List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Defining trained immunity and its role in health and disease. Nature Reviews Immunology, 2020, 20, 375-388.	10.6	1,345
2	TLR3 Deficiency in Patients with Herpes Simplex Encephalitis. Science, 2007, 317, 1522-1527.	6.0	970
3	Herd Immunity: Understanding COVID-19. Immunity, 2020, 52, 737-741.	6.6	877
4	BCG Educates Hematopoietic Stem Cells to Generate Protective Innate Immunity against Tuberculosis. Cell, 2018, 172, 176-190.e19.	13.5	802
5	Natural selection has driven population differentiation in modern humans. Nature Genetics, 2008, 40, 340-345.	9.4	526
6	From evolutionary genetics to human immunology: how selection shapes host defence genes. Nature Reviews Genetics, 2010, 11, 17-30.	7.7	471
7	Integration of Genetic and Immunological Insights into a Model of Celiac Disease Pathogenesis. Annual Review of Immunology, 2011, 29, 493-525.	9.5	459
8	Genetic Ancestry and Natural Selection Drive Population Differences in Immune Responses to Pathogens. Cell, 2016, 167, 657-669.e21.	13.5	419
9	Social networks predict gut microbiome composition in wild baboons. ELife, 2015, 4, .	2.8	403
10	Reovirus infection triggers inflammatory responses to dietary antigens and development of celiac disease. Science, 2017, 356, 44-50.	6.0	367
11	Evolutionary Dynamics of Human Toll-Like Receptors and Their Different Contributions to Host Defense. PLoS Genetics, 2009, 5, e1000562.	1.5	341
12	Microbial signals drive pre-leukaemic myeloproliferation in a Tet2-deficient host. Nature, 2018, 557, 580-584.	13.7	296
13	Trained immunity, tolerance, priming and differentiation: distinct immunological processes. Nature Immunology, 2021, 22, 2-6.	7.0	274
14	Social environment is associated with gene regulatory variation in the rhesus macaque immune system. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6490-6495.	3.3	257
15	Seasonal Variation in Human Gut Microbiome Composition. PLoS ONE, 2014, 9, e90731.	1.1	246
16	Deciphering the genetic architecture of variation in the immune response to <i>Mycobacterium tuberculosis</i> infection. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 1204-1209.	3.3	238
17	Social status alters immune regulation and response to infection in macaques. Science, 2016, 354, 1041-1045.	6.0	235
18	Genome-Wide Association Studies of the Human Gut Microbiota. PLoS ONE, 2015, 10, e0140301.	1.1	228

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19	Bacterial infection remodels the DNA methylation landscape of human dendritic cells. Genome Research, 2015, 25, 1801-1811.	2.4	195
20	The macrophage IRF8/IRF1 regulome is required for protection against infections and is associated with chronic inflammation. Journal of Experimental Medicine, 2016, 213, 585-603.	4.2	194
21	Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America. Science, 2017, 356, 543-546.	6.0	188
22	Evolutionary genetic dissection of human interferons. Journal of Experimental Medicine, 2011, 208, 2747-2759.	4.2	170
23	Promoter Variation in the DC-SIGN–Encoding Gene CD209 Is Associated with Tuberculosis. PLoS Medicine, 2006, 3, e20.	3.9	166
24	Genetic regulatory effects modified by immune activation contribute to autoimmune disease associations. Nature Communications, 2017, 8, 266.	5.8	157
25	M.Âtuberculosis Reprograms Hematopoietic Stem Cells to Limit Myelopoiesis and Impair Trained Immunity. Cell, 2020, 183, 752-770.e22.	13.5	148
26	Inferring the Demographic History of African Farmers and Pygmy Hunter–Gatherers Using a Multilocus Resequencing Data Set. PLoS Genetics, 2009, 5, e1000448.	1.5	142
27	Vaginal microbiome in early pregnancy and subsequent risk of spontaneous preterm birth: a case–control study. BJOG: an International Journal of Obstetrics and Gynaecology, 2019, 126, 349-358.	1.1	132
28	Deciphering the Ancient and Complex Evolutionary History of Human Arylamine N-Acetyltransferase Genes. American Journal of Human Genetics, 2006, 78, 423-436.	2.6	127
29	Gene activation precedes DNA demethylation in response to infection in human dendritic cells. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 6938-6943.	3.3	127
30	Chronic Inflammation Permanently Reshapes Tissue-Resident Immunity in Celiac Disease. Cell, 2019, 176, 967-981.e19.	13.5	126
31	Gut microbiome heritability is nearly universal but environmentally contingent. Science, 2021, 373, 181-186.	6.0	126
32	IL-15, gluten and HLA-DQ8 drive tissue destruction in coeliac disease. Nature, 2020, 578, 600-604.	13.7	122
33	Adaptively introgressed Neandertal haplotype at the OAS locus functionally impacts innate immune responses in humans. Genome Biology, 2016, 17, 246.	3.8	117
34	Evolutionary insights into the high worldwide prevalence of MBL2 deficiency alleles. Human Molecular Genetics, 2006, 15, 2650-2658.	1.4	114
35	Reservoir Host Immune Responses to Emerging Zoonotic Viruses. Cell, 2015, 160, 20-35.	13.5	114
36	The impact of agricultural emergence on the genetic history of African rainforest hunter-gatherers and agriculturalists. Nature Communications, 2014, 5, 3163.	5.8	96

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37	Genome-wide quantification of the effects of DNA methylation on human gene regulation. ELife, 2018, 7, .	2.8	96
38	Functional Comparison of Innate Immune Signaling Pathways in Primates. PLoS Genetics, 2010, 6, e1001249.	1.5	94
39	Adaptive, convergent origins of the pygmy phenotype in African rainforest hunter-gatherers. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E3596-603.	3.3	91
40	Widespread Shortening of 3' Untranslated Regions and Increased Exon Inclusion Are Evolutionarily Conserved Features of Innate Immune Responses to Infection. PLoS Genetics, 2016, 12, e1006338.	1.5	90
41	Efficient and Robust NK-Cell Transduction With Baboon Envelope Pseudotyped Lentivector. Frontiers in Immunology, 2019, 10, 2873.	2.2	84
42	Signatures of Purifying and Local Positive Selection in Human miRNAs. American Journal of Human Genetics, 2009, 84, 316-327.	2.6	83
43	The Heritage of Pathogen Pressures and Ancient Demography in the Human Innate-Immunity CD209/CD209L Region. American Journal of Human Genetics, 2005, 77, 869-886.	2.6	81
44	The epigenomic landscape of African rainforest hunter-gatherers and farmers. Nature Communications, 2015, 6, 10047.	5.8	75
45	Fecal microbiota transplant rescues mice from human pathogen mediated sepsis by restoring systemic immunity. Nature Communications, 2020, 11, 2354.	5.8	75
46	Formulating a Historical and Demographic Model of Recent Human Evolution Based on Resequencing Data from Noncoding Regions. PLoS ONE, 2010, 5, e10284.	1.1	74
47	Exploring the Occurrence of Classic Selective Sweeps in Humans Using Whole-Genome Sequencing Data Sets. Molecular Biology and Evolution, 2014, 31, 1850-1868.	3.5	72
48	The contribution of natural selection to present-day susceptibility to chronic inflammatory and autoimmune disease. Current Opinion in Immunology, 2014, 31, 66-78.	2.4	72
49	Social status alters chromatin accessibility and the gene regulatory response to glucocorticoid stimulation in rhesus macaques. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 1219-1228.	3.3	71
50	Signature-Tagged Transposon Mutagenesis Identifies Novel Mycobacterium tuberculosis Genes Involved in the Parasitism of Human Macrophages. Infection and Immunity, 2007, 75, 504-507.	1.0	69
51	Genetic ancestry effects on the response to viral infection are pervasive but cell type specific. Science, 2021, 374, 1127-1133.	6.0	68
52	Annexin1 regulates DC efferocytosis and cross-presentation during Mycobacterium tuberculosis infection. Journal of Clinical Investigation, 2015, 125, 752-768.	3.9	65
53	A multilayered immune system through the lens of unconventional T cells. Nature, 2021, 595, 501-510.	13.7	64
54	Mycobacterial infection induces a specific human innate immune response. Scientific Reports, 2015, 5, 16882.	1.6	63

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55	Common methods for fecal sample storage in field studies yield consistent signatures of individual identity in microbiome sequencing data. Scientific Reports, 2016, 6, 31519.	1.6	63
56	Gene-body 5-hydroxymethylation is associated with gene expression changes in the prefrontal cortex of depressed individuals. Translational Psychiatry, 2017, 7, e1119-e1119.	2.4	63
5 7	A genomic portrait of the genetic architecture and regulatory impact of microRNA expression in response to infection. Genome Research, 2014, 24, 850-859.	2.4	60
58	Bacterial Infection Drives the Expression Dynamics of microRNAs and Their isomiRs. PLoS Genetics, 2015, 11, e1005064.	1.5	60
59	Alu repeats as transcriptional regulatory platforms in macrophage responses to <i>M. tuberculosis</i> infection. Nucleic Acids Research, 2016, 44, 10571-10587.	6.5	52
60	Lack of Association between Genetic Polymorphisms in Enzymes Associated with Folate Metabolism and Unexplained Reduced Sperm Counts. PLoS ONE, 2009, 4, e6540.	1.1	51
61	Different selective pressures shape the evolution of Toll-like receptors in human and African great ape populations. Human Molecular Genetics, 2013, 22, 4829-4840.	1.4	49
62	Social status drives social relationships in groups of unrelated female rhesus macaques. Animal Behaviour, 2016, 111, 307-317.	0.8	47
63	Age-Dependent Association between Pulmonary Tuberculosis and Common TOX Variants in the 8q12–13 Linkage Region. American Journal of Human Genetics, 2013, 92, 407-414.	2.6	46
64	The contribution of admixture to primate evolution. Current Opinion in Genetics and Development, 2017, 47, 61-68.	1.5	44
65	Fetal microglial phenotype in vitro carries memory of prior in vivo exposure to inflammation. Frontiers in Cellular Neuroscience, 2015, 9, 294.	1.8	43
66	pncA Mutations in Pyrazinamide-Resistant Mycobacterium tuberculosis Isolates in Portugal. Antimicrobial Agents and Chemotherapy, 2004, 48, 2736-2738.	1.4	41
67	Evolution of the TIR Domain-Containing Adaptors in Humans: Swinging between Constraint and Adaptation. Molecular Biology and Evolution, 2011, 28, 3087-3097.	3.5	40
68	Genomic Evidence for Local Adaptation of Hunter-Gatherers to the African Rainforest. Current Biology, 2019, 29, 2926-2935.e4.	1.8	40
69	Promoter and neck region length variation of DC-SIGN is not associated with susceptibility to tuberculosis in Tunisian patients. Human Immunology, 2007, 68, 908-912.	1.2	39
70	Characterizing 5-hydroxymethylcytosine in human prefrontal cortex at single base resolution. BMC Genomics, 2015, 16, 672.	1.2	38
71	The demographic history and mutational load of African hunter-gatherers and farmers. Nature Ecology and Evolution, 2018, 2, 721-730.	3.4	38
72	Deciphering the genetic control of gene expression following Mycobacterium leprae antigen stimulation. PLoS Genetics, 2017, 13, e1006952.	1.5	37

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73	Dominance rank causally affects personality and glucocorticoid regulation in female rhesus macaques. Psychoneuroendocrinology, 2016, 74, 179-188.	1.3	34
74	Social history and exposure to pathogen signals modulate social status effects on gene regulation in rhesus macaques. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23317-23322.	3.3	33
75	Gene Set Signature of Reversal Reaction Type I in Leprosy Patients. PLoS Genetics, 2013, 9, e1003624.	1.5	32
76	Polygenic adaptation and convergent evolution on growth and cardiac genetic pathways in African and Asian rainforest hunter-gatherers. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E11256-E11263.	3.3	30
77	Primate innate immune responses to bacterial and viral pathogens reveals an evolutionary trade-off between strength and specificity. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	30
78	Functional characterization of naturally occurring genetic variants in the human TLR1-2-6 gene family. Human Mutation, 2011, 32, 643-652.	1.1	28
79	Human NKG2E Is Expressed and Forms an Intracytoplasmic Complex with CD94 and DAP12. Journal of Immunology, 2014, 193, 610-616.	0.4	28
80	Genetic and Transcriptional Analysis of Human Host Response to Healthy Gut Microbiota. MSystems, 2016, 1, .	1.7	28
81	Natural selection contributed to immunological differences between hunter-gatherers and agriculturalists. Nature Ecology and Evolution, 2019, 3, 1253-1264.	3.4	28
82	Evolutionary and population (epi)genetics of immunity to infection. Human Genetics, 2020, 139, 723-732.	1.8	28
83	High-Throughput SNP Genotyping: Combining Tag SNPs and Molecular Beacons. Methods in Molecular Biology, 2009, 578, 255-276.	0.4	27
84	DC-SIGN Interacts with Mycobacterium leprae but Sequence Variation in This Lectin Is Not Associated with Leprosy in the Pakistani Population. Human Immunology, 2006, 67, 102-107.	1.2	26
85	The role played by natural selection on Mendelian traits in humans. Annals of the New York Academy of Sciences, 2010, 1214, 1-17.	1.8	25
86	The epigenetically-encoded memory of the innate immune system. Current Opinion in Immunology, 2020, 65, 7-13.	2.4	24
87	High molecular weight DNA extraction strategies for longâ€read sequencing of complex metagenomes. Molecular Ecology Resources, 2022, 22, 1786-1802.	2.2	24
88	Identification of a $\hat{1}^3$ c Receptor Antagonist That Prevents Reprogramming of Human Tissue-resident Cytotoxic T Cells by IL15 and IL21. Gastroenterology, 2020, 158, 625-637.e13.	0.6	23
89	Evolutionary genetics evidence of an essential, nonredundant role of the IFN-γ pathway in protective immunity. Human Mutation, 2011, 32, 633-642.	1.1	22
90	A Short-Term High-Fat Diet Alters Glutathione Levels and IL-6 Gene Expression in Oxidative Skeletal Muscles of Young Rats. Frontiers in Physiology, 2019, 10, 372.	1.3	22

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91	Length Variation of DC-SIGN and L-SIGN Neck-Region has no Impact on Tuberculosis Susceptibility. Human Immunology, 2007, 68, 106-112.	1.2	21
92	Genetic and evolutionary determinants of human population variation in immune responses. Current Opinion in Genetics and Development, 2018, 53, 28-35.	1.5	20
93	Transposable elements have contributed human regulatory regions that are activated upon bacterial infection. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190332.	1.8	20
94	Pre-existing chromatin accessibility and gene expression differences among naive CD4+ TÂcells influence effector potential. Cell Reports, 2021, 37, 110064.	2.9	20
95	Alveolar macrophages from persons living with HIV show impaired epigenetic response to Mycobacterium tuberculosis. Journal of Clinical Investigation, 2021, 131, .	3.9	19
96	Extracellular Adenosine Triphosphate Affects the Response of Human Macrophages Infected With Mycobacterium tuberculosis. Journal of Infectious Diseases, 2014, 210, 824-833.	1.9	18
97	Synchrony and idiosyncrasy in the gut microbiome of wild baboons. Nature Ecology and Evolution, 2022, 6, 955-964.	3.4	18
98	Proteomic Characterization of Phagosomal Membrane Microdomains During Phagolysosome Biogenesis and Evolution. Molecular and Cellular Proteomics, 2012, 11, 1365-1377.	2.5	17
99	Lack of evidence for intergenerational inheritance of immune resistance to infections. Nature Immunology, 2022, 23, 203-207.	7.0	17
100	Quantitative Trait Loci (QTL) Study Identifies Novel Genomic Regions Associated to Chiari-Like Malformation in Griffon Bruxellois Dogs. PLoS ONE, 2014, 9, e89816.	1.1	16
101	DC‣IGNRNeckâ€Region Polymorphisms and HIVâ€1 Susceptibility: From Population Stratification to a Possible Advantage of the 7/5 Heterozygous Genotype. Journal of Infectious Diseases, 2006, 194, 1184-1185.	1.9	14
102	Protective Role of DCâ€SIGN(CD209)Neckâ€Region Alleles with <5 Repeat Units in HIVâ€1 Transmission. Journal of Infectious Diseases, 2008, 198, 68-71.	1.9	13
103	When genetics meets epigenetics: deciphering the mechanisms controlling inter-individual variation in immune responses to infection. Current Opinion in Immunology, 2014, 29, 119-126.	2.4	13
104	Holy Immune Tolerance, Batman!. Immunity, 2018, 48, 1074-1076.	6.6	13
105	Agonism and grooming behaviour explain social status effects on physiology and gene regulation in rhesus macaques. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20210132.	1.8	13
106	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. Journal of Neuroscience Methods, 2017, 276, 23-32.	1.3	11
107	Molecular Signature of CAID Syndrome: Noncanonical Roles of SGO1 in Regulation of TGF-Î ² Signaling and Epigenomics. Cellular and Molecular Gastroenterology and Hepatology, 2019, 7, 411-431.	2.3	11
108	Lung Epithelial Signaling Mediates Early Vaccine-Induced CD4 ⁺ T Cell Activation and <i>Mycobacterium tuberculosis</i> Control. MBio, 2021, 12, e0146821.	1.8	11

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109	Don't move: LRRK2 arrests NFAT in the cytoplasm. Nature Immunology, 2011, 12, 1029-1030.	7.0	8
110	Predicting susceptibility to tuberculosis based on gene expression profiling in dendritic cells. Scientific Reports, 2017, 7, 5702.	1.6	8
111	Social affiliation predicts mitochondrial DNA copy number in female rhesus macaques. Biology Letters, 2019, 15, 20180643.	1.0	8
112	A signature of Neanderthal introgression on molecular mechanisms of environmental responses. PLoS Genetics, 2021, 17, e1009493.	1.5	5
113	Mitochondrial cyclophilin D promotes disease tolerance by licensing NK cell development and IL-22 production against influenza virus. Cell Reports, 2022, 39, 110974.	2.9	5
114	Epidemiologia molecular de Mycobacterium tuberculosis em Lisboa. Revista Portuguesa De Pneumologia, 2008, 14, 239-259.	0.7	4
115	Getting under—and through—the skin: ecological genomics of chytridiomycosis infection in frogs. Molecular Ecology, 2012, 21, 3095-3097.	2.0	2
116	Editorial Overview: Immunogenetics and transplantation: Bringing evolution and genomics to human immunology. Current Opinion in Immunology, 2014, 30, v-vii.	2.4	0
117	My Old World chap, this α-gal is not for you. Cell Host and Microbe, 2021, 29, 315-317.	5.1	0
118	The macrophage IRF8/IRF1 regulome is required for protection against infections and is associated with chronic inflammation. Journal of Cell Biology, 2016, 212, 2127OIA59.	2.3	0