

Stephane Boissinot

List of Publications by Year in descending order

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66
papers

3,116
citations

236925

25
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175258

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all docs

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docs citations

75
times ranked

3688
citing authors

#	ARTICLE	IF	CITATIONS
1	Habitat determines convergent evolution of cephalic horns in vipers. <i>Biological Journal of the Linnean Society</i> , 2022, 135, 652-664.	1.6	2
2	Varied diversification patterns and distinct demographic trajectories in Ethiopian montane forest bird (Aves: Passeriformes) populations separated by the Great Rift Valley. <i>Molecular Ecology</i> , 2022, 31, 2664-2678.	3.9	3
3	On the Base Composition of Transposable Elements. <i>International Journal of Molecular Sciences</i> , 2022, 23, 4755.	4.1	11
4	Linked-Read Sequencing of Eight Falcons Reveals a Unique Genomic Architecture in Flux. <i>Genome Biology and Evolution</i> , 2022, 14, .	2.5	3
5	Taxonomic revision of grass frogs (Ptychadenidae, Ptychadena) endemic to the Ethiopian highlands. <i>ZooKeys</i> , 2021, 1016, 77-141.	1.1	8
6	The Structural, Functional and Evolutionary Impact of Transposable Elements in Eukaryotes. <i>Genes</i> , 2021, 12, 918.	2.4	31
7	Mitogenomics of historical type specimens clarifies the taxonomy of Ethiopian Boulenger, 1917 (Anura, Tj ETQq1 1 0.784314 rgBT /Qv 1.1	1.1	5
8	Disentangling the determinants of transposable elements dynamics in vertebrate genomes using empirical evidences and simulations. <i>PLoS Genetics</i> , 2020, 16, e1009082.	3.5	15
9	Genome-wide SNPs clarify lineage diversity confused by coloration in coral snakes of the <i>Micrurus diastema</i> species complex (Serpentes: Elapidae). <i>Molecular Phylogenetics and Evolution</i> , 2020, 147, 106770.	2.7	20
10	Variation in base composition underlies functional and evolutionary divergence in non-LTR retrotransposons. <i>Mobile DNA</i> , 2020, 11, 14.	3.6	4
11	Title is missing!. , 2020, 16, e1009082.		0
12	Title is missing!. , 2020, 16, e1009082.		0
13	Title is missing!. , 2020, 16, e1009082.		0
14	Title is missing!. , 2020, 16, e1009082.		0
15	On the Population Dynamics of Junk: A Review on the Population Genomics of Transposable Elements. <i>Genes</i> , 2019, 10, 419.	2.4	94
16	Selection at behavioural, developmental and metabolic genes is associated with the northward expansion of a successful tropical colonizer. <i>Molecular Ecology</i> , 2019, 28, 3523-3543.	3.9	7
17	Recent Secondary Contacts, Linked Selection, and Variable Recombination Rates Shape Genomic Diversity in the Model Species <i>Anolis carolinensis</i> . <i>Genome Biology and Evolution</i> , 2019, 11, 2009-2022.	2.5	29
18	The Mobilome of Reptiles: Evolution, Structure, and Function. <i>Cytogenetic and Genome Research</i> , 2019, 157, 21-33.	1.1	14

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19	Biodiversity genomics of North American <i>Dryobates woodpeckers</i> reveals little gene flow across the <i>D. nuttallii</i> x <i>D. scalaris</i> contact zone. <i>Auk</i> , 2019, 136, .	1.4	2
20	The 2019 FASEB Science Research Conference on The Mobile DNA Conference: 25 Years of Discussion and Research, June 23â€“28, Palm Springs, California, USA. <i>FASEB Journal</i> , 2019, 33, 11625-11628.	0.5	1
21	Falcon genomics in the context of conservation, speciation, and human culture. <i>Ecology and Evolution</i> , 2019, 9, 14523-14537.	1.9	14
22	A new species of puddle frog from an unexplored mountain in southwestern Ethiopia (Anura,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622	1.1	5
23	Diversification of African tree frogs (genus <i>Leptopelis</i>) in the highlands of Ethiopia. <i>Molecular Ecology</i> , 2018, 27, 2256-2270.	3.9	14
24	Differential Effect of Selection against LINE Retrotransposons among Vertebrates Inferred from Whole-Genome Data and Demographic Modeling. <i>Genome Biology and Evolution</i> , 2018, 10, 1265-1281.	2.5	19
25	Contrasted patterns of evolution of the LINE-1 retrotransposon in perissodactyls: the history of a LINE-1 extinction. <i>Mobile DNA</i> , 2018, 9, 12.	3.6	10
26	Multiple and Independent Phases of Transposable Element Amplification in the Genomes of Piciformes (Woodpeckers and Allies). <i>Genome Biology and Evolution</i> , 2018, 10, 1445-1456.	2.5	34
27	Contrasting Rates of LINE-1 Amplification among New World Primates of the Atelidae Family. <i>Cytogenetic and Genome Research</i> , 2018, 154, 217-228.	1.1	5
28	Contrasted patterns of divergence and gene flow among five fish species in a Mongolian rift lake following glaciation. <i>Biological Journal of the Linnean Society</i> , 2018, 125, 115-125.	1.6	12
29	Revisiting the phylogeography, demography and taxonomy of the frog genus <i>Ptychadena</i> in the Ethiopian highlands with the use of genome-wide SNP data. <i>PLoS ONE</i> , 2018, 13, e0190440.	2.5	19
30	Diversification in a biodiversity hotspot: genomic variation in the river frog <i>Amietia nutti</i> across the Ethiopian Highlands. <i>Biological Journal of the Linnean Society</i> , 2017, 122, 801-813.	1.6	10
31	LINE Insertion Polymorphisms are Abundant but at Low Frequencies across Populations of <i>Anolis carolinensis</i> . <i>Frontiers in Genetics</i> , 2017, 8, 44.	2.3	23
32	Chloride intracellular channel proteins respond to heat stress in <i>Caenorhabditis elegans</i> . <i>PLoS ONE</i> , 2017, 12, e0184308.	2.5	12
33	Comparative Phylogeography of Ethiopian anurans: impact of the Great Rift Valley and Pleistocene climate change. <i>BMC Evolutionary Biology</i> , 2016, 16, 206.	3.2	30
34	Functional evolution of the OAS1 viral sensor: Insights from old world primates. <i>Infection, Genetics and Evolution</i> , 2016, 44, 341-350.	2.3	7
35	Diversification in wild populations of the model organism <i>Anolis carolinensis</i> : A genome-wide phylogeographic investigation. <i>Ecology and Evolution</i> , 2016, 6, 8115-8125.	1.9	17
36	The Evolution of Line-1 in Vertebrates. <i>Genome Biology and Evolution</i> , 2016, 8, eww247.	2.5	54

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37	Contrasted patterns of variation and evolutionary convergence at the antiviral OAS1 gene in old world primates. <i>Immunogenetics</i> , 2015, 67, 487-499.	2.4	11
38	Neutral nuclear variation in <i>Baboons</i> (genus <i>Papio</i>) provides insights into their evolutionary and demographic histories. <i>American Journal of Physical Anthropology</i> , 2014, 155, 621-634.	2.1	20
39	Genetic variation in the green anole lizard (<i>Anolis carolinensis</i>) reveals island refugia and a fragmented Florida during the quaternary. <i>Genetica</i> , 2014, 142, 59-72.	1.1	32
40	Hiding in the highlands: Evolution of a frog species complex of the genus <i>Ptychadena</i> in the Ethiopian highlands. <i>Molecular Phylogenetics and Evolution</i> , 2014, 71, 157-169.	2.7	34
41	Revisiting the evolution of mouse LINE-1 in the genomic era. <i>Mobile DNA</i> , 2013, 4, 3.	3.6	149
42	Lizards and LINEs: Selection and Demography Affect the Fate of L1 Retrotransposons in the Genome of the Green Anole (<i>Anolis carolinensis</i>). <i>Genome Biology and Evolution</i> , 2013, 5, 1754-1768.	2.5	29
43	Long-Term Balancing Selection at the Antiviral Gene OAS1 in Central African Chimpanzees. <i>Molecular Biology and Evolution</i> , 2012, 29, 1093-1103.	8.9	22
44	Accumulation and Rapid Decay of Non-LTR Retrotransposons in the Genome of the Three-Spine Stickleback. <i>Genome Biology and Evolution</i> , 2012, 4, 687-702.	2.5	48
45	Multi-Locus Phylogeographic and Population Genetic Analysis of <i>Anolis carolinensis</i> : Historical Demography of a Genomic Model Species. <i>PLoS ONE</i> , 2012, 7, e38474.	2.5	40
46	The genome of the green anole lizard and a comparative analysis with birds and mammals. <i>Nature</i> , 2011, 477, 587-591.	27.8	575
47	The Evolution and Diversity of DNA Transposons in the Genome of the Lizard <i>Anolis carolinensis</i> . <i>Genome Biology and Evolution</i> , 2011, 3, 1-14.	2.5	39
48	Developing a community-based genetic nomenclature for anole lizards. <i>BMC Genomics</i> , 2011, 12, 554.	2.8	23
49	The transposable element profile of the <i>Anolis</i> genome. <i>Mobile Genetic Elements</i> , 2011, 1, 107-111.	1.8	27
50	Efficient and exact maximum likelihood quantisation of genomic features using dynamic programming. <i>International Journal of Data Mining and Bioinformatics</i> , 2010, 4, 123.	0.1	3
51	Independent and parallel lateral transfer of DNA transposons in tetrapod genomes. <i>Gene</i> , 2010, 449, 85-94.	2.2	57
52	The Evolutionary Dynamics of Autonomous Non-LTR Retrotransposons in the Lizard <i>Anolis carolinensis</i> Shows More Similarity to Fish Than Mammals. <i>Molecular Biology and Evolution</i> , 2009, 26, 1811-1822.	8.9	58
53	Long-Term Balancing Selection at the West Nile Virus Resistance Gene, <i>Oas1b</i> , Maintains Transspecific Polymorphisms in the House Mouse. <i>Molecular Biology and Evolution</i> , 2008, 25, 1609-1618.	8.9	30
54	Selection against LINE-1 retrotransposons results principally from their ability to mediate ectopic recombination. <i>Gene</i> , 2007, 390, 206-213.	2.2	71

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55	Molecular evolution and tempo of amplification of human LINE-1 retrotransposons since the origin of primates. <i>Genome Research</i> , 2006, 16, 78-87.	5.5	304
56	The Genomic Distribution of L1 Elements: The Role of Insertion Bias and Natural Selection. <i>Journal of Biomedicine and Biotechnology</i> , 2006, 2006, 1-5.	3.0	49
57	Fitness cost of LINE-1 (L1) activity in humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 9590-9594.	7.1	124
58	The Insertional History of an Active Family of L1 Retrotransposons in Humans. <i>Genome Research</i> , 2004, 14, 1221-1231.	5.5	100
59	L1 (LINE-1) retrotransposon diversity differs dramatically between mammals and fish. <i>Trends in Genetics</i> , 2004, 20, 9-14.	6.7	137
60	Different Rates of LINE-1 (L1) Retrotransposon Amplification and Evolution in New World Monkeys. <i>Journal of Molecular Evolution</i> , 2004, 58, 122-130.	1.8	38
61	Adaptive Evolution in LINE-1 Retrotransposons. <i>Molecular Biology and Evolution</i> , 2001, 18, 2186-2194.	8.9	100
62	L1 (LINE-1) Retrotransposon Evolution and Amplification in Recent Human History. <i>Molecular Biology and Evolution</i> , 2000, 17, 915-928.	8.9	285
63	Molecular Genetics of Spectral Tuning in New World Monkey Color Vision. <i>Journal of Molecular Evolution</i> , 1998, 46, 697-702.	1.8	64
64	Hybrid Origin and Clonal Diversity in the Parthenogenetic Gecko, <i>Lepidodactylus lugubris</i> in French Polynesia. <i>Journal of Herpetology</i> , 1997, 31, 295.	0.5	9
65	Discordant Phylogeographic Patterns Between the <i>Y</i> Chromosome and Mitochondrial DNA in the House Mouse: Selection on the <i>Y</i> Chromosome?. <i>Genetics</i> , 1997, 146, 1019-1034.	2.9	91
66	Allozyme Evidence for Specific Status of the Two French Polynesian Skink Species in the Genus <i>Emoia</i> (Reptilia: Lacertilia). <i>Copeia</i> , 1994, 1994, 1042.	1.3	7