

Lluís Quintana-Murci

List of Publications by Year in descending order

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Version: 2024-02-01

165
papers

16,765
citations

17440

63
h-index

18647

119
g-index

202
all docs

202
docs citations

202
times ranked

25000
citing authors

#	ARTICLE	IF	CITATIONS
1	Autoantibodies against type I IFNs in patients with life-threatening COVID-19. Science, 2020, 370, .	12.6	1,983
2	TLR3 Deficiency in Patients with Herpes Simplex Encephalitis. Science, 2007, 317, 1522-1527.	12.6	970
3	An epigenetic clock analysis of race/ethnicity, sex, and coronary heart disease. Genome Biology, 2016, 17, 171.	8.8	535
4	Natural selection has driven population differentiation in modern humans. Nature Genetics, 2008, 40, 340-345.	21.4	526
5	From evolutionary genetics to human immunology: how selection shapes host defence genes. Nature Reviews Genetics, 2010, 11, 17-30.	16.3	471
6	Genetic evidence of an early exit of Homo sapiens sapiens from Africa through eastern Africa. Nature Genetics, 1999, 23, 437-441.	21.4	461
7	Where West Meets East: The Complex mtDNA Landscape of the Southwest and Central Asian Corridor. American Journal of Human Genetics, 2004, 74, 827-845.	6.2	375
8	Genetic Adaptation and Neandertal Admixture Shaped the Immune System of Human Populations. Cell, 2016, 167, 643-656.e17.	28.9	373
9	Autoantibodies neutralizing type I IFNs are present in ~4% of uninfected individuals over 70 years old and account for ~20% of COVID-19 deaths. Science Immunology, 2021, 6, .	11.9	357
10	Evolutionary Dynamics of Human Toll-Like Receptors and Their Different Contributions to Host Defense. PLoS Genetics, 2009, 5, e1000562.	3.5	341
11	Human TLRs and IL-1Rs in Host Defense: Natural Insights from Evolutionary, Epidemiological, and Clinical Genetics. Annual Review of Immunology, 2011, 29, 447-491.	21.8	316
12	X-linked recessive TLR7 deficiency in ~1% of men under 60 years old with life-threatening COVID-19. Science Immunology, 2021, 6, .	11.9	267
13	The mutation significance cutoff: gene-level thresholds for variant predictions. Nature Methods, 2016, 13, 109-110.	19.0	249
14	Genomic Signatures of Selective Pressures and Introgression from Archaic Hominins at Human Innate Immunity Genes. American Journal of Human Genetics, 2016, 98, 5-21.	6.2	243
15	Human genetic and immunological determinants of critical COVID-19 pneumonia. Nature, 2022, 603, 587-598.	27.8	216
16	The human gene damage index as a gene-level approach to prioritizing exome variants. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13615-13620.	7.1	213
17	Natural variation in the parameters of innate immune cells is preferentially driven by genetic factors. Nature Immunology, 2018, 19, 302-314.	14.5	205
18	Functional Analysis via Standardized Whole-Blood Stimulation Systems Defines the Boundaries of a Healthy Immune Response to Complex Stimuli. Immunity, 2014, 40, 436-450.	14.3	192

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19	Dispersals and genetic adaptation of Bantu-speaking populations in Africa and North America. <i>Science</i> , 2017, 356, 543-546.	12.6	188
20	A Global Effort to Define the Human Genetics of Protective Immunity to SARS-CoV-2 Infection. <i>Cell</i> , 2020, 181, 1194-1199.	28.9	185
21	Evidence for Polygenic Adaptation to Pathogens in the Human Genome. <i>Molecular Biology and Evolution</i> , 2013, 30, 1544-1558.	8.9	181
22	Distinctive roles of age, sex, and genetics in shaping transcriptional variation of human immune responses to microbial challenges. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E488-E497.	7.1	181
23	Origins and Genetic Diversity of Pygmy Hunter-Gatherers from Western Central Africa. <i>Current Biology</i> , 2009, 19, 312-318.	3.9	177
24	Ribosomal Protein SA Haploinsufficiency in Humans with Isolated Congenital Asplenia. <i>Science</i> , 2013, 340, 976-978.	12.6	176
25	The Genetic Legacy of Religious Diversity and Intolerance: Paternal Lineages of Christians, Jews, and Muslims in the Iberian Peninsula. <i>American Journal of Human Genetics</i> , 2008, 83, 725-736.	6.2	174
26	Evolutionary genetic dissection of human interferons. <i>Journal of Experimental Medicine</i> , 2011, 208, 2747-2759.	8.5	170
27	Maternal traces of deep common ancestry and asymmetric gene flow between Pygmy hunter-gatherers and Bantu-speaking farmers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 1596-1601.	7.1	157
28	Immunology in natura: clinical, epidemiological and evolutionary genetics of infectious diseases. <i>Nature Immunology</i> , 2007, 8, 1165-1171.	14.5	155
29	Life-threatening infectious diseases of childhood: single gene inborn errors of immunity?. <i>Annals of the New York Academy of Sciences</i> , 2010, 1214, 18-33.	3.8	154
30	Human IFN- γ immunity to mycobacteria is governed by both IL-12 and IL-23. <i>Science Immunology</i> , 2018, 3, .	11.9	152
31	Positively Selected <i>G6PD</i> -Mahidol Mutation Reduces <i>Plasmodium vivax</i> Density in Southeast Asians. <i>Science</i> , 2009, 326, 1546-1549.	12.6	150
32	Tuberculosis and impaired IL-23-dependent IFN- γ immunity in humans homozygous for a common <i>TYK2</i> missense variant. <i>Science Immunology</i> , 2018, 3, .	11.9	148
33	Inferring the Demographic History of African Farmers and Pygmy Hunter-Gatherers Using a Multilocus Resequencing Data Set. <i>PLoS Genetics</i> , 2009, 5, e1000448.	3.5	142
34	The Matrilineal Ancestry of Ashkenazi Jewry: Portrait of a Recent Founder Event. <i>American Journal of Human Genetics</i> , 2006, 78, 487-497.	6.2	140
35	Deciphering the Ancient and Complex Evolutionary History of Human Arylamine N-Acetyltransferase Genes. <i>American Journal of Human Genetics</i> , 2006, 78, 423-436.	6.2	127
36	Population genetic tools for dissecting innate immunity in humans. <i>Nature Reviews Immunology</i> , 2013, 13, 280-293.	22.7	119

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37	Dual T cellâ€ and B cellâ€intrinsic deficiency in humans with biallelic <i>RLTPR</i> mutations. Journal of Experimental Medicine, 2016, 213, 2413-2435.	8.5	117
38	Genetic and Demographic Implications of the Bantu Expansion: Insights from Human Paternal Lineages. Molecular Biology and Evolution, 2009, 26, 1581-1589.	8.9	114
39	Human genetic variants and age are the strongest predictors of humoral immune responses to common pathogens and vaccines. Genome Medicine, 2018, 10, 59.	8.2	113
40	Systematic evaluation of DNA methylation age estimation with common preprocessing methods and the Infinium MethylationEPIC BeadChip array. Clinical Epigenetics, 2018, 10, 123.	4.1	111
41	The risk of COVID-19 death is much greater and age dependent with type I IFN autoantibodies. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2200413119.	7.1	110
42	Strong Maternal Khoisan Contribution to the South African Coloured Population: A Case of Gender-Biased Admixture. American Journal of Human Genetics, 2010, 86, 611-620.	6.2	107
43	Insights into the Demographic History of African Pygmies from Complete Mitochondrial Genomes. Molecular Biology and Evolution, 2011, 28, 1099-1110.	8.9	105
44	Human Immunology through the Lens of Evolutionary Genetics. Cell, 2019, 177, 184-199.	28.9	105
45	Exploring the genetic basis of human population differences in DNA methylation and their causal impact on immune gene regulation. Genome Biology, 2018, 19, 222.	8.8	101
46	A comprehensive assessment of demographic, environmental, and host genetic associations with gut microbiome diversity in healthy individuals. Microbiome, 2019, 7, 130.	11.1	101
47	Genomic insights into population history and biological adaptation in Oceania. Nature, 2021, 592, 583-589.	27.8	100
48	From Social to Genetic Structures in Central Asia. Current Biology, 2007, 17, 43-48.	3.9	98
49	MtDNA evidence for a genetic bottleneck in the early history of the Ashkenazi Jewish population. European Journal of Human Genetics, 2004, 12, 355-364.	2.8	96
50	The impact of agricultural emergence on the genetic history of African rainforest hunter-gatherers and agriculturalists. Nature Communications, 2014, 5, 3163.	12.8	96
51	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.	7.1	91
52	Homozygosity for <i>TYK2</i> P1104A underlies tuberculosis in about 1% of patients in a cohort of European ancestry. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10430-10434.	7.1	87
53	Standardized Whole-Blood Transcriptional Profiling Enables the Deconvolution of Complex Induced Immune Responses. Cell Reports, 2016, 16, 2777-2791.	6.4	84
54	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84

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55	Signatures of Purifying and Local Positive Selection in Human miRNAs. American Journal of Human Genetics, 2009, 84, 316-327.	6.2	83
56	Human T-bet Governs Innate and Innate-like Adaptive IFN- γ Immunity against Mycobacteria. Cell, 2020, 183, 1826-1847.e31.	28.9	83
57	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.	6.2	81
58	The human gene connectome as a map of short cuts for morbid allele discovery. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 5558-5563.	7.1	79
59	Understanding rare and common diseases in the context of human evolution. Genome Biology, 2016, 17, 225.	8.8	76
60	Human SNORA31 variations impair cortical neuron-intrinsic immunity to HSV-1 and underlie herpes simplex encephalitis. Nature Medicine, 2019, 25, 1873-1884.	30.7	76
61	Sociocultural Behavior, Sex-Biased Admixture, and Effective Population Sizes in Central African Pygmies and Non-Pygmies. Molecular Biology and Evolution, 2013, 30, 918-937.	8.9	75
62	Y-chromosome descent clusters and male differential reproductive success: young lineage expansions dominate Asian pastoral nomadic populations. European Journal of Human Genetics, 2015, 23, 1413-1422.	2.8	75
63	The epigenomic landscape of African rainforest hunter-gatherers and farmers. Nature Communications, 2015, 6, 10047.	12.8	75
64	Formulating a Historical and Demographic Model of Recent Human Evolution Based on Resequencing Data from Noncoding Regions. PLoS ONE, 2010, 5, e10284.	2.5	74
65	Exploring the Occurrence of Classic Selective Sweeps in Humans Using Whole-Genome Sequencing Data Sets. Molecular Biology and Evolution, 2014, 31, 1850-1868.	8.9	72
66	The Milieu Intérieur study – An integrative approach for study of human immunological variance. Clinical Immunology, 2015, 157, 277-293.	3.2	71
67	Trends in DNA Methylation with Age Replicate Across Diverse Human Populations. Genetics, 2017, 206, 1659-1674.	2.9	69
68	Population genetic diversity of the NAT2 gene supports a role of acetylation in human adaptation to farming in Central Asia. European Journal of Human Genetics, 2008, 16, 243-251.	2.8	66
69	Associations between usual diet and gut microbiota composition: results from the Milieu Intérieur cross-sectional study. American Journal of Clinical Nutrition, 2019, 109, 1472-1483.	4.7	66
70	Sub-Saharan African coding sequence variation and haplotype diversity at the NAT2 gene. Human Mutation, 2006, 27, 720-720.	2.5	61
71	A genomic portrait of the genetic architecture and regulatory impact of microRNA expression in response to infection. Genome Research, 2014, 24, 850-859.	5.5	60
72	Bacterial Infection Drives the Expression Dynamics of microRNAs and Their isomiRs. PLoS Genetics, 2015, 11, e1005064.	3.5	60

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73	Associations between consumption of dietary fibers and the risk of cardiovascular diseases, cancers, type 2 diabetes, and mortality in the prospective NutriNet-Sant� cohort. American Journal of Clinical Nutrition, 2020, 112, 195-207.	4.7	60
74	Recessive inborn errors of type I IFN immunity in children with COVID-19 pneumonia. Journal of Experimental Medicine, 2022, 219, .	8.5	59
75	Human ancient DNA analyses reveal the high burden of tuberculosis in Europeans over the last 2,000 years. American Journal of Human Genetics, 2021, 108, 517-524.	6.2	58
76	Genetic diversity and the emergence of ethnic groups in Central Asia. BMC Genetics, 2009, 10, 49.	2.7	56
77	The Genetic or Mythical Ancestry of Descent Groups: Lessons from the Y Chromosome. American Journal of Human Genetics, 2004, 75, 1113-1116.	6.2	55
78	Immunology Taught by Human Genetics. Cold Spring Harbor Symposia on Quantitative Biology, 2013, 78, 157-172.	1.1	55
79	Defining the genetic and evolutionary architecture of alternative splicing in response to infection. Nature Communications, 2019, 10, 1671.	12.8	52
80	Blacklisting variants common in private cohorts but not in public databases optimizes human exome analysis. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 950-959.	7.1	52
81	Multiple Advantageous Amino Acid Variants in the NAT2 Gene in Human Populations. PLoS ONE, 2008, 3, e3136.	2.5	50
82	Evolutionary Trajectories of Primate Genes Involved in HIV Pathogenesis. Molecular Biology and Evolution, 2009, 26, 2865-2875.	8.9	50
83	Different selective pressures shape the evolution of Toll-like receptors in human and African great ape populations. Human Molecular Genetics, 2013, 22, 4829-4840.	2.9	49
84	Parkinson's disease-related LRRK2 G2019S mutation results from independent mutational events in humans. Human Molecular Genetics, 2010, 19, 1998-2004.	2.9	48
85	Study of Human RIG-I Polymorphisms Identifies Two Variants with an Opposite Impact on the Antiviral Immune Response. PLoS ONE, 2009, 4, e7582.	2.5	48
86	Origins, admixture and founder lineages in European Roma. European Journal of Human Genetics, 2016, 24, 937-943.	2.8	45
87	The selective footprints of viral pressures at the human RIG-I-like receptor family. Human Molecular Genetics, 2011, 20, 4462-4474.	2.9	44
88	The Red Queen's long race: human adaptation to pathogen pressure. Current Opinion in Genetics and Development, 2014, 29, 31-38.	3.3	44
89	HGCS: an online tool for prioritizing disease-causing gene variants by biological distance. BMC Genomics, 2014, 15, 256.	2.8	43
90	IRF4 haploinsufficiency in a family with Whipple��s disease. ELife, 2018, 7, .	6.0	43

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91	Impact and Evolutionary Determinants of Neanderthal Introgression on Transcriptional and Post-Transcriptional Regulation. American Journal of Human Genetics, 2019, 104, 1241-1250.	6.2	42
92	A global effort to dissect the human genetic basis of resistance to SARS-CoV-2 infection. Nature Immunology, 2022, 23, 159-164.	14.5	41
93	Evolution of the TIR Domain-Containing Adaptors in Humans: Swinging between Constraint and Adaptation. Molecular Biology and Evolution, 2011, 28, 3087-3097.	8.9	40
94	Human Genetic Data Reveal Contrasting Demographic Patterns between Sedentary and Nomadic Populations That Predate the Emergence of Farming. Molecular Biology and Evolution, 2013, 30, 2629-2644.	8.9	40
95	Semi-automated and standardized cytometric procedures for multi-panel and multi-parametric whole blood immunophenotyping. Clinical Immunology, 2015, 157, 261-276.	3.2	40
96	A Call for Bloodâ€™In Human Immunology. Immunity, 2019, 50, 1335-1336.	14.3	40
97	Genomic Evidence for Local Adaptation of Hunter-Gatherers to the African Rainforest. Current Biology, 2019, 29, 2926-2935.e4.	3.9	40
98	Diversity in immunogenomics: the value and the challenge. Nature Methods, 2021, 18, 588-591.	19.0	40
99	The Genetic Legacy of the Indian Ocean Slave Trade: Recent Admixture and Post-admixture Selection in the Makranis of Pakistan. American Journal of Human Genetics, 2017, 101, 977-984.	6.2	39
100	The demographic history and mutational load of African hunter-gatherers and farmers. Nature Ecology and Evolution, 2018, 2, 721-730.	7.8	38
101	Lactase Persistence in Central Asia: Phenotype, Genotype, and Evolution. Human Biology, 2011, 83, 379-392.	0.2	37
102	Gut microbiome stability and dynamics in healthy donors and patients with non-gastrointestinal cancers. Journal of Experimental Medicine, 2021, 218, .	8.5	37
103	The impact of natural selection on health and disease: uses of the population genetics approach in humans. Evolutionary Applications, 2013, 6, 596-607.	3.1	35
104	Vaccine breakthrough hypoxemic COVID-19 pneumonia in patients with auto-Abs neutralizing type I IFNs. Science Immunology, 2023, 8, .	11.9	35
105	The Evolutionary Landscape of Cytosolic Microbial Sensors in Humans. American Journal of Human Genetics, 2012, 91, 27-37.	6.2	34
106	Living in an adaptive world: Genomic dissection of the genus Homo and its immune response. Journal of Experimental Medicine, 2017, 214, 877-894.	8.5	34
107	Human thymopoiesis is influenced by a common genetic variant within the <i>TCRA-TCRD</i> locus. Science Translational Medicine, 2018, 10, .	12.4	33
108	Recent Adaptive Acquisition by African Rainforest Hunter-Gatherers of the Late Pleistocene Sickle-Cell Mutation Suggests Past Differences in Malaria Exposure. American Journal of Human Genetics, 2019, 104, 553-561.	6.2	33

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109	Negative selection on human genes underlying inborn errors depends on disease outcome and both the mode and mechanism of inheritance. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	33
110	Towards a crucial role for DC-SIGN in tuberculosis and beyond. Trends in Microbiology, 2006, 14, 383-387.	7.7	32
111	miR-222 isoforms are differentially regulated by type-I interferon. Rna, 2018, 24, 332-341.	3.5	31
112	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.	7.1	30
113	Natural selection contributed to immunological differences between hunter-gatherers and agriculturalists. Nature Ecology and Evolution, 2019, 3, 1253-1264.	7.8	28
114	Evolutionary and population (epi)genetics of immunity to infection. Human Genetics, 2020, 139, 723-732.	3.8	28
115	A loss-of-function <i>IFNAR1</i> allele in Polynesia underlies severe viral diseases in homozygotes. Journal of Experimental Medicine, 2022, 219, .	8.5	28
116	Genetic traces of east-to-west human expansion waves in Eurasia. American Journal of Physical Anthropology, 2008, 136, 309-317.	2.1	27
117	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.	2.4	26
118	A Genome-Wide Perspective of Human Diversity and Its Implications in Infectious Disease. Cold Spring Harbor Perspectives in Medicine, 2013, 3, a012450-a012450.	6.2	26
119	Automated flow cytometric analysis across large numbers of samples and cell types. Clinical Immunology, 2015, 157, 249-260.	3.2	26
120	Diversity of KIR, HLA Class I, and Their Interactions in Seven Populations of Sub-Saharan Africans. Journal of Immunology, 2019, 202, 2636-2647.	0.8	26
121	The role played by natural selection on Mendelian traits in humans. Annals of the New York Academy of Sciences, 2010, 1214, 1-17.	3.8	25
122	Deconvolution of the Response to Bacillus Calmette-Guérin Reveals NF- κ B-Induced Cytokines As Autocrine Mediators of Innate Immunity. Frontiers in Immunology, 2017, 8, 796.	4.8	25
123	Demeter's legacy: rapid changes to our genome imposed by diet. Trends in Ecology and Evolution, 2008, 23, 56-59.	8.7	22
124	Evolutionary genetics evidence of an essential, nonredundant role of the IFN- γ pathway in protective immunity. Human Mutation, 2011, 32, 633-642.	2.5	22
125	Preserving immune diversity through ancient inheritance and admixture. Current Opinion in Immunology, 2014, 30, 79-84.	5.5	22
126	Length Variation of DC-SIGN and L-SIGN Neck-Region has no Impact on Tuberculosis Susceptibility. Human Immunology, 2007, 68, 106-112.	2.4	21

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127	Population variation in NAIP functional copy number confers increased cell death upon <i>Legionella pneumophila</i> infection. <i>Human Immunology</i> , 2012, 73, 196-200.	2.4	21
128	The genomic signatures of natural selection in admixed human populations. <i>American Journal of Human Genetics</i> , 2022, 109, 710-726.	6.2	21
129	Respiratory viral infections in otherwise healthy humans with inherited IRF7 deficiency. <i>Journal of Experimental Medicine</i> , 2022, 219, .	8.5	21
130	The Genetics of Innate Immunity Sensors and Human Disease. <i>International Reviews of Immunology</i> , 2013, 32, 157-208.	3.3	19
131	Functional consequences of archaic introgression and their impact on fitness. <i>Genome Biology</i> , 2020, 21, 3.	8.8	18
132	Immune Profiling Enables Stratification of Patients With Active Tuberculosis Disease or <i>Mycobacterium tuberculosis</i> Infection. <i>Clinical Infectious Diseases</i> , 2021, 73, e3398-e3408.	5.8	18
133	Common homozygosity for predicted loss-of-function variants reveals both redundant and advantageous effects of dispensable human genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13626-13636.	7.1	18
134	The demographic and adaptive history of central African hunter-gatherers and farmers. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 90-97.	3.3	17
135	New insights into human immunity from ancient genomics. <i>Current Opinion in Immunology</i> , 2021, 72, 116-125.	5.5	17
136	Recent Common Origin, Reduced Population Size, and Marked Admixture Have Shaped European Roma Genomes. <i>Molecular Biology and Evolution</i> , 2020, 37, 3175-3187.	8.9	16
137	DC-SIGN/CD209 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, 1184-1185.	4.0	14
138	Population variation in miRNAs and isomiRs and their impact on human immunity to infection. <i>Genome Biology</i> , 2020, 21, 187.	8.8	14
139	The Counteracting Effects of Demography on Functional Genomic Variation: The Roma Paradigm. <i>Molecular Biology and Evolution</i> , 2021, 38, 2804-2817.	8.9	14
140	Single-Cell and Bulk RNA-Sequencing Reveal Differences in Monocyte Susceptibility to Influenza A Virus Infection Between Africans and Europeans. <i>Frontiers in Immunology</i> , 2021, 12, 768189.	4.8	14
141	Protective Role of DC-SIGN(CD209)Neck-Region Alleles with <5 Repeat Units in HIV-1 Transmission. <i>Journal of Infectious Diseases</i> , 2008, 198, 68-71.	4.0	13
142	Genetic and epigenetic variation of human populations: An adaptive tale. <i>Comptes Rendus - Biologies</i> , 2016, 339, 278-283.	0.2	12
143	Genetic origins, singularity, and heterogeneity of Basques. <i>Current Biology</i> , 2021, 31, 2167-2177.e4.	3.9	11
144	Gene Losses in the Human Genome. <i>Science</i> , 2012, 335, 806-807.	12.6	8

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145	Quantitative genetic analysis deciphers the impact of cis and trans regulation on cell-to-cell variability in protein expression levels. <i>PLoS Genetics</i> , 2020, 16, e1008686.	3.5	8
146	Integrative genetic and immune cell analysis of plasma proteins in healthy donors identifies novel associations involving primary immune deficiency genes. <i>Genome Medicine</i> , 2022, 14, 28.	8.2	8
147	Might Interspecific Interactions between Pathogens Drive Host Evolution? The Case of <i>Plasmodium</i> Species and Duffy-Negativity in Human Populations. <i>Trends in Parasitology</i> , 2017, 33, 21-29.	3.3	7
148	Counting Oceanians of Non-European, Non-Asian Descent (ONENA) in the South Pacific to Make Them Count in Global Health.. <i>Tropical Medicine and Infectious Disease</i> , 2019, 4, 114.	2.3	7
149	The genetic and evolutionary determinants of COVID-19 susceptibility. <i>European Journal of Human Genetics</i> , 2022, 30, 915-921.	2.8	7
150	Associations between untargeted plasma metabolomic signatures and gut microbiota composition in the Milieu Intérieur population of healthy adults. <i>British Journal of Nutrition</i> , 2020, 126, 1-11.	2.3	4
151	Ancestral diversity is limited in published T cell receptor sequencing studies. <i>Immunity</i> , 2021, 54, 2177-2179.	14.3	3
152	A genetic variant controls interferon- γ gene expression in human myeloid cells by preventing C/EBP- γ binding on a conserved enhancer. <i>PLoS Genetics</i> , 2020, 16, e1009090.	3.5	3
153	PERSPECTIVE: Evolutionary genetics as a tool to target genes involved in phenotypes of medical relevance. <i>Evolutionary Applications</i> , 2009, 2, 71-80.	3.1	2
154	Host and viral genetic diversity can help explain mortality during the 1918-21 influenza pandemic in the Pacific region. <i>Lancet Infectious Diseases</i> , The, 2018, 18, 833-834.	9.1	2
155	Reconstructing 50,000 years of human history from our DNA: lessons from modern genomics. <i>Comptes Rendus - Biologies</i> , 2021, 344, 177-187.	0.2	2
156	Sporadic occurrence of recent selective sweeps from standing variation in humans as revealed by an approximate Bayesian computation approach. <i>Genetics</i> , 2021, 219, .	2.9	2
157	Rhesus negative males have an enhanced IFN γ -mediated immune response to influenza A virus. <i>Genes and Immunity</i> , 2022, 23, 93-98.	4.1	2
158	Editorial overview: Evolutionary and systems immunology “ methods to understand human immune system variation. <i>Current Opinion in Immunology</i> , 2020, 65, iv.	5.5	1
159	Dangerous liaisons: human genetic adaptation to infectious agents. <i>Comptes Rendus - Biologies</i> , 2020, 343, 297-309.	0.2	1
160	Human Genome Diversity: a Host Genomic Perspective of Host-Pathogen Interactions and Infectious Diseases. , 0, , 39-49.		0
161	Editorial Overview: Immunogenetics and transplantation: Bringing evolution and genomics to human immunology. <i>Current Opinion in Immunology</i> , 2014, 30, v-vii.	5.5	0
162	Une perspective génétique sur notre histoire: migrations humaines et adaptation à l'environnement. , 2017, , 33-60.		0

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163	Les espaces et le temps de l'adaptation génétique. , 2012, , 34-37.		0
164	Towards a functional understanding of adaptive phenotypes in humans. Journal of Anthropological Sciences, 2021, 99, .	0.4	0
165	Paleogenomics: The demographic past of prehistoric Europeans. Current Biology, 2022, 32, R535-R538.	3.9	0