

AVAILABLE POSITIONS

Principal Investigator	BEATRICE BODEGA
Institute of Affiliation	Fondazione Istituto Nazionale Genetica Molecolare "Romeo ed Enrica Invernizzi" (INGM)

PROJECT INFO	
Title of the proposed project:	Decoding RNA Programs of therapy resistance in cancer
Short description of the project	Cancer therapy resistance is increasingly driven by adaptive RNA programs that extend beyond genetic alterations and include alternative isoforms, non-coding RNAs, chromatin-associated RNAs and retrotransposon-derived transcripts. This PhD project will investigate how these RNA programs regulate tumor adaptation, genome stability, immune visibility and response to therapy. The student will combine computational analysis of genomic, transcriptomic and long-read sequencing data, integration with public cancer genomics datasets, functional perturbation and RNA-binding protein prioritization to identify candidate RNA programs, define their mechanistic contribution to therapy resistance and nominate RNA-based biomarkers or therapeutic vulnerabilities.
Main research area for the project	RNA biology, Cancer biology
Second research area for the project	Functional genomics, computational biology
3 key words for the project	Cancer, RNA biology, therapy resistance

LAB INFO	
Main topic/s of the lab	RNA biology, immune regulation and cancer; Epigenetic and regulatory mechanisms mediated by Retrotransposons
Short description of the lab activity	The Genome Biology Lab investigates the complexity of human transcriptome with a particular focus on how retrotransposon-derived RNAs contribute to gene regulation, cell identity and disease-relevant cellular states. By combining molecular biology, genomics, long-read and single-cell transcriptomics, imaging and computational approaches, the lab aims to uncover the regulatory potential of these repetitive elements and their implications for human disease.
Recent bibliography	• LINE1 modulate human T cell function by regulating protein synthesis during the life span. Burattin FV, Vadalà R, Panepuccia M, Ranzani V, Crosti M, Colombo FA, Ruberti C, Erba E, Prati D, Nittoli T, Montini G, Ronchi A, Pugni L, Mosca F, Ricciardi S, Abrignani S, Pietrasanta C, Marasca F, Bodega B. <i>Sci Adv.</i> 2024 Oct 11;10(41):eado2134. • IRescue: uncertainty-aware quantification of transposable elements expression at single cell level. Polimeni B, Marasca F, Ranzani V, Bodega B. <i>Nucleic Acids Res.</i> 2024 Oct 28;52(19):e93.

AVAILABLE POSITIONS

	• A Versatile Pipeline for Analyzing Dynamic Changes in Nuclear Bodies in a Variety of Cell Types. Di Gioia V, Zamporlini J, Vadalà R, Parmigiani E, Bodega B, Marasca F. <i>J Vis Exp.</i> 2024 Jun 28;(208). • LINE1 elements are spliced in non-canonical transcript variants to control gene expression in human T cell quiescence and exhaustion. Marasca F, Sinha S, Vadalà R, Polimeni B, Ranzani V, Paraboschi E, Burattin FV, Ghilotti M, Crosti MC, Negri ML, Campagnoli S, Notarbartolo S, Bianchi AS, Siena S, Prati D, Montini G, Viale G, Torre O, Harari S, Grifantini R, Soldà G, Biffo S, Abrignani S, Bodega B. <i>Nat Genet.</i> 2022 Jan 17, doi: 10.1038/s41588-021-00989-7.
Group composition	Beatrice Bodega, PI Federica Marasca, Project Leader and Research Scientist Valeria Ranzani, Project Leader and Research Scientist (Bioinformatician) Rebecca Vadalà, PhD Valeria Di Gioia, PhD Helena Costa Verdera, PhD Francesco Panariello, PhD (Bioinformatician) Michele Panepuccia, 3rd year SEMM PhD student, (Bioinformatician) Alen Stambolliu, 2nd year SEMM PhD student (Bioinformatician) Jan Zamporlini, Pre-doctoral fellow Giulia Solbiati, Pre-doctoral fellow Flaminia Mazza, Pre-doctoral fellow Marco Cominelli, Pre-doctoral fellow (Bioinformatician) Jhon Villis, Master student (Bioinformatician) Davide Sandrelli, Master student (Bioinformatician) Thashini Thennakoon, Master student Federico De Santis, Bachelor student (wet)
Institutional page link	https://ingm.org/bodega_lab_ita/
Lab website link	https://bodegalab.org/