

Jean-Christophe Grenier

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/1407279/jean-christophe-grenier-publications-by-year.pdf>

Version: 2024-04-09

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

41 papers	2,168 citations	19 h-index	46 g-index
51 ext. papers	2,958 ext. citations	17.2 avg, IF	4.38 L-index

#	Paper	IF	Citations
41	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	3.7	0
40	The mutational landscape of SARS-CoV-2 variants diversifies T cell targets in an HLA-supertype-dependent manner. <i>Cell Systems</i> , 2021 ,	10.6	6
39	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,	11.5	11
38	Genomic epidemiology and associated clinical outcomes of a SARS-CoV-2 outbreak in a general adult hospital in Quebec 2021 ,		1
37	Differential modulation of polyunsaturated fatty acids in patients with myocardial infarction treated with ticagrelor or clopidogrel. <i>Cell Reports Medicine</i> , 2021 , 2, 100299	18	
36	Non-CG methylation and multiple histone profiles associate child abuse with immune and small GTPase dysregulation. <i>Nature Communications</i> , 2021 , 12, 1132	17.4	5
35	Gut microbiome heritability is nearly universal but environmentally contingent. <i>Science</i> , 2021 , 373, 181-186	35.3	22
34	IL-15, gluten and HLA-DQ8 drive tissue destruction in coeliac disease. <i>Nature</i> , 2020 , 578, 600-604	50.4	65
33	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	4.6	10
32	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	11.5	62
31	Chronic Inflammation Permanently Reshapes Tissue-Resident Immunity in Celiac Disease. <i>Cell</i> , 2019 , 176, 967-981.e19	56.2	72
30	Natural selection contributed to immunological differences between hunter-gatherers and agriculturalists. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1253-1264	12.3	15
29	Gene-by-environment interactions in urban populations modulate risk phenotypes. <i>Nature Communications</i> , 2018 , 9, 827	17.4	50
28	BCG Educates Hematopoietic Stem Cells to Generate Protective Innate Immunity against Tuberculosis. <i>Cell</i> , 2018 , 172, 176-190.e19	56.2	471
27	Relaxed Selection During a Recent Human Expansion. <i>Genetics</i> , 2018 , 208, 763-777	4	28
26	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.e1-7	3.8	13
25	Social status alters immune regulation and response to infection in macaques. <i>Science</i> , 2016 , 354, 1041-1045	35.5	154

24	Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. <i>Cell</i> , 2016 , 167, 657-669.e21	56.2	264
23	Widespread Shortening of 3' Untranslated Regions and Increased Exon Inclusion Are Evolutionarily Conserved Features of Innate Immune Responses to Infection. <i>PLoS Genetics</i> , 2016 , 12, e1006338	6	53
22	A haplotype-based normalization technique for the analysis and detection of allele specific expression. <i>BMC Bioinformatics</i> , 2016 , 17, 364	3.6	5
21	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015 , 25, 1801-11	9.7	138
20	Social networks predict gut microbiome composition in wild baboons. <i>ELife</i> , 2015 , 4,	8.9	294
19	Recombination affects accumulation of damaging and disease-associated mutations in human populations. <i>Nature Genetics</i> , 2015 , 47, 400-4	36.3	63
18	High-resolution genomic analysis of human mitochondrial RNA sequence variation. <i>Science</i> , 2014 , 344, 413-5	33.3	72
17	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	11.5	70
16	Human NKG2E is expressed and forms an intracytoplasmic complex with CD94 and DAP12. <i>Journal of Immunology</i> , 2014 , 193, 610-6	5.3	26
15	Genomic architecture of sickle cell disease in West African children. <i>Frontiers in Genetics</i> , 2014 , 5, 26	4.5	9
14	Selective constraint, background selection, and mutation accumulation variability within and between human populations. <i>BMC Genomics</i> , 2013 , 14, 495	4.5	13
13	Rare allelic forms of PRDM9 associated with childhood leukemogenesis. <i>Genome Research</i> , 2013 , 23, 419-30	9.7	37
12	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	6	52
11	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, 16786-93	11.5	66
10	Natural selection contributed to immunological differences between human hunter-gatherers and agriculturalists		
9	Bacterial Infection Remodels the DNA Methylation Landscape of Human Dendritic Cells		3
8	Genomic and Environmental Contributions to Chronic Diseases in Urban Populations		1
7	Primate innate immune responses to bacterial and viral pathogens reveals an evolutionary trade-off between strength and specificity		1

6	Multiscale PHATE Exploration of SARS-CoV-2 Data Reveals Multimodal Signatures of Disease	1
5	Single-cell RNA-sequencing reveals pervasive but highly cell type-specific genetic ancestry effects on the response to viral infection	3
4	Gene activation precedes DNA demethylation in response to infection in human dendritic cells	2
3	Non-CG methylation and multiple epigenetic layers associate child abuse with immune and small GTPase dysregulation	1
2	Widespread shortening of 3'UTR untranslated regions and increased exon inclusion are evolutionarily conserved features of innate immune responses to infection	2
1	ImputeCoVNet: 2D ResNet Autoencoder for Imputation of SARS-CoV-2 Sequences	3