

Maddalena Pacelli

PhD Student

Curriculum Vitae

Scientific Interests

I am interested in characterizing molecular mechanisms in health and disease, specifically in the context of cancer immunology, where single cell technologies opened new possibilities to study functional niches in tissues in terms of cell types, states, and interactions, certainly improving our understanding and ability to treat patients. I would like to study the immune response over the course of tumor progression and treatment, focusing on changes in cellular interactions and signaling mechanisms and how these reshape the tumor microenvironment, with temporal and spatial resolution. In addition to tackle biological questions, I am interested in developing new therapeutic strategies and innovative platforms for their delivery, making therapy specific and localized to pathological site; to this aim, I have focused on synthetic biology approaches, and I believe that genetic engineering of hematopoietic stem cells for the development of innovative cell-based cancer therapies is a very promising field. I worked on a CRISPR screening on immunosuppressive macrophages and on a macrophage-based platform for studying the tumor-microenvironment changes in response to a specific signal and for the treatment of solid tumors. Recently I have been focusing on modeling synthetic receptors and designing inhibitors and strategies for their targeted delivery.

Work Experience

2023-10 -
Current

Paiardini A. Lab

Sapienza University Of Rome - Department Of Biochemical Sciences, Rome

PhD Student | Structural Bioinformatics and Drug Delivery strategies

2021-10 -
2023-09

Amit I. Lab

Weizmann Institute of Science, Rehovot - Israel

PhD Student | Novel immunotherapeutic approaches to reshape the TME

2021-07 -
2021-09

Tartaglia G.G. Lab

Italian Institute of Technology, IIT, Genoa - Italy

External collaborator for the eQTLs analysis of genetic variants associated with Schizophrenia and Bipolar Disorder from the

personal details

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Skills

Bulk / scRNA sequencing techniques.

CRISPR-KO screening.

Cell lines: HEK293T, HeLa, SH-SY5Y.

Primary cells: mouse BMDMs and BMDCs, T cells extracted from mouse spleen, PBMCs, iPSCs, mESCs.

Other techniques: cloning and transduction, RNA/DNA extraction, PCR, library preparation for different sequencing methods, ELISA, Western Blot, biochemical fractionation of cellular compartments (cytoplasm/nucleus/chromatin), flow cytometry, cell culture.

Specific assays: motor neuron differentiation from iPSCs and mESCs. Nuclei extraction from P0 mouse brain and cellular dissociation of tumor samples. T cells and macrophages coculture assay.

Computational skills: Bash, R and Python programming. Brief experience in sequencing and GWAS data analysis. Programs for protein sequence alignment and protein structure determination, molecular docking, drug design.

Psychencode database.

2019-10 -
2020-12

Rajewsky N. Lab

Berlin Institute for Medical Systems Biology - MDC, Berlin - Germany

Master thesis project (for a short description see below).

2019-03 -
2019-09

Bozzoni I. Lab

Italian Institute of Technology, IIT, Rome - Italy

Master internship project on single cell RNA sequencing during motor neuron differentiation of Amyotrophic Lateral Sclerosis (SLA) patients derived iPSCs and correlative mESCs mutant.

2018-03 -
2018-07

Presutti C. Lab

Sapienza University of Rome, Rome - Italy

Bachelor thesis project.

Education

2023-10 -
Current

PhD Student

Sapienza University of Rome - Italy

Life Sciences, curricula in Bioinformatics and Omics, Macromolecule Structure and Function and Drug Discovery

2021-10 -
2023-09

PhD Student

Weizmann Institute of Science - Israel

Systems Immunology Department, Immunogenomics

2018-10 -
2021-05

Master degree: Genetics and Molecular Biology

Sapienza University of Rome, Berlin Institute For Medical Systems Biology - Max Delbrück Center For Molecular Medicine - Rome And Berlin

Final score: 110 with honors/110

Thesis project: "Genome-wide analysis of poly(A) tails length in cytoplasm/nucleus reveals nuclear shortening with functional implications" – Berlin Institute for Medical Systems Biology - Max Delbrück Center for Molecular Medicine, Berlin – Germany

2015-01 -
2018-04

Bachelor degree: Biotechnology

Sapienza University of Rome - Rome, Italy

Final score: 110 with honors/110

Thesis project: "Characterization of the HIVEP2 circular RNA isoform, isolated from hippocampus of model mice for Autism Spectrum Disorders" – Department of Biology and Biotechnology "Charles Darwin" – Sapienza University of Rome, Rome – Italy

Teaching Experiences

Mediterranean Institute for Life Sciences - Split, Croatia

summer school teaching homology modeling and protein structure prediction rational and tools

Languages

English



Advanced

Italian



Advanced

French



Intermediate

German



Beginner

Hebrew



Beginner

Fellowships

- Project fellowship "Borsa Prof.ssa M.A. Pozio, 2020" – Sapienza Foundation, Rome, Italy
- Project Fellowship "Torno Subito, 2019" – DiSCo - Regione Lazio, Italy
- Academic Fellowship for "Scientific Research European Festival – Trieste Next 2018" – Trieste, Italy
- Academic Fellowship for "Scientific Research European Festival – Trieste Next 2016", Trieste, Italy

Trainings and Conferences

Training on Handling and Maintenance of human Pluripotent Stem Cells – Berlin Institute of Health (BIH), Berlin – Germany.

Training course on Statistics for Animal Proposal – Max Delbrück Center, Berlin – Germany.

"R" Statistical Analysis II Advanced – Max Delbrück Center, Berlin –

Publications

Rapid nuclear deadenylation of mammalian messenger RNA

under revision

doi: <https://doi.org/10.1101/2021.11.16.468655>

Master Thesis Project

Poly(A) tails are known to be important for the stability and the half-life of transcripts, being synthesized to a specie-specific fixed length during transcription and gradually shortened after the export in the cytoplasm, until degradation occurs.

Knowledge in the field mostly comes from studies performed in vitro or on few representative transcripts, due to technical challenges in sequencing homopolymers that have limited genome scale investigation of poly(A) tails until very recently.

Global poly(A) tail length profiling in vivo reported unexpected findings, such as the absence of correlation between poly(A) tails length and mRNAs stability or translation efficiency, highlighting the need for a new perspective on such a central regulatory mechanism of gene expression. My project aims to study poly(A) tails length regulation from a systems biology perspective, by taking advantage of Full-Length poly(A) and mRNAs sequencing (FLAM-seq) to sequence the poly(A) tails genome-wide. As investigation on bulk sequencing can affect spatial and functional resolution on the mechanisms regulating the poly(A) tails length, FLAM-seq libraries were accurately prepared following cytoplasmic/nuclear fractionation from HeLa, SH-SY5Y cell lines and primary mouse brain tissue. My bioinformatic analysis shows that poly(A) tails length regulation in the nucleus is linked to export and splicing and is affected by nuclear decay pathways, as part of a complex mechanism by which the cell distinguishes efficiently spliced molecules that need to be exported from nuclear retained molecules which are either stabilized or degraded, determining transcripts' fate decision.

Germany.

"La formazione in Biotecnologie in Italia" – Presidenza del Consiglio dei Ministri, Rome- Italy.

"I brevetti in biotecnologie in Italia e la loro valorizzazione economica" – Ministry of Economic Development, Rome – Italy.

"New Technologies and Strategies to Fight Cancer"- Alliance Against Cancer, Milan – Italy.

"LifeTime meets industry" – EU LifeTime Consortium, Basel – Switzerland.

2Nd Immune-oncological meeting: Immunity, Cancer and Microenvironment – Israel Immunological Society (IIS), Haifa – Israel.

Quantum Leap: how Quantum Computing is advancing from Lab to Industry – Weizmann Institute of Science, Rehovot – Israel.

BioMed 2022 – Tel Aviv, Israel.

Single Cell Genomics – Utrecht, The Netherlands.

"High Performance Bioinformatics" at CINECA - Rome, Italy