

# Jonathan Romiguier

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3605877/publications.pdf>

Version: 2024-02-01

22  
papers

2,306  
citations

567281

15  
h-index

752698

20  
g-index

29  
all docs

29  
docs citations

29  
times ranked

2687  
citing authors

#	ARTICLE	IF	CITATIONS
1	MitoFinder: Efficient automated large-scale extraction of mitogenomic data in target enrichment phylogenomics. <i>Molecular Ecology Resources</i> , 2020, 20, 892-905.	4.8	785
2	Shedding Light on the Grey Zone of Speciation along a Continuum of Genomic Divergence. <i>PLoS Biology</i> , 2016, 14, e2000234.	5.6	381
3	Contrasting GC-content dynamics across 33 mammalian genomes: Relationship with life-history traits and chromosome sizes. <i>Genome Research</i> , 2010, 20, 1001-1009.	5.5	195
4	Less Is More in Mammalian Phylogenomics: AT-Rich Genes Minimize Tree Conflicts and Unravel the Root of Placental Mammals. <i>Molecular Biology and Evolution</i> , 2013, 30, 2134-2144.	8.9	158
5	Extensive recent secondary contacts between four European white oak species. <i>New Phytologist</i> , 2017, 214, 865-878.	7.3	113
6	Codon Usage Bias in Animals: Disentangling the Effects of Natural Selection, Effective Population Size, and GC-Biased Gene Conversion. <i>Molecular Biology and Evolution</i> , 2018, 35, 1092-1103.	8.9	111
7	Phylogenomics Controlling for Base Compositional Bias Reveals a Single Origin of Eusociality in Corbiculate Bees. <i>Molecular Biology and Evolution</i> , 2016, 33, 670-678.	8.9	80
8	OrthoMaM v8: A Database of Orthologous Exons and Coding Sequences for Comparative Genomics in Mammals. <i>Molecular Biology and Evolution</i> , 2014, 31, 1923-1928.	8.9	77
9	Biased Gene Conversion and GC-Content Evolution in the Coding Sequences of Reptiles and Vertebrates. <i>Genome Biology and Evolution</i> , 2015, 7, 240-250.	2.5	67
10	Efficient Selection of Branch-Specific Models of Sequence Evolution. <i>Molecular Biology and Evolution</i> , 2012, 29, 1861-1874.	8.9	56
11	Analytical Biases Associated with GC-Content in Molecular Evolution. <i>Frontiers in Genetics</i> , 2017, 8, 16.	2.3	50
12	Fast and Robust Characterization of Time-Heterogeneous Sequence Evolutionary Processes Using Substitution Mapping. <i>PLoS ONE</i> , 2012, 7, e33852.	2.5	47
13	DILS: Demographic inferences with linked selection by using ABC. <i>Molecular Ecology Resources</i> , 2021, 21, 2629-2644.	4.8	32
14	Convergent evolution of social hybridogenesis in <i>Messor</i> harvester ants. <i>Molecular Ecology</i> , 2017, 26, 1108-1117.	3.9	27
15	The divergence history of European blue mussel species reconstructed from Approximate Bayesian Computation: the effects of sequencing techniques and sampling strategies. <i>PeerJ</i> , 2018, 6, e5198.	2.0	26
16	Ant phylogenomics reveals a natural selection hotspot preceding the origin of complex eusociality. <i>Current Biology</i> , 2022, 32, 2942-2947.e4.	3.9	20
17	Gene expression is more strongly influenced by age than caste in the ant <i>Lasius niger</i> . <i>Molecular Ecology</i> , 2017, 26, 5058-5073.	3.9	18
18	Phylogenomics of palearctic <i>Formica</i> species suggests a single origin of temporary parasitism and gives insights to the evolutionary pathway toward slave-making behaviour. <i>BMC Evolutionary Biology</i> , 2018, 18, 40.	3.2	15

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19	Molecular evolutionary rates are not correlated with temperature and latitude in Squamata: an exception to the metabolic theory of ecology?. <i>BMC Evolutionary Biology</i> , 2016, 16, 95.	3.2	12
20	Vulnerability to Fishing and Life History Traits Correlate with the Load of Deleterious Mutations in Teleosts. <i>Molecular Biology and Evolution</i> , 2020, 37, 2192-2196.	8.9	12
21	Relaxation of purifying selection suggests low effective population size in eusocial Hymenoptera and solitary pollinating bees. , 0, 1, .		8
22	Hybridization enables the fixation of selfish queen genotypes in eusocial colonies. <i>Evolution Letters</i> , 2021, 5, 582-594.	3.3	4