

ECCB 2026 Accepted abstracts

Genomics, epigenomics and genome editing

CREsted: modeling genomic and synthetic cell-type-specific enhancers across tissues and species.

Niklas Kempynck, Seppe De Winter, Cas Blaauw, Vasilieios Konstantakos, Eren Can Ekşi, Sam Dieltiens, Darina Abaffyová, Valérie Bercier, Ibrahim Taskiran, Gert Hulselmans, Valerie Christiaens, Ludo Van Den Bosch, Lukas Mahieu and Stein Aerts.

From Transcripts to Cells: Dissecting Sensitivity, Signal Contamination, and Specificity in Xenium Spatial Transcriptomics.

Mariia Bilous, Daria Buszta, Jonathan Bac, Senbai Kang, Yixing Dong, Stephanie Tissot, Sylvie Andre, Marina Alexandre-Gaveta, Christel Voize, Solange Peters, Krisztian Homicsko and Raphael Gottardo.

Improved RNA–DNA interaction calling suggests RNA-based gene regulation of phenotypic transitions.

Simonida Zehr, Ralf Brandes, Marcel Schulz and Timothy Warwick.

k-mer manifold approximation and projection for visualizing DNA sequences.

Chengbo Fu, Einari Niskanen, Gong Hong Wei, Zhirong Yang, Marta Sanvicente-García, Marc Güell and Lu Cheng.

Locityper enables biobank-scale genotyping of structurally complex loci.

Timofey Prodanov and Tobias Marschall.

Ultrafast and accurate sequence alignment and clustering of viral genomes.

Andrzej Zieleziński, Adam Gudyś, Jakub Barylski, Krzysztof Simiński, Piotr Rozwalak, Bas E. Dutilh and Sebastian Deorowicz.

Transcriptomics and gene regulation

From enhancer-scale to locus-scale: modelling gene regulation with sequence-to-function models.

Casper H. Blaauw, Niklas Kempynck, Seppe De Winter, Vasilieios Konstantakos, Eren Can Ekşi, Sam Dieltiens, Darina Abaffyová, Valérie Bercier, Ibrahim Taskiran, Gert Hulselmans, Valerie Christiaens, Ludo Van Den Bosch, Lukas Mahieu, Alexander van Oudenaarden, Oliver Hobert, David R. Kelley and Stein Aerts.

Prognostic RNA-splicing archetypes in breast cancer identified by extended pre-training of histopathology foundation models.

Lisa Fournier, Garance Haefliger, Albin Vernhes, Vincent Jung, Lena Loye, Valentine Du Bois, Intidhar Labidi-Galy, Pascal Frossard, Igor Letovanec, Cédric Vincent-Cuaz and Raphaëlle Luisier.

STAN, a computational framework for inferring spatially informed transcription factor activity.

Linan Zhang, April Sagan, Bin Qin, Haoyu Wang, Elena Kim, Baoli Hu and Hatice Ulku Osmanbeyoglu.

Unexpectedly high intrinsic sequence specificity and complex DNA binding of human transcription factors.

Arttu Jolma, Aldo Hernandez-Corchado, Ally Yang, Ali Fathi, Kaitlin Laverty, Alexander Brechalov, Rozita Razavi, Mihai Albu, Hong Zheng, Ivan Kulakovskiy, Hamed Najafabadi and Tim Hughes.

Proteins and structural biology

Accurate identification and mechanistic evaluation of pathogenic missense variants with Rhapsody-2.

Anupam Banerjee, Anthony Bogetti and Ivet Bahar.

DRLiPS: A Novel Computational Method for Identifying Druggable Small Molecule Binding Pockets in RNA.

Sowmya Ramaswamy Krishnan and Michael Gromiha.

Efficient sampling of large-scale transition pathways and intermediate conformations in sub-mesoscopic protein complexes.

Domenico Scaramozzino, Byung Ho Lee and Laura Orellana.

Exploring functional insights into the human gut microbiome via the structural proteome.

Hongbin Liu, Jiuming Wang, Yu Li and Lei Dai.

ImmunoMatch learns and predicts cognate pairing of heavy and light immunoglobulin chains.

Dongjun Guo, Deborah Dunn-Walters, Franca Fraternali and Joseph Ng.

Rapid Proteome-Wide Discovery of Protein-Protein Interactions With ppIRIS.

Luiz Felipe Piochi, Di Tang, Johan Malmström, Yasaman Karami and Hamed Khakzad.

Reconstructing Atomistic Biomolecular Dynamics from High-Speed Atomic Force Microscopy Data.

Florence Tama.

Systems biology, multi-omics integration and modelling

Charting spatial ligand-target activity using Renoir.

Narein Rao, Tanush Kumar, Dina Kazemi, Shaozhi Hou, Atefeh Khakpoor, Merrin Mary Eapen, Rhea Pai, Liang Qiao, Archita Mishra, Florent Ginhoux, Jerry Chan, Jacob George, Ankur Sharma and Hamim Zafar.

Decoding non-coding SNPs: systems genomics modelling dissects the heterogeneity of IBD.

Dezso Modos, John Thomas, Johanne Brooks-Warburton, Martina Poletti, Balazs Bohar, Yufan Liu, Matthew Madgwick, Wen-Xin Kang, Benjamin Alexander-Dann, Azedine Zoufir, Padhmanand Sudhakar, Domenico Cozzetto, David Fazekas, Shamith Samarajiwa, Simon R Carding, Nicholas Powell, Bram Verstockt, Andreas Bender and Tamas Korcsmaros.

Machine learning and data-driven inverse modeling of metabolomics unveil key processes of active aging.

Jiahang Li, Steffen Waldherr and Wolfram Weckwerth.

PatientProfiler, from multi-omic data to clinical insight: patient-specific models to derive signalling-based biomarkers.

Veronica Lombardi, Lorenzo Di Rocco, Eleonora Meo, Veronica Venafrà, Elena Di Nisio, Velerio Perticaroli, Mihail Lorentz Nicolaeasa, Chiara Cencioni, Francesco Spallotta, Rodolfo Negri, Francesca Sacco and Livia Perfetto.

Reusable Generative Models for Mechanistic Studies of Metabolic Dynamics.

Ljubisa Miskovic, Subham Choudhury, Ilias Toumpe, Ousaama Gabouj, Jakob Behler and Vassily Hatzimanikatis.

Shortcomings of silhouette in single-cell integration benchmarking.

Pia Rautenstrauch and Uwe Ohler.

Unifying non-Markovian dynamics and agent heterogeneity in scalable stochastic networks.

Aurelien Pelissier, Miroslav Phan, Didier Le Bail, Niko Beerenwinkel and Maria Rodriguez Martinez.

Biodiversity, sustainability, and environmental bioinformatics

Cleanifier: contamination removal from microbial sequences using spaced seeds of a human pangenome index.

Johanna Elena Schmitz, Jens Zentgraf and Sven Rahmann.

Coral microbiomes as reservoirs of unknown genomic and biosynthetic diversity.

Fabienne Wiederkehr, Daniel Richter, Lucas Paoli, Dora Racunica, Hans-Joachim Ruscheweyh, Martin Sperfeld, James O'Brien, Samuel Miravet-Verde, Alena Streiff, Jessica Ransome, Clara Chepkirui, Taylor Priest, Anna Sintsova, Guillem Salazar, Kalia Bistolas, Teresa Sawyer, Karine Labadie, Kim-Isabelle Mayer, Didier Forcioli, Pierre Galand, Fabien Lombard, Pedro Oliveira, Olivier Thomas, Rebecca Vega Thurber, Romain Troublé, Christian Voolstra, Patrick Wincker, Maren Ziegler, Jörn Piel and Shinichi Sunagawa.

Improving metagenome binning by integrating intrinsic features and taxonomy

Simon Rasmussen, Svetlana Kutuzova, Jakob Nybo Andersen, Mads Nielsen, Lars Hestbjerg Hansen and Knud Nor Nielsen.

ProteomeLM: A proteome-scale language model enables accurate and rapid prediction of protein-protein interactions and gene essentiality across taxa.

Cyril Malbranke, Gionata Paolo Zalaffi and Anne-Florence Bitbol.