Loukas Moutsianas

List of Publications by Year
in descending order

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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	Whole-genome sequencing reveals host factors underlying critical COVID-19. Nature, 2022, 607, 97-103.	27.8	174
2	An ancestral 10-bp repeat expansion in VWA1 causes recessive hereditary motor neuropathy. Brain, 2021, 144, 584-600.	7.6	20
3	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
4	Genetic mechanisms of critical illness in COVID-19. Nature, 2021, 591, 92-98.	27.8	1,014
5	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
6	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
7	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
8	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
9	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
10	Genetic Association in the HLA Region. Methods in Molecular Biology, 2018, 1793, 111-134.	0.9	9
11	Genome-wide association study implicates immune activation of multiple integrin genes in inflammatory bowel disease. Nature Genetics, 2017, 49, 256-261.	21.4	943
12	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
13	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
14	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
15	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
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	Class II HLA interactions modulate genetic risk for multiple sclerosis. Nature Genetics, 2015, 47, 1107-1113.	21.4	312
18	Hypoxia induces a lipogenic cancer cell phenotype via HIF1Î±-dependent and -independent pathways. Oncotarget, 2015, 6, 1920-1941.	1.8	72

#	Article	IF	Citations
19	Power of Rare Variant Aggregate Tests. , 2015, , 185-199.		1
20	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
21	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
22	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
23	Analysis of immune-related loci identifies 48 new susceptibility variants for multiple sclerosis. Nature Genetics, 2013, 45, 1353-1360.	21.4	1,213
24	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. Nature Communications, 2013, 4, 2872.	12.8	77
25	Multi-Population Classical HLA Type Imputation. PLoS Computational Biology, 2013, 9, e1002877.	3.2	157
26	Genetic risk and a primary role for cell-mediated immune mechanisms in multiple sclerosis. Nature, 2011, 476, 214-219.	27.8	2,400
27	MHC variation and risk of childhood B-cell precursor acute lymphoblastic leukemia. Blood, 2011, 117, 1633-1640.	1.4	24
28	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
29	HLA*IMPâ€"an integrated framework for imputing classical HLA alleles from SNP genotypes. Bioinformatics, 2011, 27, 968-972.	4.1	151
30	Integrating common and rare genetic variation in diverse human populations. Nature, 2010, 467, 52-58.	27.8	2,625
31	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
32	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
33	Grid Methodology for Identifying Co-Regulated Genes and Transcription Factor Binding Sites. IEEE Transactions on Nanobioscience, 2007, 6, 162-167.	3.3	4