

Eric Coissac

List of Publications by Year in descending order

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Version: 2024-02-01

120
papers

17,085
citations

23879

60
h-index

31191

106
g-index

130
all docs

130
docs citations

130
times ranked

17608
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | Towards next-generation biodiversity assessment using DNA metabarcoding. <i>Molecular Ecology</i> , 2012, 21, 2045-2050. | 2.0 | 1,253 |
| 2 | Environmental DNA. <i>Molecular Ecology</i> , 2012, 21, 1789-1793. | 2.0 | 926 |
| 3 | Next-generation monitoring of aquatic biodiversity using environmental DNA metabarcoding. <i>Molecular Ecology</i> , 2016, 25, 929-942. | 2.0 | 873 |
| 4 | Power and limitations of the chloroplast trnL (UAA) intron for plant DNA barcoding. <i>Nucleic Acids Research</i> , 2007, 35, e14-e14. | 6.5 | 842 |
| 5 | ITS as an environmental DNA barcode for fungi: an in silico approach reveals potential PCR biases. <i>BMC Microbiology</i> , 2010, 10, 189. | 1.3 | 792 |
| 6 | obitools: a UNIX-inspired software package for DNA metabarcoding. <i>Molecular Ecology Resources</i> , 2016, 16, 176-182. | 2.2 | 765 |
| 7 | Replication levels, false presences and the estimation of the presence/absence from eDNA metabarcoding data. <i>Molecular Ecology Resources</i> , 2015, 15, 543-556. | 2.2 | 517 |
| 8 | Fifty thousand years of Arctic vegetation and megafaunal diet. <i>Nature</i> , 2014, 506, 47-51. | 13.7 | 505 |
| 9 | DNA metabarcoding and the cytochrome c oxidase subunit I marker: not a perfect match. <i>Biology Letters</i> , 2014, 10, 20140562. | 1.0 | 445 |
| 10 | DNA metabarcoding multiplexing and validation of data accuracy for diet assessment: application to omnivorous diet. <i>Molecular Ecology Resources</i> , 2014, 14, 306-323. | 2.2 | 431 |
| 11 | ecoPrimers: inference of new DNA barcode markers from whole genome sequence analysis. <i>Nucleic Acids Research</i> , 2011, 39, e145-e145. | 6.5 | 416 |
| 12 | An In silico approach for the evaluation of DNA barcodes. <i>BMC Genomics</i> , 2010, 11, 434. | 1.2 | 370 |
| 13 | New perspectives in diet analysis based on DNA barcoding and parallel pyrosequencing: the trnL approach. <i>Molecular Ecology Resources</i> , 2009, 9, 51-60. | 2.2 | 358 |
| 14 | From barcodes to genomes: extending the concept of DNA barcoding. <i>Molecular Ecology</i> , 2016, 25, 1423-1428. | 2.0 | 322 |
| 15 | DNA metabarcoding: Need for robust experimental designs to draw sound ecological conclusions. <i>Molecular Ecology</i> , 2019, 28, 1857-1862. | 2.0 | 300 |
| 16 | Long livestock farming history and human landscape shaping revealed by lake sediment DNA. <i>Nature Communications</i> , 2014, 5, 3211. | 5.8 | 297 |
| 17 | Glacial Survival of Boreal Trees in Northern Scandinavia. <i>Science</i> , 2012, 335, 1083-1086. | 6.0 | 287 |
| 18 | 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. | 2.0 | 264 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 19 | DNA from soil mirrors plant taxonomic and growth form diversity. <i>Molecular Ecology</i> , 2012, 21, 3647-3655. | 2.0 | 262 |
| 20 | New environmental metabarcodes for analysing soil DNA: potential for studying past and present ecosystems. <i>Molecular Ecology</i> , 2012, 21, 1821-1833. | 2.0 | 259 |
| 21 | Carnivore diet analysis based on next-generation sequencing: application to the leopard cat (<i>Prionailurus bengalensis</i>) in Pakistan. <i>Molecular Ecology</i> , 2012, 21, 1951-1965. | 2.0 | 244 |
| 22 | Bioinformatic challenges for DNA metabarcoding of plants and animals. <i>Molecular Ecology</i> , 2012, 21, 1834-1847. | 2.0 | 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. <i>Frontiers in Zoology</i> , 2009, 6, 16. | 0.9 | 233 |
| 24 | Convergent genomic signatures of domestication in sheep and goats. <i>Nature Communications</i> , 2018, 9, 813. | 5.8 | 220 |
| 25 | Using next-generation sequencing for molecular reconstruction of past Arctic vegetation and climate. <i>Molecular Ecology Resources</i> , 2010, 10, 1009-1018. | 2.2 | 196 |
| 26 | How to limit false positives in environmental <i>scp</i> DNA and metabarcoding?. <i>Molecular Ecology Resources</i> , 2016, 16, 604-607. | 2.2 | 166 |
| 27 | Deep-Sea, Deep-Sequencing: Metabarcoding Extracellular DNA from Sediments of Marine Canyons. <i>PLoS ONE</i> , 2015, 10, e0139633. | 1.1 | 163 |
| 28 | 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. | 1.4 | 154 |
| 29 | 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 |
| 30 | A comparative study of ancient sedimentary DNA, pollen and macrofossils from permafrost sediments of northern Siberia reveals long-term vegetational stability. <i>Molecular Ecology</i> , 2012, 21, 1989-2003. | 2.0 | 144 |
| 31 | Conservation genetics of cattle, sheep, and goats. <i>Comptes Rendus - Biologies</i> , 2011, 334, 247-254. | 0.1 | 137 |
| 32 | Body size determines soil community assembly in a tropical forest. <i>Molecular Ecology</i> , 2019, 28, 528-543. | 2.0 | 129 |
| 33 | Blocking human contaminant DNA during PCR allows amplification of rare mammal species from sedimentary ancient DNA. <i>Molecular Ecology</i> , 2012, 21, 1806-1815. | 2.0 | 120 |
| 34 | Fungal palaeodiversity revealed using high-throughput metabarcoding of ancient <i>scp</i> DNA from arctic permafrost. <i>Environmental Microbiology</i> , 2013, 15, 1176-1189. | 1.8 | 115 |
| 35 | Evaluating the impact of domestication and captivity on the horse gut microbiome. <i>Scientific Reports</i> , 2017, 7, 15497. | 1.6 | 112 |
| 36 | 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. | 1.2 | 111 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 37 | Testing the potential of a ribosomal 16S marker for DNA metabarcoding of insects. PeerJ, 2016, 4, e1966. | 0.9 | 111 |
| 38 | Prey Preference of Snow Leopard (<i>Panthera uncia</i>) in South Gobi, Mongolia. PLoS ONE, 2012, 7, e32104. | 1.1 | 110 |
| 39 | Tracking earthworm communities from soil DNA. Molecular Ecology, 2012, 21, 2017-2030. | 2.0 | 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. | 2.4 | 109 |
| 41 | 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. | 1.1 | 108 |
| 42 | Spatio-temporal monitoring of deep-sea communities using metabarcoding of sediment DNA and RNA. PeerJ, 2016, 4, e2807. | 0.9 | 103 |
| 43 | Genome skimming by shotgun sequencing helps resolve the phylogeny of a pantropical tree family. Molecular Ecology Resources, 2014, 14, 966-975. | 2.2 | 102 |
| 44 | Sedimentary ancient DNA from Lake Skartj rna, Svalbard: Assessing the resilience of arctic flora to Holocene climate change. Holocene, 2016, 26, 627-642. | 0.9 | 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 <i>Lupinus</i> . DNA Research, 2017, 24, 343-358. | 1.5 | 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. | 0.4 | 90 |
| 47 | Mitochondrial Phylogenomics Resolves the Global Spread of Higher Termites, Ecosystem Engineers of the Tropics. Molecular Biology and Evolution, 2017, 34, msw253. | 3.5 | 89 |
| 48 | Comparative Genomic Analysis of Three Strains of <i>Ehrlichia ruminantium</i> Reveals an Active Process of Genome Size Plasticity. Journal of Bacteriology, 2006, 188, 2533-2542. | 1.0 | 86 |
| 49 | UniPathway: a resource for the exploration and annotation of metabolic pathways. Nucleic Acids Research, 2012, 40, D761-D769. | 6.5 | 83 |
| 50 | Unsuspected prophage like elements in <i>Salmonella typhimurium</i> . Molecular Microbiology, 1997, 25, 161-173. | 1.2 | 82 |
| 51 | Effect of DNA extraction and sample preservation method on rumen bacterial population. Anaerobe, 2014, 29, 80-84. | 1.0 | 81 |
| 52 | Late Quaternary dynamics of Arctic biota from ancient environmental genomics. Nature, 2021, 600, 86-92. | 13.7 | 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. | 2.4 | 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. | 4.2 | 71 |

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|----|---|-----|-----------|
| 55 | Associations Between Inverted Repeats and the Structural Evolution of Bacterial Genomes. <i>Genetics</i> , 2003, 164, 1279-1289. | 1.2 | 70 |
| 56 | 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. | 3.5 | 69 |
| 57 | Repseek, a tool to retrieve approximate repeats from large DNA sequences. <i>Bioinformatics</i> , 2007, 23, 119-121. | 1.8 | 69 |
| 58 | Plant functional traits reveal the relative contribution of habitat and food preferences to the diet of grasshoppers. <i>Oecologia</i> , 2013, 173, 1459-1470. | 0.9 | 69 |
| 59 | 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. | 2.0 | 67 |
| 60 | New insights on diet variability revealed by DNA barcoding and highâ€throughput pyrosequencing: chamois diet in autumn as a case study. <i>Ecological Research</i> , 2011, 26, 265-276. | 0.7 | 64 |
| 61 | Assessment of soil fungal diversity in different alpine tundra habitats by means of pyrosequencing. <i>Fungal Diversity</i> , 2011, 49, 113-123. | 4.7 | 63 |
| 62 | DNA metabarcoding diet analysis for species with parapatric vs sympatric distribution: a case study on subterranean rodents. <i>Heredity</i> , 2015, 114, 525-536. | 1.2 | 60 |
| 63 | 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. | 1.6 | 59 |
| 64 | 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. | 1.1 | 56 |
| 65 | Whole mitochondrial genomes unveil the impact of domestication on goat matrilineal variability. <i>BMC Genomics</i> , 2015, 16, 1115. | 1.2 | 56 |
| 66 | Conservation of the Prion Properties of Ure2p through Evolution. <i>Molecular Biology of the Cell</i> , 2003, 14, 3449-3458. | 0.9 | 55 |
| 67 | 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. | 1.4 | 55 |
| 68 | Forest without prey: livestock sustain a leopard <i>Panthera pardus</i> population in Pakistan. <i>Oryx</i> , 2015, 49, 248-253. | 0.5 | 53 |
| 69 | Metabarcoding of modern soil DNA gives a highly local vegetation signal in Svalbard tundra. <i>Holocene</i> , 2018, 28, 2006-2016. | 0.9 | 52 |
| 70 | Phylogenomics and taxonomy of Lecomtelleae (Poaceae), an isolated panicoid lineage from Madagascar. <i>Annals of Botany</i> , 2013, 112, 1057-1066. | 1.4 | 51 |
| 71 | Study of Intrachromosomal Duplications Among the Eukaryote Genomes. <i>Molecular Biology and Evolution</i> , 2001, 18, 2280-2288. | 3.5 | 50 |
| 72 | Microrefugia, Climate Change, and Conservation of <i>Cedrus atlantica</i> in the Rif Mountains, Morocco. <i>Frontiers in Ecology and Evolution</i> , 2017, 5, . | 1.1 | 45 |

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|----|--|-----|-----------|
| 73 | Shotgun assembly of the assassin bug <i>Brontostoma colossus</i> mitochondrial genome (Heteroptera, Tj ETQq1 1 0.784314 rgBT ₄₁ /Overl | 1.0 | 41 |
| 74 | Mapping the imprint of biotic interactions on β -diversity. <i>Ecology Letters</i> , 2018, 21, 1660-1669. | 3.0 | 40 |
| 75 | 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. | 1.4 | 39 |
| 76 | Upscaling the niche variation hypothesis from the intra- to the inter-specific level. <i>Oecologia</i> , 2015, 179, 835-842. | 0.9 | 35 |
| 77 | Comparing three types of dietary samples for prey $\langle scp \rangle$ DNA $\langle /scp \rangle$ decay in an insect generalist predator. <i>Molecular Ecology Resources</i> , 2018, 18, 966-973. | 2.2 | 31 |
| 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. | 1.5 | 27 |
| 79 | 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. | 2.0 | 26 |
| 80 | Ancient environmental DNA reveals shifts in dominant mutualisms during the late Quaternary. <i>Nature Communications</i> , 2018, 9, 139. | 5.8 | 24 |
| 81 | Chloroplast genome assembly of <i>Handroanthus impetiginosus</i> : comparative analysis and molecular evolution in Bignoniaceae. <i>Planta</i> , 2020, 252, 91. | 1.6 | 24 |
| 82 | Altitudinal Zonation of Green Algae Biodiversity in the French Alps. <i>Frontiers in Plant Science</i> , 2021, 12, 679428. | 1.7 | 22 |
| 83 | 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. | 1.4 | 21 |
| 84 | Environmental and biotic drivers of soil microbial β -diversity across spatial and phylogenetic scales. <i>Ecography</i> , 2019, 42, 2144-2156. | 2.1 | 21 |
| 85 | Unraveling the biogeographical history of Chrysobalanaceae from plastid genomes. <i>American Journal of Botany</i> , 2016, 103, 1089-1102. | 0.8 | 20 |
| 86 | Comparative Genomics of Three Strains of <i>Ehrlichia ruminantium</i> . <i>Annals of the New York Academy of Sciences</i> , 2006, 1081, 417-433. | 1.8 | 19 |
| 87 | 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. | 0.9 | 19 |
| 88 | Ecological specialization and niche overlap of subterranean rodents inferred from DNA metabarcoding diet analysis. <i>Molecular Ecology</i> , 2020, 29, 3143-3153. | 2.0 | 18 |
| 89 | Effects of organochlorines on microbial diversity and community structure in <i>Phragmites australis</i> rhizosphere. <i>Applied Microbiology and Biotechnology</i> , 2014, 98, 4257-4266. | 1.7 | 17 |
| 90 | 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. | 2.2 | 16 |

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|-----|--|-----|-----------|
| 91 | Biodiversity monitoring using environmental DNA. <i>Molecular Ecology Resources</i> , 2021, 21, 1405-1409. | 2.2 | 15 |
| 92 | Inferring neutral biodiversity parameters using environmental DNA data sets. <i>Scientific Reports</i> , 2016, 6, 35644. | 1.6 | 13 |
| 93 | Brazilian montane rainforest expansion induced by Heinrich Stadial 1 event. <i>Scientific Reports</i> , 2019, 9, 17912. | 1.6 | 13 |
| 94 | 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. | 1.4 | 13 |
| 95 | Complete mitochondrial genome of <i>Lutzomyia</i> (<i>Nyssomyia</i>) <i>umbratilis</i> (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 <i>Aedes aegypti</i> . <i>Evolutionary Applications</i> , 2013, 6, 1012-1027. | 1.5 | 9 |
| 97 | 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 |
| 98 | 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. | 1.4 | 8 |
| 99 | ORTHOSKIM: In silico sequence capture from genomic and transcriptomic libraries for phylogenomic and barcoding applications. <i>Molecular Ecology Resources</i> , 2022, 22, 2018-2037. | 2.2 | 7 |
| 100 | Two Methods to Easily Obtain Nucleotide Sequences from AFLP Loci of Interest. <i>Methods in Molecular Biology</i> , 2012, 888, 91-108. | 0.4 | 6 |
| 101 | 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 |
| 102 | Interspecific coprophagia by wild red foxes: DNA metabarcoding reveals a potentially widespread form of commensalism among animals. <i>Ecology and Evolution</i> , 2022, 12, . | 0.8 | 6 |
| 103 | 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. | 0.8 | 5 |
| 104 | Differential strain-specific diagnosis of the heartwater agent: <i>Ehrlichia ruminantium</i> . <i>Infection, Genetics and Evolution</i> , 2008, 8, 459-466. | 1.0 | 5 |
| 105 | DNA amplification and multiplexing. , 2018, , . | | 5 |
| 106 | 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. | 1.1 | 4 |
| 107 | Environmental DNA for functional diversity. , 2018, , . | | 4 |
| 108 | Priority conservation areas for <i>Cedrus atlantica</i> in the Atlas Mountains, Morocco. <i>Conservation Science and Practice</i> , 0, , . | 0.9 | 3 |

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|-----|--|----|-----------|
| 109 | DNA metabarcoding 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 |