

Eric Coissac

List of Publications by Year in descending order

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Version: 2024-02-01

120
papers

17,085
citations

20817

60
h-index

27406

106
g-index

130
all docs

130
docs citations

130
times ranked

15888
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary origins and species delineation of the two Pyrenean endemics <i>Campanula jaubertiana</i> and <i>C. andorrana</i> (Campanulaceae): evidence for transverse alpine speciation. <i>Alpine Botany</i> , 2022, 132, 51-64.	2.4	4
2	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
3	Interspecific coprophagia by wild red foxes: DNA metabarcoding reveals a potentially widespread form of commensalism among animals. <i>Ecology and Evolution</i> , 2022, 12, .	1.9	6
4	How do forest management and wolf space-use affect diet composition of the wolf's main prey, the red deer versus a non-prey species, the European bison?. <i>Forest Ecology and Management</i> , 2021, 479, 118620.	3.2	8
5	Small shrubs with large importance? Smaller deer may increase the moose-forestry conflict through feeding competition over <i>Vaccinium</i> shrubs in the field layer. <i>Forest Ecology and Management</i> , 2021, 480, 118768.	3.2	13
6	Connecting high-throughput biodiversity inventories: Opportunities for a site-based genomic framework for global integration and synthesis. <i>Molecular Ecology</i> , 2021, 30, 1120-1135.	3.9	26
7	Biodiversity monitoring using environmental DNA. <i>Molecular Ecology Resources</i> , 2021, 21, 1405-1409.	4.8	15
8	Altitudinal Zonation of Green Algae Biodiversity in the French Alps. <i>Frontiers in Plant Science</i> , 2021, 12, 679428.	3.6	22
9	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. <i>Nature</i> , 2021, 600, 86-92.	27.8	81
10	Latent Dirichlet Allocation reveals spatial and taxonomic structure in a DNA-based census of soil biodiversity from a tropical forest. <i>Molecular Ecology Resources</i> , 2020, 20, 371-386.	4.8	16
11	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
12	Chloroplast genome assembly of <i>Handroanthus impetiginosus</i> : comparative analysis and molecular evolution in Bignoniaceae. <i>Planta</i> , 2020, 252, 91.	3.2	24
13	The Treasure Vault Can be Opened: Large-Scale Genome Skimming Works Well Using Herbarium and Silica Gel Dried Material. <i>Plants</i> , 2020, 9, 432.	3.5	59
14	Foraging plasticity allows a large herbivore to persist in a sheltering forest habitat: DNA metabarcoding diet analysis of the European bison. <i>Forest Ecology and Management</i> , 2019, 449, 117474.	3.2	39
15	DNA metabarcoding: Need for robust experimental designs to draw sound ecological conclusions. <i>Molecular Ecology</i> , 2019, 28, 1857-1862.	3.9	300
16	Environmental and biotic drivers of soil microbial α -diversity across spatial and phylogenetic scales. <i>Ecography</i> , 2019, 42, 2144-2156.	4.5	21
17	Brazilian montane rainforest expansion induced by Heinrich Stadial 1 event. <i>Scientific Reports</i> , 2019, 9, 17912.	3.3	13
18	Body size determines soil community assembly in a tropical forest. <i>Molecular Ecology</i> , 2019, 28, 528-543.	3.9	129

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19	Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018, 9, 813.	12.8	220
20	Comparing three types of dietary samples for prey <scp>DNA</scp> decay in an insect generalist predator. <i>Molecular Ecology Resources</i> , 2018, 18, 966-973.	4.8	31
21	Ancient environmental DNA reveals shifts in dominant mutualisms during the late Quaternary. <i>Nature Communications</i> , 2018, 9, 139.	12.8	24
22	Metabarcoding of modern soil DNA gives a highly local vegetation signal in Svalbard tundra. <i>Holocene</i> , 2018, 28, 2006-2016.	1.7	52
23	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
24	Mapping the imprint of biotic interactions on β -diversity. <i>Ecology Letters</i> , 2018, 21, 1660-1669.	6.4	40
25	DNA amplification and multiplexing. , 2018, , .		5
26	Environmental DNA for functional diversity. , 2018, , .		4
27	DNA metabarcode choice and design. , 2018, , 7-20.		2
28	Analysis of bulk samples. , 2018, , .		1
29	Host-associated microbiota. , 2018, , .		0
30	Terrestrial ecosystems. , 2018, , .		0
31	Diet analysis. , 2018, , 131-139.		1
32	The future of eDNA metabarcoding. , 2018, , .		0
33	DNA metabarcoding data analysis. , 2018, , .		0
34	Reference databases. , 2018, , 21-27.		1
35	Freshwater ecosystems. , 2018, , .		0
36	Marine environments. , 2018, , .		0

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37	Some early landmark studies. , 2018, , .		0
38	Single-species detection. , 2018, , .		0
39	Mitochondrial Phylogenomics Resolves the Global Spread of Higher Termites, Ecosystem Engineers of the Tropics. <i>Molecular Biology and Evolution</i> , 2017, 34, msw253.	8.9	89
40	Evaluating the impact of domestication and captivity on the horse gut microbiome. <i>Scientific Reports</i> , 2017, 7, 15497.	3.3	112
41	The evolutionary fate of the chloroplast and nuclear <i>rps16</i> genes as revealed through the sequencing and comparative analyses of four novel legume chloroplast genomes from <i>Lupinus</i> . <i>DNA Research</i> , 2017, 24, 343-358.	3.4	96
42	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
43	Shotgun assembly of the complete mitochondrial genome of the neotropical cracker butterfly <i>Hamadryas epinome</i> . <i>Mitochondrial DNA</i> , 2016, 27, 1-3.	0.6	8
44	Next-generation monitoring of aquatic biodiversity using environmental DNA metabarcoding. <i>Molecular Ecology</i> , 2016, 25, 929-942.	3.9	873
45	From barcodes to genomes: extending the concept of DNA barcoding. <i>Molecular Ecology</i> , 2016, 25, 1423-1428.	3.9	322
46	How to limit false positives in environmental DNA and metabarcoding?. <i>Molecular Ecology Resources</i> , 2016, 16, 604-607.	4.8	166
47	Inferring neutral biodiversity parameters using environmental DNA data sets. <i>Scientific Reports</i> , 2016, 6, 35644.	3.3	13
48	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
49	Unraveling the biogeographical history of Chrysobalanaceae from plastid genomes. <i>American Journal of Botany</i> , 2016, 103, 1089-1102.	1.7	20
50	Complete mitochondrial genome of <i>Lutzomyia</i> (<i>Nyssomyia</i>) <i>umbratilis</i> (Diptera: Tj ETQq0 0 0 rgBT /Overlock 10 Tf Mapping, Sequencing, and Analysis, 2016, 27, 4219-4221.	0.7	12
51	Sedimentary ancient DNA from Lake Skartjvna, Svalbard: Assessing the resilience of arctic flora to Holocene climate change. <i>Holocene</i> , 2016, 26, 627-642.	1.7	97
52	Extracellular DNA extraction is a fast, cheap and reliable alternative for multi-taxa surveys based on soil DNA. <i>Soil Biology and Biochemistry</i> , 2016, 96, 16-19.	8.8	71
53	obitools: a unix-inspired software package for DNA metabarcoding. <i>Molecular Ecology Resources</i> , 2016, 16, 176-182.	4.8	765
54	PCR-free shotgun sequencing of the stone loach mitochondrial genome (<i>Barbatula barbatula</i>). <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 4211-4212.	0.7	6

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55	Testing the potential of a ribosomal 16S marker for DNA metabarcoding of insects. PeerJ, 2016, 4, e1966.	2.0	111
56	Spatio-temporal monitoring of deep-sea communities using metabarcoding of sediment DNA and RNA. PeerJ, 2016, 4, e2807.	2.0	103
57	Whole mitochondrial genomes unveil the impact of domestication on goat matrilineal variability. BMC Genomics, 2015, 16, 1115.	2.8	56
58	Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats (<i>Capra hircus</i>) using WGS data. Frontiers in Genetics, 2015, 6, 107.	2.3	108
59	Upscaling the niche variation hypothesis from the intra- to the inter-specific level. Oecologia, 2015, 179, 835-842.	2.0	35
60	DNA metabarcoding diet analysis for species with parapatric vs sympatric distribution: a case study on subterranean rodents. Heredity, 2015, 114, 525-536.	2.6	60
61	Replication levels, false presences and the estimation of the presence/absence from <scp>eDNA</scp> metabarcoding data. Molecular Ecology Resources, 2015, 15, 543-556.	4.8	517
62	Forest without prey: livestock sustain a leopard <i>Panthera pardus</i> population in Pakistan. Oryx, 2015, 49, 248-253.	1.0	53
63	Deep-Sea, Deep-Sequencing: Metabarcoding Extracellular DNA from Sediments of Marine Canyons. PLoS ONE, 2015, 10, e0139633.	2.5	163
64	From museums to genomics: old herbarium specimens shed light on a C3 to C4 transition. Journal of Experimental Botany, 2014, 65, 6711-6721.	4.8	109
65	Genome skimming by shotgun sequencing helps resolve the phylogeny of a pantropical tree family. Molecular Ecology Resources, 2014, 14, 966-975.	4.8	102
66	Effects of organochlorines on microbial diversity and community structure in <i>Phragmites australis</i> rhizosphere. Applied Microbiology and Biotechnology, 2014, 98, 4257-4266.	3.6	17
67	Long livestock farming history and human landscape shaping revealed by lake sediment DNA. Nature Communications, 2014, 5, 3211.	12.8	297
68	Fifty thousand years of Arctic vegetation and megafaunal diet. Nature, 2014, 506, 47-51.	27.8	505
69	Shotgun assembly of the assassin bug <i>Brontostoma colossus</i> mitochondrial genome (Heteroptera.) Tj ETQq1 1 0.784314 rgBT /Overl	2.2	41
70	DNA metabarcoding multiplexing and validation of data accuracy for diet assessment: application to omnivorous diet. Molecular Ecology Resources, 2014, 14, 306-323.	4.8	431
71	DNA metabarcoding and the cytochrome <i>c</i> oxidase subunit I marker: not a perfect match. Biology Letters, 2014, 10, 20140562.	2.3	445
72	Effect of DNA extraction and sample preservation method on rumen bacterial population. Anaerobe, 2014, 29, 80-84.	2.1	81

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73	Plant functional traits reveal the relative contribution of habitat and food preferences to the diet of grasshoppers. <i>Oecologia</i> , 2013, 173, 1459-1470.	2.0	69
74	Fungal palaeodiversity revealed using high-throughput metabarcoding of ancient <scp>DNA</scp> from arctic permafrost. <i>Environmental Microbiology</i> , 2013, 15, 1176-1189.	3.8	115
75	Phylogenomics and taxonomy of <i>Lecomtelleae</i> (Poaceae), an isolated panicoid lineage from Madagascar. <i>Annals of Botany</i> , 2013, 112, 1057-1066.	2.9	51
76	Investigating the genetics of Bti resistance using mRNA tag sequencing: application on laboratory strains and natural populations of the dengue vector <i>Aedes aegypti</i> . <i>Evolutionary Applications</i> , 2013, 6, 1012-1027.	3.1	9
77	UniPathway: a resource for the exploration and annotation of metabolic pathways. <i>Nucleic Acids Research</i> , 2012, 40, D761-D769.	14.5	83
78	Transcription profiling of resistance to Bti toxins in the mosquito <i>Aedes aegypti</i> using next-generation sequencing. <i>Journal of Invertebrate Pathology</i> , 2012, 109, 201-208.	3.2	27
79	Glacial Survival of Boreal Trees in Northern Scandinavia. <i>Science</i> , 2012, 335, 1083-1086.	12.6	287
80	Assessment of the Food Habits of the Moroccan Dorcas Gazelle in Mâ€™Sabih Talaa, West Central Morocco, Using the trnL Approach. <i>PLoS ONE</i> , 2012, 7, e35643.	2.5	56
81	OligoTag: A Program for Designing Sets of Tags for Next-Generation Sequencing of Multiplexed Samples. <i>Methods in Molecular Biology</i> , 2012, 888, 13-31.	0.9	90
82	Two Methods to Easily Obtain Nucleotide Sequences from AFLP Loci of Interest. <i>Methods in Molecular Biology</i> , 2012, 888, 91-108.	0.9	6
83	Prey Preference of Snow Leopard (<i>Panthera uncia</i>) in South Gobi, Mongolia. <i>PLoS ONE</i> , 2012, 7, e32104.	2.5	110
84	Islands in the ice: detecting past vegetation on Greenlandic nunataks using historical records and sedimentary ancient DNA Metaâ€barcoding. <i>Molecular Ecology</i> , 2012, 21, 1980-1988.	3.9	67
85	A comparative study of ancient sedimentary DNA, pollen and microfossils from permafrost sediments of northern Siberia reveals longâ€term vegetational stability. <i>Molecular Ecology</i> , 2012, 21, 1989-2003.	3.9	144
86	Blocking human contaminant DNA during PCR allows amplification of rare mammal species from sedimentary ancient DNA. <i>Molecular Ecology</i> , 2012, 21, 1806-1815.	3.9	120
87	Soil sampling and isolation of extracellular DNA from large amount of starting material suitable for metabarcoding studies. <i>Molecular Ecology</i> , 2012, 21, 1816-1820.	3.9	264
88	Tracking earthworm communities from soil DNA. <i>Molecular Ecology</i> , 2012, 21, 2017-2030.	3.9	109
89	Carnivore diet analysis based on nextâ€generation sequencing: application to the leopard cat (<i>Prionailurus bengalensis</i>) in Pakistan. <i>Molecular Ecology</i> , 2012, 21, 1951-1965.	3.9	244
90	Towards nextâ€generation biodiversity assessment using DNA metabarcoding. <i>Molecular Ecology</i> , 2012, 21, 2045-2050.	3.9	1,253

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91	New environmental metabarcodes for analysing soil DNA: potential for studying past and present ecosystems. <i>Molecular Ecology</i> , 2012, 21, 1821-1833.	3.9	259
92	Environmental DNA. <i>Molecular Ecology</i> , 2012, 21, 1789-1793.	3.9	926
93	DNA from soil mirrors plant taxonomic and growth form diversity. <i>Molecular Ecology</i> , 2012, 21, 3647-3655.	3.9	262
94	Bioinformatic challenges for DNA metabarcoding of plants and animals. <i>Molecular Ecology</i> , 2012, 21, 1834-1847.	3.9	243
95	ecoPrimers: inference of new DNA barcode markers from whole genome sequence analysis. <i>Nucleic Acids Research</i> , 2011, 39, e145-e145.	14.5	416
96	Conservation genetics of cattle, sheep, and goats. <i>Comptes Rendus - Biologies</i> , 2011, 334, 247-254.	0.2	137
97	Influence of management practices on large herbivore diet – Case of European bison in BiaÅ,owieÅ¼a Primeval Forest (Poland). <i>Forest Ecology and Management</i> , 2011, 261, 821-828.	3.2	154
98	New insights on diet variability revealed by DNA barcoding and high-throughput pyrosequencing: chamois diet in autumn as a case study. <i>Ecological Research</i> , 2011, 26, 265-276.	1.5	64
99	Assessment of soil fungal diversity in different alpine tundra habitats by means of pyrosequencing. <i>Fungal Diversity</i> , 2011, 49, 113-123.	12.3	63
100	ITS as an environmental DNA barcode for fungi: an in silico approach reveals potential PCR biases. <i>BMC Microbiology</i> , 2010, 10, 189.	3.3	792
101	Transcriptome response to pollutants and insecticides in the dengue vector <i>Aedes aegypti</i> using next-generation sequencing technology. <i>BMC Genomics</i> , 2010, 11, 216.	2.8	111
102	An In silico approach for the evaluation of DNA barcodes. <i>BMC Genomics</i> , 2010, 11, 434.	2.8	370
103	Using next-generation sequencing for molecular reconstruction of past Arctic vegetation and climate. <i>Molecular Ecology Resources</i> , 2010, 10, 1009-1018.	4.8	196
104	Assessment of Microbial Communities by Graph Partitioning in a Study of Soil Fungi in Two Alpine Meadows. <i>Applied and Environmental Microbiology</i> , 2009, 75, 5863-5870.	3.1	21
105	Analysing diet of small herbivores: the efficiency of DNA barcoding coupled with high-throughput pyrosequencing for deciphering the composition of complex plant mixtures. <i>Frontiers in Zoology</i> , 2009, 6, 16.	2.0	233
106	Universal DNA-Based Methods for Assessing the Diet of Grazing Livestock and Wildlife from Feces. <i>Journal of Agricultural and Food Chemistry</i> , 2009, 57, 5700-5706.	5.2	80
107	New perspectives in diet analysis based on DNA barcoding and parallel pyrosequencing: the <i>in silico</i> approach. <i>Molecular Ecology Resources</i> , 2009, 9, 51-60.	4.8	358
108	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

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109	Repseek, a tool to retrieve approximate repeats from large DNA sequences. <i>Bioinformatics</i> , 2007, 23, 119-121.	4.1	69
110	Power and limitations of the chloroplast trnL (UAA) intron for plant DNA barcoding. <i>Nucleic Acids Research</i> , 2007, 35, e14-e14.	14.5	842
111	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
112	Comparative Genomic Analysis of Three Strains of <i>Ehrlichia ruminantium</i> Reveals an Active Process of Genome Size Plasticity. <i>Journal of Bacteriology</i> , 2006, 188, 2533-2542.	2.2	86
113	Conservation of the Prion Properties of Ure2p through Evolution. <i>Molecular Biology of the Cell</i> , 2003, 14, 3449-3458.	2.1	55
114	Associations Between Inverted Repeats and the Structural Evolution of Bacterial Genomes. <i>Genetics</i> , 2003, 164, 1279-1289.	2.9	70
115	Study of Intrachromosomal Duplications Among the Eukaryote Genomes. <i>Molecular Biology and Evolution</i> , 2001, 18, 2280-2288.	8.9	50
116	Analysis of Intrachromosomal Duplications in Yeast <i>Saccharomyces cerevisiae</i> : A Possible Model for Their Origin. <i>Molecular Biology and Evolution</i> , 2000, 17, 1268-1275.	8.9	69
117	Unsuspected prophage-like elements in <i>Salmonella typhimurium</i> . <i>Molecular Microbiology</i> , 1997, 25, 161-173.	2.5	82
118	Sequence of a 39 411 bp DNA fragment covering the left end of chromosome VII of <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 1996, 12, 1555-1562.	1.7	5
119	DNAqua-Net: Developing new genetic tools for bioassessment and monitoring of aquatic ecosystems in Europe. <i>Research Ideas and Outcomes</i> , 0, 2, e11321.	1.0	154
120	Priority conservation areas for <i>Cedrus atlantica</i> in the Atlas Mountains, Morocco. <i>Conservation Science and Practice</i> , 0, , .	2.0	3