

# Maria Luisa Ratto

Researcher



## About me

My interest in genetics brought me into biotechnology, then, during my university years, I fell in love with bioinformatics. I spent all my practicals hours training first in bulk RNAseq experiments and then with single cell RNAseq.

## Personal

Maria Luisa Ratto  
nationality: Italian  
1998

## Areas of specialization

RNAseq • DNaseq •  
Single cell • Omics

## Interests

I enjoy facing complex biological problems with the powerful tools of computational biology, especially when integrating different technologies. I most of all like working in close contact with the biological questions at hand. I find cancer to be the most interesting disease.

## Extra

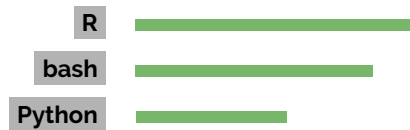
I spend my free time in nerdy activities. I love playing RPGs such as Dungeon and Dragons.

[Maria Luisa Ratto](#)  
 [MariaLuisaRatto](#)  
 [ResearchGate Profile](#)

## DEGREES

- 2020 **Biotechnology**  
BACHELOR • University of Turin
- 2022 **Molecular Biotechnology**  
MASTER DEGREE • University of Turin

## PROGRAMMING



## LANGUAGES

Italian	C2	mother tongue
English	C1	
German	A1	

## CURRICULUM

11/2022-10/2025

### Complex Systems for Quantitative Biomedicine

PHD STUDENT • University of Turin, Turin, IT

Data scientist in [Calogero Lab](#) and [Bertero Lab](#).

My project focuses on dissecting data for the optimization of iPS2-seq (iPS-optimized inducible Postranscriptional Silencing in pool deconvoluted by single cell sequencing) method and developing a tailored pipeline for specific and user-friendly analysis of these results.



01/2025-06/2025

### GeneCore

VISITING FELLOW • EMBL, Heidelberg, DE

Data scientist in the [Genomics Core Facility](#).

I worked on long reads DNaseq data of ALT+ primary tumors, investigating the role of telomeres maintenance and intrachromosomal telomeric repeats.



## PUBLICATIONS

- 2024** Arigoni, M. and Ratto, M.L. et al., *A single cell RNAseq benchmark experiment embedding "controlled" cancer heterogeneity*, Sci Data 11, 159. [10.1038/s41597-024-03002-y](https://doi.org/10.1038/s41597-024-03002-y)
- 2024** Alessandri, S. et al., *CREDO: a friendly Customizable, REproducible, DOcker file generator for bioinformatics applications*, BMC Bioinformatics 25, 110. [10.1186/s12859-024-05695-9](https://doi.org/10.1186/s12859-024-05695-9)
- 2024** Balmas, E. and Ratto, M.L. et al., *Single Cell Transcriptional Perturbome in Pluripotent Stem Cell Models*, preprint available at [SSRN](#)
- 2023** Balmas, E. et al., *Manipulating and studying gene function in human pluripotent stem cell models*, Febs Letters, Volume597, Issue18, <https://doi.org/10.1002/1873-3468.14709>
- 2021** Alessandri, L. et al., *Sparsely Connected Autoencoders: A Multi-Purpose Tool for Single Cell omics Analysis*, International Journal of Molecular Sciences (IJMS), 22(23):12755, [10.3390/ijms222312755](https://doi.org/10.3390/ijms222312755)

## CERTIFICATES

- 2023** Trainer at EMBL Course: Whole transcriptome data analysis
- 2023** Trainer at IFOM, Istituto Fondazione Oncologia Molecolare: Whole transcriptome data analysis
- 2024** Poster at BITS - Bioinformatics Italian Society Annual Meeting
- 2024** Poster at ISSCR Annual Meeting - International Society for Stem Cell Research
- 2025** Trainer at EMBL Course: Analysis and integration of transcriptome and proteome data

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