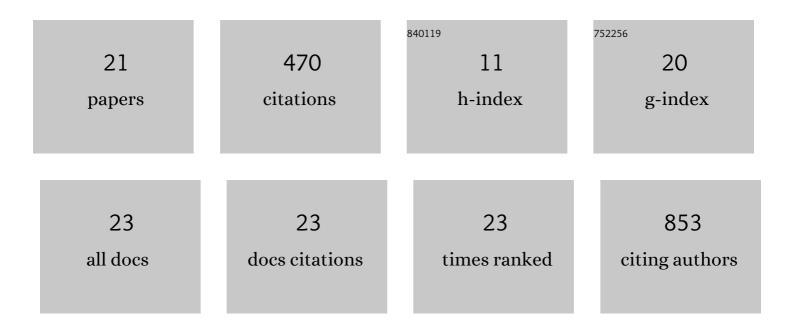
Mariano Avino

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5648271/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	OpenProt 2021: deeper functional annotation of the coding potential of eukaryotic genomes. Nucleic Acids Research, 2021, 49, D380-D388.	6.5	71
2	Hemeprotein Tpx1 interacts with cellâ€surface heme transporter Str3 in <i>Schizosaccharomyces pombe</i> . Molecular Microbiology, 2021, 115, 699-722.	1.2	3
3	High-level resistance to bictegravir and cabotegravir in subtype A- and D-infected HIV-1 patients failing raltegravir with multiple resistance mutations. Journal of Antimicrobial Chemotherapy, 2021, 76, 2965-2974.	1.3	13
4	Janus Kinase Mutations in Mice Lacking PU.1 and Spi-B Drive B Cell Leukemia through Reactive Oxygen Species-Induced DNA Damage. Molecular and Cellular Biology, 2020, 40, .	1.1	8
5	A targeted reactivation of latent HIV-1 using an activator vector in patient samples from acute infection. EBioMedicine, 2020, 59, 102853.	2.7	12
6	Accumulation of integrase strand transfer inhibitor resistance mutations confers high-level resistance to dolutegravir in non-B subtype HIV-1 strains from patients failing raltegravir in Uganda. Journal of Antimicrobial Chemotherapy, 2020, 75, 3525-3533.	1.3	12
7	Human Hepatocyte Nuclear Factor 4-α Encodes Isoforms with Distinct Transcriptional Functions. Molecular and Cellular Proteomics, 2020, 19, 808-827.	2.5	31
8	Genetic diversity in a collection of Italian long storage tomato landraces as revealed by SNP markers array. Plant Biosystems, 2019, 153, 288-297.	0.8	17
9	Tree shapeâ€based approaches for the comparative study of cophylogeny. Ecology and Evolution, 2019, 9, 6756-6771.	0.8	14
10	Evidence for a recombinant origin of HIV-1 Group M from genomic variation. Virus Evolution, 2019, 5, vey039.	2.2	13
11	First-line HIV treatment failures in non-B subtypes and recombinants: a cross-sectional analysis of multiple populations in Uganda. AIDS Research and Therapy, 2019, 16, 3.	0.7	8
12	Detecting Amino Acid Coevolution with Bayesian Graphical Models. Methods in Molecular Biology, 2019, 1851, 105-122.	0.4	5
13	Absence of HIV-1 Drug Resistance Mutations Supports the Use of Dolutegravir in Uganda. AIDS Research and Human Retroviruses, 2018, 34, 404-414.	0.5	23
14	An open-source k-mer based machine learning tool for fast and accurate subtyping of HIV-1 genomes. PLoS ONE, 2018, 13, e0206409.	1.1	70
15	Sanger and next generation sequencing in the characterisation of arbuscular mycorrhizal fungi (AMF) in Pancratium maritimum L. (Amaryllidaceae), a representative plant species of Mediterranean sand dunes. Planta, 2018, 248, 1443-1453.	1.6	4
16	Beta-Binomial Model for the Detection of Rare Mutations in Pooled Next-Generation Sequencing Experiments. Journal of Computational Biology, 2017, 24, 357-367.	0.8	7
17	Understanding the basis of a novel fruit type in Brassicaceae: conservation and deviation in expression patterns of six genes. EvoDevo, 2012, 3, 20.	1.3	34
18	Historical biogeography of the coffee family (Rubiaceae, Gentianales) in Madagascar: case studies from the tribes Knoxieae, Naucleeae, Paederieae and Vanguerieae. Journal of Biogeography, 2010, 37, 1094-1113.	1.4	35

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#	Article	IF	CITATIONS
19	Chitin Synthases from Saprolegnia Are Involved in Tip Growth and Represent a Potential Target for Anti-Oomycete Drugs. PLoS Pathogens, 2010, 6, e1001070.	2.1	61
20	A phylogenetic analysis of Dipsacaceae based on four DNA regions. Plant Systematics and Evolution, 2009, 279, 69-86.	0.3	26
21	Isolation and characterization of nuclear microsatellite loci from <i>Ceratopetalum apetalum</i> (Cunoniaceae). Molecular Ecology Resources, 2009, 9, 566-568.	2.2	1