Alexandre Alcais

List of Publications by Year
in descending order

103	6,367	81839 39	71651 76
papers	citations	h-index	g-index

120	120	120	7640
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Herpes Simplex Virus Encephalitis in Human UNC-93B Deficiency. Science, 2006, 314, 308-312.	6.0	674
2	Susceptibility to leprosy is associated with PARK2 and PACRG. Nature, 2004, 427, 636-640.	13.7	426
3	Evolutionary Dynamics of Human Toll-Like Receptors and Their Different Contributions to Host Defense. PLoS Genetics, 2009, 5, e1000562.	1.5	341
4	Partial MCM4 deficiency in patients with growth retardation, adrenal insufficiency, and natural killer cell deficiency. Journal of Clinical Investigation, 2012, 122, 821-832.	3.9	272
5	Autoimmune and inflammatory manifestations occur frequently in patients with primary immunodeficiencies. Journal of Allergy and Clinical Immunology, 2017, 140, 1388-1393.e8.	1.5	222
6	Tuberculosis in children and adults. Journal of Experimental Medicine, 2005, 202, 1617-1621.	4.2	209
7	Gains of glycosylation comprise an unexpectedly large group of pathogenic mutations. Nature Genetics, 2005, 37, 692-700.	9.4	198
8	A Missense LRRK2 Variant Is a Risk Factor for Excessive Inflammatory Responses in Leprosy. PLoS Neglected Tropical Diseases, 2016, 10, e0004412.	1.3	181
9	Chromosome 6q25 is linked to susceptibility to leprosy in a Vietnamese population. Nature Genetics, 2003, 33, 412-415.	9.4	164
10	Immunology in natura: clinical, epidemiological and evolutionary genetics of infectious diseases. Nature Immunology, 2007, 8, 1165-1171.	7.0	155
11	Lifeâ€threatening infectious diseases of childhood: singleâ€gene inborn errors of immunity?. Annals of the New York Academy of Sciences, 2010, 1214, 18-33.	1.8	154
12	Stepwise replication identifies a low-producing lymphotoxin-Î± allele as a major risk factor for early-onset leprosy. Nature Genetics, 2007, 39, 517-522.	9.4	152
13	Human genetics of infectious diseases: between proof of principle and paradigm. Journal of Clinical Investigation, 2009, 119, 2506-2514.	3.9	151
14	Two loci control tuberculin skin test reactivity in an area hyperendemic for tuberculosis. Journal of Experimental Medicine, 2009, 206, 2583-2591.	4.2	142
15	Immunological and Genetic Evidence for a Crucial Role of IL-10 in Cutaneous Lesions in Humans Infected with Leishmania braziliensis. Journal of Immunology, 2008, 180, 6139-6148.	0.4	138
16	Bacillus Calmette GuÃ©rin triggers the IL-12/IFN-Î³ axis by an IRAK-4- and NEMO-dependent, non-cognate interaction between monocytes, NK, and Tâ€„lymphocytes. European Journal of Immunology, 2004, 34, 3276-3284.	1.6	133
17	IL-12RÎ²1 Deficiency in Two of Fifty Children with Severe Tuberculosis from Iran, Morocco, and Turkey. PLoS ONE, 2011, 6, e18524.	1.1	111
18	Leprosy as a genetic disease. Mammalian Genome, 2011, 22, 19-31.	1.0	94

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19	Clinical epidemiology of laboratory-confirmed Buruli ulcer in Benin: a cohort study. The Lancet Global Health, 2014, 2, e422-e430.	2.9	94
20	IgM+IgD+CD27+ B cells are markedly reduced in IRAK-4â€“, MyD88-, and TIRAP- but not UNC-93Bâ€“deficient patients. Blood, 2012, 120, 4992-5001.	0.6	87
21	Age-Dependent Mendelian Predisposition to Herpes Simplex Virus Type 1 Encephalitis in Childhood. Journal of Pediatrics, 2010, 157, 623-629.e1.	0.9	85
22	Granulomatous Reaction to Intradermal Injection of Lepromin (Mitsuda Reaction) Is Linked to the HumanNRAMP1Gene in Vietnamese Leprosy Sibships. Journal of Infectious Diseases, 2000, 181, 302-308.	1.9	81
23	Genetic dissection of immunity in leprosy. Current Opinion in Immunology, 2005, 17, 44-48.	2.4	80
24	Leprosy as a genetic model for susceptibility to common infectious diseases. Human Genetics, 2008, 123, 227-235.	1.8	79
25	Crohn's Disease Susceptibility Genes are Associated With Leprosy in the Vietnamese Population. Journal of Infectious Diseases, 2012, 206, 1763-1767.	1.9	70
26	Genetic and functional analysis of common MRC1 exon 7 polymorphisms in leprosy susceptibility. Human Genetics, 2010, 127, 337-348.	1.8	69
27	Longitudinal changes in the ductus venosus, cerebral transverse sinus and cardiotocogram in fetal growth restriction. Ultrasound in Obstetrics and Gynecology, 2000, 16, 19-24.	0.9	67
28	Age Is an Important Risk Factor for Onset and Sequelae of Reversal Reactions in Vietnamese Patients with Leprosy. Clinical Infectious Diseases, 2007, 44, 33-40.	2.9	64
29	Complementation of a pathogenic IFNGR2 misfolding mutation with modifiers of N-glycosylation. Journal of Experimental Medicine, 2008, 205, 1729-1737.	4.2	59
30	High Heritability of Antimycobacterial Immunity in an Area of Hyperendemicity for Tuberculosis Disease. Journal of Infectious Diseases, 2010, 201, 15-19.	1.9	57
31	Pauci- and Multibacillary Leprosy: Two Distinct, Genetically Neglected Diseases. PLoS Neglected Tropical Diseases, 2016, 10, e0004345.	1.3	57
32	Whole-exome sequencing to analyze population structure, parental inbreeding, and familial linkage. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6713-6718.	3.3	53
33	Pleiotropic effects for Parkin and LRRK2 in leprosy type-1 reactions and Parkinsonâ€™s disease. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15616-15624.	3.3	50
34	Maximum-likelihood-binomial method for genetic model-free linkage analysis of quantitative traits in sibships. Genetic Epidemiology, 1999, 17, 102-117.	0.6	49
35	Human Leukocyte Antigen Class I Region Single-Nucleotide Polymorphisms are Associated with Leprosy Susceptibility in Vietnam and India. Journal of Infectious Diseases, 2011, 203, 1274-1281.	1.9	49
36	Comparison of four sib-pair linkage methods for analyzing sibships with more than two affecteds: Interest of the binomial maximum likelihood approach. Genetic Epidemiology, 1998, 15, 371-390.	0.6	46

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37	Risk Factors for Onset of Cutaneous and Mucocutaneous Leishmaniasis in Bolivia. American Journal of Tropical Medicine and Hygiene, 1997, 57, 79-84.	0.6	46
38	PARK2 Mediates Interleukin 6 and Monocyte Chemoattractant Protein 1 Production by Human Macrophages. PLoS Neglected Tropical Diseases, 2013, 7, e2015.	1.3	45
39	Tuberculin Skin Test Negativity Is Under Tight Genetic Control of Chromosomal Region 11p14-15 in Settings With Different Tuberculosis Endemicities. Journal of Infectious Diseases, 2015, 211, 317-321.	1.9	42
40	Genetic predisposition to leprosy: A major gene reveals novel pathways of immunity to Mycobacterium leprae. Seminars in Immunology, 2006, 18, 404-410.	2.7	41
41	Genetics of leprosy reactions: an overview. Memorias Do Instituto Oswaldo Cruz, 2012, 107, 132-142.	0.8	41
42	Evidence for a Major Gene Controlling Susceptibility to Tegumentary Leishmaniasis in a Recently Exposed Bolivian Population. American Journal of Human Genetics, 1997, 61, 968-979.	2.6	39
43	A Major Gene Controls Leprosy Susceptibility in a Hyperendemic Isolated Population from North of Brazil. Journal of Infectious Diseases, 2010, 201, 1598-1605.	1.9	38
44	Tuberculin Skin Test and In Vitro Assays Provide Complementary Measures of Antimycobacterial Immunity in Children and Adolescents. Chest, 2010, 137, 1071-1077.	0.4	35
45	Identification of a Major Locus, TNF1, That Controls BCG-Triggered Tumor Necrosis Factor Production by Leukocytes in an Area Hyperendemic for Tuberculosis. Clinical Infectious Diseases, 2013, 57, 963-970.	2.9	33
46	Linkage disequilibrium pattern and age-at-diagnosis are critical for replicating genetic associations across ethnic groups in leprosy. Human Genetics, 2013, 132, 107-116.	1.8	32
47	Gene Set Signature of Reversal Reaction Type I in Leprosy Patients. PLoS Genetics, 2013, 9, e1003624.	1.5	32
48	Dental Caries and Enamelin Haplotype. Journal of Dental Research, 2014, 93, 360-365.	2.5	32
49	Prevalence of primary immunodeficiencies in France is underestimated. Journal of Allergy and Clinical Immunology, 2017, 140, 1731-1733.	1.5	32
50	Familial NK Cell Deficiency Associated with Impaired IL-2- and IL-15-Dependent Survival of Lymphocytes. Journal of Immunology, 2006, 177, 8835-8843.	0.4	31
51	Highly Significant Association between Two Common Single Nucleotide Polymorphisms in CORIN Gene and Preeclampsia in Caucasian Women. PLoS ONE, 2014, 9, e113176.	1.1	31
52	Segregation of HLA/TNF region is linked to leprosy clinical spectrum in families displaying mixed leprosy subtypes. Genes and Immunity, 2003, 4, 67-73.	2.2	30
53	Tuberculin Skin Test Reactivity Is Dependent on Host Genetic Background in Colombian Tuberculosis Household Contacts. Clinical Infectious Diseases, 2012, 54, 968-971.	2.9	30
54	Association of TNFSF8 Regulatory Variants With Excessive Inflammatory Responses but not Leprosy Per Se. Journal of Infectious Diseases, 2015, 211, 968-977.	1.9	29

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55	A genome wide association study identifies a lncRna as risk factor for pathological inflammatory responses in leprosy. PLoS Genetics, 2017, 13, e1006637.	1.5	29
56	Findings in Patients From Benin With Osteomyelitis and Polymerase Chain Reactionâ€“Confirmed Mycobacterium ulcerans Infection. Clinical Infectious Diseases, 2014, 59, 1256-1264.	2.9	27
57	Human Genetics of Common Mycobacterial Infections. Immunologic Research, 2003, 28, 109-130.	1.3	26
58	Mycolactone toxin induces an inflammatory response by targeting the IL-1Î² pathway: Mechanistic insight into Buruli ulcer pathophysiology. PLoS Pathogens, 2020, 16, e1009107.	2.1	25
59	A Major Gene Effect Controls Resistance to Caries. Journal of Dental Research, 2011, 90, 735-739.	2.5	24
60	A General Efficient and Flexible Approach for Genome-Wide Association Analyses of Imputed Genotypes in Family-Based Designs. Genetic Epidemiology, 2014, 38, 560-571.	0.6	23
61	Age-Dependent Association of TNFSF15/TNFSF8 Variants and Leprosy Type 1 Reaction. Frontiers in Immunology, 2017, 8, 155.	2.2	23
62	Somatic Hypermutation at A/T-Rich Oligonucleotide Substrates Shows Different Strand Polarities in Ung-Deficient or -Proficient Backgrounds. Molecular and Cellular Biology, 2014, 34, 2176-2187.	1.1	22
63	Impact of age and sex on mycobacterial immunity in an area of high tuberculosis incidence. International Journal of Tuberculosis and Lung Disease, 2010, 14, 952-9.	0.6	22
64	Genetic diagnosis of primary immunodeficiencies: AÂsurvey of the French national registry. Journal of Allergy and Clinical Immunology, 2019, 143, 1646-1649.e10.	1.5	20
65	HIV infection and Buruli ulcer in Africa. Lancet Infectious Diseases, The, 2014, 14, 796-797.	4.6	19
66	The dissection of complex susceptibility to infectious disease: bacterial, viral and parasitic infections. Current Opinion in Immunology, 2014, 30, 72-78.	2.4	19
67	Clinical Features of Spontaneous Partial Healing During Mycobacterium ulcerans Infection. Open Forum Infectious Diseases, 2016, 3, ofw013.	0.4	19
68	Combined Linkage and Association Studies Show that HLA Class II Variants Control Levels of Antibodies against Epstein-Barr Virus Antigens. PLoS ONE, 2014, 9, e102501.	1.1	17
69	Improving the diagnostic efficiency of primary immunodeficiencies with targeted next-generation sequencing. Journal of Allergy and Clinical Immunology, 2021, 147, 734-737.	1.5	17
70	Genome-wide association study of resistance to Mycobacterium tuberculosis infection identifies a locus at 10q26.2 in three distinct populations. PLoS Genetics, 2021, 17, e1009392.	1.5	17
71	A Recessive Major Gene Controls the Mitsuda Reaction in a Region Endemic for Leprosy. Journal of Infectious Diseases, 2005, 192, 1475-1482.	1.9	16
72	Genome-wide association study of Buruli ulcer in rural Benin highlights role of two LncRNAs and the autophagy pathway. Communications Biology, 2020, 3, 177.	2.0	16

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73	Major Loci on Chromosomes 8q and 3q Control Interferon Î³ Production Triggered by Bacillus Calmette-Guerin and 6-kDa Early Secretory Antigen Target, Respectively, in Various Populations. Journal of Infectious Diseases, 2016, 213, 1173-1179.	1.9	15
74	The complex pattern of genetic associations of leprosy with HLA class I and class II alleles can be reduced to four amino acid positions. PLoS Pathogens, 2020, 16, e1008818.	2.1	14
75	Linkage Analysis of Quantitative Trait Loci: Sib Pairs or Sibships?. Human Heredity, 2000, 50, 251-256.	0.4	13
76	Skin-specific antibodies neutralizing mycolactone toxin during the spontaneous healing of Mycobacterium ulcerans infection. Science Advances, 2020, 6, eaax7781.	4.7	13
77	CUBN and NEBL common variants in the chromosome 10p13 linkage region are associated with multibacillary leprosy in Vietnam. Human Genetics, 2014, 133, 883-93.	1.8	12
78	Genetic model-free linkage analysis using the maximum-likelihood-binomial method for categorical traits. Genetic Epidemiology, 1999, 17, S467-S472.	0.6	11
79	Incorporation of covariates in multipoint model-free linkage analysis of binary traits: how important are unaffecteds?. European Journal of Human Genetics, 2001, 9, 613-620.	1.4	11
80	An Extensive Comparison of Quantitative Trait Loci Mapping Methods. Human Heredity, 2010, 69, 202-211.	0.4	11
81	Microdeletion on chromosome 8p23.1 in a familial form of severe Buruli ulcer. PLoS Neglected Tropical Diseases, 2018, 12, e0006429.	1.3	11
82	Estimating and Comparing Reduction in HIV-1 RNA in Clinical Trials Using Methods for Interval Censored Data. Journal of Acquired Immune Deficiency Syndromes (1999), 2004, 35, 286-292.	0.9	9
83	Quantifying Genomic Imprinting in the Presence of Linkage. Biometrics, 2006, 62, 1071-1080.	0.8	8
84	Genomewide Linkage Analysis of the Granulomatous Mitsuda Reaction Implicates Chromosomal Regions 2q35 and 17q21. Journal of Infectious Diseases, 2007, 196, 1248-1252.	1.9	8
85	Mycobacterial infections:PARK2andPACRGassociations in leprosy. Tissue Antigens, 2007, 69, 231-233.	1.0	8
86	Family-based genome-wide association study of leprosy in Vietnam. PLoS Pathogens, 2020, 16, e1008565.	2.1	8
87	The Maximum-Likelihood-Binomial method revisited: a robust approach for model-free linkage analysis of quantitative traits in large sibships. Genetic Epidemiology, 2011, 35, 46-56.	0.6	7
88	An Autosomeâ€Wide Search for Loci Underlying Wheezing Age of Onset in German Asthmatic Children Identifies a New Region of Interest on 6q24â€“q25. Genetic Epidemiology, 2001, 21, S168-73.	0.6	6
89	Robustness of the maximum-likelihood-binomial approach for linkage analysis of quantitative trait loci with non-normal phenotypic data. GeneScreen, 2000, 1, 47-50.	0.7	5
90	An eQTL variant of ZXDC is associated with IFN-Î³ production following Mycobacterium tuberculosis antigen-specific stimulation. Scientific Reports, 2017, 7, 12800.	1.6	5

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91	Deep resequencing identifies candidate functional genes in leprosy GWAS loci. PLoS Neglected Tropical Diseases, 2021, 15, e0010029.	1.3	5
92	Evaluation of Approaches to Identify Associated SNPs That Explain the Linkage Evidence in Nuclear Families with Affected Siblings. Human Heredity, 2010, 69, 104-119.	0.4	4
93	Application of genetic epidemiology to dissecting host susceptibility/resistance to infection illustrated with the study of common mycobacterial infections. , 2003, , 7-44.		3
94	Inclusion of unaffected sibs increases power in model-free linkage analysis of a behavioral trait. BMC Genetics, 2005, 6, S22.	2.7	3
95	La lÃ¨pre, une maladie Ã©liminÃ©eâ€¦ ou nÃ©gligÃ©e ?. Antibiotiques, 2007, 9, 99-114.	0.1	3
96	Reply to Zhang et al.: The differential role of LRRK2 variants in nested leprosy phenotypes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10124-10125.	3.3	3
97	Implicit Hypotheses Are Hidden Power Droppers in Family-Based Association Studies of Secondary Outcomes. Open Journal of Statistics, 2015, 05, 35-45.	0.3	3
98	Removing phenotypic distribution assumptions from tests of linkage disequilibrium for quantitative traits. Genetic Epidemiology, 2003, 24, 191-199.	0.6	2
99	â€˜Brown sugarâ€™ heroin intoxication and improvement of surrogate immunologic markers in HIV infection. Clinical Microbiology and Infection, 1999, 5, 244-252.	2.8	1
100	Introduction: Linkage Analyses in Single (Nonâ€Hutterite) Populations. Genetic Epidemiology, 2001, 21, S166-7.	0.6	1
101	Defining and targeting high-risk populations in Buruli ulcerâ€“Authors' reply. The Lancet Global Health, 2014, 2, e630.	2.9	1
102	Complementation of a pathogenic IFNGR2 misfolding mutation with modifiers of N-glycosylation. Journal of Biotechnology, 2008, 136, S176.	1.9	0
103	ComplementationofapathogenicIFNGR2misfolding mutation with modifiers of N-glycosylation. Journal of Cell Biology, 2008, 182, i6-i6.	2.3	0