

CIBB 2026 – Accepted Posters

Poster Sessions

Preliminary Schedule

Last update: August 3, 2026

Venue: Museo di Arte Classica (Museum of Classical Art), Sapienza University of Rome

The following list includes all accepted posters. Presentation in the poster session may differ from the final on-site poster exhibition.

Session A - Sept 2, 2026 (from 16:45 to 18:30)

Bioinformatics (30)

ID	Title
5265	A ML-powered Multiscale Computational Platform Based on QSP and PBPK Modeling to Support the Development of mRNA-based Therapies
0022	A Network Story: tumor educated platelets transcriptome and Glioblastoma
3745	Analysis of Prompt Engineering for Drug Toxicity Prediction
0059	Autoresearch Discovery of Interpretable Filter Rules for Antibody Binder Classification
0087	Benchmarking LLMs for automated systems biology model replication
0070	Beyond Differential Expression: Network Centrality measures reveal Tissue-Specific Signatures in Tumor-Educated Platelets
0029	Computational Framework for the Design of Second-Generation Pharmacochaperones Targeting Allosteric Pockets
0023	Computational Prediction of Pathogenic FMR1 Variants in Fragile X Syndrome
0031	Development and Internal Validation of a Multimodal Machine Learning Model Integrating Omics, Clinical and Psychosocial Data for Heart Failure Risk Prediction

0033	FLiCoN: Friendship Like differential Coexpression Network for the identification of Tumor-Educated Platelets Driver Genes in Glioma via structural Imbalance
0050	geneslator: a R package for comprehensive gene identifier mapping and annotation
0039	High-Performance Tensor-Based HSMM Decoding for Genome-Scale CpG Island Detection
0094	Integrated genomic analysis of corpus callosum malformations in a Tunisian cohort reveals extensive genetic heterogeneity and improves genotype-phenotype characterization
0030	Integrative analysis of multi-modal single-cell data reveals chromosome alterations underlying critical disease development stages: a proof-of-principle in MDS
0066	Investigating Immunotherapy Response in Non-Small Cell Lung Cancer Using Machine Learning and Differential Networks
0089	Large-scale analysis and clustering of RNA 3D structures
0086	Learning Read-Level joint genomic and epigenomic status representations from Nanopore sequencing data using Jesica-Fetcher and NTV3-like architecture
0062	Machine learning approaches for predicting functional lncRNAs and key regulatory interactions in plant gene networks
0079	Mutational signature in Mycobacterium tuberculosis under pretomanid and nitric oxide exposure
0077	Pathway-Mediated Networks for Drug Repurposing in Breast Cancer
0034	Quantum Annealing for De Novo Genome Assembly
0072	Quantum Optimization for Protein-Protein Interaction Network Alignment
0095	Repeats Enrichment Analysis of sequencing Datasets (READs) reveals unique repair and transcription dynamics of human satellites
0044	REV-AGE and REV-AGE 2.0: From Systematic Evidence Mapping to AI-Guided Mechanistic Discovery in Aging Research
0036	Single-cell multi-omics integration for TCR-epitope binding inference in acute myeloid leukemia
0083	Single-Molecule Tissue-of-Origin Profiling for Prenatal and Oncology cfDNA Applications

5995	Statistical Model Checking of Uncertain Continuous Time Markov Chain in Systems Biology
0035	Toward Accessible and Reproducible Bioinformatics Workflows for Nanopore-Based Virus Surveillance
0047	VISMA: Vector Integration Site Mutation Analysis

Biostatistics (7)

ID	Title
8845	Comparative Deep Learning and Statistical Analysis for Spatial Prediction of Lymph Node Metastasis in Gastric Cancer
0078	Early Warning of Extremely Rare Events from Pediatric Cardiac Intensive Care Electronic Health Records
5486	Functional Shapley Representations for Longitudinal Random Survival Forests using Hierarchical FPCA
0040	GLM-Based Parametric Survival Modeling Under Two-Phase Sampling: A Computational Framework with Application to High-Dimensional Methylation Data
0024	Modified Gompertz Function in Quantitative Evaluation of Endolysin Lytic Activity in Physiological Fluids
0060	QFARM - hierarchical quantitative association rule mining
4182	Spatial host pathogen transcriptomics maps bacterial burden linked urothelial injury and repair in bladder infection

Medical Informatics (10)

ID	Title
3784	A new MRI-based feature for quantifying the Diffuse Low-Grade Glioma brain infiltration and discriminating patterns of patients
0056	Advancing Facial Recognition for Next-Generation Phenotyping in Africa
0085	AEGLOS V7: Hyperbolic Digital Pathology for Morphology-to-Genomics Prediction in Advanced Non-Small Cell Lung Cancer
0046	Artificial Intelligence in Oncology: Trends and Insights from Systematic Evidence
0054	Beyond the Diagnosis: Semi-Automated Risk Analysis of Inappropriate Antibiotic Prescribing in Mexico and the Potential for Real-Time Alerts
0001	Contour-Guided Segmentation and X-Ray Image Validation for Pneumonia Detection Using Mobile Deep Learning in Low-Resource Settings
0027	Development of an AI-Based Assistive Technology for Neurodivergent Children: Enhancing Learning and Social Engagement in African Language Contexts
0068	FFPE-Open-ST: high-resolution, unbiased spatial transcriptomics profiling of archival samples
6293	On the adoption of Quantum Machine Learning for Privacy-Preserving and Explainable Diabetic Retinopathy Detection and Localisation

Session B - Sept 3, 2026 (from 10:15 to 12:30)

Bioinformatics (29)

ID	Title
0065	A Multiplex Graph Framework for Higher-Order Gene Interactions in Lung Cancer Pathway Analysis
0038	A tumor-agnostic network medicine framework reveals topological rewiring of systemic T-cell immunity in long-surviving cancer patients
0073	An atlas of gene expression and alternative splicing across stress conditions in microalgal species: a focus on CO2 capture
0055	An LLM-RAG System for Interactive Multi-Omic Exploration of 3D Genome Organization and Gene Expression during Mouse Cortical Neurogenesis
0048	Analytical variability across computational workflows in assessing tumor mutational burden and microsatellite instability from NGS data in male breast cancer
0045	Closing the Design-Validation Loop for AI-Driven mRNA Therapeutics via Structured Knowledge Accumulation
0061	Doski-nf: an integrated computational pipeline for consensus variant calling and comprehensive cancer genomic profiling
1805	DQIS: Byzantine Fault Tolerance for Multi-Channel Immune Surveillance - A Quantum-Inspired Quorum-Based Framework
0075	Evaluating Genome Language Model Embeddings as Transferable Priors for Metagenomic Binning
0042	From hepatosome to interactome: network-based discovery of UBIAD1 as a lipid-metabolism target in hepatocellular carcinoma
0043	G4REP: A deep learning framework for the prediction of human RNA G-quadruplex-binding proteins
0049	Gene expression models for Alzheimer's Disease vs Mild Cognitive Impairment classification
0088	HIC-Sutra: Inferring 3D genome organization from condition-specific transcriptomic signals

0092	Hypothesis-driven integrative transcriptomics reveals distinct Z-disc gene signatures in ischemic and non-ischemic cardiomyopathy
0080	Integration of computational and functional screening reveals novel R-loop-inducing drugs for triple-negative breast cancer treatment
3383	Learning Invariant Biological Dynamics Across Environments with Physics-Aware Neural Differential Equations
0082	Liquid biopsy-based multi-omics data integration for triple-negative breast cancer
0052	MErlin - Methylation-driven Expression & Regulation Linkage in Interacting Nuclear-domains
0091	MoonLitDB: An LLM-powered database annotating moonlighting proteins from scientific literature
7280	NARCOD: Non-Arbitrarily Reproducible Clustering of transcriptOmics Data
0071	Network-Based Comparison of Solid Tissue and Tumor-Educated Platelet Transcriptomes in Glioblastoma
0028	OMICS-query: An AI Agent-Based Chatbot for Bioinformatics Pipelines
0067	SOPHYSM: More Steps towards Digital Twins of Solid Tumours
0032	Spatial GeoMx NGS profiling to map molecular drivers of pathological response in the tumor microenvironment of pleural mesothelioma patients
0026	TensorPLS: an R package for tensor-aware PLS-based discriminant analysis of longitudinal multi-omics data
0058	Torch-eCpG v2: A Scalable and Interpretable Framework for eQTM Mapping and Multi-Omic Network Analysis
0037	Towards Full Bioinformatics Automation at the National Facility for Genomics of Human Technopole
0093	Whole-Genome Sequencing Reveals Novel De Novo and Familial Variants Underlying Syndromic and Isolated Congenital Heart Defects in Tunisian Patients

Biostatistics (8)

ID	Title
2618	Exploring the potential of Bayesian Gaussian Mixture integration for Variational Autoencoders in the generation of synthetic tabular data
0025	Exploring the role of marital status in Depression-Free Life Expectancy among older adults
0084	Federated Real World Data, Zero Exchange Framework for Transportability
9768	Gimme a rainy week life more: a computational study on the signal-to-noise ratio of epigenetic aging associations
0064	Impact of Non-Informative Censoring on the Performance of Propensity Scores Methods for Estimating Absolute Treatment Effects on Survival Outcome
8282	Joint Bayesian Modelling for Neuroimaging Meta-Analysis
0057	Mixture-based Nonparametric Estimation of Spatial Covariance Functions with Applications to HIV Key Population Size Estimation across Sub-Saharan Africa
0004	Piecewise Regression Mixture Models with Skewness

Medical Informatics (9)

ID	Title
0041	A unified Medical Informatics black-box framework for integrating environmental sampling and laboratory analytical data at the Luxembourg National Health Laboratory (LNS)
9287	An unsupervised clustering analysis of breast cancer data derived from electronic health records enhanced through UMAP dimensionality reduction
0069	Automation of Prescription Analysis in Older Adults: A Big Data Approach in Mexico
0311	ClinAgent: A ReAct-Based Agent for Conversational Access to Clinical Trial Information
0076	High-Resolution Spatial Transcriptomics Using Open-ST Reveals Alterations across Midbrain Subregions in an Alzheimer's Disease Mouse Model
7510	Multimodal Learning from Temporally Grounded Narrative Events
0005	Predicting Third-Generation Cephalosporin Resistance in Hospitalised Patients Using Machine Learning: Evidence from Tanzania's AMR Surveillance Data, 2021-2025
9549	Privacy-Preserving Detection of Rare Disease-Associated Cell Subsets via Secure Multi-Party Computation
0090	Proteogenomic insights into complex human diseases
0053	The voice as a diagnostic tool: Machine Learning-based speech model in discriminating patients with acute mental disorders

This is a preliminary program. Assignments may be subject to minor adjustments.