Dipartimento di Chimica e Tecnologie del Farmaco

Sapienza Università di Roma

Epigenetic Seminars

Tuesday Jul 15, 2025
Room A, Plesso Tecce
CU018, h 3.00-5.00 pm

Prof. Mark T. Bedford

The University of Texas MD Anderson Cancer Center, Houston, TX, USA

Characterizing Methylarginine Effector Proteins

Arginine methylation is a ubiquitous and relatively stable post-translational modification (PTM) that occurs in three types: monomethylarginine (MMA), asymmetric dimethylarginine (ADMA) and symmetric dimethylarginine (SDMA). Methylarginine marks are catalyzed by members of the **protein arginine methyltransferases (PRMTs**) family of enzymes. Substrates for arginine methylation are found in most cellular compartments, with RNA-binding proteins forming the majority of PRMT targets. Arginine methylation often occurs in intrinsically disordered regions of proteins, which impacts biological processes like protein-protein interactions and phase separation, to modulate **gene transcription, mRNA splicing and signal transduction**. With regards to protein-protein interactions, the major **"readers"** of methylarginine marks are Tudor domain-containing proteins, although additional domain types and unique protein folds have also recently been identified as methylarginine readers. Here I will describe the identification and characterization of a new effector protein for methylarginine marks called SART3 and I will also address how the known effector SND1 likely functions as an oncogene.

Prof. Christian A. Olsen

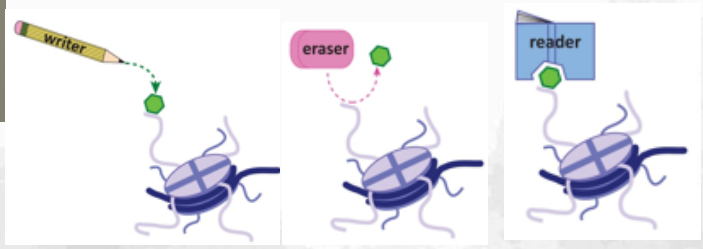
University of Copenhagen, Copenhagen, Denmark

Inhibitors of Class III and IV Histone Deacetylases (HDACs)

Histone deacetylases (HDACs) are validated targets for treatment of certain cancer types and play numerous regulatory roles in biology, ranging from epigenetics to metabolism. Small molecules are highly important as tool compounds to probe these mechanisms as well as for the development of new medicines. Therefore, detailed mechanistic information and precise characterization of the **enzyme substrate preference** as well as **development of chemical probes** to investigate the effects of HDAC enzymes are vital.

Through profiling of both sirtuins and zinc-dependent HDACs, we have developed efficient assay formats for inhibitor characterization and discovered enzymatic activities against novel ε-*N*-acyllysine posttranslational modifications, most recently ε-*N*-lactyllysine.

In this presentation, I will focus on our advances in the selective targeting of **SIRT5**, **SIRT7** and **HDAC11**, using different strategies including **covalent targeting and macrocyclic peptide inhibitors**.



Proponent: Prof. Antonello Mai