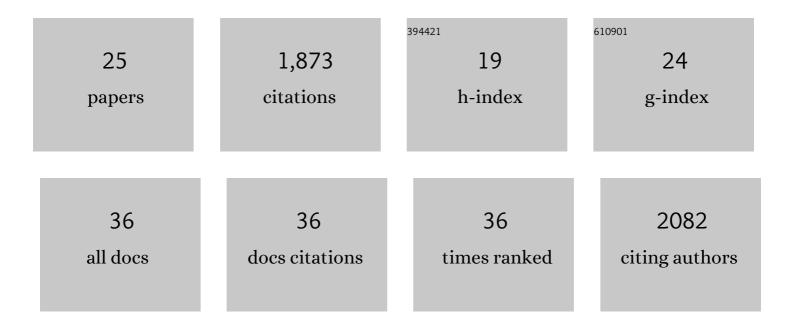
## Fabrizio Menardo

List of Publications by Year in descending order

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FARRIZIO MENARDO

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

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#	Article	IF	CITATIONS
19	Multiple Introductions of Mycobacterium tuberculosis Lineage 2–Beijing Into Africa Over Centuries. Frontiers in Ecology and Evolution, 2019, 7, .	2.2	29
20	Local adaptation in populations of Mycobacterium tuberculosis endemic to the Indian Ocean Rim. F1000Research, 2021, 10, 60.	1.6	21
21	Local adaptation in populations of Mycobacterium tuberculosis endemic to the Indian Ocean Rim. F1000Research, 2021, 10, 60.	1.6	13
22	Multiple Merger Genealogies in Outbreaks of <i>Mycobacterium tuberculosis</i> . Molecular Biology and Evolution, 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. Lancet Microbe, The, 2021, 2, e584-e593.	7.3	9
24	Understanding drivers of phylogenetic clustering and terminal branch lengths distribution in epidemics of Mycobacterium tuberculosis. ELife, 0, 11, .	6.0	7
25	The making of a genomic parasite - the Mothra family sheds light on the evolution of Helitrons in plants. Mobile DNA, 2015, 6, 23.	3.6	4