# Mattia Pelizzola

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/800645/publications.pdf

Version: 2024-02-01

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|---|---|---|---|
| 61 papers | 11,976 citations | 147726 31 h-index | 133188 59 g-index |
| 68 all docs | 68 docs citations | 68 times ranked | 19104 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Identification, semantic annotation and comparison of combinations of functional elements in multiple biological conditions. Bioinformatics, 2022, 38, 1183-1190. | 1.8 | 1 |
| 2 | Dynamics of transcriptional and post-transcriptional regulation. Briefings in Bioinformatics, 2021, 22, . | 3.2 | 19 |
| 3 | Identification of Genes Post-Transcriptionally Regulated from RNA-seq: The Case Study of Liver Hepatocellular Carcinoma. Methods in Molecular Biology, 2021, 2284, 271-287. | 0.4 | 0 |
| 4 | Computational methods for RNA modification detection from nanopore direct RNA sequencing data. RNA Biology, 2021, 18, 31-40. | 1.5 | 48 |
| 5 | Translation is required for miRNAâ€dependent decay of endogenous transcripts. EMBO Journal, 2021, 40, e104569. | 3.5 | 22 |
| 6 | New insight into the catalytic -dependent and -independent roles of METTL3 in sustaining aberrant translation in chronic myeloid leukemia. Cell Death and Disease, 2021, 12, 870. | 2.7 | 25 |
| 7 | A dual role of dLsd1 in oogenesis: regulating developmental genes and repressing transposons. Nucleic Acids Research, 2020, 48, 1206-1224. | 6.5 | 5 |
| 8 | Genome-wide dynamics of RNA synthesis, processing, and degradation without RNA metabolic labeling. Genome Research, 2020, 30, 1492-1507. | 2.4 | 26 |
| 9 | INSPEcT-GUI Reveals the Impact of the Kinetic Rates of RNA Synthesis, Processing, and Degradation, on Premature and Mature RNA Species. Frontiers in Genetics, 2020, 11, 759. | 1.1 | 7 |
| 10 | Direct RNA Sequencing for the Study of Synthesis, Processing, and Degradation of Modified Transcripts. Frontiers in Genetics, 2020, 11, 394. | 1.1 | 11 |
| 11 | Ontology-driven integrative analysis of omics data through Onassis. Scientific Reports, 2020, 10, 703. | 1.6 | 9 |
| 12 | Macrophages fine tune satellite cell fate in dystrophic skeletal muscle of mdx mice. PLoS Genetics, 2019, 15, e1008408. | 1.5 | 35 |
| 13 | An early Mycâ€dependent transcriptional program orchestrates cell growth during Bâ€cell activation. EMBO Reports, 2019, 20, e47987. | 2.0 | 44 |
| 14 | m6A-Dependent RNA Dynamics in T Cell Differentiation. Genes, 2019, 10, 28. | 1.0 | 32 |
| 15 | Positioning Europe for the EPITRANSCRIPTOMICS challenge. RNA Biology, 2018, 15, 1-3. | 1.5 | 18 |
| 16 | Identification of Differentially Methylated Regions in the Genome of Arabidopsis thaliana. Methods in Molecular Biology, 2018, 1675, 61-69. | 0.4 | 5 |
| 17 | DNA methylation dynamics during embryonic development and postnatal maturation of the mouse auditory sensory epithelium. Scientific Reports, 2018, 8, 17348. | 1.6 | 27 |
| 18 | Ontology-based annotations and semantic relations in large-scale (epi)genomics data. Briefings in Bioinformatics, 2017, 18, bbw036. | 3.2 | 21 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Integrative analysis of RNA polymerase II and transcriptional dynamics upon MYC activation. Genome Research, 2017, 27, 1658-1664. | 2.4 | 50 |
| 20 | Compensatory RNA polymerase 2 loading determines the efficacy and transcriptional selectivity of JQ1 in Myc-driven tumors. Leukemia, 2017, 31, 479-490. | 3.3 | 37 |
| 21 | Integrative classification of human coding and noncoding genes through RNA metabolism profiles. Nature Structural and Molecular Biology, 2017, 24, 86-96. | 3.6 | 157 |
| 22 | DNA methylation variations are required for epithelial-to-mesenchymal transition induced by cancer-associated fibroblasts in prostate cancer cells. Oncogene, 2017, 36, 5551-5566. | 2.6 | 88 |
| 23 | Integrated Systems for NGS Data Management and Analysis: Open Issues and Available Solutions. Frontiers in Genetics, 2016, 7, 75. | 1.1 | 45 |
| 24 | Mycobacterium tuberculosis exploits the formation of new blood vessels for its dissemination. Scientific Reports, 2016, 6, 33162. | 1.6 | 86 |
| 25 | LowMACA: exploiting protein family analysis for the identification of rare driver mutations in cancer. BMC Bioinformatics, 2016, 17, 80. | 1.2 | 16 |
| 26 | Degradation dynamics of microRNAs revealed by a novel pulse-chase approach. Genome Research, 2016, 26, 554-565. | 2.4 | 155 |
| 27 | methylPipe and compEpiTools: a suite of R packages for the integrative analysis of epigenomics data. BMC Bioinformatics, 2015, 16, 313. | 1.2 | 68 |
| 28 | INSPEcT: a computational tool to infer mRNA synthesis, processing and degradation dynamics from RNA- and 4sU-seq time course experiments. Bioinformatics, 2015, 31, 2829-2835. | 1.8 | 60 |
| 29 | Computational epigenomics: challenges and opportunities. Frontiers in Genetics, 2015, 6, 88. | 1.1 | 8 |
| 30 | Selective transcriptional regulation by Myc: Experimental design and computational analysis of high-throughput sequencing data. Data in Brief, 2015, 3, 40-46. | 0.5 | 3 |
| 31 | Transcription of Mammalian cis-Regulatory Elements Is Restrained by Actively Enforced Early Termination. Molecular Cell, 2015, 60, 460-474. | 4.5 | 80 |
| 32 | Systematic mapping of occluded genes by cell fusion reveals prevalence and stability of cis-mediated silencing in somatic cells. Genome Research, 2014, 24, 267-280. | 2.4 | 12 |
| 33 | Computational and experimental methods to decipher the epigenetic code. Frontiers in Genetics, 2014, 5, 335. | 1.1 | 7 |
| 34 | DOTS-Finder: a comprehensive tool for assessing driver genes in cancer genomes. Genome Medicine, 2014, 6, 44. | 3.6 | 25 |
| 35 | Relationship between genome and epigenome - challenges and requirements for future research. BMC Genomics, 2014, 15, 487. | 1.2 | 24 |
| 36 | Selective transcriptional regulation by Myc in cellular growth control and lymphomagenesis. Nature, 2014, 511, 488-492. | 13.7 | 411 |

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|---|---|---|---|
| 37 | Patterns of population epigenomic diversity. Nature, 2013, 495, 193-198. | 13.7 | 543 |
| 38 | Temporal transcriptional response to ethylene gas drives growth hormone cross-regulation in Arabidopsis. ELife, 2013, 2, e00675. | 2.8 | 379 |
| 39 | Global DNA hypomethylation coupled to repressive chromatin domain formation and gene silencing in breast cancer. Genome Research, 2012, 22, 246-258. | 2.4 | 476 |
| 40 | Widespread dynamic DNA methylation in response to biotic stress. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E2183-91. | 3.3 | 878 |
| 41 | Hotspots of aberrant epigenomic reprogramming in human induced pluripotent stem cells. Nature, 2011, 471, 68-73. | 13.7 | 1,442 |
| 42 | The DNA methylome. FEBS Letters, 2011, 585, 1994-2000. | 1.3 | 80 |
| 43 | Germline competency of parthenogenetic embryonic stem cells from immature oocytes of adult mouse ovary. Human Molecular Genetics, 2011, 20, 1339-1352. | 1.4 | 15 |
| 44 | Methylated DNA Immunoprecipitation Genome-Wide Analysis. Methods in Molecular Biology, 2011, 791, 113-123. | 0.4 | 2 |
| 45 | Temporal gene expression profile of the hippocampus following trace fear conditioning. Brain Research, 2010, 1308, 14-23. | 1.1 | 13 |
| 46 | Comparison of sequencing-based methods to profile DNA methylation and identification of monoallelic epigenetic modifications. Nature Biotechnology, 2010, 28, 1097-1105. | 9.4 | 647 |
| 47 | Distinct Epigenomic Landscapes of Pluripotent and Lineage-Committed Human Cells. Cell Stem Cell, 2010, 6, 479-491. | 5.2 | 747 |
| 48 | Integrative Analysis of Epigenetic Modulation in Melanoma Cell Response to Decitabine: Clinical Implications. PLoS ONE, 2009, 4, e4563. | 1.1 | 56 |
| 49 | Genome-wide screen of promoter methylation identifies novel markers in melanoma. Genome Research, 2009, 19, 1462-1470. | 2.4 | 179 |
| 50 | Human DNA methylomes at base resolution show widespread epigenomic differences. Nature, 2009, 462, 315-322. | 13.7 | 4,063 |
| 51 | MEDME: An experimental and analytical methodology for the estimation of DNA methylation levels based on microarray derived MeDIP-enrichment. Genome Research, 2008, 18, 1652-1659. | 2.4 | 105 |
| 52 | Statistical Similarities between Transcriptomics and Quantitative Shotgun Proteomics Data. Molecular and Cellular Proteomics, 2008, 7, 631-644. | 2.5 | 146 |
| 53 | Probing Host Pathogen Cross-Talk by Transcriptional Profiling of Both Mycobacterium tuberculosis and Infected Human Dendritic Cells and Macrophages. PLoS ONE, 2008, 3, e1403. | 1.1 | 172 |
| 54 | The Genopolis Microarray Database. BMC Bioinformatics, 2007, 8, S21. | 1.2 | 8 |

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|---|---|---|---|
| 55 | Transcriptional Profiling of Dendritic Cells in Response to Pathogens. , 2006, , 461-486. | | 0 |
| 56 | AMDA: an R package for the automated microarray data analysis. BMC Bioinformatics, 2006, 7, 335. | 1.2 | 33 |
| 57 | Effects of dexamethazone on LPS-induced activationand migration of mouse dendritic cells revealed by a genome-wide transcriptional analysis. European Journal of Immunology, 2006, 36, 1504-1515. | 1.6 | 51 |
| 58 | Dendritic cells in pathogen recognition and induction of immune responses: a functional genomics approach. Journal of Leukocyte Biology, 2006, 79, 913-916. | 1.5 | 33 |
| 59 | A critical role for lipophosphoglycan in proinflammatory responses of dendritic cells toLeishmania mexicana. European Journal of Immunology, 2005, 35, 476-486. | 1.6 | 43 |
| 60 | A Type I IFN-Dependent Pathway Induced by Schistosoma mansoni Eggs in Mouse Myeloid Dendritic Cells Generates an Inflammatory Signature. Journal of Immunology, 2004, 172, 3011-3017. | 0.4 | 63 |
| 61 | A power law global error model for the identification of differentially expressed genes in microarray data. BMC Bioinformatics, 2004, 5, 203. | 1.2 | 105 |