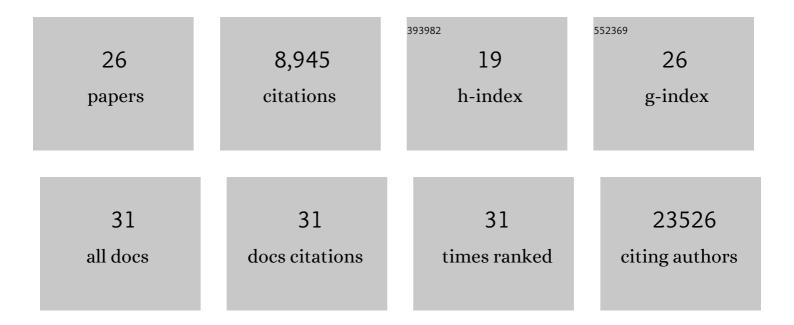
## Marta Mele

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1856507/publications.pdf Version: 2024-02-01



Μλάτλ Μειε

#	Article	IF	CITATIONS
1	Whole genome sequencing delineates regulatory, copy number, and cryptic splice variants in early onset cardiomyopathy. Npj Genomic Medicine, 2022, 7, 18.	1.7	14
2	Population-scale tissue transcriptomics maps long non-coding RNAs to complex disease. Cell, 2021, 184, 2633-2648.e19.	13.5	94
3	A Quantitative Proteome Map of the Human Body. Cell, 2020, 183, 269-283.e19.	13.5	243
4	Cis and trans effects differentially contribute to the evolution of promoters and enhancers. Genome Biology, 2020, 21, 210.	3.8	35
5	Single-Cell Profiling of Ebola Virus Disease InÂVivo Reveals Viral and Host Dynamics. Cell, 2020, 183, 1383-1401.e19.	13.5	79
6	High-throughput functional analysis of IncRNA core promoters elucidates rules governing tissue specificity. Genome Research, 2019, 29, 344-355.	2.4	100
7	Spatiotemporal allele organization by allele-specific CRISPR live-cell imaging (SNP-CLING). Nature Structural and Molecular Biology, 2018, 25, 176-184.	3.6	75
8	Chromatin environment, transcriptional regulation, and splicing distinguish lincRNAs and mRNAs. Genome Research, 2017, 27, 27-37.	2.4	207
9	Molecular and cellular reorganization of neural circuits in the human lineage. Science, 2017, 358, 1027-1032.	6.0	192
10	In vivo Ebola virus infection leads to a strong innate response in circulating immune cells. BMC Genomics, 2016, 17, 707.	1.2	54
11	"Cat's Cradling―the 3D Genome by the Act of LncRNA Transcription. Molecular Cell, 2016, 62, 657-664.	4.5	128
12	Functional Implications of Human-Specific Changes in Great Ape microRNAs. PLoS ONE, 2016, 11, e0154194.	1.1	12
13	Extreme selective sweeps independently targeted the X chromosomes of the great apes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6413-6418.	3.3	75
14	The human transcriptome across tissues and individuals. Science, 2015, 348, 660-665.	6.0	1,127
15	The Genotype-Tissue Expression (GTEx) pilot analysis: Multitissue gene regulation in humans. Science, 2015, 348, 648-660.	6.0	4,659
16	Effect of predicted protein-truncating genetic variants on the human transcriptome. Science, 2015, 348, 666-669.	6.0	252
17	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. BMC Genomics, 2013, 14, 363.	1.2	48
18	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	13.7	768

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#	Article	IF	CITATIONS
19	Recombination Gives a New Insight in the Effective Population Size and the History of the Old World Human Populations. Molecular Biology and Evolution, 2012, 29, 25-30.	3.5	31
20	Recombination networks as genetic markers in a human variation study of the Old World. Human Genetics, 2012, 131, 601-613.	1.8	7
21	The genome of melon ( <i>Cucumis melo</i> L.). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11872-11877.	3.3	654
22	Similarity in Recombination Rate Estimates Highly Correlates with Genetic Differentiation in Humans. PLoS ONE, 2011, 6, e17913.	1.1	18
23	IRiS: Construction of ARG networks at genomic scales. Bioinformatics, 2011, 27, 2448-2450.	1.8	14
24	A New Method to Reconstruct Recombination Events at a Genomic Scale. PLoS Computational Biology, 2010, 6, e1001010.	1.5	14
25	Minimizing recombinations in consensus networks for phylogeographic studies. BMC Bioinformatics, 2009, 10, S72.	1.2	12
26	Estimating the Ancestral Recombinations Graph (ARG) as Compatible Networks of SNP Patterns. Journal of Computational Biology, 2008, 15, 1133-1153.	0.8	27