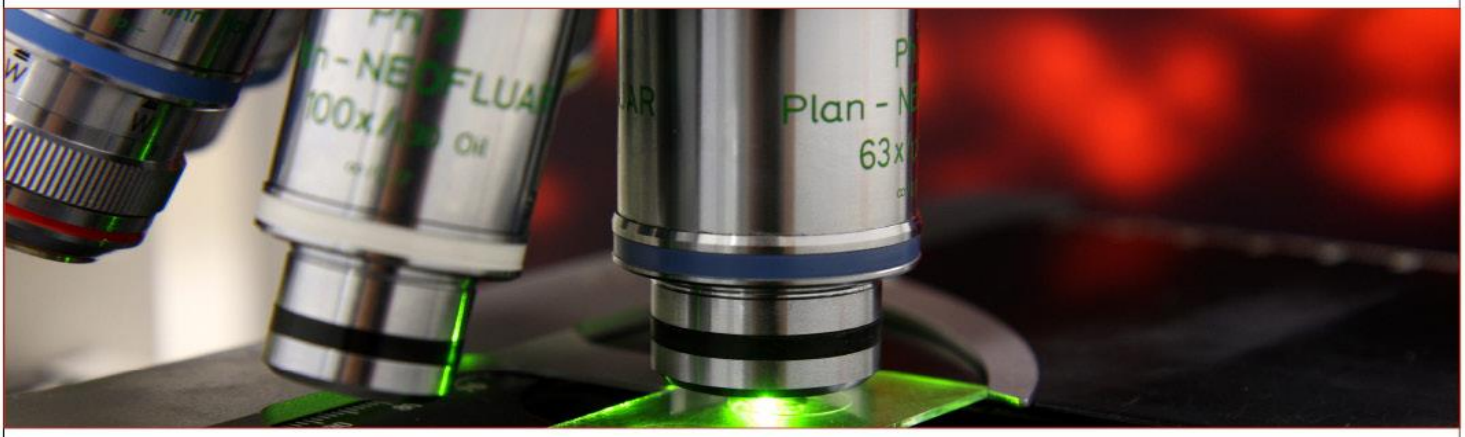
SÉMINAIRES ET CONFÉRENCES



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'' A Complete Map of Specificity Encoding for a Partially Dynamic Protein interaction ''

Thousands of human proteins function by binding short linear motifs embedded in intrinsically disordered regions. How affinity and specificity are encoded in these binding domains and the motifs themselves is not well understood. The evolvability of binding specificity - how rapidly and extensively it can change upon mutation - is also largely unexplored, as is the contribution of 'fuzzy' dynamic residues to affinity and specificity in protein-protein interactions. To address these questions, we constructed a complete map of specificity encoding for a globular protein domain binding to a disordered ligand. Quantifying >200,000 energetic interactions revealed 20 major energetically coupled pairs of sites that control specificity. These are organized into six modules, with most mutations in each module reprogramming specificity for a single position in the ligand. The dynamic, or "fuzzy" tail of the ligand is more robust to mutation than the non-dynamic residues but contributes additively to binding affinity and communicates with non-dynamic residues to enable changes in specificity. Our results quantify the binding specificities of >1,800 globular proteins to reveal how specificity is encoded and provide a direct comparison of the encoding of affinity and specificity in structured and dynamic molecular recognition.

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Université de Montréal

Le lundi 22 septembre, 11h30

Pavillon Joseph-Armand-Bombardier, Salle : 1035

Et

Zoom

invité de Stephen Michnick et Adrian Serohijos