

# Laurent GuÃ©guen

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/10812944/publications.pdf>

Version: 2024-02-01

24  
papers

895  
citations

623734

14  
h-index

610901

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g-index

31  
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31  
docs citations

31  
times ranked

1427  
citing authors

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

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