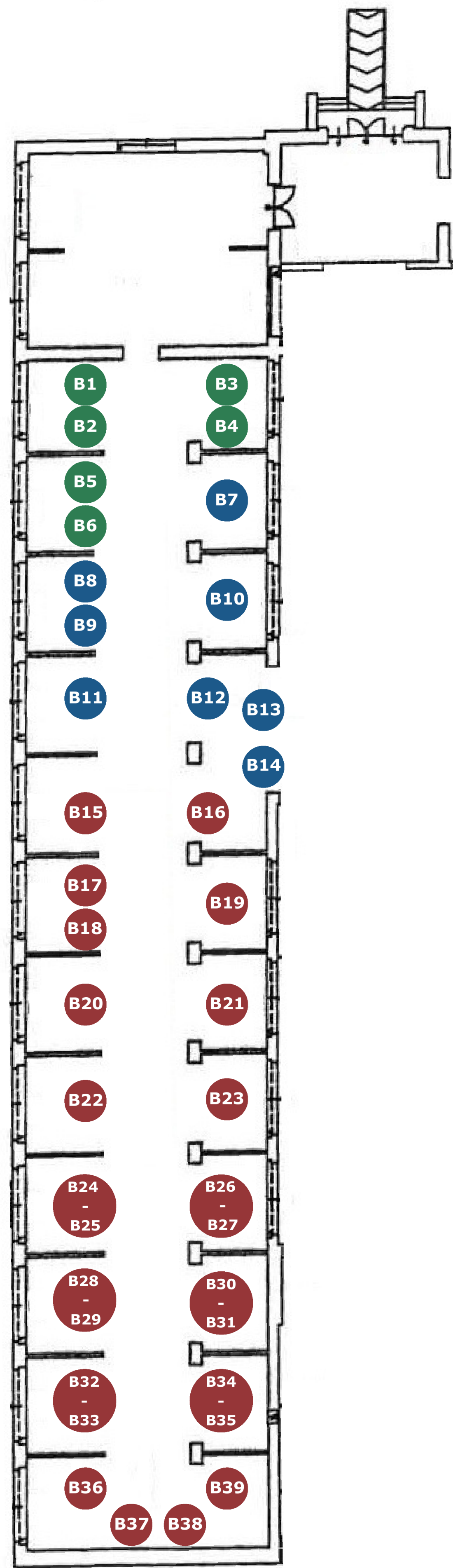




BIOSTATISTICS

- B1** ID 0004  
Piecewise Regression Mixture Models with Skewness
- B2** ID 2618  
Exploring the potential of Bayesian Gaussian Mixture integration for Variational Autoencoders in the generation of synthetic tabular data
- B3** ID 0064  
Impact of Non-Informative Censoring on the Performance of Propensity Scores Methods for Estimating Absolute Treatment Effects on Survival Outcome; Simulation study
- B4** ID 0084  
Federated Real World Data, Zero Exchange Framework for Transportability
- B5** ID 0025  
Exploring the role of marital status in Depression-Free Life Expectancy among older adults
- B6** ID 9768  
Gimme a rainy week life more: a computational study on the signal-to-noise ratio of epigenetic aging associations

MEDICAL INFORMATICS

- B7** ID 0311  
ClinAgent: A ReAct-Based Agent for Conversational Access to Clinical Trial Information
- B8** ID 7510  
Multimodal Learning from Temporally Grounded Narrative Events
- B9** ID 9287  
An unsupervised clustering analysis of breast cancer data derived from electronic health records enhanced through UMAP dimensionality reduction
- B10** ID 0069  
Automation of Prescription Analysis in Older Adults: A Big Data Approach in Mexico
- B11** ID 9549  
Privacy-Preserving Detection of Rare Disease-Associated Cell Subsets via Secure Multi-Party Computation
- B12** ID 0041  
A unified Medical Informatics black-box framework for integrating environmental sampling and laboratory analytical data at the Luxembourg National Health Laboratory (LNS)
- B13** ID 0076  
High-Resolution Spatial Transcriptomics Using Open-ST Reveals Alterations across Midbrain Subregions in an Alzheimer's Disease Mouse Model
- B14** ID 0090  
Proteogenomic insights into complex human diseases

BIOINFORMATICS

- B15** ID 0026  
TensorPLS: an R package for tensor-aware PLS-based discriminant analysis of longitudinal multi-omics data
- B16** ID 7280  
NARCOD: Non-Arbitrarily Reproducible Clustering of transcriptOmics Data
- B17** ID 0031  
Development and Internal Validation of a Multimodal Machine Learning Model Integrating Omics, Clinical and Psychosocial Data for Heart Failure Risk Prediction
- B18** ID 0092  
Hypothesis-driven integrative transcriptomics reveals distinct Z-disc gene signatures in ischemic and non-ischemic cardiomyopathy
- B19** ID 0049  
Gene expression models for Alzheimer's Disease vs Mild Cognitive Impairment classification
- B20** ID 0043  
G4REP: A deep learning framework for the prediction of human RNA G-quadruplex-binding proteins
- B21** ID 0045  
Closing the Design-Validation Loop for AI-Driven mRNA Therapeutics via Structured Knowledge Accumulation
- B22** ID 0082  
Liquid biopsy-based multi-omics data integration for triple-negative breast cancer
- B23** ID 1805  
DQIS: Byzantine Fault Tolerance for Multi-Channel Immune Surveillance - A Quantum-Inspired Quorum-Based Framework Grounded on Melanoma, GBM, and PDAC Single-Cell RNA-Seq Data
- B24** ID 0071  
Network-Based Comparison of Solid Tissue and Tumor-Educated Platelet Transcriptomes in Glioblastoma
- B25** ID 0080  
Integration of computational and functional screening reveals novel R-loop-inducing drugs for triple-negative breast cancer treatment
- B26** ID 0038  
A tumor-agnostic network medicine framework reveals topological rewiring of systemic T-cell immunity in long-surviving cancer patients
- B27** ID 0042  
From hepatosome to interactome: network-based discovery of UBIAD1 as a lipid-metabolism target in hepatocellular carcinoma
- B28** ID 0028  
OMICS-query: An AI Agent-Based Chatbot for Bioinformatics Pipelines
- B29** ID 0091  
MoonLitDB: An LLM-powered database annotating moonlighting proteins from scientific literature
- B30** ID 0055  
An LLM-RAG System for Interactive Multi-Omic Exploration of 3D Genome Organization and Gene Expression during Mouse Cortical Neurogenesis
- B31** ID 0075  
Evaluating Genome Language Model Embeddings as Transferable Priors for Metagenomic Binning
- B32** ID 0052  
MERlin - Methylation-driven Expression & Regulation Linkage in Interacting Nuclear-domains
- B33** ID 0058  
Torch-eCpG v2: A Scalable and Interpretable Framework for eQTM Mapping and Multi-Omic Network Analysis
- B34** ID 0032  
Spatial GeoMx NGS profiling to map molecular drivers of pathological response in the tumor microenvironment of pleural mesothelioma patients receiving neoadjuvant chemo-immunotherapy
- B35** ID 0067  
SOPHYSM: More Steps towards Digital Twins of Solid Tumours
- B36** ID 0061  
Doski-nf: an integrated computational pipeline for consensus variant calling and comprehensive cancer genomic profiling
- B37** ID 0048  
Analytical variability across computational workflows in assessing tumor mutational burden and microsatellite instability from NGS data in male breast cancer
- B38** ID 0037  
Towards Full Bioinformatics Automation at the National Facility for Genomics of Human Technopole
- B39** ID 0073  
An atlas of gene expression and alternative splicing across stress conditions in microalgal species: a focus on CO2 capture