

Paul J McLaren

List of Publications by Year in descending order

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Version: 2024-02-01

75
papers

7,139
citations

126708

33
h-index

82410

72
g-index

87
all docs

87
docs citations

87
times ranked

16451
citing authors

#	ARTICLE	IF	CITATIONS
1	Increased prevalence of clonal hematopoiesis of indeterminate potential amongst people living with HIV. <i>Scientific Reports</i> , 2022, 12, 577.	1.6	27
2	Expansion of cytotoxic tissue-resident CD8+ T cells and CCR6+CD161+ CD4+ T cells in the nasal mucosa following mRNA COVID-19 vaccination. <i>Nature Communications</i> , 2022, 13, .	5.8	51
3	Genetic variation near CXCL12 is associated with susceptibility to HIV-related non-Hodgkin lymphoma. <i>Haematologica</i> , 2021, 106, 2233-2241.	1.7	4
4	Rectal microbiota diversity in Kenyan MSM is inversely associated with frequency of receptive anal sex, independent of HIV status. <i>Aids</i> , 2021, 35, 1091-1101.	1.0	5
5	Dissemination of <i>Mycobacterium tuberculosis</i> is associated to a <i>SIGLEC1</i> null variant that limits antigen exchange via trafficking extracellular vesicles. <i>Journal of Extracellular Vesicles</i> , 2021, 10, e12046.	5.5	9
6	The influence of human genetic variation on Epstein-Barr virus sequence diversity. <i>Scientific Reports</i> , 2021, 11, 4586.	1.6	8
7	HIV-1 and human genetic variation. <i>Nature Reviews Genetics</i> , 2021, 22, 645-657.	7.7	39
8	A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. <i>Nature Genetics</i> , 2021, 53, 1504-1516.	9.4	69
9	HLA Heterozygote Advantage against HIV-1 Is Driven by Quantitative and Qualitative Differences in HLA Allele-Specific Peptide Presentation. <i>Molecular Biology and Evolution</i> , 2020, 37, 639-650.	3.5	60
10	Sex Work Is Associated With Increased Vaginal Microbiome Diversity in Young Women From Mombasa, Kenya. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2020, 85, 79-87.	0.9	10
11	Minding the gap in HIV host genetics: opportunities and challenges. <i>Human Genetics</i> , 2020, 139, 865-875.	1.8	9
12	CCR5AS lncRNA variation differentially regulates CCR5, influencing HIV disease outcome. <i>Nature Immunology</i> , 2019, 20, 824-834.	7.0	87
13	HIV peptidome-wide association study reveals patient-specific epitope repertoires associated with HIV control. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 944-949.	3.3	26
14	Are privacy-enhancing technologies for genomic data ready for the clinic? A survey of medical experts of the Swiss HIV Cohort Study. <i>Journal of Biomedical Informatics</i> , 2018, 79, 1-6.	2.5	5
15	Interaction of the Host and Viral Genome and Their Influence on HIV Disease. <i>Frontiers in Genetics</i> , 2018, 9, 720.	1.1	24
16	<i>Systems Biology.</i> , 2018, , 1949-1956.		0
17	<i>Host Genetics and Genomics.</i> , 2018, , 1015-1022.		0
18	No Evidence for Association of Defensin Genomic Copy Number with HIV Susceptibility, HIV Load during Clinical Latency, or Progression to AIDS. <i>Annals of Human Genetics</i> , 2017, 81, 27-34.	0.3	4

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19	Systemic inflammation before and after antiretroviral therapy initiation as a predictor of immune response among HIV-infected individuals in Manitoba. <i>Cytokine</i> , 2017, 91, 74-81.	1.4	11
20	A Genome-wide Association Study Identifies Risk Alleles in Plasminogen and P4HA2 Associated with Giant Cell Arteritis. <i>American Journal of Human Genetics</i> , 2017, 100, 64-74.	2.6	78
21	Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. <i>Journal of Infectious Diseases</i> , 2017, 216, 1063-1069.	1.9	20
22	Severe viral respiratory infections in children with <i>IFIH1</i> loss-of-function mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 8342-8347.	3.3	111
23	Retroviruses As Myeloid Cell Riders: What Natural Human Siglec-1 "Knockouts" Tell Us About Pathogenesis. <i>Frontiers in Immunology</i> , 2017, 8, 1593.	2.2	14
24	Estimating the Respective Contributions of Human and Viral Genetic Variation to HIV Control. <i>PLoS Computational Biology</i> , 2017, 13, e1005339.	1.5	28
25	Exome Sequencing Reveals Primary Immunodeficiencies in Children with Community-Acquired <i>Pseudomonas aeruginosa</i> Sepsis. <i>Frontiers in Immunology</i> , 2016, 7, 357.	2.2	21
26	Host genetic predictors of the kynurenine pathway of tryptophan catabolism among treated HIV-infected Ugandans. <i>Aids</i> , 2016, 30, 1807-1815.	1.0	13
27	Privacy-preserving genomic testing in the clinic: a model using HIV treatment. <i>Genetics in Medicine</i> , 2016, 18, 814-822.	1.1	36
28	Identification of Siglec-1 null individuals infected with HIV-1. <i>Nature Communications</i> , 2016, 7, 12412.	5.8	38
29	Guanylate Binding Protein (GBP) 5 Is an Interferon-Inducible Inhibitor of HIV-1 Infectivity. <i>Cell Host and Microbe</i> , 2016, 19, 504-514.	5.1	211
30	Vitamin D Time Profile Based on the Contribution of Non-Genetic and Genetic Factors in HIV-Infected Individuals of European Ancestry. <i>Antiviral Therapy</i> , 2015, 20, 261-269.	0.6	5
31	The Characteristics of Heterozygous Protein Truncating Variants in the Human Genome. <i>PLoS Computational Biology</i> , 2015, 11, e1004647.	1.5	34
32	Identification of potential HIV restriction factors by combining evolutionary genomic signatures with functional analyses. <i>Retrovirology</i> , 2015, 12, 41.	0.9	78
33	Polymorphisms of large effect explain the majority of the host genetic contribution to variation of HIV-1 virus load. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14658-14663.	3.3	154
34	The impact of host genetic variation on infection with HIV-1. <i>Nature Immunology</i> , 2015, 16, 577-583.	7.0	119
35	Additive effects of HLA alleles and innate immune genes determine viral outcome in HCV infection. <i>Gut</i> , 2015, 64, 813-819.	6.1	65
36	Human genetic variation in HIV disease. <i>Current Opinion in HIV and AIDS</i> , 2015, 10, 110-115.	1.5	9

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37	Genome-wide association study of virologic response with efavirenz-containing or abacavir-containing regimens in AIDS clinical trials group protocols. <i>Pharmacogenetics and Genomics</i> , 2015, 25, 51-59.	0.7	13
38	Amino Acid Variation in HLA Class II Proteins Is a Major Determinant of Humoral Response to Common Viruses. <i>American Journal of Human Genetics</i> , 2015, 97, 738-743.	2.6	63
39	A Novel Acute Retroviral Syndrome Severity Score Predicts the Key Surrogate Markers for HIV-1 Disease Progression. <i>PLoS ONE</i> , 2014, 9, e114111.	1.1	17
40	Disentangling Human Tolerance and Resistance Against HIV. <i>PLoS Biology</i> , 2014, 12, e1001951.	2.6	53
41	HIV-1 Capture and Transmission by Dendritic Cells: The Role of Viral Glycolipids and the Cellular Receptor Siglec-1. <i>PLoS Pathogens</i> , 2014, 10, e1004146.	2.1	108
42	Analysis of Stop-Gain and Frameshift Variants in Human Innate Immunity Genes. <i>PLoS Computational Biology</i> , 2014, 10, e1003757.	1.5	32
43	GuavaH: a compendium of host genomic data in HIV biology and disease. <i>Retrovirology</i> , 2014, 11, 6.	0.9	13
44	Genomewide association study of atazanavir pharmacokinetics and hyperbilirubinemia in AIDS Clinical Trials Group protocol A5202. <i>Pharmacogenetics and Genomics</i> , 2014, 24, 195-203.	0.7	37
45	Genome-Wide Association Study of Human Immunodeficiency Virus (HIV)-1 Coreceptor Usage in Treatment-Naïve Patients from An AIDS Clinical Trials Group Study. <i>Open Forum Infectious Diseases</i> , 2014, 1, ofu018.	0.4	7
46	Genome-wide association study of peripheral neuropathy with D-drug-containing regimens in AIDS Clinical Trials Group protocol 384. <i>Journal of NeuroVirology</i> , 2014, 20, 304-308.	1.0	14
47	HLA Class I and KIR Genes Do Not Protect Against HIV Type 1 Infection in Highly Exposed Uninfected Individuals With Hemophilia A. <i>Journal of Infectious Diseases</i> , 2014, 210, 1047-1051.	1.9	16
48	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
49	Influence of HLA-C Expression Level on HIV Control. <i>Science</i> , 2013, 340, 87-91.	6.0	352
50	Susceptibility and adaptation to human TRIM5 α alleles at positive selected sites in HIV-1 capsid. <i>Virology</i> , 2013, 441, 162-170.	1.1	12
51	Association Study of Common Genetic Variants and HIV-1 Acquisition in 6,300 Infected Cases and 7,200 Controls. <i>PLoS Pathogens</i> , 2013, 9, e1003515.	2.1	109
52	A genome-wide association study of resistance to HIV infection in highly exposed uninfected individuals with hemophilia A. <i>Human Molecular Genetics</i> , 2013, 22, 1903-1910.	1.4	38
53	Genetic interplay between HLA-C and MIR148A in HIV control and Crohn disease. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 20705-20710.	3.3	109
54	Genetic Predictors of Cervical Dysplasia in African American HIV-Infected Women: ACTG DACS 268. <i>HIV Clinical Trials</i> , 2013, 14, 292-302.	2.0	1

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55	On stand by. Aids, 2013, 27, 2831-2839.	1.0	10
56	European Genetic Diversity and Susceptibility to Pathogens. Human Heredity, 2013, 76, 187-193.	0.4	3
57	HIV and innate immunity â€“ a genomics perspective. F1000prime Reports, 2013, 5, 29.	5.9	10
58	A genome-to-genome analysis of associations between human genetic variation, HIV-1 sequence diversity, and viral control. ELife, 2013, 2, e01123.	2.8	126
59	Systems Biology. , 2013, , 1-9.		0
60	GWAS Identifies Novel Susceptibility Loci on 6p21.32 and 21q21.3 for Hepatocellular Carcinoma in Chronic Hepatitis B Virus Carriers. PLoS Genetics, 2012, 8, e1002791.	1.5	177
61	Genome-wide association study of plasma efavirenz pharmacokinetics in AIDS Clinical Trials Group protocols implicates several CYP2B6 variants. Pharmacogenetics and Genomics, 2012, 22, 858-867.	0.7	128
62	Fine-mapping classical HLA variation associated with durable host control of HIV-1 infection in African Americans. Human Molecular Genetics, 2012, 21, 4334-4347.	1.4	61
63	Microarray Analysis of HIV Resistant Female Sex Workers Reveal a Gene Expression Signature Pattern Reminiscent of a Lowered Immune Activation State. PLoS ONE, 2012, 7, e30048.	1.1	51
64	Host Genetics and Resistance to HIV-1 Infection. , 2012, , 169-209.		1
65	Extremely low-coverage sequencing and imputation increases power for genome-wide association studies. Nature Genetics, 2012, 44, 631-635.	9.4	239
66	Exome sequencing and the genetic basis of complex traits. Nature Genetics, 2012, 44, 623-630.	9.4	340
67	Comparative transcriptomics of extreme phenotypes of human HIV-1 infection and SIV infection in sooty mangabey and rhesus macaque. Journal of Clinical Investigation, 2011, 121, 2391-2400.	3.9	168
68	HIVâ€™Exposed Seronegative Commercial Sex Workers Show a Quiescent Phenotype in the CD4⁺T Cell Compartment and Reduced Expression of HIVâ€™Dependent Host Factors. Journal of Infectious Diseases, 2010, 202, S339-S344.	1.9	104
69	Genomic Approaches to the Study of HIVâ€™1 Acquisition. Journal of Infectious Diseases, 2010, 202, S382-S386.	1.9	17
70	The Major Genetic Determinants of HIV-1 Control Affect HLA Class I Peptide Presentation. Science, 2010, 330, 1551-1557.	6.0	1,054
71	Decreased Immune Activation in Resistance to HIVâ€™1 Infection Is Associated with an Elevated Frequency of CD4⁺CD25⁺FOXP3⁺Regulatory T Cells. Journal of Infectious Diseases, 2009, 199, 1318-1322.	1.9	147
72	The Role of Regulatory T Cells in Chronic and Acute Viral Infections. Clinical Infectious Diseases, 2008, 46, 1046-1052.	2.9	63

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73	Polymorphisms in IRF-1 associated with resistance to HIV-1 infection in highly exposed uninfected Kenyan sex workers. <i>Aids</i> , 2007, 21, 1091-1101.	1.0	74
74	Antigen-Specific Gene Expression Profiles of Peripheral Blood Mononuclear Cells Do Not Reflect Those of T-Lymphocyte Subsets. <i>Vaccine Journal</i> , 2004, 11, 977-982.	3.2	15
75	CYFIP2 is highly abundant in CD4+ cells from multiple sclerosis patients and is involved in T cell adhesion. <i>European Journal of Immunology</i> , 2004, 34, 1217-1227.	1.6	34