

Guillaume Laval

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7585676/publications.pdf>

Version: 2024-02-01

34
papers

3,554
citations

236612

25
h-index

377514

34
g-index

34
all docs

34
docs citations

34
times ranked

7140
citing authors

#	ARTICLE	IF	CITATIONS
1	The genomic signatures of natural selection in admixed human populations. <i>American Journal of Human Genetics</i> , 2022, 109, 710-726.	2.6	21
2	Human ancient DNA analyses reveal the high burden of tuberculosis in Europeans over the last 2,000 years. <i>American Journal of Human Genetics</i> , 2021, 108, 517-524.	2.6	58
3	Genomic insights into population history and biological adaptation in Oceania. <i>Nature</i> , 2021, 592, 583-589.	13.7	100
4	Sporadic occurrence of recent selective sweeps from standing variation in humans as revealed by an approximate Bayesian computation approach. <i>Genetics</i> , 2021, 219, .	1.2	2
5	Genetic susceptibility to severe childhood asthma and rhinovirus-C maintained by balancing selection in humans for 150,000 years. <i>Human Molecular Genetics</i> , 2020, 29, 736-744.	1.4	5
6	Recent Common Origin, Reduced Population Size, and Marked Admixture Have Shaped European Roma Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 3175-3187.	3.5	16
7	Recent Adaptive Acquisition by African Rainforest Hunter-Gatherers of the Late Pleistocene Sickle-Cell Mutation Suggests Past Differences in Malaria Exposure. <i>American Journal of Human Genetics</i> , 2019, 104, 553-561.	2.6	33
8	Gene flow contributes to diversification of the major fungal pathogen <i>Candida albicans</i> . <i>Nature Communications</i> , 2018, 9, 2253.	5.8	131
9	Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America. <i>Science</i> , 2017, 356, 543-546.	6.0	188
10	Deciphering the genetic control of gene expression following <i>Mycobacterium leprae</i> antigen stimulation. <i>PLoS Genetics</i> , 2017, 13, e1006952.	1.5	37
11	Genetic Adaptation and Neandertal Admixture Shaped the Immune System of Human Populations. <i>Cell</i> , 2016, 167, 643-656.e17.	13.5	373
12	Detecting Genomic Signatures of Natural Selection with Principal Component Analysis: Application to the 1000 Genomes Data. <i>Molecular Biology and Evolution</i> , 2016, 33, 1082-1093.	3.5	123
13	Genomic Signatures of Selective Pressures and Introgression from Archaic Hominins at Human Innate Immunity Genes. <i>American Journal of Human Genetics</i> , 2016, 98, 5-21.	2.6	243
14	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. <i>Nature Communications</i> , 2015, 6, 8464.	5.8	304
15	Exploring the Occurrence of Classic Selective Sweeps in Humans Using Whole-Genome Sequencing Data Sets. <i>Molecular Biology and Evolution</i> , 2014, 31, 1850-1868.	3.5	72
16	A genomic portrait of the genetic architecture and regulatory impact of microRNA expression in response to infection. <i>Genome Research</i> , 2014, 24, 850-859.	2.4	60
17	The impact of agricultural emergence on the genetic history of African rainforest hunter-gatherers and agriculturalists. <i>Nature Communications</i> , 2014, 5, 3163.	5.8	96
18	Heterogeneous Pattern of Selective Pressure for PRRT2 in Human Populations, but No Association with Autism Spectrum Disorders. <i>PLoS ONE</i> , 2014, 9, e88600.	1.1	14

#	ARTICLE	IF	CITATIONS
19	Human Genetic Data Reveal Contrasting Demographic Patterns between Sedentary and Nomadic Populations That Predate the Emergence of Farming. <i>Molecular Biology and Evolution</i> , 2013, 30, 2629-2644.	3.5	40
20	Different selective pressures shape the evolution of Toll-like receptors in human and African great ape populations. <i>Human Molecular Genetics</i> , 2013, 22, 4829-4840.	1.4	49
21	The Evolutionary Landscape of Cytosolic Microbial Sensors in Humans. <i>American Journal of Human Genetics</i> , 2012, 91, 27-37.	2.6	34
22	The selective footprints of viral pressures at the human RIG-I-like receptor family. <i>Human Molecular Genetics</i> , 2011, 20, 4462-4474.	1.4	44
23	Evolutionary genetics evidence of an essential, nonredundant role of the IFN- λ 3 pathway in protective immunity. <i>Human Mutation</i> , 2011, 32, 633-642.	1.1	22
24	Evolution of the TIR Domain-Containing Adaptors in Humans: Swinging between Constraint and Adaptation. <i>Molecular Biology and Evolution</i> , 2011, 28, 3087-3097.	3.5	40
25	Evolutionary genetic dissection of human interferons. <i>Journal of Experimental Medicine</i> , 2011, 208, 2747-2759.	4.2	170
26	Formulating a Historical and Demographic Model of Recent Human Evolution Based on Resequencing Data from Noncoding Regions. <i>PLoS ONE</i> , 2010, 5, e10284.	1.1	74
27	Inferring the Demographic History of African Farmers and Pygmy Hunter-Gatherers Using a Multilocus Resequencing Data Set. <i>PLoS Genetics</i> , 2009, 5, e1000448.	1.5	142
28	Signatures of Purifying and Local Positive Selection in Human miRNAs. <i>American Journal of Human Genetics</i> , 2009, 84, 316-327.	2.6	83
29	Evolutionary Dynamics of Human Toll-Like Receptors and Their Different Contributions to Host Defense. <i>PLoS Genetics</i> , 2009, 5, e1000562.	1.5	341
30	Natural selection has driven population differentiation in modern humans. <i>Nature Genetics</i> , 2008, 40, 340-345.	9.4	526
31	An assessment of European pig diversity using molecular markers: Partitioning of diversity among breeds. <i>Conservation Genetics</i> , 2005, 6, 729-741.	0.8	40
32	CYP11B2-CYP11B1 Haplotypes Associated with Decreased 11 β -Hydroxylase Activity. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2005, 90, 1220-1225.	1.8	34
33	Stability of genetic structure and effective population size inferred from temporal changes of microsatellite DNA polymorphisms in the land snail <i>Helix aspersa</i> (Gastropoda: Helicidae). <i>Biological Journal of the Linnean Society</i> , 2004, 82, 89-102.	0.7	25
34	Maximum-Likelihood and Markov Chain Monte Carlo Approaches to Estimate Inbreeding and Effective Size From Allele Frequency Changes. <i>Genetics</i> , 2003, 164, 1189-1204.	1.2	14