Eric Coissac

List of Publications by Year
in descending order

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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	Towards nextâ€generation biodiversity assessment using DNA metabarcoding. Molecular Ecology, 2012, 21, 2045-2050.	3.9	1,253
2	Environmental DNA. Molecular Ecology, 2012, 21, 1789-1793.	3.9	926
3	Nextâ€generation monitoring of aquatic biodiversity using environmental <scp>DNA</scp> metabarcoding. Molecular Ecology, 2016, 25, 929-942.	3.9	873
4	Power and limitations of the chloroplast trnL (UAA) intron for plant DNA barcoding. Nucleic Acids Research, 2007, 35, e14-e14.	14.5	842
5	ITS as an environmental DNA barcode for fungi: an in silico approach reveals potential PCR biases. BMC Microbiology, 2010, 10, 189.	3.3	792
6	<scp>obitools</scp>: a <scp>unix</scp>â€inspired software package for <scp>DNA</scp> metabarcoding. Molecular Ecology Resources, 2016, 16, 176-182.	4.8	765
7	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
8	Fifty thousand years of Arctic vegetation and megafaunal diet. Nature, 2014, 506, 47-51.	27.8	505
9	DNA metabarcoding and the cytochrome c oxidase subunit I marker: not a perfect match. Biology Letters, 2014, 10, 20140562.	2.3	445
10	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
11	ecoPrimers: inference of new DNA barcode markers from whole genome sequence analysis. Nucleic Acids Research, 2011, 39, e145-e145.	14.5	416
12	An In silico approach for the evaluation of DNA barcodes. BMC Genomics, 2010, 11, 434.	2.8	370
13	New perspectives in diet analysis based on DNA barcoding and parallel pyrosequencing: the trnL approach. Molecular Ecology Resources, 2009, 9, 51-60.	4.8	358
14	From barcodes to genomes: extending the concept of DNA barcoding. Molecular Ecology, 2016, 25, 1423-1428.	3.9	322
15	DNA metabarcodingâ€"Need for robust experimental designs to draw sound ecological conclusions. Molecular Ecology, 2019, 28, 1857-1862.	3.9	300
16	Long livestock farming history and human landscape shaping revealed by lake sediment DNA. Nature Communications, 2014, 5, 3211.	12.8	297
17	Glacial Survival of Boreal Trees in Northern Scandinavia. Science, 2012, 335, 1083-1086.	12.6	287
18	Soil sampling and isolation of extracellular DNA from large amount of starting material suitable for metabarcoding studies. Molecular Ecology, 2012, 21, 1816-1820.	3.9	264

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19	DNA from soil mirrors plant taxonomic and growth form diversity. Molecular Ecology, 2012, 21, 3647-3655.	3.9	262
20	New environmental metabarcodes for analysing soil DNA: potential for studying past and present ecosystems. Molecular Ecology, 2012, 21, 1821-1833.	3.9	259
21	Carnivore diet analysis based on nextâ€generation sequencing: application to the leopard cat (Prionailurus bengalensis) in Pakistan. Molecular Ecology, 2012, 21, 1951-1965.	3.9	244
22	Bioinformatic challenges for DNA metabarcoding of plants and animals. Molecular Ecology, 2012, 21, 1834-1847.	3.9	243
23	Analysing diet of small herbivores: the efficiency of DNA barcoding coupled with high-throughput pyrosequencing for deciphering the composition of complex plant mixtures. Frontiers in Zoology, 2009, 6, 16.	2.0	233
24	Convergent genomic signatures of domestication in sheep and goats. Nature Communications, 2018, 9, 813.	12.8	220
25	Using nextâ€generation sequencing for molecular reconstruction of past Arctic vegetation and climate. Molecular Ecology Resources, 2010, 10, 1009-1018.	4.8	196
26	How to limit false positives in environmental <scp>DNA</scp> and metabarcoding?. Molecular Ecology Resources, 2016, 16, 604-607.	4.8	166
27	Deep-Sea, Deep-Sequencing: Metabarcoding Extracellular DNA from Sediments of Marine Canyons. PLoS ONE, 2015, 10, e0139633.	2.5	163
28	Influence of management practices on large herbivore dietâ€"Case of European bison in BiaÅ‚owieÅ¼a Primeval Forest (Poland). Forest Ecology and Management, 2011, 261, 821-828.	3.2	154
29	DNAqua-Net: Developing new genetic tools for bioassessment and monitoring of aquatic ecosystems in Europe. Research Ideas and Outcomes, 0, 2, e11321.	1.0	154
30	A comparative study of ancient sedimentary DNA, pollen and macrofossils from permafrost sediments of northern Siberia reveals longâ€term vegetational stability. Molecular Ecology, 2012, 21, 1989-2003.	3.9	144
31	Conservation genetics of cattle, sheep, and goats. Comptes Rendus - Biologies, 2011, 334, 247-254.	0.2	137
32	Body size determines soil community assembly in a tropical forest. Molecular Ecology, 2019, 28, 528-543.	3.9	129
33	Blocking human contaminant DNA during PCR allows amplification of rare mammal species from sedimentary ancient DNA. Molecular Ecology, 2012, 21, 1806-1815.	3.9	120
34	Fungal palaeodiversity revealed using highâ€throughput metabarcoding of ancient <scp>DNA</scp> from arctic permafrost. Environmental Microbiology, 2013, 15, 1176-1189.	3.8	115
35	Evaluating the impact of domestication and captivity on the horse gut microbiome. Scientific Reports, 2017, 7, 15497.	3.3	112
36	Transcriptome response to pollutants and insecticides in the dengue vector Aedes aegypti using next-generation sequencing technology. BMC Genomics, 2010, 11, 216.	2.8	111

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37	Testing the potential of a ribosomal 16S marker for DNA metabarcoding of insects. PeerJ, 2016, 4, e1966.	2.0	111
38	Prey Preference of Snow Leopard (Panthera uncia) in South Gobi, Mongolia. PLoS ONE, 2012, 7, e32104.	2.5	110
39	Tracking earthworm communities from soil DNA. Molecular Ecology, 2012, 21, 2017-2030.	3.9	109
40	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
41	Characterizing neutral genomic diversity and selection signatures in indigenous populations of Moroccan goats (Capra hircus) using WGS data. Frontiers in Genetics, 2015, 6, 107.	2.3	108
42	Spatio-temporal monitoring of deep-sea communities using metabarcoding of sediment DNA and RNA. PeerJ, 2016, 4, e2807.	2.0	103
43	Genome skimming by shotgun sequencing helps resolve the phylogeny of a pantropical tree family. Molecular Ecology Resources, 2014, 14, 966-975.	4.8	102
44	Sedimentary ancient DNA from Lake SkartjÃ¸rna, Svalbard: Assessing the resilience of arctic flora to Holocene climate change. Holocene, 2016, 26, 627-642.	1.7	97
45	The evolutionary fate of the chloroplast and nuclear rps16 genes as revealed through the sequencing and comparative analyses of four novel legume chloroplast genomes from Lupinus. DNA Research, 2017, 24, 343-358.	3.4	96
46	OligoTag: A Program for Designing Sets of Tags for Next-Generation Sequencing of Multiplexed Samples. Methods in Molecular Biology, 2012, 888, 13-31.	0.9	90
47	Mitochondrial Phylogenomics Resolves the Global Spread of Higher Termites, Ecosystem Engineers of the Tropics. Molecular Biology and Evolution, 2017, 34, msw253.	8.9	89
48	Comparative Genomic Analysis of Three Strains of Ehrlichia ruminantium Reveals an Active Process of Genome Size Plasticity. Journal of Bacteriology, 2006, 188, 2533-2542.	2.2	86
49	UniPathway: a resource for the exploration and annotation of metabolic pathways. Nucleic Acids Research, 2012, 40, D761-D769.	14.5	83
50	Unsuspected prophageâ€like elements in Salmonella typhimurium. Molecular Microbiology, 1997, 25, 161-173.	2.5	82
51	Effect of DNA extraction and sample preservation method on rumen bacterial population. Anaerobe, 2014, 29, 80-84.	2.1	81
52	Late Quaternary dynamics of Arctic biota from ancient environmental genomics. Nature, 2021, 600, 86-92.	27.8	81
53	Universal DNA-Based Methods for Assessing the Diet of Grazing Livestock and Wildlife from Feces. Journal of Agricultural and Food Chemistry, 2009, 57, 5700-5706.	5.2	80
54	Extracellular DNA extraction is a fast, cheap and reliable alternative for multi-taxa surveys based on soil DNA. Soil Biology and Biochemistry, 2016, 96, 16-19.	8.8	71

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55	Associations Between Inverted Repeats and the Structural Evolution of Bacterial Genomes. Genetics, 2003, 164, 1279-1289.	2.9	70
56	Analysis of Intrachromosomal Duplications in Yeast Saccharomyces cerevisiae: A Possible Model for Their Origin. Molecular Biology and Evolution, 2000, 17, 1268-1275.	8.9	69
57	Repseek, a tool to retrieve approximate repeats from large DNA sequences. Bioinformatics, 2007, 23, 119-121.	4.1	69
58	Plant functional traits reveal the relative contribution of habitat and food preferences to the diet of grasshoppers. Oecologia, 2013, 173, 1459-1470.	2.0	69
59	Islands in the ice: detecting past vegetation on Greenlandic nunataks using historical records and sedimentary ancient DNA Metaâ€barcoding. Molecular Ecology, 2012, 21, 1980-1988.	3.9	67
60	New insights on diet variability revealed by DNA barcoding and highâ€throughput pyrosequencing: chamois diet in autumn as a case study. Ecological Research, 2011, 26, 265-276.	1.5	64
61	Assessment of soil fungal diversity in different alpine tundra habitats by means of pyrosequencing. Fungal Diversity, 2011, 49, 113-123.	12.3	63
62	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
63	The Treasure Vault Can be Opened: Large-Scale Genome Skimming Works Well Using Herbarium and Silica Gel Dried Material. Plants, 2020, 9, 432.	3.5	59
64	Assessment of the Food Habits of the Moroccan Dorcas Gazelle in Mâ€™Sabih Talaa, West Central Morocco, Using the trnL Approach. PLoS ONE, 2012, 7, e35643.	2.5	56
65	Whole mitochondrial genomes unveil the impact of domestication on goat matrilineal variability. BMC Genomics, 2015, 16, 1115.	2.8	56
66	Conservation of the Prion Properties of Ure2p through Evolution. Molecular Biology of the Cell, 2003, 14, 3449-3458.	2.1	55
67	Understanding the evolution of holoparasitic plants: the complete plastid genome of the holoparasiteCytinus hypocistis(Cytinaceae). Annals of Botany, 2016, 118, 885-896.	2.9	55
68	Forest without prey: livestock sustain a leopard Panthera pardus population in Pakistan. Oryx, 2015, 49, 248-253.	1.0	53
69	Metabarcoding of modern soil DNA gives a highly local vegetation signal in Svalbard tundra. Holocene, 2018, 28, 2006-2016.	1.7	52
70	Phylogenomics and taxonomy of Lecomtelleae (Poaceae), an isolated panicoid lineage from Madagascar. Annals of Botany, 2013, 112, 1057-1066.	2.9	51
71	Study of Intrachromosomal Duplications Among the Eukaryote Genomes. Molecular Biology and Evolution, 2001, 18, 2280-2288.	8.9	50
72	Microrefugia, Climate Change, and Conservation of Cedrus atlantica in the Rif Mountains, Morocco. Frontiers in Ecology and Evolution, 2017, 5, .	2.2	45

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73	Shotgun assembly of the assassin bug Brontostoma colossus mitochondrial genome (Heteroptera,) Tj ETQq1 1 0.784314 rgBT /Overl	2.2	41
74	Mapping the imprint of biotic interactions on Î²â€diversity. Ecology Letters, 2018, 21, 1660-1669.	6.4	40
75	Foraging plasticity allows a large herbivore to persist in a sheltering forest habitat: DNA metabarcoding diet analysis of the European bison. Forest Ecology and Management, 2019, 449, 117474.	3.2	39
76	Upscaling the niche variation hypothesis from the intra- to the inter-specific level. Oecologia, 2015, 179, 835-842.	2.0	35
77	Comparing three types of dietary samples for prey <scp>DNA</scp> decay in an insect generalist predator. Molecular Ecology Resources, 2018, 18, 966-973.	4.8	31
78	Transcription profiling of resistance to Bti toxins in the mosquito Aedes aegypti using next-generation sequencing. Journal of Invertebrate Pathology, 2012, 109, 201-208.	3.2	27
79	Connecting highâ€throughput biodiversity inventories: Opportunities for a siteâ€based genomic framework for global integration and synthesis. Molecular Ecology, 2021, 30, 1120-1135.	3.9	26
80	Ancient environmental DNA reveals shifts in dominant mutualisms during the lateÂQuaternary. Nature Communications, 2018, 9, 139.	12.8	24
81	Chloroplast genome assembly of Handroanthus impetiginosus: comparative analysis and molecular evolution in Bignoniaceae. Planta, 2020, 252, 91.	3.2	24
82	Altitudinal Zonation of Green Algae Biodiversity in the French Alps. Frontiers in Plant Science, 2021, 12, 679428.	3.6	22
83	Assessment of Microbial Communities by Graph Partitioning in a Study of Soil Fungi in Two Alpine Meadows. Applied and Environmental Microbiology, 2009, 75, 5863-5870.	3.1	21
84	Environmental and biotic drivers of soil microbial Î²â€diversity across spatial and phylogenetic scales. Ecography, 2019, 42, 2144-2156.	4.5	21
85	Unraveling the biogeographical history of Chrysobalanaceae from plastid genomes. American Journal of Botany, 2016, 103, 1089-1102.	1.7	20
86	Comparative Genomics of Three Strains ofEhrlichia ruminantium. Annals of the New York Academy of Sciences, 2006, 1081, 417-433.	3.8	19
87	Diet shifts by adult flightless dung beetles Circellium bacchus, revealed using DNA metabarcoding, reflect complex life histories. Oecologia, 2018, 188, 107-115.	2.0	19
88	Ecological specialization and niche overlap of subterranean rodents inferred from DNA metabarcoding diet analysis. Molecular Ecology, 2020, 29, 3143-3153.	3.9	18
89	Effects of organochlorines on microbial diversity and community structure in Phragmites australis rhizosphere. Applied Microbiology and Biotechnology, 2014, 98, 4257-4266.	3.6	17
90	Latent Dirichlet Allocation reveals spatial and taxonomic structure in a DNAâ€based census of soil biodiversity from a tropical forest. Molecular Ecology Resources, 2020, 20, 371-386.	4.8	16

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91	Biodiversity monitoring using environmental DNA. Molecular Ecology Resources, 2021, 21, 1405-1409.	4.8	15
92	Inferring neutral biodiversity parameters using environmental DNA data sets. Scientific Reports, 2016, 6, 35644.	3.3	13
93	Brazilian montane rainforest expansion induced by Heinrich Stadial 1 event. Scientific Reports, 2019, 9, 17912.	3.3	13
94	Small shrubs with large importance? Smaller deer may increase the moose-forestry conflict through feeding competition over Vaccinium shrubs in the field layer. Forest Ecology and Management, 2021, 480, 118768.	3.2	13
95	Complete mitochondrial genome of Lutzomyia (Nyssomyia) umbratilis (Diptera:) Tj ETQq1 1 0.784314 rgBT /Ove Mapping, Sequencing, and Analysis, 2016, 27, 4219-4221.	0.7	12
96	Investigating the genetics of B ti resistance using m RNA tag sequencing: application on laboratory strains and natural populations of the dengue vector A edes aegypti. Evolutionary Applications, 2013, 6, 1012-1027.	3.1	9
97	Shotgun assembly of the complete mitochondrial genome of the neotropical cracker butterflyHamadryas epinome. Mitochondrial DNA, 2016, 27, 1-3.	0.6	8
98	How do forest management and wolf space-use affect diet composition of the wolfâ€™s main prey, the red deer versus a non-prey species, the European bison?. Forest Ecology and Management, 2021, 479, 118620.	3.2	8
99	ORTHOSKIM: In silico sequence capture from genomic and transcriptomic libraries for phylogenomic and barcoding applications. Molecular Ecology Resources, 2022, 22, 2018-2037.	4.8	7
100	Two Methods to Easily Obtain Nucleotide Sequences from AFLP Loci of Interest. Methods in Molecular Biology, 2012, 888, 91-108.	0.9	6
101	PCR-free shotgun sequencing of the stone loach mitochondrial genome (Barbatula barbatula). Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis, 2016, 27, 4211-4212.	0.7	6
102	Interspecific coprophagia by wild red foxes:<scp>DNA</scp>metabarcoding reveals a potentially widespread form of commensalism among animals. Ecology and Evolution, 2022, 12, .	1.9	6
103	Sequence of a 39 411 bp DNA fragment covering the left end of chromosome VII of Saccharomyces cerevisiae. Yeast, 1996, 12, 1555-1562.	1.7	5
104	Differential strain-specific diagnosis of the heartwater agent: Ehrlichia ruminantium. Infection, Genetics and Evolution, 2008, 8, 459-466.	2.3	5
105	DNA amplification and multiplexing. , 2018, , .		5
106	Evolutionary origins and species delineation of the two Pyrenean endemics Campanula jaubertiana and C. andorrana (Campanulaceae): evidence for transverse alpine speciation. Alpine Botany, 2022, 132, 51-64.	2.4	4
107	Environmental DNA for functional diversity. , 2018, , .		4
108	Priority conservation areas for Cedrus atlantica in the Atlas Mountains, Morocco. Conservation Science and Practice, 0, , .	2.0	3

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109	DNA metabarcode choice and design. , 2018, , 7-20.		2
110	Analysis of bulk samples. , 2018, , .		1
111	Diet analysis. , 2018, , 131-139.		1
112	Reference databases. , 2018, , 21-27.		1
113	Host-associated microbiota. , 2018, , .		0
114	Terrestrial ecosystems. , 2018, , .		0
115	The future of eDNA metabarcoding. , 2018, , .		0
116	DNA metabarcoding data analysis. , 2018, , .		0
117	Freshwater ecosystems. , 2018, , .		0
118	Marine environments. , 2018, , .		0
119	Some early landmark studies. , 2018, , .		0
120	Single-species detection. , 2018, , .		0