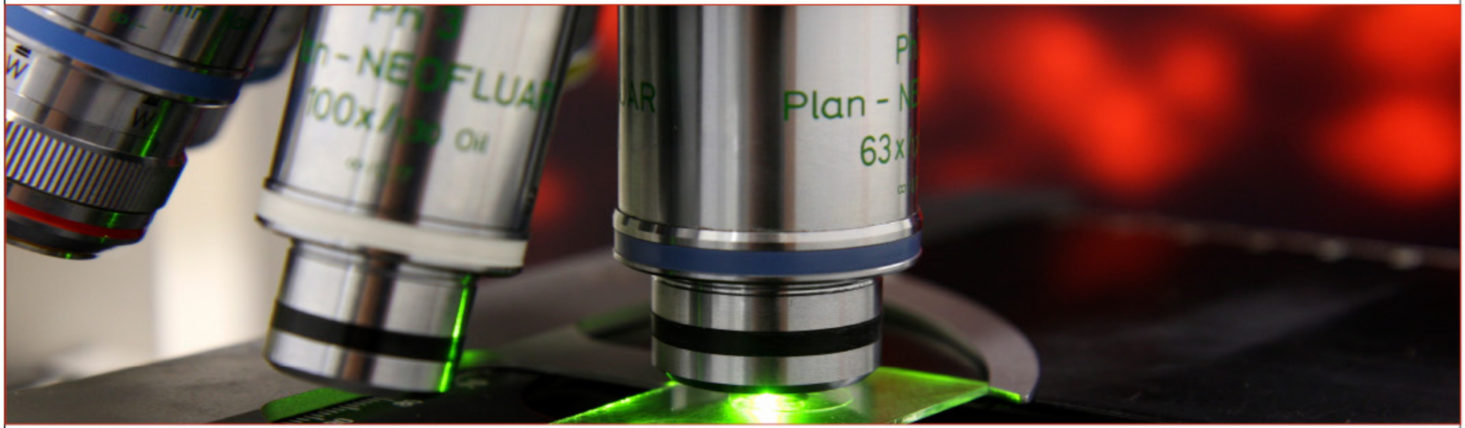
SÉMINAIRES ET CONFÉRENCES



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Multiscale deep phenotyping and optimization of mammalian developmental cis-regulatory elements

Gene expression control in space and time in metazoans is collectively mediated by non-coding regions called cis-regulatory elements (CREs). Despite its fundamental and practical importance, key features of the transcriptional 'regulatory code', the sequence-to-function relationship for CREs, remain empirically uncharacterized: What length of DNA is sufficient to capture complete regulatory activity? How much synergy exists between transcription factor binding sites? Can the flexibility of the regulatory grammar be statistically assessed? Focusing on select cell-type specific CREs as models, we functionally profiled diverse classes of variant libraries using massively parallel reporter assays to provide a comprehensive, multi-scale, and quantitative view of regulatory sequence-to-function maps. Further, leveraging CRE 'derivatization' and model-driven mutagenesis, we provide a roadmap for the engineering of compact, highly active CREs.

Lundi 7 avril 2025, 11h30

Pavillon Joseph-Armand-Bombardier, Salle : 1035

ET

LIEN ZOOM

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