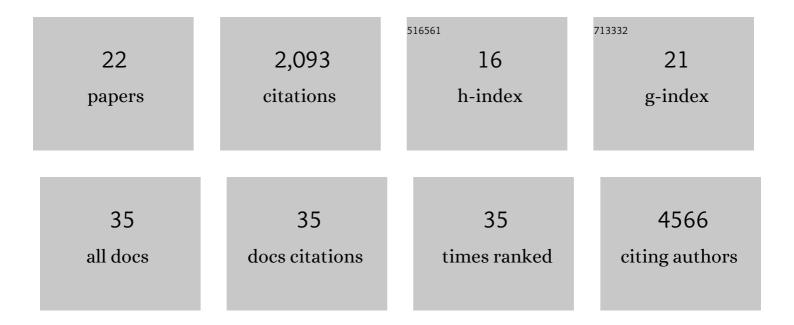
Maud Fagny

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6099595/publications.pdf Version: 2024-02-01



MAUD FACNY

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

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