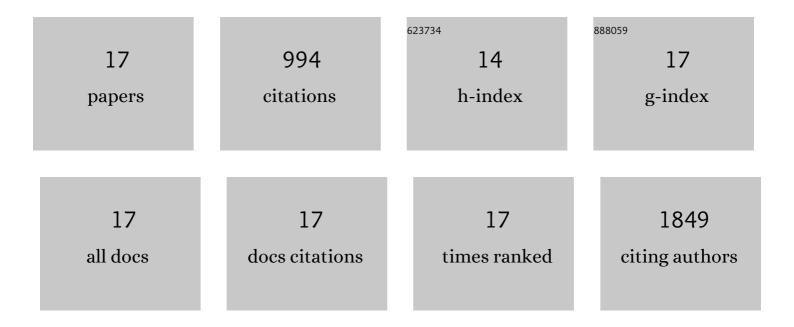
Isabelle Casademont

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3920987/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A variant in the CD209 promoter is associated with severity of dengue disease. Nature Genetics, 2005, 37, 507-513.	21.4	267
2	Positively Selected <i>G6PD</i> -Mahidol Mutation Reduces <i>Plasmodium vivax</i> Density in Southeast Asians. Science, 2009, 326, 1546-1549.	12.6	150
3	Autochthonous Japanese Encephalitis with Yellow Fever Coinfection in Africa. New England Journal of Medicine, 2017, 376, 1483-1485.	27.0	99
4	The large form of human 2′,5′-Oligoadenylate Synthetase (OAS3) exerts antiviral effect against Chikungunya virus. Virology, 2009, 384, 216-222.	2.4	90
5	Increased adaptive immune responses and proper feedback regulation protect against clinical dengue. Science Translational Medicine, 2017, 9, .	12.4	68
6	A Modified mRNA Vaccine Targeting Immunodominant NS Epitopes Protects Against Dengue Virus Infection in HLA Class I Transgenic Mice. Frontiers in Immunology, 2019, 10, 1424.	4.8	59
7	Genetic Determination and Linkage Mapping of Plasmodium falciparum Malaria Related Traits in Senegal. PLoS ONE, 2008, 3, e2000.	2.5	49
8	Heritability of the Human Infectious Reservoir of Malaria Parasites. PLoS ONE, 2010, 5, e11358.	2.5	39
9	High Anti–Dengue Virus Activity of the <i>OAS</i> Gene Family Is Associated With Increased Severity of Dengue. Journal of Infectious Diseases, 2015, 212, 2011-2020.	4.0	37
10	A Blood RNA Signature Detecting Severe Disease in Young Dengue Patients at Hospital Arrival. Journal of Infectious Diseases, 2018, 217, 1690-1698.	4.0	27
11	Impact of Mosquito Bites on Asexual Parasite Density and Gametocyte Prevalence in Asymptomatic Chronic Plasmodium falciparum Infections and Correlation with IgE and IgG Titers. Infection and Immunity, 2012, 80, 2240-2246.	2.2	25
12	Host Genetic Variation Does Not Determine Spatio-Temporal Patterns of European Bat 1 Lyssavirus. Genome Biology and Evolution, 2017, 9, 3202-3213.	2.5	19
13	Joint ancestry and association test indicate two distinct pathogenic pathways involved in classical dengue fever and dengue shock syndrome. PLoS Neglected Tropical Diseases, 2018, 12, e0006202.	3.0	17
14	Population genetics-informed meta-analysis in seven genes associated with risk to dengue fever disease. Infection, Genetics and Evolution, 2018, 62, 60-72.	2.3	16
15	Interaction of RNA viruses of the natural virome with the African malaria vector, Anopheles coluzzii. Scientific Reports, 2019, 9, 6319.	3.3	15
16	Heritability of P. falciparum and P. vivax Malaria in a Karen Population in Thailand. PLoS ONE, 2008, 3, e3887.	2.5	13
17	Detecting multi-way epistasis in family-based association studies. Briefings in Bioinformatics, 2016, 18, bbw039.	6.5	4