

# Maud Fagny

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6099595/publications.pdf>

Version: 2024-02-01

22  
papers

2,093  
citations

516561

16  
h-index

713332

21  
g-index

35  
all docs

35  
docs citations

35  
times ranked

4566  
citing authors

#	ARTICLE	IF	CITATIONS
1	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. <i>Genome Biology</i> , 2016, 17, 171.	3.8	535
2	Understanding Tissue-Specific Gene Regulation. <i>Cell Reports</i> , 2017, 21, 1077-1088.	2.9	314
3	Genomic Signatures of Selective Pressures and Introgression from Archaic Hominins at Human Innate Immunity Genes. <i>American Journal of Human Genetics</i> , 2016, 98, 5-21.	2.6	243
4	Sex Differences in Gene Expression and Regulatory Networks across 29 Human Tissues. <i>Cell Reports</i> , 2020, 31, 107795.	2.9	207
5	Exploring the genetic basis of human population differences in DNA methylation and their causal impact on immune gene regulation. <i>Genome Biology</i> , 2018, 19, 222.	3.8	101
6	Exploring regulation in tissues with eQTL networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7841-E7850.	3.3	82
7	The epigenomic landscape of African rainforest hunter-gatherers and farmers. <i>Nature Communications</i> , 2015, 6, 10047.	5.8	75
8	Exploring the Occurrence of Classic Selective Sweeps in Humans Using Whole-Genome Sequencing Data Sets. <i>Molecular Biology and Evolution</i> , 2014, 31, 1850-1868.	3.5	72
9	Trends in DNA Methylation with Age Replicate Across Diverse Human Populations. <i>Genetics</i> , 2017, 206, 1659-1674.	1.2	69
10	Regulatory network changes between cell lines and their tissues of origin. <i>BMC Genomics</i> , 2017, 18, 723.	1.2	51
11	Epigenetic clock analysis in long-term meditators. <i>Psychoneuroendocrinology</i> , 2017, 85, 210-214.	1.3	48
12	Tissue-aware RNA-Seq processing and normalization for heterogeneous and sparse data. <i>BMC Bioinformatics</i> , 2017, 18, 437.	1.2	45
13	Differential DNA methylation in experienced meditators after an intensive day of mindfulness-based practice: Implications for immune-related pathways. <i>Brain, Behavior, and Immunity</i> , 2020, 84, 36-44.	2.0	44
14	Polygenic Adaptation: Integrating Population Genetics and Gene Regulatory Networks. <i>Trends in Genetics</i> , 2021, 37, 631-638.	2.9	41
15	Nongenic cancer-risk SNPs affect oncogenes, tumour-suppressor genes, and immune function. <i>British Journal of Cancer</i> , 2020, 122, 569-577.	2.9	22
16	Deregulation of microRNA expression in monocytes and CD4+ T lymphocytes from patients with axial spondyloarthritis. <i>Arthritis Research and Therapy</i> , 2019, 21, 51.	1.6	21
17	Epigenome-wide DNA methylation profiling in Progressive Supranuclear Palsy reveals major changes at DLX1. <i>Nature Communications</i> , 2018, 9, 2929.	5.8	20
18	Histopathological Image QTL Discovery of Immune Infiltration Variants. <i>IScience</i> , 2018, 5, 80-89.	1.9	19

#	ARTICLE	IF	CITATIONS
19	PUMA: PANDA Using MicroRNA Associations. <i>Bioinformatics</i> , 2020, 36, 4765-4773.	1.8	17
20	Identification of Key Tissue-Specific, Biological Processes by Integrating Enhancer Information in Maize Gene Regulatory Networks. <i>Frontiers in Genetics</i> , 2020, 11, 606285.	1.1	11
21	An online notebook resource for reproducible inference, analysis and publication of gene regulatory networks. <i>Nature Methods</i> , 2022, 19, 511-513.	9.0	7
22	Connectivity in eQTL networks dictates reproducibility and genomic properties. <i>Cell Reports Methods</i> , 2022, 2, 100218.	1.4	3