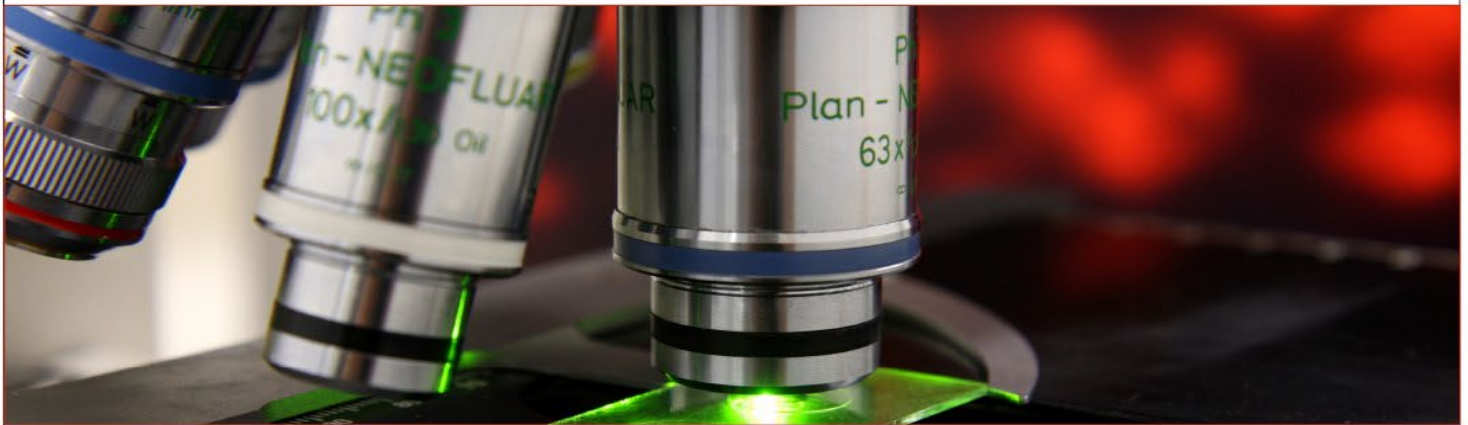


SÉMINAIRES ET CONFÉRENCES



Anne-Ruxandra Carvunis

Department of Computational and Systems Biology

University of Pittsburgh School of Medicine

“Systems Approaches to Decipher the Molecular Mechanisms of Evolutionary Innovation”

The yeast genome contains more than 200,000 open reading frames (ORFs), of which ~5,000 are annotated with confidence as protein-coding genes. Most yeast ORFs are short and lack evidence of conservation between closely related species or between isolates. These sequence properties are consistent with the notion that these ORFs transiently emerge and then disappear with random mutations in the absence of selection. As a result, these ORFs remain unannotated. However, we show by integrative ribosome profiling analyses that up to 20,000 unannotated yeast ORFs are translated. Through systematic analyses of gain- and loss-of-function mutants, high-content microscopy and integrative transcriptomics, we are uncovering evidence that transiently emerging ORFs carry a surprisingly profound impact on cell biology and fitness despite their seemingly random evolutionary patterns. We discuss the implications of our findings for the systems biology of evolutionary innovation.



Faculté de médecine
Département de biochimie
et médecine moléculaire

Université 
de Montréal

Le lundi 16 octobre, 11h30

Pavillon Joseph-Armand-Bombardier, Salle : 1035

ET

[Lien Zoom](#)

Invité de Stephen Michnick
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