Mattia Pelizzola

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	Istituto Italiano di Tecnologia Center for Genomic Science of IIT Via Adamello 16, Milano, Italy 20139	office: +39 02 9437 5019 e-mail: mattia.pelizzola@iit.it
Research Interests	I lead a research group studying how co- and post-transcriptional events shape gene expression pro- grams, through an interdisciplinary approach combining cutting edge experimental and computational methods.	
	Keywords: computational biology, transcriptional regulation, cancer genomics, epigenetics, RNA dynamics, RNA metabolism, RNA modifications, single-molecule sequencing, Nanopore sequencing, nascent RNA	
Education	PhD in Complexity in Post-Genomic Biology University of Torino, Physics Department (Advisor: N	2004 - 2006 M. Caselle)
	Master in Bioinformatics University of Milano Bicocca, Biotechnology Departm	2002 - 2003 nent (Advisor: P. Castagnoli)
	Master's degree in Industrial Biotechnologies University of Milano Bicocca, Biotechnology Departm	1995 - 2001 nent (Advisor: D. Porro)
	Computer Science and Engineering Politecnico di Milano	1994 - 1995
Professional Experience	Associate Professor – University of Milano-Bicocca Department of Biotechnology and Biosciences	$2023 - { m present}$
	Affiliated scientist – Istituto Italiano di Tecnologia (III Head of the Epigenomics and Transcriptional Regulat (2 computational postdocs, 2 experimental postdocs)	$\frac{1}{1} \frac{2023 - present}{1 PhD student 1 Master student}$
	Researcher – Istituto Italiano di Tecnologia (IIT)	2011 - 2023
	Postdoctoral Research Associate	2009 - 2011
	 Saik Institute, Genomic Analysis Lab, La Joha, CA Postdoctoral Research Associate Yale University, Biostatistics Division, New Haven, C 	2007 – 2009 T
	Computational Biologist University of Milano Bicocca, Biotechnology Departm	2001 - 2006 nent, Italy
	Molecular Biologist University of Milano Bicocca, Biotechnology Departm	1999 – 2001 nent, Italy
Editorial activity	Editor for Frontiers in Genetics (ISSN: 1664-8021) and Epigenomes (MDPI, ISSN: 2075-4655). <i>Reviewer</i> for the ERC-Synergy program , MSCA-EF program , Ireland Science Foundation, and Estonian Research Council. <i>Referee</i> for various journals, including Genome Research (12 articles), Bioinformatics (7), and Nature Communications (5). See details at <u>Publons</u> .	
Publications INFO	61 publications indexed in Pubmed (since 2004), including 13 as first author and 16 as last and corresponding author (since 2011). According to <u>Google Scholar</u> the total number of citations is ¿18K and the H-index is 36.	

Selected Publications

AWARDS

Furlan M, de Pretis S, Pelizzola M, "Dynamics of transcriptional and post-transcriptional regulation." **Briefings in Bioinformatics** (IF 13.9; 23 citations). 2021.

Furlan M, ... Pelizzola M, "Genome-wide dynamics of RNA synthesis, processing and degradation without RNA metabolic labeling." **Genome Research** (IF 9.4; 29 citations). 2020; We developed a tool to quantify the dynamics of RNA metabolism on total RNA-seq datasets.

de Pretis S, .. Pelizzola M, "Integrative analysis of RNA Polymerase II and transcriptional dynamics upon MYC activation." **Genome Research** (IF 9.4; 55 citations). 2017; In this study, which was selected as cover for the October issue, we provided an unprecedented analysis of RNA and RNAPII dynamics upon MYC activation.

de Pretis S, .. Pelizzola M. "INSPECT: a Computational Tool to Infer RNA Synthesis, Processing and Degradation Dynamics from RNA- and 4sU-seq Time Course Experiments." **Bioinformatics** (IF 6.9; 67 citations). 2015; In this study we provided the first software able to comprehensively quantify the RNA dynamics through the integrative analysis of total and nascent RNAs.

Sabo A*, Kress TR*, Pelizzola M*, et al. "Selective transcriptional regulation by Myc in cellular growth control and lymphomagenesis." **Nature** (IF 69.5; 497 citations). 2014; In this study we comprehensively characterized MYC-dependent transcriptional and epigenetic landscapes, thus revising the recent concept of MYC as transcriptional amplifier.

Lister R^{*}, Pelizzola M^{*}, et al. "Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells." **Nature** (IF 43; 1742 citations). 2011; In this study, which was recognized by ScienceWatch as the #4 hottest paper of 2011, we characterized the limits of epigenome reprogramming in the generation of iPSCs.

Lister R^{*}, Pelizzola M^{*}, et al. "Human DNA methylomes at base resolution show widespread epigenomic differences." **Nature** (IF 69.5; 5000 citations). 2009; In this study, which was nominated as the #2 scientific discovery of the year 2009 by the TIME Magazine, we described for the first time whole-genome DNA methylation maps for human, and the occurrence and reprogramming of non-CpG methylation in pluripotent cells.

Koga Y^{*}, Pelizzola M^{*}, et al. "Genome-wide screen of promoter methylation identifies novel markers in melanoma." *Genome Research* (IF 9.4; 220 citations). 2009

Pelizzola M^{*}, Koga Y^{*}, et al. "MEDME: an experimental and analytical methodology for the estimation of DNA methylation levels based on microarray derived MeDIP-enrichment." **Genome Research** (IF 9.4; 127 citations). 2008

HONOURS AND AIRC Investigator grant (PI), 499,000 euro, 2021-2025

ERC Consolidator finalist, 2018

Best Paper Selection by the International Medical Informatics Association, 2018

Cover of the October 2017 issue of Genome Research (de Pretis et al., Genome Research, 2017)

 $\underline{EPITRAN}\,\mathrm{COST}$ Action (European Epitranscriptomics Network), funding member and Management Committee member, 2017-2022

Abilitazione Scientifica Nazionale (eligibility to Associate Professorship): 05/E1 (General Biochemistry), 05/E2 (Molecular Biology), 05/F1 (Applied Biology), 05/I1 (Genetics), 2017-2023

Epigenesys, Associate membership, 2013-2015

European FP7 collaborative grant (co-PI) <u>RADIANT</u> (Rapid development and distribution of statistical tools for high-throughput sequencing data), 256,862 euro, 2013-2015

#4 hottest paper of 2011, ScienceWatch (Lister R, Pelizzola M et al, Nature 2011)

Selected in the 2010 Programma Giovani Ricercatori "Rita Levi Montalcini" (declined)

Catharina Foundation Postdoctoral Fellowship Award, \$34,300, 2010

#2 Scientific Discovery of the Year 2009, <u>TIME Magazine</u> (Lister R, Pelizzola M et al, Nature 2009)