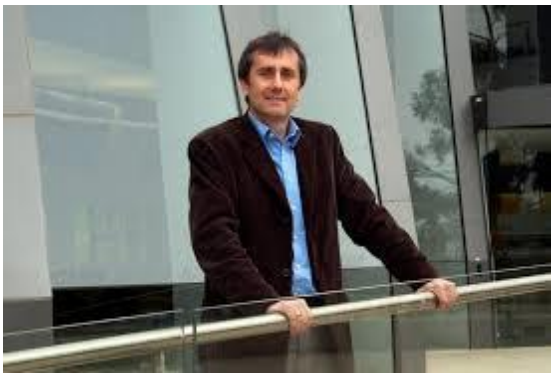
# SFB 960-/BZR – Kolloquium

## Sondertermin: 29.05.2017, 13:30 Uhr

## Neubau Biologie: DE 1.113



# Prof. Dr. Thomas Preiss

## Australian National University

**"Translation cycle dynamics and compendia of RNA-protein interactions"**

Eukaryotic mRNAs form dynamic and complexes with RNA-binding proteins (RBPs), frequently through regulatory motifs situated in their untranslated regions (UTRs). Such combinatorial mRNP formation acutely regulates mRNA function and represents a key aspect of gene expression control.
We have incomplete knowledge of RBPs that are active in a given cellular context. Addressing this, we employed two in vivo proteomic methods, mRNA interactome capture and RBDmap, to identify 1148 proteins as the RBP repertoire of beating cardiomyocytic HL-1 cells. Included were many proteins with known roles in RNA biology but those with roles in cardiovascular physiology or disease, mitochondrial function and intermediary metabolism were also highly represented. Notably, we identified 73 metabolic enzymes as RBPs. RNA-enzyme contacts frequently involve Rossmann fold domains with examples for mutual exclusivity of, or compatibility between, RNA-binding and enzymatic function. The findings suggest previously hidden RNA-mediated regulatory interactions between cardiomyocyte gene expression, physiology and metabolism.

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