Loukas Moutsianas

List of Publications by Year
in descending order

33 papers	13,200 citations	257450 24 h-index	434195 31 g-index

36 all docs	36 docs citations	36 times ranked	25730 citing authors

#	Article	IF	Citations
1	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	27.8	2,625
2	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	27.8	2,400
3	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	21.4	1,213
4	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	27.8	1,014
5	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
6	Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease. Nature Genetics, 2017, 49, 256-261.	21.4	943
7	A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. Nature Genetics, 2010, 42, 985-990.	21.4	918
8	Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. Nature Genetics, 2011, 43, 761-767.	21.4	778
9	100,000 Genomes Pilot on Rare-Disease Diagnosis in Health Care â€" Preliminary Report. New England Journal of Medicine, 2021, 385, 1868-1880.	27.0	352
10	Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113.	21.4	312
11	HLA-DQA1*05 Carriage Associated With Development of Anti-Drug Antibodies to Infliximab and Adalimumab in Patients With Crohnâ€™s Disease. Gastroenterology, 2020, 158, 189-199.	1.3	249
12	Whole-genome sequencing reveals host factors underlying critical COVID-19. Nature, 2022, 607, 97-103.	27.8	174
13	Multi-Population Classical HLA Type Imputation. PLoS Computational Biology, 2013, 9, e1002877.	3.2	157
14	Exploring the genetic architecture of inflammatory bowel disease by whole-genome sequencing identifies association at ADCY7. Nature Genetics, 2017, 49, 186-192.	21.4	153
15	HLA*IMPâ€"an integrated framework for imputing classical HLA alleles from SNP genotypes. Bioinformatics, 2011, 27, 968-972.	4.1	151
16	The Power of Gene-Based Rare Variant Methods to Detect Disease-Associated Variation and Test Hypotheses About Complex Disease. PLoS Genetics, 2015, 11, e1005165.	3.5	124
17	Genome-wide analysis of 53,400 people with irritable bowel syndrome highlights shared genetic pathways with mood and anxiety disorders. Nature Genetics, 2021, 53, 1543-1552.	21.4	96
18	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. Nature Communications, 2013, 4, 2872.	12.8	77

#	Article	IF	Citations
19	Revisiting the Thrifty Gene Hypothesis via 65 Loci Associated with Susceptibility to Type 2 Diabetes. American Journal of Human Genetics, 2014, 94, 176-185.	6.2	72
20	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. American Journal of Human Genetics, 2021, 108, 1350-1355.	6.2	72
21	Hypoxia induces a lipogenic cancer cell phenotype via HIF1Î±-dependent and -independent pathways. Oncotarget, 2015, 6, 1920-1941.	1.8	72
22	Founder population-specific HapMap panel increases power in GWA studies through improved imputation accuracy and CNV tagging. Genome Research, 2010, 20, 1344-1351.	5.5	52
23	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47
24	Somatic mosaicism and common genetic variation contribute to the risk of very-early-onset inflammatory bowel disease. Nature Communications, 2020, 11, 995.	12.8	37
25	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
26	MHC variation and risk of childhood B-cell precursor acute lymphoblastic leukemia. Blood, 2011, 117, 1633-1640.	1.4	24
27	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. American Journal of Human Genetics, 2014, 94, 710-720.	6.2	24
28	An ancestral 10-bp repeat expansion in VWA1 causes recessive hereditary motor neuropathy. Brain, 2021, 144, 584-600.	7.6	20
29	Methodology for the analysis of rare genetic variation in genome-wide association and re-sequencing studies of complex human traits. Briefings in Functional Genomics, 2014, 13, 362-370.	2.7	18
30	Genetic Association in the HLA Region. Methods in Molecular Biology, 2018, 1793, 111-134.	0.9	9
31	Grid Methodology for Identifying Co-Regulated Genes and Transcription Factor Binding Sites. IEEE Transactions on Nanobioscience, 2007, 6, 162-167.	3.3	4
32	Power of Rare Variant Aggregate Tests. , 2015, , 185-199.		1
33	Transcriptome and colocalisation analysis of CCR9+ gut-homing T cells and other immune cells identifies important genes and biological pathways potentiating primary sclerosing cholangitis risk. Journal of Hepatology, 2020, 73, S42-S43.	3.7	0