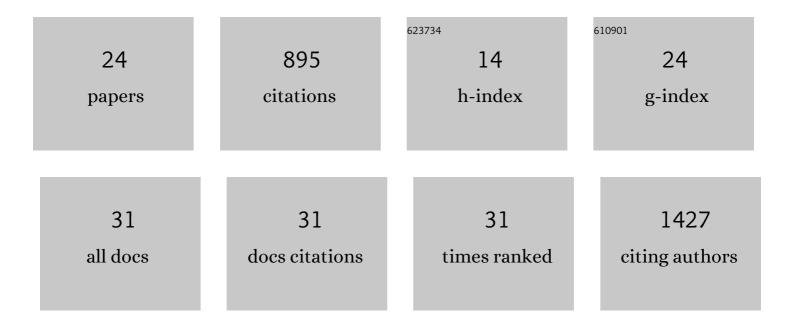
Laurent Guéguen

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10812944/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Bio++: Efficient Extensible Libraries and Tools for Computational Molecular Evolution. Molecular Biology and Evolution, 2013, 30, 1745-1750.	8.9	163
2	Genomic Species Are Ecological Species as Revealed by Comparative Genomics in Agrobacterium tumefaciens. Genome Biology and Evolution, 2011, 3, 762-781.	2.5	110
3	MareyMap: an R-based tool with graphical interface for estimating recombination rates. Bioinformatics, 2007, 23, 2188-2189.	4.1	101
4	Less effective selection leads to larger genomes. Genome Research, 2017, 27, 1016-1028.	5.5	75
5	Accurate Detection of Convergent Amino-Acid Evolution with PCOC. Molecular Biology and Evolution, 2018, 35, 2296-2306.	8.9	50
6	Unbiased Estimate of Synonymous and Nonsynonymous Substitution Rates with Nonstationary Base Composition. Molecular Biology and Evolution, 2018, 35, 734-742.	8.9	43
7	Efficient Gene Tree Correction Guided by Genome Evolution. PLoS ONE, 2016, 11, e0159559.	2.5	42
8	Breaking Good: Accounting for Fragility of Genomic Regions in Rearrangement Distance Estimation. Genome Biology and Evolution, 2016, 8, 1427-1439.	2.5	39
9	GC-biased gene conversion conceals the prediction of the nearly neutral theory in avian genomes. Genome Biology, 2019, 20, 5.	8.8	37
10	Ancestral Genome Estimation Reveals the History of Ecological Diversification in Agrobacterium. Genome Biology and Evolution, 2017, 9, 3413-3431.	2.5	31
11	Life History Traits Impact the Nuclear Rate of Substitution but Not the Mitochondrial Rate in Isopods. Molecular Biology and Evolution, 2018, 35, 2900-2912.	8.9	28
12	MareyMap Online: A User-Friendly Web Application and Database Service for Estimating Recombination Rates Using Physical and Genetic Maps. Genome Biology and Evolution, 2017, 9, 2506-2509.	2.5	23
13	Treerecs: an integrated phylogenetic tool, from sequences to reconciliations. Bioinformatics, 2020, 36, 4822-4824.	4.1	20
14	DGINN, an automated and highly-flexible pipeline for the detection of genetic innovations on protein-coding genes. Nucleic Acids Research, 2020, 48, e103-e103.	14.5	19
15	Sarment: Python modules for HMM analysis and partitioning of sequences. Bioinformatics, 2005, 21, 3427-3428.	4.1	17
16	Accurate Estimation of Substitution Rates with Neighbor-Dependent Models in a Phylogenetic Context. Systematic Biology, 2012, 61, 510-521.	5.6	17
17	UV-Targeted Dinucleotides Are Not Depleted in Light-Exposed Prokaryotic Genomes. Molecular Biology and Evolution, 2006, 23, 2214-2219.	8.9	15
18	Detecting adaptive convergent amino acid evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20180234.	4.0	15

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#	Article	IF	CITATIONS
19	SENCA: A Multilayered Codon Model to Study the Origins and Dynamics of Codon Usage. Genome Biology and Evolution, 2016, 8, 2427-2441.	2.5	14
20	Moments of genome evolution by Double Cut-and-Join. BMC Bioinformatics, 2015, 16, S7.	2.6	12
21	A Codon Model for Associating Phenotypic Traits with Altered Selective Patterns of Sequence Evolution. Systematic Biology, 2021, 70, 608-622.	5.6	5
22	Extreme mitochondrial DNA divergence underlies genetic conflict over sex determination. Current Biology, 2022, 32, 2325-2333.e6.	3.9	4
23	Probabilistic modeling of the evolution of gene synteny within reconciled phylogenies. BMC Bioinformatics, 2015, 16, S5.	2.6	3
24	A MARKOVIAN APPROACH FOR THE ANALYSIS OF THE GENE STRUCTURE. International Journal of Foundations of Computer Science, 2008, 19, 19-35.	1.1	1