AurÃ©lie Cobat

List of Publications by Year
in descending order

98 papers	11,198 citations	81900 39 h-index	33894 99 g-index
114 all docs	114 docs citations	114 times ranked	17290 citing authors

#	Article	IF	Citations
1	Vaccine breakthrough hypoxemic COVID-19 pneumonia in patients with auto-Abs neutralizing type I IFNs. Science Immunology, 2023, 8, .	11.9	35
2	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
3	Human genetic and immunological determinants of critical COVID-19 pneumonia. Nature, 2022, 603, 587-598.	27.8	216
4	Autoantibodies Neutralizing Type I Interferons in 20% of COVID-19 Deaths in a French Hospital. Journal of Clinical Immunology, 2022, 42, 459-470.	3.8	46
5	A common TMPRSS2 variant has a protective effect against severe COVID-19. Current Research in Translational Medicine, 2022, 70, 103333.	1.8	30
6	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
7	Respiratory viral infections in otherwise healthy humans with inherited IRF7 deficiency. Journal of Experimental Medicine, 2022, 219, .	8.5	21
8	Recessive inborn errors of type I IFN immunity in children with COVID-19 pneumonia. Journal of Experimental Medicine, 2022, 219, .	8.5	59
9	Clonal hematopoiesis is not significantly associated with COVID-19 disease severity. Blood, 2022, 140, 1650-1655.	1.4	10
10	Herpes simplex encephalitis in a patient with a distinctive form of inherited IFNAR1 deficiency. Journal of Clinical Investigation, 2021, 131, .	8.2	64
11	TLR3 controls constitutive IFN-Î² antiviral immunity in human fibroblasts and cortical neurons. Journal of Clinical Investigation, 2021, 131, .	8.2	64
12	Inherited GATA2 Deficiency Is Dominant by Haploinsufficiency and Displays Incomplete Clinical Penetrance. Journal of Clinical Immunology, 2021, 41, 639-657.	3.8	30
13	Distinct antibody repertoires against endemic human coronaviruses in children and adults. JCI Insight, 2021, 6, .	5.0	40
14	Auto-antibodies to type I IFNs can underlie adverse reactions to yellow fever live attenuated vaccine. Journal of Experimental Medicine, 2021, 218, .	8.5	130
15	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.	3.5	17
16	Rare Pathogenic Variants in Mitochondrial and Inflammation-Associated Genes May Lead to Inflammatory Cardiomyopathy in Chagas Disease. Journal of Clinical Immunology, 2021, 41, 1048-1063.	3.8	11
17	Inhibition of HECT E3 ligases as potential therapy for COVID-19. Cell Death and Disease, 2021, 12, 310.	6.3	33
18	SARS-CoV-2â€“related MIS-C: A key to the viral and genetic causes of Kawasaki disease?. Journal of Experimental Medicine, 2021, 218, .	8.5	100

#	Article	IF	Citations
19	Detection of homozygous and hemizygous complete or partial exon deletions by whole-exome sequencing. NAR Genomics and Bioinformatics, 2021, 3, lqab037.	3.2	7
20	Insufficient type I IFN immunity underlies life-threatening COVID-19 pneumonia. Comptes Rendus - Biologies, 2021, 344, 19-25.	0.2	16
21	A computational approach for detecting physiological homogeneity in the midst of genetic heterogeneity. American Journal of Human Genetics, 2021, 108, 1012-1025.	6.2	6
22	Association of rare predicted loss-of-function variants of influenza-related type I IFN genes with critical COVID-19 pneumonia. Journal of Clinical Investigation, 2021, 131, .	8.2	12
23	Taking population stratification into account by local permutations in rareâ€variant association studies on small samples. Genetic Epidemiology, 2021, 45, 821-829.	1.3	4
24	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
25	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
26	Biochemically deleterious human NFKB1 variants underlie an autosomal dominant form of common variable immunodeficiency. Journal of Experimental Medicine, 2021, 218, .	8.5	32
27	Controlling for human population stratification in rare variant association studies. Scientific Reports, 2021, 11, 19015.	3.3	8
28	Single-Cell and Bulk RNA-Sequencing Reveal Differences in Monocyte Susceptibility to Influenza A Virus Infection Between Africans and Europeans. Frontiers in Immunology, 2021, 12, 768189.	4.8	14
29	Deep resequencing identifies candidate functional genes in leprosy GWAS loci. PLoS Neglected Tropical Diseases, 2021, 15, e0010029.	3.0	5
30	Life-Threatening COVID-19: Defective Interferons Unleash Excessive Inflammation. Med, 2020, 1, 14-20.	4.4	110
31	A genome-wide case-only test for the detection of digenic inheritance in human exomes. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 19367-19375.	7.1	15
32	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.	4.7	14
33	Inborn errors of type I IFN immunity in patients with life-threatening COVID-19. Science, 2020, 370, .	12.6	1,749
34	Autoantibodies against type I IFNs in patients with life-threatening COVID-19. Science, 2020, 370, .	12.6	1,983
35	Family-based genome-wide association study of leprosy in Vietnam. PLoS Pathogens, 2020, 16, e1008565.	4.7	8
36	A Global Effort to Define the Human Genetics of Protective Immunity to SARS-CoV-2 Infection. Cell, 2020, 181, 1194-1199.	28.9	185

#	Article	IF	Citations
37	Severe COVID-19 in the young and healthy: monogenic inborn errors of immunity?. Nature Reviews Immunology, 2020, 20, 455-456.	22.7	47
38	Human genetics of HCV infection phenotypes in the era of direct-acting antivirals. Human Genetics, 2020, 139, 855-863.	3.8	7
39	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.	7.1	3
40	Prevalence and risk factors for latent tuberculosis infection among healthcare workers in Morocco. PLoS ONE, 2019, 14, e0221081.	2.5	17
41	Frenchâ€style genetics v. 2.0: The â€œeâ€CohortEâ€•project. Clinical Genetics, 2019, 96, 330-340.	2.0	5
42	Inherited IFNAR1 deficiency in otherwise healthy patients with adverse reaction to measles and yellow fever live vaccines. Journal of Experimental Medicine, 2019, 216, 2057-2070.	8.5	127
43	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.	7.1	50
44	Inherited IL-18BP deficiency in human fulminant viral hepatitis. Journal of Experimental Medicine, 2019, 216, 1777-1790.	8.5	70
45	Homozygosity for TYK2 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
46	Identification of an Endoglin Variant Associated With HCV-Related Liver Fibrosis Progression by Next-Generation Sequencing. Frontiers in Genetics, 2019, 10, 1024.	2.3	6
47	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
48	Inborn Errors of RNA Lariat Metabolism in Humans with Brainstem Viral Infection. Cell, 2018, 172, 952-965.e18.	28.9	92
49	HCV-Associated Liver Fibrosis and HSD17B13. New England Journal of Medicine, 2018, 379, 1875-1876.	27.0	26
50	Tuberculosis and impaired IL-23â€“dependent IFN-Î³ immunity in humans homozygous for a common TYK2 missense variant. Science Immunology, 2018, 3, .	11.9	148
51	Biallelic mutations in DNA ligase 1 underlie a spectrum of immune deficiencies. Journal of Clinical Investigation, 2018, 128, 5489-5504.	8.2	32
52	Kaposi sarcoma, oral malformations, mitral dysplasia, and scoliosis associated with 7q34â€q36.3 heterozygous terminal deletion. American Journal of Medical Genetics, Part A, 2017, 173, 1858-1865.	1.2	4
53	Autosomal Recessive Cardiomyopathy Presenting as Acute Myocarditis. Journal of the American College of Cardiology, 2017, 69, 1653-1665.	2.8	94
54	Population Pharmacokinetic Modeling of Tenofovir in the Genital Tract of Male HIV-Infected Patients. Antimicrobial Agents and Chemotherapy, 2017, 61, .	3.2	5

#	Article	IF	Citations
55	An eQTL variant of ZXDC is associated with IFN-Î³ production following Mycobacterium tuberculosis antigen-specific stimulation. Scientific Reports, 2017, 7, 12800.	3.3	5
56	A genome wide association study identifies a lncRna as risk factor for pathological inflammatory responses in leprosy. PLoS Genetics, 2017, 13, e1006637.	3.5	29
57	Deciphering the genetic control of gene expression following Mycobacterium leprae antigen stimulation. PLoS Genetics, 2017, 13, e1006952.	3.5	37
58	BRIP1coding variants are associated with a high risk of hepatocellular carcinoma occurrence in patients with HCV- or HBV-related liver disease. Oncotarget, 2017, 8, 62842-62857.	1.8	7
59	Pauci- and Multibacillary Leprosy: Two Distinct, Genetically Neglected Diseases. PLoS Neglected Tropical Diseases, 2016, 10, e0004345.	3.0	57
60	A Missense LRRK2 Variant Is a Risk Factor for Excessive Inflammatory Responses in Leprosy. PLoS Neglected Tropical Diseases, 2016, 10, e0004412.	3.0	181
61	Refined association of melanoma differentiationâ€associated gene 5 variants with spontaneous hepatitis C virus clearance in Egypt. Hepatology, 2016, 63, 1059-1061.	7.3	3
62	A new 3p25 locus is associated with liver fibrosis progression in human immunodeficiency virus/hepatitis C virusâ€coinfected patients. Hepatology, 2016, 64, 1462-1472.	7.3	15
63	Exome and genome sequencing for inborn errors of immunity. Journal of Allergy and Clinical Immunology, 2016, 138, 957-969.	2.9	187
64	Characterization of Greater Middle Eastern genetic variation for enhanced disease gene discovery. Nature Genetics, 2016, 48, 1071-1076.	21.4	314
65	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.	7.1	53
66	Loss of B Cells in Patients with Heterozygous Mutations in IKAROS. New England Journal of Medicine, 2016, 374, 1032-1043.	27.0	217
67	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.	4.0	15
68	Human HOIP and LUBAC deficiency underlies autoinflammation, immunodeficiency, amylopectinosis, and lymphangiectasia. Journal of Experimental Medicine, 2015, 212, 939-951.	8.5	241
69	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.	4.0	42
70	Whole-genome sequencing is more powerful than whole-exome sequencing for detecting exome variants. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5473-5478.	7.1	475
71	Human TYK2 deficiency: Mycobacterial and viral infections without hyper-IgE syndrome. Journal of Experimental Medicine, 2015, 212, 1641-1662.	8.5	293
72	Association of TNFSF8 Regulatory Variants With Excessive Inflammatory Responses but not Leprosy Per Se. Journal of Infectious Diseases, 2015, 211, 968-977.	4.0	29

#	Article	IF	Citations
73	Impact of IL28B, APOH and ITPA Polymorphisms on Efficacy and Safety of TVR- or BOC-Based Triple Therapy in Treatment-Experienced HCV-1 Patients with Compensated Cirrhosis from the ANRS CO20-CUPIC Study. PLoS ONE, 2015, 10, e0145105.	2.5	4
74	Implicit Hypotheses Are Hidden Power Droppers in Family-Based Association Studies of Secondary Outcomes. Open Journal of Statistics, 2015, 05, 35-45.	0.7	3
75	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.	2.5	17
76	A General Efficient and Flexible Approach for Genome-Wide Association Analyses of Imputed Genotypes in Family-Based Designs. Genetic Epidemiology, 2014, 38, 560-571.	1.3	23
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.	3.8	12
78	Host Genomics and Control of Tuberculosis Infection. Public Health Genomics, 2013, 16, 44-49.	1.0	27
79	Inherited IL-12p40 Deficiency. Medicine (United States), 2013, 92, 190.	1.0	3
80	Gene Set Signature of Reversal Reaction Type I in Leprosy Patients. PLoS Genetics, 2013, 9, e1003624.	3.5	32
81	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.	5.8	33
82	Inherited IL-12p40 Deficiency. Medicine (United States), 2013, 92, 109-122.	1.0	151
83	PARK2 Mediates Interleukin 6 and Monocyte Chemoattractant Protein 1 Production by Human Macrophages. PLoS Neglected Tropical Diseases, 2013, 7, e2015.	3.0	45
84	Tuberculin Skin Test Reactivity Is Dependent on Host Genetic Background in Colombian Tuberculosis Household Contacts. Clinical Infectious Diseases, 2012, 54, 968-971.	5.8	30
85	Genetics of leprosy reactions: an overview. Memorias Do Instituto Oswaldo Cruz, 2012, 107, 132-142.	1.6	41
86	NEMO is a key component of NF-Î²Bâ€“ and IRF-3â€“dependent TLR3-mediated immunity to herpes simplex virus. Journal of Allergy and Clinical Immunology, 2011, 128, 610-617.e4.	2.9	66
87	A Major Gene Effect Controls Resistance to Caries. Journal of Dental Research, 2011, 90, 735-739.	5.2	24
88	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.	1.3	7
89	Revisiting Human IL-12RÎ²1 Deficiency. Medicine (United States), 2010, 89, 381-402.	1.0	367
90	Tuberculin Skin Test and In Vitro Assays Provide Complementary Measures of Antimycobacterial Immunity in Children and Adolescents. Chest, 2010, 137, 1071-1077.	0.8	35

#	Article	IF	Citations
91	A Major Gene Controls Leprosy Susceptibility in a Hyperendemic Isolated Population from North of Brazil. Journal of Infectious Diseases, 2010, 201, 1598-1605.	4.0	38
92	Autoantibodies against IL-17A, IL-17F, and IL-22 in patients with chronic mucocutaneous candidiasis and autoimmune polyendocrine syndrome type I. Journal of Experimental Medicine, 2010, 207, 291-297.	8.5	663
93	High Heritability of Antimycobacterial Immunity in an Area of Hyperendemicity for Tuberculosis Disease. Journal of Infectious Diseases, 2010, 201, 15-19.	4.0	57
94	Quantifying Latent TB Infection. Chest, 2010, 138, 461.	0.8	1
95	Genetics of Susceptibility and Resistance to Infection. Methods in Microbiology, 2010, 37, 67-99.	0.8	2
96	Two loci control tuberculin skin test reactivity in an area hyperendemic for tuberculosis. Journal of Experimental Medicine, 2009, 206, 2583-2591.	8.5	142
97	Mutations in STAT3 and IL12RB1 impair the development of human IL-17â€“producing T cells. Journal of Experimental Medicine, 2008, 205, 1543-1550.	8.5	406
98	A Common TMPRSS2 Variant Protects Against Severe COVID-19. SSRN Electronic Journal, 0, , .	0.4	2