

Affectation des sujets d'article pour les posters

ATTENTION :

-- un seul étudiant par article

-- s'il n'y a que le résumé dans les proceedings de Jobim, il faut rechercher l'article complet correspondant.

-- vous ne devez pas prendre d'article en lien direct avec votre stage de M1.

	Sujet	Nom étudiant et ordre de préférence
1	Vizitig: context-rich exploration of sequencing datasets Bastien Degardins, Charles Paperman and Camille Marchet	SECHER Quentin
3	OREO: Optimizing Read Order for practical compression Mathilde Girard, Lea Vandamme, Bastien Cazaux and Antoine Limasset	Homero SANCHEZ MOREIRA
5	GrAnnoT, a tool for efficient and reliable annotation transfer through pangenome graph Nina Marthe, François Sabot and Matthias Zytnicki-	Elio Torquet
6	Facilitating genome annotation using ANNEXA and long-read RNA sequencing Nicolai Hoffmann, Aurore Besson, Edouard Cadieu, Matthias Lorthiois, Victor Le Bars, Arnel Houel, Christophe Hitte, Catherine André, Benoit Hédan and Thomas Derrien	Ciaran Mahony
7	SpecPeptidOMS Directly and Rapidly Aligns Mass Spectra on Whole Proteomes and Identifies Peptides That Are Not Necessarily Tryptic: Implications for Peptidomics Emile Benoist, Géraldine Jean, Hélène Rogniaux, Guillaume Fertin and Dominique Tessier	Dalia Belmadi
8	SVJedi-Tag : a novel method for genotyping large inversions with linked-read data Mélody Temperville, Anne Guichard, Fantine Benoit, Claire Mérot, Fabrice Legeai and Claire Lemaitre	Tamani tiziri
10	Metatranscriptomic classification in the study of microbial translocation Antonin Colajanni, Raluca Uricaru, Rodolphe Thiebaut and Patricia Thebault	Cyril Gilbert
11	OneNet—One network to rule them all: Consensus network inference from microbiome data Camille Champion, Raphaëlle Momal, Emmanuelle Le Chatelier, Mathilde Sola, Mahendra Mariadassou and Magali Berland	Raphaël Ribes
16	Methods for a species-specific genome-scale metabolic model designed for eukaryotes and applied to the <i>Ascomyces nidulans</i> macroalga Pauline Hamon-Giraud, Anne Siegel, Gabriel Markov, Benoît Bergk Pinto, Jeanne Got, Coralie Rousseau, François Thomas, Simon Dittami and Erwan Corre	Ayoub Rayane AIT ALLAOUA
17	Predictive modelling of Acute Promyelocytic Leukaemia resistance to Retinoic Acid therapy. Jose-Antonio Sanchez-Villanueva, Lia N'Guyen, Mathilde Poplineau, Estelle Duprez, Elisabeth Remy and Denis Thieffry	Yara HOUHOU
18	Building a modular and multi-cellular virtual twin of the synovial joint in Rheumatoid Arthritis Naouel Zerrouk, Franck Augé and Anna Niarakis	Tara Guillorit
21	RNA3DClust: unsupervised segmentation of RNA 3D structures using density-based clustering Quoc Khang Le, Eric Angel, Fariza Tahi and Guillaume Postic	Loik Galtier
22	Natural selection acting on gene expression and regulation in mole-rats Maëlle Daunesse, Elise Parey, Diego Villar and Camille Berthelot	Anaïs ANDRE
23	Evolutionary dynamics of centromeric DNA in guenon might end an old anthropocentric dogma Julien Pichon, Lauriane Cacheux, Manel Ait El Hadj, Axel Jensen, Katerina Guschanski, Loïc Ponger and Christophe Escudé	Coquerelle Mickael
26	Benchmarking circRNA Detection Tools from Long-Read Sequencing Using Data-Driven and Flexible Simulation Framework Anastasia Rusakovich, Sébastien Corre, Edouard Cadieu, Rose-Marie Fraboulet, Marie-Dominique Galibert, Thomas Derrien and Yuna Blum	Olayitan Dagba Allade

28	MethMotif 2024 Suite Reveals the Epigenetic Blueprint of Context-Specific Transcription Factor Binding Sites Matthew Dyer, Quy Xiao Xuan Lin, Denis Thieffry and Touati Benoukraf	Ania Saïdani
31	Assessing bioinformatics software annotations : bio.tools case-study Ulysse Le Clanche, Sarah Cohen Boulakia, Yann Le Cunff, Alban Gaignard and Olivier Dameron	Farah Moukachar
33	Madbot, a metadata and data brokering online tool to ensure the adoption of standards and FAIR principals in an open science context Laurent Bourri, Imane Messak, Baptiste Rousseau, Anakim Gualdoni, Elora Vigo, Matéo Hiriart, Nadia Goué, Julien Seiler and Thomas Denecker	Hermine KIOSSOU
34	Benchmarking Data Leakage on Link Prediction in Biomedical Knowledge Graph Embeddings Galadriel Brière, Thomas Stosskopf, Benjamin Loire and Anaïs Baudot	Lola Condom
36	Variable selection in transcriptomics data using knockoffs in a classification framework Julie Cartier, Chloé Agathe Azencott, Adeline Fermanian and Florian Massip.	Rayane ELMEDJADJI
37	Evaluating deep learning models for plant protein function prediction Minh Ngoc Vu, Hoang Ha Nguyen, Antoine Toffano and Pierre Larmande	Alessandra Ribeiro
38	jsPCA enables fast, interpretable and parameter-free domain identification in 3D spatial transcriptomics data Ines Assali, Paul Escande and Paul Villoutreix	Anaëlle Joo
39	Leveraging multi-omics integration to uncover childhood trauma-related mechanisms in bipolar disorder. Margot Derouin, Amazigh Mokhtari, El Chérif Ibrahim, Pierre-Eric Lutz, Raoul Belzeaux, Cynthia Marie-Claire, Frank Bellivier, Bruno Etain, Cathy Philippe and Andrée Delahaye-Duriez	Najat Amoukou
41	Exhaustive Identification of Pleiotropic Loci for Serum Leptin Levels in the NHGRI-EBI Genome-Wide Association Catalog Anthony Haidamous, David Meyre and Sébastien Hergalant	Teo Guilhou
43	Explainable AI for Marine Ecological Quality Prediction: Integrating Microbiome Data, Metadata, and Diversity Houria Braikia, Sana Ben Hamida and Marta Rukoz	Corentin Leguen