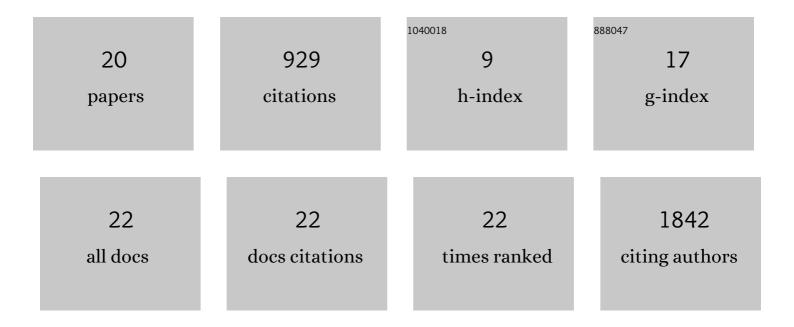
Jacques Dainat

List of Publications by Year in descending order

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ΙΛΟΟΙΙΕς ΠΛΙΝΙΑΤ

#	Article	IF	CITATIONS
1	TEsorter: An accurate and fast method to classify LTR-retrotransposons in plant genomes. Horticulture Research, 2022, 9, .	6.3	70
2	Methods to Identify and Study the Evolution of Pseudogenes Using a Phylogenetic Approach. Methods in Molecular Biology, 2021, 2324, 21-34.	0.9	1
3	Genome assemblies of three closely related leaf beetle species (<i>Galerucella</i> spp.). G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	2
4	Genome assembly of the basket willow, Salix viminalis, reveals earliest stages of sex chromosome expansion. BMC Biology, 2020, 18, 78.	3.8	39
5	Assembly and Analysis of the Genome Sequence of the Yeast Brettanomyces naardenensis CBS 7540. Microorganisms, 2019, 7, 489.	3.6	8
6	Pervasive hybridizations in the history of wheat relatives. Science Advances, 2019, 5, eaav9188.	10.3	79
7	Chromosomal genome assembly of the ethanol production strain CBS 11270 indicates a highly dynamic genome structure in the yeast species Brettanomyces bruxellensis. PLoS ONE, 2019, 14, e0215077.	2.5	8
8	The genomic footprint of sexual conflict. Nature Ecology and Evolution, 2019, 3, 1725-1730.	7.8	57
9	GUESSmyLT: Software to guess the RNA-Seq library type of paired and single end read files. Journal of Open Source Software, 2019, 4, 1344.	4.6	0
10	EMBLmyGFF3: a converter facilitating genome annotation submission to European Nucleotide Archive. BMC Research Notes, 2018, 11, 584.	1.4	19
11	Complete Genome Sequences of the Xylose-Fermenting Candida intermedia Strains CBS 141442 and PYCC 4715. Genome Announcements, 2017, 5, .	0.8	8
12	Global analysis of biosynthetic gene clusters reveals vast potential of secondary metabolite production in Penicillium species. Nature Microbiology, 2017, 2, 17044.	13.3	198
13	The genetic basis for ecological adaptation of the Atlantic herring revealed by genome sequencing. ELife, 2016, 5, .	6.0	143
14	The Bee Microbiome: Impact on Bee Health and Model for Evolution and Ecology of Host-Microbe Interactions. MBio, 2016, 7, e02164-15.	4.1	215
15	A universal genomic coordinate translator for comparative genomics. BMC Bioinformatics, 2014, 15, 227.	2.6	7
16	Impact of recurrent gene duplication on adaptation of plant genomes. BMC Plant Biology, 2014, 14, 151.	3.6	32
17	Methods to Study the Occurrence and the Evolution of Pseudogenes Through a Phylogenetic Approach. Methods in Molecular Biology, 2014, 1167, 87-99.	0.9	0
18	The Chordate Proteome History Database. Evolutionary Bioinformatics, 2012, 8, EBO.S9186.	1.2	5

#	Article	IF	CITATIONS
19	GLADX: An Automated Approach to Analyze the Lineage-Specific Loss and Pseudogenization of Genes. PLoS ONE, 2012, 7, e38792.	2.5	9
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²⁰ Integration of Evolutionary Biology Concepts for Functional Annotation and Automation of Complex Research in Evolution: The Multi-Agent Software System DAGOBAH. , 2011, , 71-87.

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