

# Mattia Pelizzola

## List of Publications by Year in Descending Order

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**Version:** 2024-04-27

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

65  
papers

9,590  
citations

30  
h-index

68  
g-index

68  
ext. papers

11,089  
ext. citations

10.4  
avg, IF

5.3  
L-index

#	Paper	IF	Citations
65	Dynamics of transcriptional and post-transcriptional regulation. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	5
64	Translation is required for miRNA-dependent decay of endogenous transcripts. <i>EMBO Journal</i> , <b>2021</b> , 40, e104569	13	5
63	New insight into the catalytic -dependent and -independent roles of METTL3 in sustaining aberrant translation in chronic myeloid leukemia. <i>Cell Death and Disease</i> , <b>2021</b> , 12, 870	9.8	7
62	Identification of Genes Post-Transcriptionally Regulated from RNA-seq: The Case Study of Liver Hepatocellular Carcinoma. <i>Methods in Molecular Biology</i> , <b>2021</b> , 2284, 271-287	1.4	
61	Computational methods for RNA modification detection from nanopore direct RNA sequencing data. <i>RNA Biology</i> , <b>2021</b> , 1-10	4.8	8
60	Direct RNA Sequencing for the Study of Synthesis, Processing, and Degradation of Modified Transcripts. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 394	4.5	9
59	Ontology-driven integrative analysis of omics data through Onassis. <i>Scientific Reports</i> , <b>2020</b> , 10, 703	4.9	5
58	A dual role of dLsd1 in oogenesis: regulating developmental genes and repressing transposons. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, 1206-1224	20.1	1
57	Genome-wide dynamics of RNA synthesis, processing, and degradation without RNA metabolic labeling. <i>Genome Research</i> , <b>2020</b> , 30, 1492-1507	9.7	9
56	INSPECT-GUI Reveals the Impact of the Kinetic Rates of RNA Synthesis, Processing, and Degradation, on Premature and Mature RNA Species. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 759	4.5	4
55	Macrophages fine tune satellite cell fate in dystrophic skeletal muscle of mdx mice. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008408	6	19
54	An early Myc-dependent transcriptional program orchestrates cell growth during B-cell activation. <i>EMBO Reports</i> , <b>2019</b> , 20, e47987	6.5	20
53	m6A-Dependent RNA Dynamics in T Cell Differentiation. <i>Genes</i> , <b>2019</b> , 10,	4.2	20
52	Positioning Europe for the EPITRANSCRIPTOMICS challenge. <i>RNA Biology</i> , <b>2018</b> , 15, 829-831	4.8	14
51	Identification of Differentially Methylated Regions in the Genome of <i>Arabidopsis thaliana</i> . <i>Methods in Molecular Biology</i> , <b>2018</b> , 1675, 61-69	1.4	5
50	DNA methylation dynamics during embryonic development and postnatal maturation of the mouse auditory sensory epithelium. <i>Scientific Reports</i> , <b>2018</b> , 8, 17348	4.9	17
49	Computational Epigenomics <b>2017</b> , 19-35		

48	Dendritic Cells Inflammatory Signature Induced by Microbial Pathogens <b>2017</b> , 23-44		
47	Integrative analysis of RNA polymerase II and transcriptional dynamics upon MYC activation. <i>Genome Research</i> , <b>2017</b> , 27, 1658-1664	9.7	35
46	Compensatory RNA polymerase 2 loading determines the efficacy and transcriptional selectivity of JQ1 in Myc-driven tumors. <i>Leukemia</i> , <b>2017</b> , 31, 479-490	10.7	30
45	Integrative classification of human coding and noncoding genes through RNA metabolism profiles. <i>Nature Structural and Molecular Biology</i> , <b>2017</b> , 24, 86-96	17.6	106
44	DNA methylation variations are required for epithelial-to-mesenchymal transition induced by cancer-associated fibroblasts in prostate cancer cells. <i>Oncogene</i> , <b>2017</b> , 36, 5551-5566	9.2	59
43	Ontology-based annotations and semantic relations in large-scale (epi)genomics data. <i>Briefings in Bioinformatics</i> , <b>2017</b> , 18, 403-412	13.4	13
42	Mycobacterium tuberculosis exploits the formation of new blood vessels for its dissemination. <i>Scientific Reports</i> , <b>2016</b> , 6, 33162	4.9	51
41	LowMACA: exploiting protein family analysis for the identification of rare driver mutations in cancer. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 80	3.6	11
40	Degradation dynamics of microRNAs revealed by a novel pulse-chase approach. <i>Genome Research</i> , <b>2016</b> , 26, 554-65	9.7	98
39	Integrated Systems for NGS Data Management and Analysis: Open Issues and Available Solutions. <i>Frontiers in Genetics</i> , <b>2016</b> , 7, 75	4.5	27
38	Computational epigenomics: challenges and opportunities. <i>Frontiers in Genetics</i> , <b>2015</b> , 6, 88	4.5	5
37	Selective transcriptional regulation by Myc: Experimental design and computational analysis of high-throughput sequencing data. <i>Data in Brief</i> , <b>2015</b> , 3, 40-6	1.2	2
36	Transcription of Mammalian cis-Regulatory Elements Is Restrained by Actively Enforced Early Termination. <i>Molecular Cell</i> , <b>2015</b> , 60, 460-74	17.6	53
35	methylPipe and compEpiTools: a suite of R packages for the integrative analysis of epigenomics data. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 313	3.6	48
34	INSPECT: a computational tool to infer mRNA synthesis, processing and degradation dynamics from RNA- and 4sU-seq time course experiments. <i>Bioinformatics</i> , <b>2015</b> , 31, 2829-35	7.2	40
33	Relationship between genome and epigenome--challenges and requirements for future research. <i>BMC Genomics</i> , <b>2014</b> , 15, 487	4.5	21
32	Selective transcriptional regulation by Myc in cellular growth control and lymphomagenesis. <i>Nature</i> , <b>2014</b> , 511, 488-492	50.4	308
31	Systematic mapping of occluded genes by cell fusion reveals prevalence and stability of cis-mediated silencing in somatic cells. <i>Genome Research</i> , <b>2014</b> , 24, 267-80	9.7	5

30	Computational and experimental methods to decipher the epigenetic code. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 335	4.5	6
29	DOTS-Finder: a comprehensive tool for assessing driver genes in cancer genomes. <i>Genome Medicine</i> , <b>2014</b> , 6, 44	14.4	21
28	Patterns of population epigenomic diversity. <i>Nature</i> , <b>2013</b> , 495, 193-8	50.4	406
27	Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in <i>Arabidopsis</i> . <i>ELife</i> , <b>2013</b> , 2, e00675	8.9	265
26	Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. <i>Genome Research</i> , <b>2012</b> , 22, 246-58	9.7	385
25	Widespread dynamic DNA methylation in response to biotic stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, E2183-91	11.5	640
24	Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. <i>Nature</i> , <b>2011</b> , 471, 68-73	50.4	1241
23	The DNA methylome. <i>FEBS Letters</i> , <b>2011</b> , 585, 1994-2000	3.8	63
22	Germline competency of parthenogenetic embryonic stem cells from immature oocytes of adult mouse ovary. <i>Human Molecular Genetics</i> , <b>2011</b> , 20, 1339-52	5.6	15
21	Methylated DNA immunoprecipitation genome-wide analysis. <i>Methods in Molecular Biology</i> , <b>2011</b> , 791, 113-23	1.4	1
20	Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 1097-105	44.5	570
19	Distinct epigenomic landscapes of pluripotent and lineage-committed human cells. <i>Cell Stem Cell</i> , <b>2010</b> , 6, 479-91	18	630
18	Temporal gene expression profile of the hippocampus following trace fear conditioning. <i>Brain Research</i> , <b>2010</b> , 1308, 14-23	3.7	13
17	Integrative analysis of epigenetic modulation in melanoma cell response to decitabine: clinical implications. <i>PLoS ONE</i> , <b>2009</b> , 4, e4563	3.7	50
16	Genome-wide screen of promoter methylation identifies novel markers in melanoma. <i>Genome Research</i> , <b>2009</b> , 19, 1462-70	9.7	144
15	Human DNA methylomes at base resolution show widespread epigenomic differences. <i>Nature</i> , <b>2009</b> , 462, 315-22	50.4	3401
14	MEDME: an experimental and analytical methodology for the estimation of DNA methylation levels based on microarray derived MeDIP-enrichment. <i>Genome Research</i> , <b>2008</b> , 18, 1652-9	9.7	93
13	Statistical similarities between transcriptomics and quantitative shotgun proteomics data. <i>Molecular and Cellular Proteomics</i> , <b>2008</b> , 7, 631-44	7.6	134

12	Probing host pathogen cross-talk by transcriptional profiling of both Mycobacterium tuberculosis and infected human dendritic cells and macrophages. <i>PLoS ONE</i> , <b>2008</b> , 3, e1403	3.7	148
11	The genopolis microarray database. <i>BMC Bioinformatics</i> , <b>2007</b> , 8 Suppl 1, S21	3.6	8
10	AMDA: an R package for the automated microarray data analysis. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 335	3.6	31
9	Effects of dexamethazone on LPS-induced activation and migration of mouse dendritic cells revealed by a genome-wide transcriptional analysis. <i>European Journal of Immunology</i> , <b>2006</b> , 36, 1504-15	6.1	46
8	Dendritic cells in pathogen recognition and induction of immune responses: a functional genomics approach. <i>Journal of Leukocyte Biology</i> , <b>2006</b> , 79, 913-6	6.5	32
7	Transcriptional Profiling of Dendritic Cells in Response to Pathogens <b>2006</b> , 461-486		
6	A critical role for lipophosphoglycan in proinflammatory responses of dendritic cells to <i>Leishmania mexicana</i> . <i>European Journal of Immunology</i> , <b>2005</b> , 35, 476-86	6.1	41
5	A type I IFN-dependent pathway induced by <i>Schistosoma mansoni</i> eggs in mouse myeloid dendritic cells generates an inflammatory signature. <i>Journal of Immunology</i> , <b>2004</b> , 172, 3011-7	5.3	56
4	A power law global error model for the identification of differentially expressed genes in microarray data. <i>BMC Bioinformatics</i> , <b>2004</b> , 5, 203	3.6	82
3	Gene Profiling of Dendritic cells during HostPathogen Interactions 175-197		
2	DNA methylation dynamics during embryonic development and postnatal maturation of the mouse auditory organ of Corti		1
1	Genome-wide dynamics of RNA synthesis, processing and degradation without RNA metabolic labeling		4