

Luis B Barreiro

List of Publications by Citations

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

128
papers

9,516
citations

49
h-index

97
g-index

146
ext. papers

12,463
ext. citations

13.8
avg, IF

6.61
L-index

#	Paper	IF	Citations
128	TLR3 deficiency in patients with herpes simplex encephalitis. <i>Science</i> , 2007 , 317, 1522-7	33.3	842
127	Defining trained immunity and its role in health and disease. <i>Nature Reviews Immunology</i> , 2020 , 20, 375-388	38.5	587
126	Herd Immunity: Understanding COVID-19. <i>Immunity</i> , 2020 , 52, 737-741	32.3	484
125	BCG Educates Hematopoietic Stem Cells to Generate Protective Innate Immunity against Tuberculosis. <i>Cell</i> , 2018 , 172, 176-190.e19	56.2	471
124	Natural selection has driven population differentiation in modern humans. <i>Nature Genetics</i> , 2008 , 40, 340-5	36.3	436
123	From evolutionary genetics to human immunology: how selection shapes host defence genes. <i>Nature Reviews Genetics</i> , 2010 , 11, 17-30	30.1	352
122	Integration of genetic and immunological insights into a model of celiac disease pathogenesis. <i>Annual Review of Immunology</i> , 2011 , 29, 493-525	34.7	351
121	Social networks predict gut microbiome composition in wild baboons. <i>ELife</i> , 2015 , 4,	8.9	294
120	Evolutionary dynamics of human Toll-like receptors and their different contributions to host defense. <i>PLoS Genetics</i> , 2009 , 5, e1000562	6	272
119	Reovirus infection triggers inflammatory responses to dietary antigens and development of celiac disease. <i>Science</i> , 2017 , 356, 44-50	33.3	264
118	Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. <i>Cell</i> , 2016 , 167, 657-669.e21	56.2	264
117	Social environment is associated with gene regulatory variation in the rhesus macaque immune system. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 6490-5	11.5	208
116	Seasonal variation in human gut microbiome composition. <i>PLoS ONE</i> , 2014 , 9, e90731	3.7	179
115	Deciphering the genetic architecture of variation in the immune response to Mycobacterium tuberculosis infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 1204-9	11.5	179
114	Microbial signals drive pre-leukaemic myeloproliferation in a Tet2-deficient host. <i>Nature</i> , 2018 , 557, 580-584	58.4	163
113	Social status alters immune regulation and response to infection in macaques. <i>Science</i> , 2016 , 354, 1041-1045	39.5	154
112	Genome-Wide Association Studies of the Human Gut Microbiota. <i>PLoS ONE</i> , 2015 , 10, e0140301	3.7	153

111	Promoter variation in the DC-SIGN-encoding gene CD209 is associated with tuberculosis. <i>PLoS Medicine</i> , 2006 , 3, e20	11.6	152
110	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. <i>Genome Research</i> , 2015 , 25, 1801-11	9.7	138
109	Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America. <i>Science</i> , 2017 , 356, 543-546	33.3	128
108	Evolutionary genetic dissection of human interferons. <i>Journal of Experimental Medicine</i> , 2011 , 208, 2747-2756	15.6	118
107	Inferring the demographic history of African farmers and pygmy hunter-gatherers using a multilocus resequencing data set. <i>PLoS Genetics</i> , 2009 , 5, e1000448	6	117
106	The macrophage IRF8/IRF1 regulome is required for protection against infections and is associated with chronic inflammation. <i>Journal of Experimental Medicine</i> , 2016 , 213, 585-603	16.6	112
105	Deciphering the ancient and complex evolutionary history of human arylamine N-acetyltransferase genes. <i>American Journal of Human Genetics</i> , 2006 , 78, 423-36	11	100
104	Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations. <i>Nature Communications</i> , 2017 , 8, 266	17.4	93
103	Evolutionary insights into the high worldwide prevalence of MBL2 deficiency alleles. <i>Human Molecular Genetics</i> , 2006 , 15, 2650-8	5.6	91
102	Trained immunity, tolerance, priming and differentiation: distinct immunological processes. <i>Nature Immunology</i> , 2021 , 22, 2-6	19.1	85
101	Reservoir host immune responses to emerging zoonotic viruses. <i>Cell</i> , 2015 , 160, 20-35	56.2	80
100	The heritage of pathogen pressures and ancient demography in the human innate-immunity CD209/CD209L region. <i>American Journal of Human Genetics</i> , 2005 , 77, 869-86	11	79
99	The macrophage IRF8/IRF1 regulome is required for protection against infections and is associated with chronic inflammation. <i>Journal of Cell Biology</i> , 2016 , 212, 2127OIA59	7.3	78
98	Vaginal microbiome in early pregnancy and subsequent risk of spontaneous preterm birth: a case-control study. <i>BJOG: an International Journal of Obstetrics and Gynaecology</i> , 2019 , 126, 349-358	3.7	73
97	The impact of agricultural emergence on the genetic history of African rainforest hunter-gatherers and agriculturalists. <i>Nature Communications</i> , 2014 , 5, 3163	17.4	73
96	Chronic Inflammation Permanently Reshapes Tissue-Resident Immunity in Celiac Disease. <i>Cell</i> , 2019 , 176, 967-981.e19	56.2	72
95	Functional comparison of innate immune signaling pathways in primates. <i>PLoS Genetics</i> , 2010 , 6, e1001269	14.9	71
94	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

93	Formulating a historical and demographic model of recent human evolution based on resequencing data from noncoding regions. <i>PLoS ONE</i> , 2010 , 5, e10284	3.7	70
92	Adaptively introgressed Neandertal haplotype at the OAS locus functionally impacts innate immune responses in humans. <i>Genome Biology</i> , 2016 , 17, 246	18.3	70
91	Signatures of purifying and local positive selection in human miRNAs. <i>American Journal of Human Genetics</i> , 2009 , 84, 316-27	11	68
90	IL-15, gluten and HLA-DQ8 drive tissue destruction in coeliac disease. <i>Nature</i> , 2020 , 578, 600-604	50.4	65
89	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
88	M. tuberculosis Reprograms Hematopoietic Stem Cells to Limit Myelopoiesis and Impair Trained Immunity. <i>Cell</i> , 2020 , 183, 752-770.e22	56.2	60
87	Signature-tagged transposon mutagenesis identifies novel Mycobacterium tuberculosis genes involved in the parasitism of human macrophages. <i>Infection and Immunity</i> , 2007 , 75, 504-7	3.7	59
86	Exploring the occurrence of classic selective sweeps in humans using whole-genome sequencing data sets. <i>Molecular Biology and Evolution</i> , 2014 , 31, 1850-68	8.3	57
85	The epigenomic landscape of African rainforest hunter-gatherers and farmers. <i>Nature Communications</i> , 2015 , 6, 10047	17.4	55
84	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
83	bacterial infection drives the expression dynamics of microRNAs and their isomiRs. <i>PLoS Genetics</i> , 2015 , 11, e1005064	6	50
82	The contribution of natural selection to present-day susceptibility to chronic inflammatory and autoimmune disease. <i>Current Opinion in Immunology</i> , 2014 , 31, 66-78	7.8	50
81	A genomic portrait of the genetic architecture and regulatory impact of microRNA expression in response to infection. <i>Genome Research</i> , 2014 , 24, 850-9	9.7	49
80	Annexin1 regulates DC efferocytosis and cross-presentation during Mycobacterium tuberculosis infection. <i>Journal of Clinical Investigation</i> , 2015 , 125, 752-68	15.9	49
79	Social status alters chromatin accessibility and the gene regulatory response to glucocorticoid stimulation in rhesus macaques. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 1219-1228	11.5	47
78	Genome-wide quantification of the effects of DNA methylation on human gene regulation. <i>ELife</i> , 2018 , 7,	8.9	44
77	Efficient and Robust NK-Cell Transduction With Baboon Envelope Pseudotyped Lentivector. <i>Frontiers in Immunology</i> , 2019 , 10, 2873	8.4	43
76	Age-dependent association between pulmonary tuberculosis and common TOX variants in the 8q12-13 linkage region. <i>American Journal of Human Genetics</i> , 2013 , 92, 407-14	11	42

75	Fecal microbiota transplant rescues mice from human pathogen mediated sepsis by restoring systemic immunity. <i>Nature Communications</i> , 2020 , 11, 2354	17.4	40
74	Common methods for fecal sample storage in field studies yield consistent signatures of individual identity in microbiome sequencing data. <i>Scientific Reports</i> , 2016 , 6, 31519	4.9	40
73	Mycobacterial infection induces a specific human innate immune response. <i>Scientific Reports</i> , 2015 , 5, 16882	4.9	40
72	Lack of association between genetic polymorphisms in enzymes associated with folate metabolism and unexplained reduced sperm counts. <i>PLoS ONE</i> , 2009 , 4, e6540	3.7	40
71	pncA mutations in pyrazinamide-resistant Mycobacterium tuberculosis isolates in Portugal. <i>Antimicrobial Agents and Chemotherapy</i> , 2004 , 48, 2736-8	5.9	40
70	Different selective pressures shape the evolution of Toll-like receptors in human and African great ape populations. <i>Human Molecular Genetics</i> , 2013 , 22, 4829-40	5.6	38
69	Social status drives social relationships in groups of unrelated female rhesus macaques. <i>Animal Behaviour</i> , 2016 , 111, 307-317	2.8	38
68	Promoter and neck region length variation of DC-SIGN is not associated with susceptibility to tuberculosis in Tunisian patients. <i>Human Immunology</i> , 2007 , 68, 908-12	2.3	37
67	Gene-body 5-hydroxymethylation is associated with gene expression changes in the prefrontal cortex of depressed individuals. <i>Translational Psychiatry</i> , 2017 , 7, e1119	8.6	36
66	Fetal microglial phenotype in vitro carries memory of prior in vivo exposure to inflammation. <i>Frontiers in Cellular Neuroscience</i> , 2015 , 9, 294	6.1	35
65	Characterizing 5-hydroxymethylcytosine in human prefrontal cortex at single base resolution. <i>BMC Genomics</i> , 2015 , 16, 672	4.5	34
64	Alu repeats as transcriptional regulatory platforms in macrophage responses to M. tuberculosis infection. <i>Nucleic Acids Research</i> , 2016 , 44, 10571-10587	20.1	30
63	Evolution of the TIR domain-containing adaptors in humans: swinging between constraint and adaptation. <i>Molecular Biology and Evolution</i> , 2011 , 28, 3087-97	8.3	30
62	The demographic history and mutational load of African hunter-gatherers and farmers. <i>Nature Ecology and Evolution</i> , 2018 , 2, 721-730	12.3	29
61	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
60	Genomic Evidence for Local Adaptation of Hunter-Gatherers to the African Rainforest. <i>Current Biology</i> , 2019 , 29, 2926-2935.e4	6.3	25
59	The contribution of admixture to primate evolution. <i>Current Opinion in Genetics and Development</i> , 2017 , 47, 61-68	4.9	25
58	Dominance rank causally affects personality and glucocorticoid regulation in female rhesus macaques. <i>Psychoneuroendocrinology</i> , 2016 , 74, 179-188	5	24

57	Genetic and transcriptional analysis of human host response to healthy gut microbiota. <i>MSystems</i> , 2016 , 1,	7.6	24
56	Social history and exposure to pathogen signals modulate social status effects on gene regulation in rhesus macaques. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 23317-23322	11.5	23
55	Gene set signature of reversal reaction type I in leprosy patients. <i>PLoS Genetics</i> , 2013 , 9, e1003624	6	23
54	Functional characterization of naturally occurring genetic variants in the human TLR1-2-6 gene family. <i>Human Mutation</i> , 2011 , 32, 643-52	4.7	23
53	DC-SIGN interacts with <i>Mycobacterium leprae</i> but sequence variation in this lectin is not associated with leprosy in the Pakistani population. <i>Human Immunology</i> , 2006 , 67, 102-7	2.3	23
52	High-throughput SNP genotyping: combining tag SNPs and molecular beacons. <i>Methods in Molecular Biology</i> , 2009 , 578, 255-76	1.4	23
51	Gut microbiome heritability is nearly universal but environmentally contingent. <i>Science</i> , 2021 , 373, 181-186	3.5	22
50	Length variation of DC-SIGN and L-SIGN neck-region has no impact on tuberculosis susceptibility. <i>Human Immunology</i> , 2007 , 68, 106-12	2.3	21
49	Polygenic adaptation and convergent evolution on growth and cardiac genetic pathways in African and Asian rainforest hunter-gatherers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E11256-E11263	11.5	21
48	Evolutionary genetics evidence of an essential, nonredundant role of the IFN- γ pathway in protective immunity. <i>Human Mutation</i> , 2011 , 32, 633-42	4.7	20
47	Deciphering the genetic control of gene expression following <i>Mycobacterium leprae</i> antigen stimulation. <i>PLoS Genetics</i> , 2017 , 13, e1006952	6	17
46	Extracellular adenosine triphosphate affects the response of human macrophages infected with <i>Mycobacterium tuberculosis</i> . <i>Journal of Infectious Diseases</i> , 2014 , 210, 824-33	7	16
45	Evolutionary and population (epi)genetics of immunity to infection. <i>Human Genetics</i> , 2020 , 139, 723-732	6.3	15
44	Natural selection contributed to immunological differences between hunter-gatherers and agriculturalists. <i>Nature Ecology and Evolution</i> , 2019 , 3, 1253-1264	12.3	15
43	The role played by natural selection on Mendelian traits in humans. <i>Annals of the New York Academy of Sciences</i> , 2010 , 1214, 1-17	6.5	15
42	Proteomic characterization of phagosomal membrane microdomains during phagolysosome biogenesis and evolution. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1365-77	7.6	14
41	DC-SIGNR neck-region polymorphisms and HIV-1 susceptibility: From population stratification to a possible advantage of the 7/5 heterozygous genotype. <i>Journal of Infectious Diseases</i> , 2006 , 194, 1184-5; author reply 1185-7	7	14
40	Protective role of DC-SIGN (CD209) neck-region alleles with . <i>Journal of Infectious Diseases</i> , 2008 , 198, 68-71	7	13

39	Identification of a β Receptor Antagonist That Prevents Reprogramming of Human Tissue-resident Cytotoxic T Cells by IL15 and IL21. <i>Gastroenterology</i> , 2020 , 158, 625-637.e13	13.3	13
38	Genetic and evolutionary determinants of human population variation in immune responses. <i>Current Opinion in Genetics and Development</i> , 2018 , 53, 28-35	4.9	13
37	Quantitative trait loci (QTL) study identifies novel genomic regions associated to Chiari-like malformation in Griffon Bruxellois dogs. <i>PLoS ONE</i> , 2014 , 9, e89816	3.7	12
36	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
35	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
34	The epigenetically-encoded memory of the innate immune system. <i>Current Opinion in Immunology</i> , 2020 , 65, 7-13	7.8	10
33	A multilayered immune system through the lens of unconventional T cells. <i>Nature</i> , 2021 , 595, 501-510	50.4	9
32	Transposable elements have contributed human regulatory regions that are activated upon bacterial infection. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2020 , 375, 20190332	5.8	8
31	RNAseq profiling of primary microglia and astrocyte cultures in near-term ovine fetus: A glial in vivo-in vitro multi-hit paradigm in large mammalian brain. <i>Journal of Neuroscience Methods</i> , 2017 , 276, 23-32	3	7
30	Molecular Signature of CAID Syndrome: Noncanonical Roles of SGO1 in Regulation of TGF- β Signaling and Epigenomics. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2019 , 7, 411-431	7.9	6
29	When genetics meets epigenetics: deciphering the mechanisms controlling inter-individual variation in immune responses to infection. <i>Current Opinion in Immunology</i> , 2014 , 29, 119-26	7.8	6
28	Predicting susceptibility to tuberculosis based on gene expression profiling in dendritic cells. <i>Scientific Reports</i> , 2017 , 7, 5702	4.9	6
27	Agonism and grooming behaviour explain social status effects on physiology and gene regulation in rhesus macaques.. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2022 , 377, 20210132	5.8	5
26	Pre-existing chromatin accessibility and gene expression differences among naive CD4 T cells influence effector potential. <i>Cell Reports</i> , 2021 , 37, 110064	10.6	5
25	Genetic ancestry effects on the response to viral infection are pervasive but cell type specific. <i>Science</i> , 2021 , 374, 1127-1133	33.3	5
24	Social status alters chromatin accessibility and the gene regulatory response to glucocorticoid stimulation in rhesus macaques		5
23	Social affiliation predicts mitochondrial DNA copy number in female rhesus macaques. <i>Biology Letters</i> , 2019 , 15, 20180643	3.6	4
22	Molecular epidemiology of Mycobacterium tuberculosis in Lisbon. <i>Revista Portuguesa De Pneumologia</i> , 2008 , 14, 239-59		4

21	Lung Epithelial Signaling Mediates Early Vaccine-Induced CD4 T Cell Activation and Control. <i>MBio</i> , 2021 , 12, e0146821	7.8	4
20	Alveolar macrophages from persons living with HIV show impaired epigenetic response to <i>Mycobacterium tuberculosis</i> . <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	4
19	Holy Immune Tolerance, Batman!. <i>Immunity</i> , 2018 , 48, 1074-1076	32.3	3
18	Lack of evidence for intergenerational inheritance of immune resistance to infections.. <i>Nature Immunology</i> , 2022 ,	19.1	3
17	Author response: Genome-wide quantification of the effects of DNA methylation on human gene regulation 2018 ,		3
16	Bacterial Infection Remodels the DNA Methylation Landscape of Human Dendritic Cells		3
15	Single-cell RNA-sequencing reveals pervasive but highly cell type-specific genetic ancestry effects on the response to viral infection		3
14	Genome-wide quantification of the effects of DNA methylation on human gene regulation		2
13	Gene activation precedes DNA demethylation in response to infection in human dendritic cells		2
12	Social history and exposure to pathogen signals modulate social status effects on gene regulation in rhesus macaques		2
11	Widespread shortening of 3' untranslated regions and increased exon inclusion are evolutionarily conserved features of innate immune responses to infection		2
10	Mycobacterial infection induces a specific human innate immune response 2015 ,		1
9	Getting under and through the skin: ecological genomics of chytridiomycosis infection in frogs. <i>Molecular Ecology</i> , 2012 , 21, 3095-7	5.7	1
8	Natural selection contributed to immunological differences between human hunter-gatherers and agriculturalists		
7	Transposable elements have contributed human regulatory regions that are activated upon bacterial infection		1
6	Primate innate immune responses to bacterial and viral pathogens reveals an evolutionary trade-off between strength and specificity		1
5	Adaptively introgressed Neandertal haplotype at the OAS locus functionally impacts innate immune responses in humans		1
4	Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations		1

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| 3 | Agonism and grooming behavior explain social status effects on physiology and gene regulation in rhesus macaques | | 1 |
| 2 | A signature of Neanderthal introgression on molecular mechanisms of environmental responses. <i>PLoS Genetics</i> , 2021, 17, e1009493 | 6 | 0 |
| 1 | My Old World chap, this Egal is not for you. <i>Cell Host and Microbe</i> , 2021, 29, 315-317 | | 23.4 |