

Frédéric Boyer

List of Publications by Year in descending order

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Version: 2024-02-01

56
papers

6,313
citations

186265

28
h-index

161849

54
g-index

62
all docs

62
docs citations

62
times ranked

8700
citing authors

#	ARTICLE	IF	CITATIONS
1	ORTHOSKIM: In silico sequence capture from genomic and transcriptomic libraries for phylogenomic and barcoding applications. <i>Molecular Ecology Resources</i> , 2022, 22, 2018-2037.	4.8	7
2	Tempo and drivers of plant diversification in the European mountain system. <i>Nature Communications</i> , 2022, 13, 2750.	12.8	15
3	Comparison of markers for the monitoring of freshwater benthic biodiversity through DNA metabarcoding. <i>Molecular Ecology</i> , 2021, 30, 3189-3202.	3.9	35
4	Morphological vs. DNA metabarcoding approaches for the evaluation of stream ecological status with benthic invertebrates: Testing different combinations of markers and strategies of data filtering. <i>Molecular Ecology</i> , 2021, 30, 3203-3220.	3.9	27
5	Double-digest RAD-sequencing: do pre- and post-sequencing protocol parameters impact biological results?. <i>Molecular Genetics and Genomics</i> , 2021, 296, 457-471.	2.1	13
6	metabaR: An <code>scpr</code> package for the evaluation and improvement of DNA metabarcoding data quality. <i>Methods in Ecology and Evolution</i> , 2021, 12, 586-592.	5.2	32
7	Altitudinal Zonation of Green Algae Biodiversity in the French Alps. <i>Frontiers in Plant Science</i> , 2021, 12, 679428.	3.6	22
8	Environmental DNA for biomonitoring. <i>Molecular Ecology</i> , 2021, 30, 2931-2936.	3.9	38
9	Genome-Wide Detection of Structural Variations Reveals New Regions Associated with Domestication in Small Ruminants. <i>Genome Biology and Evolution</i> , 2021, 13, .	2.5	7
10	Genetic Variations and Differential DNA Methylation to Face Contrasted Climates in Small Ruminants: An Analysis on Traditionally-Managed Sheep and Goats. <i>Frontiers in Genetics</i> , 2021, 12, 745284.	2.3	4
11	Genomic Uniqueness of Local Sheep Breeds From Morocco. <i>Frontiers in Genetics</i> , 2021, 12, 723599.	2.3	2
12	From environmental DNA sequences to ecological conclusions: How strong is the influence of methodological choices?. <i>Journal of Biogeography</i> , 2020, 47, 193-206.	3.0	76
13	Ecological specialization and niche overlap of subterranean rodents inferred from DNA metabarcoding diet analysis. <i>Molecular Ecology</i> , 2020, 29, 3143-3153.	3.9	18
14	Adult survival in migratory caribou is negatively associated with MHC functional diversity. <i>Heredity</i> , 2020, 125, 290-303.	2.6	5
15	Diverging landscape impacts on macronutrient status despite overlapping diets in managed (<i>Apis</i>) Tj ETQq1 1 0.784314 rgBT /Ove		
16	Old origin of a protective endogenous retrovirus (enJSRV) in the <i>Ovis</i> genus. <i>Heredity</i> , 2019, 122, 187-194.	2.6	10
17	An evaluation of sequencing coverage and genotyping strategies to assess neutral and adaptive diversity. <i>Molecular Ecology Resources</i> , 2019, 19, 1497-1515.	4.8	31
18	A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions. <i>Science Advances</i> , 2019, 5, eaav8391.	10.3	218

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19	DNA metabarcoding: Need for robust experimental designs to draw sound ecological conclusions. <i>Molecular Ecology</i> , 2019, 28, 1857-1862.	3.9	300
20	Environmental and biotic drivers of soil microbial diversity across spatial and phylogenetic scales. <i>Ecography</i> , 2019, 42, 2144-2156.	4.5	21
21	Brazilian montane rainforest expansion induced by Heinrich Stadial 1 event. <i>Scientific Reports</i> , 2019, 9, 17912.	3.3	13
22	Body size determines soil community assembly in a tropical forest. <i>Molecular Ecology</i> , 2019, 28, 528-543.	3.9	129
23	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018, 9, 813.	12.8	220
24	Phylogenomic Analysis of the Explosive Adaptive Radiation of the Espeletia Complex (Asteraceae) in the Tropical Andes. <i>Systematic Biology</i> , 2018, 67, 1041-1060.	5.6	118
25	Diet shifts by adult flightless dung beetles <i>Circellium bacchus</i> , revealed using DNA metabarcoding, reflect complex life histories. <i>Oecologia</i> , 2018, 188, 107-115.	2.0	19
26	Microrefugia, Climate Change, and Conservation of <i>Cedrus atlantica</i> in the Rif Mountains, Morocco. <i>Frontiers in Ecology and Evolution</i> , 2017, 5, .	2.2	45
27	In the hunt for genomic markers of metabolic resistance to pyrethroids in the mosquito <i>Aedes aegypti</i> : An integrated next-generation sequencing approach. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005526.	3.0	73
28	Next-generation monitoring of aquatic biodiversity using environmental DNA metabarcoding. <i>Molecular Ecology</i> , 2016, 25, 929-942.	3.9	873
29	Understanding the evolution of holoparasitic plants: the complete plastid genome of the holoparasite <i>Cytinus hypocistis</i> (Cytinaceae). <i>Annals of Botany</i> , 2016, 118, 885-896.	2.9	55
30	obitools: a unix-inspired software package for DNA metabarcoding. <i>Molecular Ecology Resources</i> , 2016, 16, 176-182.	4.8	765
31	Testing the potential of a ribosomal 16S marker for DNA metabarcoding of insects. <i>PeerJ</i> , 2016, 4, e1966.	2.0	111
32	Whole mitochondrial genomes unveil the impact of domestication on goat matrilineal variability. <i>BMC Genomics</i> , 2015, 16, 1115.	2.8	56
33	Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats (<i>Capra hircus</i>) using WGS data. <i>Frontiers in Genetics</i> , 2015, 6, 107.	2.3	108
34	The Type VI Secretion TssEFGK-VgrG Phage-Like Baseplate Is Recruited to the TssJLM Membrane Complex via Multiple Contacts and Serves As Assembly Platform for Tail Tube/Sheath Polymerization. <i>PLoS Genetics</i> , 2015, 11, e1005545.	3.5	148
35	Upscaling the niche variation hypothesis from the intra- to the inter-specific level. <i>Oecologia</i> , 2015, 179, 835-842.	2.0	35
36	Reconstructing long-term human impacts on plant communities: an ecological approach based on lake sediment DNA. <i>Molecular Ecology</i> , 2015, 24, 1485-1498.	3.9	109

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37	DNA metabarcoding diet analysis for species with parapatric vs sympatric distribution: a case study on subterranean rodents. <i>Heredity</i> , 2015, 114, 525-536.	2.6	60
38	Identifying genomic changes associated with insecticide resistance in the dengue mosquito <i>Aedes aegypti</i> by deep targeted sequencing. <i>Genome Research</i> , 2015, 25, 1347-1359.	5.5	151
39	Replication levels, false presences and the estimation of the presence/absence from eDNA metabarcoding data. <i>Molecular Ecology Resources</i> , 2015, 15, 543-556.	4.8	517
40	DNA metabarcoding multiplexing and validation of data accuracy for diet assessment: application to omnivorous diet. <i>Molecular Ecology Resources</i> , 2014, 14, 306-323.	4.8	431
41	Effect of DNA extraction and sample preservation method on rumen bacterial population. <i>Anaerobe</i> , 2014, 29, 80-84.	2.1	81
42	An ABC transporter and an outer membrane lipoprotein participate in posttranslational activation of type VI secretion in <i>Pseudomonas aeruginosa</i> . <i>Environmental Microbiology</i> , 2013, 15, 471-486.	3.8	84
43	Microprocessor, Setx, Xrn2, and Rrp6 Co-operate to Induce Premature Termination of Transcription by RNAPII. <i>Cell</i> , 2012, 150, 1147-1157.	28.9	156
44	Bacterial synteny: an exact approach with gene quorum. <i>BMC Bioinformatics</i> , 2011, 12, 193.	2.6	9
45	Burkholderia Type VI Secretion Systems Have Distinct Roles in Eukaryotic and Bacterial Cell Interactions. <i>PLoS Pathogens</i> , 2010, 6, e1001068.	4.7	328
46	Dissecting the bacterial type VI secretion system by a genome wide in silico analysis: what can be learned from available microbial genomic resources?. <i>BMC Genomics</i> , 2009, 10, 104.	2.8	502
47	Multiple Alignment of Biological Networks: A Flexible Approach. <i>Lecture Notes in Computer Science</i> , 2009, , 263-273.	1.3	10
48	Lossless filter for multiple repetitions with Hamming distance. <i>Journal of Discrete Algorithms</i> , 2008, 6, 497-509.	0.7	12
49	Differential strain-specific diagnosis of the heartwater agent: <i>Ehrlichia ruminantium</i> . <i>Infection, Genetics and Evolution</i> , 2008, 8, 459-466.	2.3	5
50	Emergence and Potential of High-Throughput and Integrative Approaches in Pathology. <i>Annals of the New York Academy of Sciences</i> , 2008, 1149, 62-65.	3.8	0
51	Repseek, a tool to retrieve approximate repeats from large DNA sequences. <i>Bioinformatics</i> , 2007, 23, 119-121.	4.1	69
52	<i>Ehrlichia ruminantium</i> : genomic and evolutionary features. <i>Trends in Parasitology</i> , 2007, 23, 414-419.	3.3	28
53	Comparative Genomics of Three Strains of <i>Ehrlichia ruminantium</i> . <i>Annals of the New York Academy of Sciences</i> , 2006, 1081, 417-433.	3.8	19
54	Syntons, metabolons and interactons: an exact graph-theoretical approach for exploring neighbourhood between genomic and functional data. <i>Bioinformatics</i> , 2005, 21, 4209-4215.	4.1	44

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55	Ab initio reconstruction of metabolic pathways. <i>Bioinformatics</i> , 2003, 19, ii26-ii34.	4.1	23
56	Priority conservation areas for <i>Cedrus atlantica</i> in the Atlas Mountains, Morocco. <i>Conservation Science and Practice</i> , 0, , .	2.0	3