

# 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  
• Functional screens  
• Oncology

## 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.

## Contacts

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

## DEGREES

2020	<b>Biotechnology</b> BACHELOR · University of Turin 106/110
2022	<b>Molecular Biotechnology</b> MASTER DEGREE · University of Turin 110/110 Cum Laude

## 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. DOI: [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. DOI: [10.1186/s12859-024-05695-9](https://doi.org/10.1186/s12859-024-05695-9)
- 2024** Balmas, E. and Ratto, ML et al. *Single Cell Transcriptional Perturbome in Pluripotent Stem Cell Models*, preprint available at [SSRN](#) and now accepted for publication at Molecular Systems Biology.
- 2023** Balmas, E. et al. *Manipulating and studying gene function in human pluripotent stem cell models*, Febs Letters, Volume597, Issue18, DOI: [10.1002/1873-3468.14709](https://doi.org/10.1002/1873-3468.14709)
- 2021** Alessandri, L. et al. *Sparingly Connected Autoencoders: A Multi-Purpose Tool for Single Cell omics Analysis*, International Journal of Molecular Sciences (IJMS), 22(23):12755, DOI: [10.3390/ijms222312755](https://doi.org/10.3390/ijms222312755)

## SKILLS

- Computational** Scripting • Containerization • Git • Packaging (R) • Reproducibility • Documentation • Machine learning • Statistical analysis • Visualization • High-throughput data processing • Seurat • Monocle3
- Transferable** Effective communication • Presentations • Critical thinking • Problem-solving • Teamwork • Independent work • Organization • Bridging disciplines

## 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