

# Fabrizio Menardo

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6169011/publications.pdf>

Version: 2024-02-01

25  
papers

1,873  
citations

394421

19  
h-index

610901

24  
g-index

36  
all docs

36  
docs citations

36  
times ranked

2082  
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole genome sequencing of <i>Mycobacterium tuberculosis</i> : current standards and open issues. <i>Nature Reviews Microbiology</i> , 2019, 17, 533-545.	28.6	237
2	Hybridization of powdery mildew strains gives rise to pathogens on novel agricultural crop species. <i>Nature Genetics</i> , 2016, 48, 201-205.	21.4	192
3	A New Phylogenetic Framework for the Animal-Adapted <i>Mycobacterium tuberculosis</i> Complex. <i>Frontiers in Microbiology</i> , 2018, 9, 2820.	3.5	145
4	A sister lineage of the <i>Mycobacterium tuberculosis</i> complex discovered in the African Great Lakes region. <i>Nature Communications</i> , 2020, 11, 2917.	12.8	136
5	Multiple Avirulence Loci and Allele-Specific Effector Recognition Control the <i>Pm3</i> Race-Specific Resistance of Wheat to Powdery Mildew. <i>Plant Cell</i> , 2015, 27, tpc.15.00171.	6.6	135
6	Treemmer: a tool to reduce large phylogenetic datasets with minimal loss of diversity. <i>BMC Bioinformatics</i> , 2018, 19, 164.	2.6	121
7	<i>AvrPm2</i> encodes an <i>RNase</i> -like avirulence effector which is conserved in the two different specialized forms of wheat and rye powdery mildew fungus. <i>New Phytologist</i> , 2017, 213, 1301-1314.	7.3	112
8	The molecular clock of <i>Mycobacterium tuberculosis</i> . <i>PLoS Pathogens</i> , 2019, 15, e1008067.	4.7	107
9	The <i>AvrPm3-Pm3</i> effector-NLR interactions control both race-specific resistance and host-specificity of cereal mildews on wheat. <i>Nature Communications</i> , 2019, 10, 2292.	12.8	103
10	A chromosome-scale genome assembly reveals a highly dynamic effector repertoire of wheat powdery mildew. <i>New Phytologist</i> , 2019, 221, 2176-2189.	7.3	79
11	Phylogenomics of <i>Mycobacterium africanum</i> reveals a new lineage and a complex evolutionary history. <i>Microbial Genomics</i> , 2021, 7, .	2.0	71
12	Rapid turnover of effectors in grass powdery mildew ( <i>Blumeria graminis</i> ). <i>BMC Evolutionary Biology</i> , 2017, 17, 223.	3.2	52
13	Genetic and molecular characterization of a locus involved in avirulence of <i>Blumeria graminis</i> f. sp. <i>tritici</i> on wheat <i>Pm3</i> resistance alleles. <i>Fungal Genetics and Biology</i> , 2015, 82, 181-192.	2.1	50
14	Transition bias influences the evolution of antibiotic resistance in <i>Mycobacterium tuberculosis</i> . <i>PLoS Biology</i> , 2019, 17, e3000265.	5.6	50
15	An African origin for <i>Mycobacterium bovis</i> . <i>Evolution, Medicine and Public Health</i> , 2020, 2020, 49-59.	2.5	42
16	Reconstructing the Evolutionary History of Powdery Mildew Lineages ( <i>Blumeria graminis</i> ) at Different Evolutionary Time Scales with NGS Data. <i>Genome Biology and Evolution</i> , 2017, 9, 446-456.	2.5	34
17	Non-parent of Origin Expression of Numerous Effector Genes Indicates a Role of Gene Regulation in Host Adaptation of the Hybrid Triticale Powdery Mildew Pathogen. <i>Frontiers in Plant Science</i> , 2018, 9, 49.	3.6	33
18	Distinct domains of the <i>AVRPM3<sup>A2/F2</sup></i> avirulence protein from wheat powdery mildew are involved in immune receptor recognition and putative effector function. <i>New Phytologist</i> , 2018, 218, 681-695.	7.3	31

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19	Multiple Introductions of Mycobacterium tuberculosis Lineage 2â€œBeijing Into Africa Over Centuries. <i>Frontiers in Ecology and Evolution</i> , 2019, 7, .	2.2	29
20	Local adaptation in populations of Mycobacterium tuberculosis endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021, 10, 60.	1.6	21
21	Local adaptation in populations of Mycobacterium tuberculosis endemic to the Indian Ocean Rim. <i>F1000Research</i> , 2021, 10, 60.	1.6	13
22	Multiple Merger Genealogies in Outbreaks of <i>Mycobacterium tuberculosis</i> . <i>Molecular Biology and Evolution</i> , 2021, 38, 290-306.	8.9	11
23	Potential contribution of HIV during first-line tuberculosis treatment to subsequent rifampicin-monoresistant tuberculosis and acquired tuberculosis drug resistance in South Africa: a retrospective molecular epidemiology study. <i>Lancet Microbe</i> , The, 2021, 2, e584-e593.	7.3	9
24	Understanding drivers of phylogenetic clustering and terminal branch lengths distribution in epidemics of Mycobacterium tuberculosis. <i>ELife</i> , 0, 11, .	6.0	7
25	The making of a genomic parasite - the Mothra family sheds light on the evolution of Helitrons in plants. <i>Mobile DNA</i> , 2015, 6, 23.	3.6	4