

Maxime Rotival

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,816
citations

430442

18
h-index

500791

28
g-index

34
all docs

34
docs citations

34
times ranked

4607
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative genetic and immune cell analysis of plasma proteins in healthy donors identifies novel associations involving primary immune deficiency genes. <i>Genome Medicine</i> , 2022, 14, 28.	3.6	8
2	Reconstructing 50,000 years of human history from our DNA: lessons from modern genomics. <i>Comptes Rendus - Biologies</i> , 2021, 344, 177-187.	0.1	2
3	Single-Cell and Bulk RNA-Sequencing Reveal Differences in Monocyte Susceptibility to Influenza A Virus Infection Between Africans and Europeans. <i>Frontiers in Immunology</i> , 2021, 12, 768189.	2.2	14
4	Towards a functional understanding of adaptive phenotypes in humans. <i>Journal of Anthropological Sciences</i> , 2021, 99, .	0.4	0
5	Functional consequences of archaic introgression and their impact on fitness. <i>Genome Biology</i> , 2020, 21, 3.	3.8	18
6	Population variation in miRNAs and isomiRs and their impact on human immunity to infection. <i>Genome Biology</i> , 2020, 21, 187.	3.8	14
7	Two common disease-associated TYK2 variants impact exon splicing and TYK2 dosage. <i>PLoS ONE</i> , 2020, 15, e0225289.	1.1	25
8	A trans-eQTL network regulates osteoclast multinucleation and bone mass. <i>ELife</i> , 2020, 9, .	2.8	24
9	A genetic variant controls interferon- β gene expression in human myeloid cells by preventing C/EBP- β binding on a conserved enhancer. <i>PLoS Genetics</i> , 2020, 16, e1009090.	1.5	3
10	WWP2 regulates pathological cardiac fibrosis by modulating SMAD2 signaling. <i>Nature Communications</i> , 2019, 10, 3616.	5.8	44
11	Impact and Evolutionary Determinants of Neanderthal Introgression on Transcriptional and Post-Transcriptional Regulation. <i>American Journal of Human Genetics</i> , 2019, 104, 1241-1250.	2.6	42
12	Characterising the genetic basis of immune response variation to identify causal mechanisms underlying disease susceptibility. <i>Hla</i> , 2019, 94, 275-284.	0.4	5
13	Defining the genetic and evolutionary architecture of alternative splicing in response to infection. <i>Nature Communications</i> , 2019, 10, 1671.	5.8	52
14	Ethnicity-Specific Skeletal Muscle Transcriptional Signatures and Their Relevance to Insulin Resistance in Singapore. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2019, 104, 465-486.	1.8	4
15	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
16	Genome-wide analysis of differential RNA editing in epilepsy. <i>Genome Research</i> , 2017, 27, 440-450.	2.4	73
17	Identification of Ceruloplasmin as a Gene that Affects Susceptibility to Glomerulonephritis Through Macrophage Function. <i>Genetics</i> , 2017, 206, 1139-1151.	1.2	11
18	Wars2 is a determinant of angiogenesis. <i>Nature Communications</i> , 2016, 7, 12061.	5.8	45

#	ARTICLE	IF	CITATIONS
19	Genetic Adaptation and Neandertal Admixture Shaped the Immune System of Human Populations. <i>Cell</i> , 2016, 167, 643-656.e17.	13.5	373
20	Systems genetics identifies a convergent gene network for cognition and neurodevelopmental disease. <i>Nature Neuroscience</i> , 2016, 19, 223-232.	7.1	131
21	Identification of protein complexes that bind to histone H3 combinatorial modifications using super-SILAC and weighted correlation network analysis. <i>Nucleic Acids Research</i> , 2015, 43, 1418-1432.	6.5	35
22	Systems genetics identifies Sestrin 3 as a regulator of a proconvulsant gene network in human epileptic hippocampus. <i>Nature Communications</i> , 2015, 6, 6031.	5.8	158
23	Integrating Phosphoproteome and Transcriptome Reveals New Determinants of Macrophage Multinucleation. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 484-498.	2.5	27
24	The epigenomic landscape of African rainforest hunter-gatherers and farmers. <i>Nature Communications</i> , 2015, 6, 10047.	5.8	75
25	Multi-tissue Analysis of Co-expression Networks by Higher-Order Generalized Singular Value Decomposition Identifies Functionally Coherent Transcriptional Modules. <i>PLoS Genetics</i> , 2014, 10, e1004006.	1.5	54
26	Genetic Analysis of the Cardiac Methylome at Single Nucleotide Resolution in a Model of Human Cardiovascular Disease. <i>PLoS Genetics</i> , 2014, 10, e1004813.	1.5	19
27	Leveraging gene co-expression networks to pinpoint the regulation of complex traits and disease, with a focus on cardiovascular traits. <i>Briefings in Functional Genomics</i> , 2014, 13, 66-78.	1.3	40
28	Genetic Influences on Brain Gene Expression in Rats Selected for Tameness and Aggression. <i>Genetics</i> , 2014, 198, 1277-1290.	1.2	78
29	Kcnn4 Is a Regulator of Macrophage Multinucleation in Bone Homeostasis and Inflammatory Disease. <i>Cell Reports</i> , 2014, 8, 1210-1224.	2.9	53
30	A trans-acting locus regulates an anti-viral expression network and type 1 diabetes risk. <i>Nature</i> , 2010, 467, 460-464.	13.7	271