

Jean-Christophe Grenier

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

3,527
citations

331670

21
h-index

414414

32
g-index

51
all docs

51
docs citations

51
times ranked

7509
citing authors

#	ARTICLE	IF	CITATIONS
1	BCG Educates Hematopoietic Stem Cells to Generate Protective Innate Immunity against Tuberculosis. <i>Cell</i> , 2018, 172, 176-190.e19.	28.9	802
2	Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. <i>Cell</i> , 2016, 167, 657-669.e21.	28.9	419
3	Social networks predict gut microbiome composition in wild baboons. <i>ELife</i> , 2015, 4, .	6.0	403
4	Social status alters immune regulation and response to infection in macaques. <i>Science</i> , 2016, 354, 1041-1045.	12.6	235
5	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015, 25, 1801-1811.	5.5	195
6	Gene activation precedes DNA demethylation in response to infection in human dendritic cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6938-6943.	7.1	127
7	Chronic Inflammation Permanently Reshapes Tissue-Resident Immunity in Celiac Disease. <i>Cell</i> , 2019, 176, 967-981.e19.	28.9	126
8	Gut microbiome heritability is nearly universal but environmentally contingent. <i>Science</i> , 2021, 373, 181-186.	12.6	126
9	IL-15, gluten and HLA-DQ8 drive tissue destruction in coeliac disease. <i>Nature</i> , 2020, 578, 600-604.	27.8	122
10	Adaptive, convergent origins of the pygmy phenotype in African rainforest hunter-gatherers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E3596-603.	7.1	91
11	High-Resolution Genomic Analysis of Human Mitochondrial RNA Sequence Variation. <i>Science</i> , 2014, 344, 413-415.	12.6	90
12	Widespread Shortening of 3' UTRs and Increased Exon Inclusion Are Evolutionarily Conserved Features of Innate Immune Responses to Infection. <i>PLoS Genetics</i> , 2016, 12, e1006338.	3.5	90
13	Evidence for additive and interaction effects of host genotype and infection in malaria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 16786-16793.	7.1	89
14	Recombination affects accumulation of damaging and disease-associated mutations in human populations. <i>Nature Genetics</i> , 2015, 47, 400-404.	21.4	84
15	Gene-by-environment interactions in urban populations modulate risk phenotypes. <i>Nature Communications</i> , 2018, 9, 827.	12.8	84
16	Whole-Exome Sequencing Reveals a Rapid Change in the Frequency of Rare Functional Variants in a Founding Population of Humans. <i>PLoS Genetics</i> , 2013, 9, e1003815.	3.5	70
17	Relaxed Selection During a Recent Human Expansion. <i>Genetics</i> , 2018, 208, 763-777.	2.9	49
18	Rare allelic forms of <i>PRDM9</i> associated with childhood leukemogenesis. <i>Genome Research</i> , 2013, 23, 419-430.	5.5	45

#	ARTICLE	IF	CITATIONS
19	Primate innate immune responses to bacterial and viral pathogens reveals an evolutionary trade-off between strength and specificity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	30
20	Human NKG2E Is Expressed and Forms an Intracytoplasmic Complex with CD94 and DAP12. <i>Journal of Immunology</i> , 2014, 193, 610-616.	0.8	28
21	Natural selection contributed to immunological differences between hunter-gatherers and agriculturalists. <i>Nature Ecology and Evolution</i> , 2019, 3, 1253-1264.	7.8	28
22	Non-CG methylation and multiple histone profiles associate child abuse with immune and small GTPase dysregulation. <i>Nature Communications</i> , 2021, 12, 1132.	12.8	24
23	A Short-Term High-Fat Diet Alters Glutathione Levels and IL-6 Gene Expression in Oxidative Skeletal Muscles of Young Rats. <i>Frontiers in Physiology</i> , 2019, 10, 372.	2.8	22
24	The mutational landscape of SARS-CoV-2 variants diversifies T _H cell targets in an HLA-supertype-dependent manner. <i>Cell Systems</i> , 2022, 13, 143-157.e3.	6.2	22
25	Aortic Dilatation Associated With a De Novo Mutation in the SOX18 Gene: Expanding the Clinical Spectrum of Hypotrichosis-Lymphedema-Telangiectasia Syndrome. <i>Canadian Journal of Cardiology</i> , 2016, 32, 135.e1-135.e7.	1.7	19
26	Synchrony and idiosyncrasy in the gut microbiome of wild baboons. <i>Nature Ecology and Evolution</i> , 2022, 6, 955-964.	7.8	18
27	Selective constraint, background selection, and mutation accumulation variability within and between human populations. <i>BMC Genomics</i> , 2013, 14, 495.	2.8	16
28	Genomic architecture of sickle cell disease in West African children. <i>Frontiers in Genetics</i> , 2014, 5, 26.	2.3	11
29	A sex-specific evolutionary interaction between ADCY9 and CETP. <i>ELife</i> , 2021, 10, .	6.0	8
30	A haplotype-based normalization technique for the analysis and detection of allele specific expression. <i>BMC Bioinformatics</i> , 2016, 17, 364.	2.6	7
31	Patient health records and whole viral genomes from an early SARS-CoV-2 outbreak in a Quebec hospital reveal features associated with favorable outcomes. <i>PLoS ONE</i> , 2021, 16, e0260714.	2.5	5
32	Differential modulation of polyunsaturated fatty acids in patients with myocardial infarction treated with ticagrelor or clopidogrel. <i>Cell Reports Medicine</i> , 2021, 2, 100299.	6.5	2