



**Department of Anatomy and Cell Biology**  
Hosted by Dr. Susanne Bechstedt

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**"Investigating Heterogeneity and Specialization of Macromolecular Machines"**

In the last decade, RNAs have emerged as being not only conveyors of genetic information, but also important regulators of gene expression. While after transcription, all RNA species are assembled into ribonucleoprotein (RNP) complexes to get modified, processed and transported to their final destination within the cell, for each of them this occurs via a different pathway defined by very specific proteins, which form discrete subsets associating with each RNA in a dynamic fashion. Yet even for a specific RNA specie these subsets can differ, either due to alternative maturation pathways for specialized niches of gene expression, cellular perturbations, cell types, and tissues, or disease. In my lab, we are developing and applying proteomic approaches to study these different aspects of RNA metabolism. Combining fast affinity purification with semi-quantitative mass spectrometry and targeted crosslinking, we have investigated interactome variations of alternative and spatiotemporal composites during ribosome biogenesis and mRNA maturation, as well as identified vicinal intra-complex interactomes of dynamic RNPs. Further expanding our approaches, we aim to examine heterogeneity and modifications of both RNAs and proteins using mass spectrometry to determine components, niches, and functions of specialized ribosomes.

**Wednesday, February 20<sup>th</sup>, 2019**

**11:30 am**

**Strathcona Anatomy Building**  
**3640 University Street**  
**Room 2/36**

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