

# Marlo MÃ¶ller

## List of Publications by Year in descending order

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Version: 2024-02-01

66  
papers

2,445  
citations

279487

23  
h-index

233125

45  
g-index

79  
all docs

79  
docs citations

79  
times ranked

3515  
citing authors

#	ARTICLE	IF	CITATIONS
1	Deciphering Genetic Susceptibility to Tuberculous Meningitis. <i>Frontiers in Neurology</i> , 2022, 13, 820168.	1.1	2
2	African Genetic Representation in the Context of SARS-CoV-2 Infection and COVID-19 Severity. <i>Frontiers in Genetics</i> , 2022, 13, .	1.1	5
3	Characterizing epidemiological and genotypic features of <i>Mycobacterium bovis</i> infection in wild dogs ( <i>Lycaon pictus</i> ). <i>Transboundary and Emerging Diseases</i> , 2021, 68, 3433-3442.	1.3	6
4	<i>Mycobacterium tuberculosis</i> complex and human coadaptation: a two-way street complicating host susceptibility to TB. <i>Human Molecular Genetics</i> , 2021, 30, R146-R153.	1.4	3
5	Human whole genome sequencing in South Africa. <i>Scientific Reports</i> , 2021, 11, 606.	1.6	10
6	Inferring recombination patterns in African populations. <i>Human Molecular Genetics</i> , 2021, 30, R11-R16.	1.4	6
7	High diversity, inbreeding and a dynamic Pleistocene demographic history revealed by African buffalo genomes. <i>Scientific Reports</i> , 2021, 11, 4540.	1.6	11
8	Phenotype Definition for “Resisters” to <i>Mycobacterium tuberculosis</i> Infection in the Literature” A Review and Recommendations. <i>Frontiers in Immunology</i> , 2021, 12, 619988.	2.2	13
9	Shedding of <i>Mycobacterium bovis</i> in respiratory secretions of free-ranging wild dogs ( ) Tj ETQq1 1 0.784314 rgBT /Overlock <i>Diseases</i> , 2021, 68, 2581-2588.	1.3	6
10	Clinical Utility of Whole Exome Sequencing and Targeted Panels for the Identification of Inborn Errors of Immunity in a Resource-Constrained Setting. <i>Frontiers in Immunology</i> , 2021, 12, 665621.	2.2	14
11	A multi-phenotype genome-wide association study of clades causing tuberculosis in a Ghanaian- and South African cohort. <i>Genomics</i> , 2021, 113, 1802-1815.	1.3	8
12	Local ancestry inference in heterogeneous populations”Are recent recombination events more relevant?. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	2
13	Phenotypic and immune functional profiling of patients with suspected Mendelian Susceptibility to Mycobacterial Disease in South Africa. <i>BMC Immunology</i> , 2021, 22, 62.	0.9	4
14	Local Ancestry Adjusted Allelic Association Analysis Robustly Captures Tuberculosis Susceptibility Loci. <i>Frontiers in Genetics</i> , 2021, 12, 716558.	1.1	7
15	An observational study identifying highly tuberculosis-exposed, HIV-1-positive but persistently TB, tuberculin and IGRA negative persons with <i>M. tuberculosis</i> specific antibodies in Cape Town, South Africa. <i>EBioMedicine</i> , 2020, 61, 103053.	2.7	22
16	Hyperphosphatasia with mental retardation syndrome type 4 in three unrelated South African patients. <i>American Journal of Medical Genetics, Part A</i> , 2020, 182, 2230-2235.	0.7	8
17	Prospective avenues for human population genomics and disease mapping in southern Africa. <i>Molecular Genetics and Genomics</i> , 2020, 295, 1079-1089.	1.0	7
18	Identification of a novel WAS mutation in a South African patient presenting with atypical Wiskott-Aldrich syndrome: a case report. <i>BMC Medical Genetics</i> , 2020, 21, 124.	2.1	4

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19	A regulatory variant in the C1Q gene cluster is associated with tuberculosis susceptibility and C1qA plasma levels in a South African population. <i>Immunogenetics</i> , 2020, 72, 305-314.	1.2	7
20	Human global and population-specific genetic susceptibility to Mycobacterium tuberculosis infection and disease. <i>Current Opinion in Pulmonary Medicine</i> , 2020, 26, 302-310.	1.2	11
21	Putting RFMix and ADMIXTURE to the test in a complex admixed population. <i>BMC Genetics</i> , 2020, 21, 40.	2.7	29
22	Evaluating the Accuracy of Imputation Methods in a Five-Way Admixed Population. <i>Frontiers in Genetics</i> , 2019, 10, 34.	1.1	53
23	Primary immunodeficiency diseases in a tuberculosis endemic region: challenges and opportunities. <i>Genes and Immunity</i> , 2019, 20, 447-454.	2.2	14
24	The X chromosome and sex-specific effects in infectious disease susceptibility. <i>Human Genomics</i> , 2019, 13, 2.	1.4	271
25	Different Selected Mechanisms Attenuated the Inhibitory Interaction of KIR2DL1 with C2+ HLA-C in Two Indigenous Human Populations in Southern Africa. <i>Journal of Immunology</i> , 2018, 200, 2640-2655.	0.4	32
26	The arms race between man and Mycobacterium tuberculosis: Time to regroup. <i>Infection, Genetics and Evolution</i> , 2018, 66, 361-375.	1.0	17
27	Neutrophils: Innate Effectors of TB Resistance?. <i>Frontiers in Immunology</i> , 2018, 9, 2637.	2.2	59
28	Rapid evolution of a skin-lightening allele in southern African KhoeSan. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 13324-13329.	3.3	17
29	The critical needs and challenges for genetic architecture studies in Africa. <i>Current Opinion in Genetics and Development</i> , 2018, 53, 113-120.	1.5	57
30	Genetic Resistance to Mycobacterium tuberculosis Infection and Disease. <i>Frontiers in Immunology</i> , 2018, 9, 2219.	2.2	29
31	Autosomal Dominant IFN- $\beta$ R1 Deficiency Presenting with both Atypical Mycobacteriosis and Tuberculosis in a BCG-Vaccinated South African Patient. <i>Journal of Clinical Immunology</i> , 2018, 38, 460-463.	2.0	8
32	A Sex-Stratified Genome-Wide Association Study of Tuberculosis Using a Multi-Ethnic Genotyping Array. <i>Frontiers in Genetics</i> , 2018, 9, 678.	1.1	28
33	Population structure and infectious disease risk in southern Africa. <i>Molecular Genetics and Genomics</i> , 2017, 292, 499-509.	1.0	21
34	An Unexpectedly Complex Architecture for Skin Pigmentation in Africans. <i>Cell</i> , 2017, 171, 1340-1353.e14.	18.5	134
35	The role of human host genetics in tuberculosis resistance. <i>Expert Review of Respiratory Medicine</i> , 2017, 11, 721-737.	1.0	16
36	Exome sequencing identifies a novel TTC37 mutation in the first reported case of Trichohepatoenteric syndrome (THE-S) in South Africa. <i>BMC Medical Genetics</i> , 2017, 18, 26.	2.1	8

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37	Exome Sequencing Identifies a Novel MAP3K14 Mutation in Recessive Atypical Combined Immunodeficiency. <i>Frontiers in Immunology</i> , 2017, 8, 1624.	2.2	16
38	A post-GWAS analysis of predicted regulatory variants and tuberculosis susceptibility. <i>PLoS ONE</i> , 2017, 12, e0174738.	1.1	19
39	A new tool for prioritization of sequence variants from whole exome sequencing data. <i>Source Code for Biology and Medicine</i> , 2016, 11, 10.	1.7	9
40	The complete genome sequence of the African buffalo ( <i>Syncerus caffer</i> ). <i>BMC Genomics</i> , 2016, 17, 1001.	1.2	21
41	Fine-Scale Human Population Structure in Southern Africa Reflects Ecogeographic Boundaries. <i>Genetics</i> , 2016, 204, 303-314.	1.2	93
42	Polymorphisms in the Pattern Recognition Receptor Mincle Gene (CLEC4E) and Association with Tuberculosis. <i>Lung</i> , 2016, 194, 763-767.	1.4	19
43	TLR1, 2, 4, 6 and 9 Variants Associated with Tuberculosis Susceptibility: A Systematic Review and Meta-Analysis. <i>PLoS ONE</i> , 2015, 10, e0139711.	1.1	92
44	Activating KIRs alter susceptibility to pulmonary tuberculosis in a South African population. <i>Tuberculosis</i> , 2015, 95, 817-821.	0.8	21
45	Association of toll-like receptors with susceptibility to tuberculosis suggests sex-specific effects of TLR8 polymorphisms. <i>Infection, Genetics and Evolution</i> , 2015, 34, 221-229.	1.0	69
46	Investigating the Role of Gene-Gene Interactions in TB Susceptibility. <i>PLoS ONE</i> , 2015, 10, e0123970.	1.1	15
47	Using multi-way admixture mapping to elucidate TB susceptibility in the South African Coloured population. <i>BMC Genomics</i> , 2014, 15, 1021.	1.2	36
48	Associations Between Human Leukocyte Antigen Class I Variants and the Mycobacterium tuberculosis Subtypes Causing Disease. <i>Journal of Infectious Diseases</i> , 2014, 209, 216-223.	1.9	59
49	Genome-wide association study of ancestry-specific TB risk in the South African Coloured population. <i>Human Molecular Genetics</i> , 2014, 23, 796-809.	1.4	162
50	The role of ancestry in TB susceptibility of an admixed South African population. <i>Tuberculosis</i> , 2014, 94, 413-420.	0.8	32
51	Associations between human leukocyte antigen class I variants and the Mycobacterium tuberculosis subtypes causing disease. <i>International Journal of Infectious Diseases</i> , 2014, 21, 300.	1.5	1
52	Determining Ancestry Proportions in Complex Admixture Scenarios in South Africa Using a Novel Proxy Ancestry Selection Method. <i>PLoS ONE</i> , 2013, 8, e73971.	1.1	42
53	A Panel of Ancestry Informative Markers for the Complex Five-Way Admixed South African Coloured Population. <i>PLoS ONE</i> , 2013, 8, e82224.	1.1	74
54	Comparative Analysis of a Putative Tuberculosis-Susceptibility Gene, <i>MC3R</i> , and Pseudogene Sequences in Cattle, African Buffalo, Hyena, Rhinoceros and Other African Bovids and Ruminants. <i>Cytogenetic and Genome Research</i> , 2012, 136, 117-122.	0.6	4

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55	. Genetic Perspectives of Tuberculosis in Southern Africa. , 2012, , 487-499.		0
56	Polymorphisms in MC3R promoter and CTSZ 3'UTR are associated with tuberculosis susceptibility. European Journal of Human Genetics, 2011, 19, 676-681.	1.4	38
57	Genome-wide analysis of the structure of the South African Coloured Population in the Western Cape. Human Genetics, 2010, 128, 145-153.	1.8	177
58	Current findings, challenges and novel approaches in human genetic susceptibility to tuberculosis. Tuberculosis, 2010, 90, 71-83.	0.8	201
59	Analysis of eight genes modulating interferon gamma and human genetic susceptibility to tuberculosis: a case-control association study. BMC Infectious Diseases, 2010, 10, 154.	1.3	29
60	Past, present and future directions in human genetic susceptibility to tuberculosis. FEMS Immunology and Medical Microbiology, 2010, 58, 3-26.	2.7	109
61	A Functional Haplotype in the 3' Untranslated Region of <i>TNFRSF1B</i> Is Associated with Tuberculosis in Two African Populations. American Journal of Respiratory and Critical Care Medicine, 2010, 181, 388-393.	2.5	27
62	Investigation of chromosome 17 candidate genes in susceptibility to TB in a South African population. Tuberculosis, 2009, 89, 189-194.	0.8	50
63	Host susceptibility to tuberculosis: CARD15 polymorphisms in a South African population. Molecular and Cellular Probes, 2007, 21, 148-151.	0.9	24
64	Allelic variation in BTNL2 and susceptibility to tuberculosis in a South African population. Microbes and Infection, 2007, 9, 522-528.	1.0	17
65	TB epidemiology and human genetics. Novartis Foundation Symposium, 2006, 279, 17-31; discussion 31-41, 216-9.	1.2	5
66	TB Epidemiology and Human Genetics. Novartis Foundation Symposium, 0, , 17-41.	1.2	11