decryptM and decryptE technologies that measure target deconvolution, pathway engagement and cellular reprogramming in a fully dose-dependent fashion respectively. Finally, I will show how we aim to bring the two aspects together in order to arrive at individual treatment recommendations in molecular tumor boards. Beyond the clinical potential of drug and patient proteomics, it is important to share data with the scientific community so that more hypothesis may be formed and tested than any single laboratory can hope to accomplish. Our approach to this is ProteomicsDB that contains millions of dose-response curves and for >150 cancer drugs and the (phospho)proteomes of hundreds of cancer cell lines.

## SPEAKER

### Prof Bernhard Küster

Full Professor and Chair of Proteomics and Bioanalytics, TUM München
Director Bavarian Biomolecular Mass Spectrometry Center Co-director Center for Infection Prevention
Adjunct Professor, University of Southern Denmark, Odense

## HOST:

Department of Infection and Immunity (LIH)

## RESPONSIBLE SCIENTIST:

Gunnar Dittmar (gunnar.dittmar@lih.lu)

*** Please note that registration is mandatory by sending an email to carole.weis@lih.lu or michelle.roderes@lih.lu**

**Locations:**

**Lecture:**
House of BioHealth
Conference Room
*(ground floor 0)*
*29, rue Henri Koch, L-4354 Esch-sur-Alzette*

**Meet & eat:**
House of BioHealth
Salle Françoise Barré Sinoussi
*Registration mandatory*

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