Alexandre Bolze

List of Publications by Year
in descending order

34 papers	8,206 citations	185998 28 h-index	377514 34 g-index
45 all docs	45 docs citations	45 times ranked	15106 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, .	5.6	35
2	A global effort to dissect the human genetic basis of resistance to SARS-CoV-2 infection. Nature Immunology, 2022, 23, 159-164.	7.0	41
3	Human genetic and immunological determinants of critical COVID-19 pneumonia. Nature, 2022, 603, 587-598.	13.7	216
4	HLA-Aâˆ—03:01 is associated with increased risk of fever, chills, and stronger side effects from Pfizer-BioNTech COVID-19 vaccination. Human Genetics and Genomics Advances, 2022, 3, 100084.	1.0	21
5	SARS-CoV-2 variant Delta rapidly displaced variant Alpha in the United States and led to higher viral loads. Cell Reports Medicine, 2022, 3, 100564.	3.3	61
6	Respiratory viral infections in otherwise healthy humans with inherited IRF7 deficiency. Journal of Experimental Medicine, 2022, 219, .	4.2	21
7	Recessive inborn errors of type I IFN immunity in children with COVID-19 pneumonia. Journal of Experimental Medicine, 2022, 219, .	4.2	59
8	Wastewater sequencing reveals early cryptic SARS-CoV-2 variant transmission. Nature, 2022, 609, 101-108.	13.7	200
9	SARS-CoV-2â€“related MIS-C: A key to the viral and genetic causes of Kawasaki disease?. Journal of Experimental Medicine, 2021, 218, .	4.2	100
10	Emergence and rapid transmission of SARS-CoV-2 B.1.1.7 in the United States. Cell, 2021, 184, 2587-2594.e7.	13.5	285
11	Harnessing Type I IFN Immunity Against SARS-CoV-2 with Early Administration of IFN-Î². Journal of Clinical Immunology, 2021, 41, 1425-1442.	2.0	39
12	From Your Nose to Your Toes: A Review of Severe Acute Respiratory Syndrome Coronavirus 2 Pandemicâ€'Associated Pernio. Journal of Investigative Dermatology, 2021, 141, 2791-2796.	0.3	21
13	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. PLoS ONE, 2021, 16, e0255402.	1.1	6
14	Positive predictive value highlights four novel candidates for actionable genetic screening from analysis of 220,000 clinicogenomic records. Genetics in Medicine, 2021, 23, 2300-2308.	1.1	13
15	X-linked recessive TLR7 deficiency in ~1% of men under 60 years old with life-threatening COVID-19. Science Immunology, 2021, 6, .	5.6	267
16	Pathogenic variants in actionable MODY genes are associated with type 2 diabetes. Nature Metabolism, 2020, 2, 1126-1134.	5.1	43
17	Life-Threatening COVID-19: Defective Interferons Unleash Excessive Inflammation. Med, 2020, 1, 14-20.	2.2	110
18	Inborn errors of type I IFN immunity in patients with life-threatening COVID-19. Science, 2020, 370, .	6.0	1,749

#	Article	IF	Citations
19	Autoantibodies against type I IFNs in patients with life-threatening COVID-19. Science, 2020, 370, .	6.0	1,983
20	A Global Effort to Define the Human Genetics of Protective Immunity to SARS-CoV-2 Infection. Cell, 2020, 181, 1194-1199.	13.5	185
21	A 44-Year-Old Female With Overwhelming Sepsis. Clinical Infectious Diseases, 2019, 68, 712-712.	2.9	1
22	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.	3.3	52
23	Incomplete penetrance for isolated congenital asplenia in humans with mutations in translated and untranslated RPSA exons. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E8007-E8016.	3.3	31
24	Exome and genome sequencing for inborn errors of immunity. Journal of Allergy and Clinical Immunology, 2016, 138, 957-969.	1.5	187
25	Inherited IL-17RC deficiency in patients with chronic mucocutaneous candidiasis. Journal of Experimental Medicine, 2015, 212, 619-631.	4.2	162
26	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.	3.3	475
27	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.	3.3	213
28	Ribosomal Protein SA Haploinsufficiency in Humans with Isolated Congenital Asplenia. Science, 2013, 340, 976-978.	6.0	176
29	Congenital Asplenia in Mice and Humans with Mutations in a Pbx/Nkx2-5/p15 Module. Developmental Cell, 2012, 22, 913-926.	3.1	70
30	A Mild Form of SLC29A3 Disorder: A Frameshift Deletion Leads to the Paradoxical Translation of an Otherwise Noncoding mRNA Splice Variant. PLoS ONE, 2012, 7, e29708.	1.1	50
31	Isolated Congenital Asplenia: A French Nationwide Retrospective Survey of 20 Cases. Journal of Pediatrics, 2011, 158, 142-148.e1.	0.9	74
32	Gain-of-function human STAT1 mutations impair IL-17 immunity and underlie chronic mucocutaneous candidiasis. Journal of Experimental Medicine, 2011, 208, 1635-1648.	4.2	739
33	Whole-Exome-Sequencing-Based Discovery of Human FADD Deficiency. American Journal of Human Genetics, 2010, 87, 873-881.	2.6	171
34	Inflammatory tumour microenvironment is associated with superior survival in hepatocellular carcinoma patients. Journal of Hepatology, 2010, 52, 370-379.	1.8	227