

Marta Mele

List of Publications by Year in descending order

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Version: 2024-02-01

26
papers

8,945
citations

393982

19
h-index

552369

26
g-index

31
all docs

31
docs citations

31
times ranked

23526
citing authors

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

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