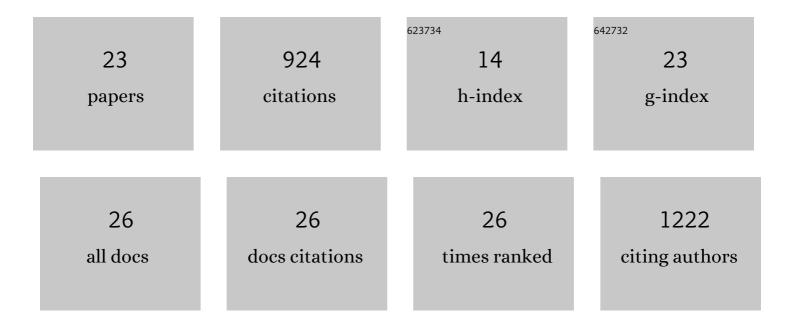
Marianna Orlova

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/6275844/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	A Missense LRRK2 Variant Is a Risk Factor for Excessive Inflammatory Responses in Leprosy. PLoS Neglected Tropical Diseases, 2016, 10, e0004412.	3.0	181
2	Stepwise replication identifies a low-producing lymphotoxin-α allele as a major risk factor for early-onset leprosy. Nature Genetics, 2007, 39, 517-522.	21.4	152
3	Crohn's Disease Susceptibility Genes are Associated With Leprosy in the Vietnamese Population. Journal of Infectious Diseases, 2012, 206, 1763-1767.	4.0	70
4	Pauci- and Multibacillary Leprosy: Two Distinct, Genetically Neglected Diseases. PLoS Neglected Tropical Diseases, 2016, 10, e0004345.	3.0	57
5	Pleiotropic effects for Parkin and LRRK2 in leprosy type-1 reactions and Parkinson's disease. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15616-15624.	7.1	50
6	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.	4.0	49
7	HIV persistence in mucosal CD4+ T cells within the lungs of adults receiving long-term suppressive antiretroviral therapy. Aids, 2018, 32, 2279-2289.	2.2	44
8	Genetics of leprosy reactions: an overview. Memorias Do Instituto Oswaldo Cruz, 2012, 107, 132-142.	1.6	41
9	Deciphering the genetic control of gene expression following Mycobacterium leprae antigen stimulation. PLoS Genetics, 2017, 13, e1006952.	3.5	37
10	Linkage disequilibrium pattern and age-at-diagnosis are critical for replicating genetic associations across ethnic groups in leprosy. Human Genetics, 2013, 132, 107-116.	3.8	32
11	Gene Set Signature of Reversal Reaction Type I in Leprosy Patients. PLoS Genetics, 2013, 9, e1003624.	3.5	32
12	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
13	A genome wide association study identifies a IncRna as risk factor for pathological inflammatory responses in leprosy. PLoS Genetics, 2017, 13, e1006637.	3.5	29
14	An observational study identifying highly tuberculosis-exposed, HIV-1-positive but persistently TB, tuberculin and IGRA negative persons with M. tuberculosis specific antibodies in Cape Town, South Africa. EBioMedicine, 2020, 61, 103053.	6.1	22
15	Alveolar macrophages from persons living with HIV show impaired epigenetic response to Mycobacterium tuberculosis. Journal of Clinical Investigation, 2021, 131, .	8.2	19
16	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
17	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
18	A systems biology approach identifies candidate drugs to reduce mortality in severely ill patients with COVID-19. Science Advances, 2022, 8, .	10.3	14

MARIANNA ORLOVA

#	Article	IF	CITATIONS
19	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
20	Family-based genome-wide association study of leprosy in Vietnam. PLoS Pathogens, 2020, 16, e1008565.	4.7	8
21	An eQTL variant of ZXDC is associated with IFN-γ production following Mycobacterium tuberculosis antigen-specific stimulation. Scientific Reports, 2017, 7, 12800.	3.3	5
22	Peculiar Phenotypic and Cytotoxic Features of Pulmonary Mucosal CD8 T Cells in People Living with HIV Receiving Long-Term Antiretroviral Therapy. Journal of Immunology, 2021, 206, 641-651.	0.8	5
23	Deep resequencing identifies candidate functional genes in leprosy GWAS loci. PLoS Neglected Tropical Diseases, 2021, 15, e0010029.	3.0	5