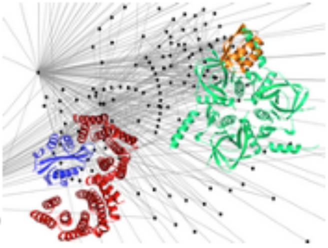

# JUNIOR CONFERENCE Computational approaches to nucleic acid and protein structure & function

*8 Nov 2017 Orsay (France)*

| **DNA Dynamics and Gene Expression** (Chair: Arach Goldar) | |
|---|---|
| 9:15 | Keynote presentation: François Major. Artificial microRNA engineering. |
| 10:05 | Improved Promoter Sequence Models for de novo Transcription Factor Binding Site Prediction in Bacteria<br>Ibrahim Sultan, Pierre Nicolas, Sophie Schbath, Vincent Fromion |
| 10:25 | Pause café |
| 10:40 | A numerical model for the spatio-temporal program of DNA replication in Xenopus early embryos<br>Ciardo Diletta, Kathrin Marheineke, Arach Goldar |
| 11:00 | Filtering techniques for feature reduction in k-mer analysis<br>Nguyen Ha, Daniel Gautheret |
| 11:20 | Dynamics of nucleotide entry into the active site of the hepatitis C virus RNA polymerase<br>Kaouther Ben Ouirane |
| **Proteins and Protein Complexes** (Chair: Anne Lopes) | |
| 11:40 | Coupling natural and artificial coevolution for the structural prediction of complexes<br>Aravindan Arun Nadaradjane, Seydou Traoré, Jessica Andreani, Raphael Guérois |
| 12:00 | Lunch |
| 14:00 | Keynote presentation: Alessandra Carbone. Learning about protein-protein interactions at the residue resolution. |
| 14:50 | La modélisation structurale en 3D : outil innovant pour la compréhension de l'expression des antigènes de groupe sanguin<br>Aline Floch, France Pirenne, Christophe Tournamille, Alexandre de Brevern |
| 15:10 | Application of robotics algorithms for the full description of the conformational landscape of cyclized peptides<br>Maud Jusot, Dirk Stratmann, Marc Vaisset, Eric Ngo, Matthias Lerbinger, Théo Torcq, Jacques Chomilier, Juan Cortes |
| 15:30 | Pause café |
| 15:45 | Studying conservation of interaction energy landscapes across structural homologs through cross-docking calculations<br>Hugo Schweke, Sophie Sacquin-Mora, Marie-Hélène Mucchielli-Giorgi, Anne Lopes |
| **RNA Structure** (chair: Daniel Gautheret) | |

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|---|---|
| 16:05 | Curating pseudoknoted RFAM families using sequence structure alignment<br>wei Wang, Matthieu Barba, Philippe Rinaudo, Alain Denise, Yann Ponty |
| 16:25 | An integrative approach for predicting the RNA secondary structure for the HIV–1 Gag UTR using probing data<br>Afaf Saaidi, Yann Ponty, bruno sargueil |
| 16:45 | Prediction de pseudonoeuds avec la programmation linéaire bi-objective<br>Audrey Legendre |

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