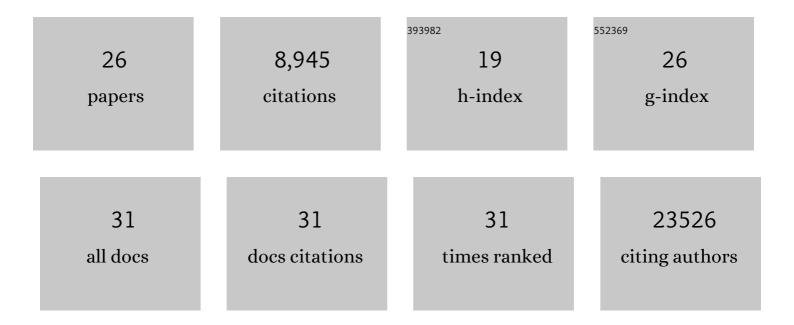
Marta Mele

List of Publications by Year in descending order

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



MADTA MELE

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

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#	Article	IF	CITATIONS
19	Estimating the Ancestral Recombinations Graph (ARG) as Compatible Networks of SNP Patterns. Journal of Computational Biology, 2008, 15, 1133-1153.	0.8	27
20	Similarity in Recombination Rate Estimates Highly Correlates with Genetic Differentiation in Humans. PLoS ONE, 2011, 6, e17913.	1.1	18
21	A New Method to Reconstruct Recombination Events at a Genomic Scale. PLoS Computational Biology, 2010, 6, e1001010.	1.5	14
22	IRiS: Construction of ARG networks at genomic scales. Bioinformatics, 2011, 27, 2448-2450.	1.8	14
23	Whole genome sequencing delineates regulatory, copy number, and cryptic splice variants in early onset cardiomyopathy. Npj Genomic Medicine, 2022, 7, 18.	1.7	14
24	Minimizing recombinations in consensus networks for phylogeographic studies. BMC Bioinformatics, 2009, 10, S72.	1.2	12
25	Functional Implications of Human-Specific Changes in Great Ape microRNAs. PLoS ONE, 2016, 11, e0154194.	1.1	12
26	Recombination networks as genetic markers in a human variation study of the Old World. Human Genetics, 2012, 131, 601-613.	1.8	7