

# Ludovic Orlando

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9065530/publications.pdf>

Version: 2024-02-01

204  
papers

31,872  
citations

5574

82  
h-index

5394

164  
g-index

221  
all docs

221  
docs citations

221  
times ranked

27944  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | A communal catalogue reveals Earth's multiscale microbial diversity. <i>Nature</i> , 2017, 551, 457-463.  | 27.8 | 1,942     |
| 2  | Whole-genome analyses resolve early branches in the tree of life of modern birds. <i>Science</i> , 2014, 346, 1320-1331.  | 12.6 | 1,583     |
| 3  | AdapterRemoval v2: rapid adapter trimming, identification, and read merging. <i>BMC Research Notes</i> , 2016, 9, 88.   | 1.4  | 1,255     |
| 4  | mapDamage2.0: fast approximate Bayesian estimates of ancient DNA damage parameters. <i>Bioinformatics</i> , 2013, 29, 1682-1684.  | 4.1  | 1,174     |
| 5  | Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015, 522, 167-172.  | 27.8 | 1,166     |
| 6  | Comparative genomics reveals insights into avian genome evolution and adaptation. <i>Science</i> , 2014, 346, 1311-1320.  | 12.6 | 895       |
| 7  | Monitoring endangered freshwater biodiversity using environmental DNA. <i>Molecular Ecology</i> , 2012, 21, 2565-2573.  | 3.9  | 882       |
| 8  | Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans. <i>Nature</i> , 2014, 505, 87-91.   | 27.8 | 821       |
| 9  | Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010, 463, 757-762.  | 27.8 | 750       |
| 10 | Recalibrating <i>Equus</i> evolution using the genome sequence of an early Middle Pleistocene horse. <i>Nature</i> , 2013, 499, 74-78.                                  | 27.8 | 717       |
| 11 | An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.   | 12.6 | 675       |
| 12 | Species-specific responses of Late Quaternary megafauna to climate and humans. <i>Nature</i> , 2011, 479, 359-364.  | 27.8 | 586       |
| 13 | Fifty thousand years of Arctic vegetation and megafaunal diet. <i>Nature</i> , 2014, 506, 47-51.  | 27.8 | 505       |
| 14 | The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.  | 27.8 | 500       |
| 15 | The Derived FOXP2 Variant of Modern Humans Was Shared with Neandertals. <i>Current Biology</i> , 2007, 17, 1908-1912.   | 3.9  | 487       |
| 16 | Early Divergent Strains of <i>Yersinia pestis</i> in Eurasia 5,000 Years Ago. <i>Cell</i> , 2015, 163, 571-582.   | 28.9 | 425       |
| 17 | Characterization of ancient and modern genomes by SNP detection and phylogenomic and metagenomic analysis using PALEOMIX. <i>Nature Protocols</i> , 2014, 9, 1056-1082. | 12.0 | 403       |
| 18 | Population Genomics Reveal Recent Speciation and Rapid Evolutionary Adaptation in Polar Bears. <i>Cell</i> , 2014, 157, 785-794.  | 28.9 | 363       |

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|----|--|------|-----------|
| 19 | Postglacial viability and colonization in North America's ice-free corridor. <i>Nature</i> , 2016, 537, 45-49.                               | 27.8 | 363       |
| 20 | 137 ancient human genomes from across the Eurasian steppes. <i>Nature</i> , 2018, 557, 369-374.  | 27.8 | 325       |
| 21 | Terminal Pleistocene Alaskan genome reveals first founding population of Native Americans. <i>Nature</i> , 2018, 553, 203-207.               | 27.8 | 304       |
| 22 | The Effects of Captivity on the Mammalian Gut Microbiome. <i>Integrative and Comparative Biology</i> , 2017, 57, 690-704.                    | 2.0  | 301       |
| 23 | DNA metabarcoding—Need for robust experimental designs to draw sound ecological conclusions. <i>Molecular Ecology</i> , 2019, 28, 1857-1862. | 3.9  | 300       |
| 24 | Investigating the Potential Use of Environmental DNA (eDNA) for Genetic Monitoring of Marine Mammals. <i>PLoS ONE</i> , 2012, 7, e41781.     | 2.5  | 294       |
| 25 | Neanderthals in central Asia and Siberia. <i>Nature</i> , 2007, 449, 902-904.  | 27.8 | 293       |
| 26 | Ancient and modern environmental DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130383.   | 4.0  | 292       |
| 27 | The prehistoric peopling of Southeast Asia. <i>Science</i> , 2018, 361, 88-92.   | 12.6 | 291       |
| 28 | mapDamage: testing for damage patterns in ancient DNA sequences. <i>Bioinformatics</i> , 2011, 27, 2153-2155.                                | 4.1  | 287       |
| 29 | Glacial Survival of Boreal Trees in Northern Scandinavia. <i>Science</i> , 2012, 335, 1083-1086.   | 12.6 | 287       |
| 30 | Genomic structure in Europeans dating back at least 36,200 years. <i>Science</i> , 2014, 346, 1113-1118.                                     | 12.6 | 287       |
| 31 | Meta-barcoding of "dirty" DNA from soil reflects vertebrate biodiversity. <i>Molecular Ecology</i> , 2012, 21, 1966-1979.                    | 3.9  | 276       |
| 32 | Ancient proteins resolve the evolutionary history of Darwin's South American ungulates. <i>Nature</i> , 2015, 522, 81-84.                    | 27.8 | 273       |
| 33 | The genetic prehistory of the New World Arctic. <i>Science</i> , 2014, 345, 1255-1258.   | 12.6 | 264       |
| 34 | Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.              | 12.6 | 263       |
| 35 | DNA from soil mirrors plant taxonomic and growth form diversity. <i>Molecular Ecology</i> , 2012, 21, 3647-3655.                             | 3.9  | 262       |
| 36 | The first horse herders and the impact of early Bronze Age steppe expansions into Asia. <i>Science</i> , 2018, 360, .                        | 12.6 | 262       |

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|----|---|------------------|-----------|
| 37 | Prehistoric genomes reveal the genetic foundation and cost of horse domestication. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5661-9. | 7.1              | 260       |
| 38 | Improving ancient DNA read mapping against modern reference genomes. BMC Genomics, 2012, 13, 178.   | 2.8              | 247       |
| 39 | The ancestry and affiliations of Kennewick Man. Nature, 2015, 523, 455-458.   | 27.8             | 241       |
| 40 | Ancient genomes revisit the ancestry of domestic and Przewalski's horses. Science, 2018, 360, 111-114.  | 12.6             | 241       |
| 41 | Population characteristics of a large whale shark aggregation inferred from seawater environmental DNA. Nature Ecology and Evolution, 2017, 1, 4.                                       | 7.8              | 223       |
| 42 | Convergent genomic signatures of domestication in sheep and goats. Nature Communications, 2018, 9, 813.   | 12.8             | 220       |
| 43 | Ancient DNA analyses exclude humans as the driving force behind late Pleistocene musk ox ( <i>Ovibos</i> ) in the States of America, 2010, 107, 5675-5680.                              | 10.784314<br>7.1 | 208       |
| 44 | Reconstructing ancient genomes and epigenomes. Nature Reviews Genetics, 2015, 16, 395-408.  | 16.3             | 197       |
| 45 | Proteomic Analysis of a Pleistocene Mammoth Femur Reveals More than One Hundred Ancient Bone Proteins. Journal of Proteome Research, 2012, 11, 917-926.                                 | 3.7              | 196       |
| 46 | Tracking Five Millennia of Horse Management with Extensive Ancient Genome Time Series. Cell, 2019, 177, 1419-1435.e31.  | 28.9             | 195       |
| 47 | Ancient genomic changes associated with domestication of the horse. Science, 2017, 356, 442-445.  | 12.6             | 185       |
| 48 | Speciation with gene flow in equids despite extensive chromosomal plasticity. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18655-18660.  | 7.1              | 183       |
| 49 | Improving access to endogenous DNA in ancient bones and teeth. Scientific Reports, 2015, 5, 11184.  | 3.3              | 182       |
| 50 | Bacterial natural transformation by highly fragmented and damaged DNA. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19860-19865.         | 7.1              | 170       |
| 51 | Genome-wide nucleosome map and cytosine methylation levels of an ancient human genome. Genome Research, 2014, 24, 454-466.  | 5.5              | 161       |
| 52 | Evolutionary Genomics and Conservation of the Endangered Przewalski's Horse. Current Biology, 2015, 25, 2577-2583.  | 3.9              | 161       |
| 53 | Ancient DNA analysis reveals divergence of the cave bear, <i>Ursus spelaeus</i> , and brown bear, <i>Ursus arctos</i> , lineages. Current Biology, 2001, 11, 200-203.                   | 3.9              | 160       |
| 54 | Genomic Affinities of Two 7,000-Year-Old Iberian Hunter-Gatherers. Current Biology, 2012, 22, 1494-1499.  | 3.9              | 160       |

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|----|--|------|-----------|
| 55 | Ancient hepatitis B viruses from the Bronze Age to the Medieval period. <i>Nature</i> , 2018, 557, 418-423.  | 27.8 | 155       |
| 56 | Improved reference genome for the domestic horse increases assembly contiguity and composition. <i>Communications Biology</i> , 2018, 1, 197.  | 4.4  | 148       |
| 57 | A comparative study of ancient sedimentary DNA, pollen and microfossils from permafrost sediments of northern Siberia reveals long-term vegetational stability. <i>Molecular Ecology</i> , 2012, 21, 1989-2003.                                | 3.9  | 144       |
| 58 | A Robust Framework for Microbial Archaeology. <i>Annual Review of Genomics and Human Genetics</i> , 2017, 18, 321-356.   | 6.2  | 144       |
| 59 | Population genomics of the Viking world. <i>Nature</i> , 2020, 585, 390-396.   | 27.8 | 143       |
| 60 | Ancient genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130387.   | 4.0  | 142       |
| 61 | The origins and spread of domestic horses from the Western Eurasian steppes. <i>Nature</i> , 2021, 598, 634-640.   | 27.8 | 142       |
| 62 | Survival and divergence in a small group: The extraordinary genomic history of the endangered Apennine brown bear stragglers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9589-E9597. | 7.1  | 140       |
| 63 | Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E6889-97.               | 7.1  | 139       |
| 64 | Revising the recent evolutionary history of equids using ancient DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21754-21759.   | 7.1  | 136       |
| 65 | Early Pleistocene enamel proteome from Dmanisi resolves <i>Stephanorhinus</i> phylogeny. <i>Nature</i> , 2019, 574, 103-107.   | 27.8 | 135       |
| 66 | Ancient DNA analysis. <i>Nature Reviews Methods Primers</i> , 2021, 1, .   | 21.2 | 133       |
| 67 | Comparing the performance of three ancient <i>DNA</i> extraction methods for high-throughput sequencing. <i>Molecular Ecology Resources</i> , 2016, 16, 459-469.   | 4.8  | 127       |
| 68 | Mitochondrial Phylogenomics of Modern and Ancient Equids. <i>PLoS ONE</i> , 2013, 8, e55950.   | 2.5  | 123       |
| 69 | Taming the Past: Ancient DNA and the Study of Animal Domestication. <i>Annual Review of Animal Biosciences</i> , 2017, 5, 329-351.   | 7.4  | 120       |
| 70 | Animal domestication in the era of ancient genomics. <i>Nature Reviews Genetics</i> , 2020, 21, 449-460.   | 16.3 | 119       |
| 71 | Revisiting Neandertal diversity with a 100,000 year old mtDNA sequence. <i>Current Biology</i> , 2006, 16, R400-R402.  | 3.9  | 116       |
| 72 | Developing a 670k genotyping array to tag ~2M SNPs across 24 horse breeds. <i>BMC Genomics</i> , 2017, 18, 565.  | 2.8  | 116       |

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|----|--|------|-----------|
| 73 | True single-molecule DNA sequencing of a pleistocene horse bone. <i>Genome Research</i> , 2011, 21, 1705-1719.   | 5.5  | 114       |
| 74 | Evaluating the impact of domestication and captivity on the horse gut microbiome. <i>Scientific Reports</i> , 2017, 7, 15497.  | 3.3  | 112       |
| 75 | Genome-wide ancestry of 17th-century enslaved Africans from the Caribbean. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 3669-3673.  | 7.1  | 110       |
| 76 | Reconstructing genome evolution in historic samples of the Irish potato famine pathogen. <i>Nature Communications</i> , 2013, 4, 2172.   | 12.8 | 103       |
| 77 | Synergistic roles of climate warming and human occupation in Patagonian megafaunal extinctions during the Last Deglaciation. <i>Science Advances</i> , 2016, 2, e1501682.  | 10.3 | 102       |
| 78 | A comparative study of ancient environmental DNA to pollen and macrofossils from lake sediments reveals taxonomic overlap and additional plant taxa. <i>Quaternary Science Reviews</i> , 2013, 75, 161-168.                            | 3.0  | 99        |
| 79 | Using paleo-archives to safeguard biodiversity under climate change. <i>Science</i> , 2020, 369, .   | 12.6 | 98        |
| 80 | Variola Virus in a 300-Year-Old Siberian Mummy. <i>New England Journal of Medicine</i> , 2012, 367, 2057-2059.   | 27.0 | 97        |
| 81 | Ancient DNA and the Population Genetics of Cave Bears ( <i>Ursus spelaeus</i> ) Through Space and Time. <i>Molecular Biology and Evolution</i> , 2002, 19, 1920-1933.  | 8.9  | 88        |
| 82 | Using Ancient DNA to Understand Evolutionary and Ecological Processes. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2014, 45, 573-598.  | 8.3  | 88        |
| 83 | Rodents of the Caribbean: origin and diversification of hutias unravelled by next-generation museomics. <i>Biology Letters</i> , 2014, 10, 20140266.   | 2.3  | 87        |
| 84 | Surprising migration and population size dynamics in ancient Iberian brown bears ( <i>Ursus arctos</i> ). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5123-5128.               | 7.1  | 86        |
| 85 | gargammel: a sequence simulator for ancient DNA. <i>Bioinformatics</i> , 2017, 33, 577-579.  | 4.1  | 85        |
| 86 | Mitogenome sequencing reveals shallow evolutionary histories and recent divergence time between morphologically and ecologically distinct European whitefish ( <i>Coregonus</i> spp.). <i>Molecular Ecology</i> , 2012, 21, 2727-2742. | 3.9  | 83        |
| 87 | Partial Genetic Turnover in Neandertals: Continuity in the East and Population Replacement in the West. <i>Molecular Biology and Evolution</i> , 2012, 29, 1893-1897.  | 8.9  | 82        |
| 88 | Morphological and genetic evidence for early Holocene cattle management in northeastern China. <i>Nature Communications</i> , 2013, 4, 2755.   | 12.8 | 82        |
| 89 | Dairy pastoralism sustained eastern Eurasian steppe populations for 5,000 years. <i>Nature Ecology and Evolution</i> , 2020, 4, 346-355.   | 7.8  | 82        |
| 90 | Early cave art and ancient DNA record the origin of European bison. <i>Nature Communications</i> , 2016, 7, 13158.   | 12.8 | 81        |

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|-----|--|------|-----------|
| 91  | Late Quaternary dynamics of Arctic biota from ancient environmental genomics. <i>Nature</i> , 2021, 600, 86-92.  | 27.8 | 81        |
| 92  | EPAS1 Gain-of-Function Mutation Contributes to High-Altitude Adaptation in Tibetan Horses. <i>Molecular Biology and Evolution</i> , 2019, 36, 2591-2603.   | 8.9  | 80        |
| 93  | Combining bleach and mild predigestion improves ancient <i>&lt;sc&gt;DNA&lt;/sc&gt;</i> recovery from bones. <i>Molecular Ecology Resources</i> , 2017, 17, 742-751.                                     | 4.8  | 77        |
| 94  | Geographic distribution of an extinct equid ( <i>Equus hydruntinus</i> : Mammalia, Equidae) revealed by morphological and genetical analyses of fossils. <i>Molecular Ecology</i> , 2006, 15, 2083-2093. | 3.9  | 76        |
| 95  | Mitogenomic phylogenetic analyses of the Delphinidae with an emphasis on the Globicephalinae. <i>BMC Evolutionary Biology</i> , 2011, 11, 65.  | 3.2  | 76        |
| 96  | Modern human incursion into Neanderthal territories 54,000 years ago at Mandrin, France. <i>Science Advances</i> , 2022, 8, eabj9496.  | 10.3 | 76        |
| 97  | Less effective selection leads to larger genomes. <i>Genome Research</i> , 2017, 27, 1016-1028.  | 5.5  | 75        |
| 98  | Two ancient human genomes reveal Polynesian ancestry among the indigenous Botocudos of Brazil. <i>Current Biology</i> , 2014, 24, R1035-R1037.   | 3.9  | 73        |
| 99  | Evolutionary Patterns and Processes: Lessons from Ancient DNA. <i>Systematic Biology</i> , 2017, 66, syw059.   | 5.6  | 73        |
| 100 | The wolf reference genome sequence ( <i>Canis lupus lupus</i> ) and its implications for <i>Canis</i> spp. population genomics. <i>BMC Genomics</i> , 2017, 18, 495.                                     | 2.8  | 73        |
| 101 | High-throughput <i>&lt;sc&gt;DNA&lt;/sc&gt;</i> sequencing of ancient wood. <i>Molecular Ecology</i> , 2018, 27, 1138-1154.  | 3.9  | 73        |
| 102 | Ancient DNA analysis reveals woolly rhino evolutionary relationships. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 485-499.  | 2.7  | 68        |
| 103 | Ligation Bias in Illumina Next-Generation DNA Libraries: Implications for Sequencing Ancient Genomes. <i>PLoS ONE</i> , 2013, 8, e78575.   | 2.5  | 68        |
| 104 | Islands in the ice: detecting past vegetation on Greenlandic nunataks using historical records and sedimentary ancient DNA Meta-barcoding. <i>Molecular Ecology</i> , 2012, 21, 1980-1988.               | 3.9  | 67        |
| 105 | Experimental conditions improving in-solution target enrichment for ancient <i>&lt;sc&gt;DNA&lt;/sc&gt;</i> . <i>Molecular Ecology Resources</i> , 2017, 17, 508-522.                                    | 4.8  | 67        |
| 106 | Planning tiger recovery: Understanding intraspecific variation for effective conservation. <i>Science Advances</i> , 2015, 1, e1400175.  | 10.3 | 63        |
| 107 | Ancient <i>&lt;sc&gt;DNA&lt;/sc&gt;</i> analysis identifies marine mollusc shells as new metagenomic archives of the past. <i>Molecular Ecology Resources</i> , 2017, 17, 835-853.                       | 4.8  | 62        |
| 108 | Pros and cons of methylation-based enrichment methods for ancient DNA. <i>Scientific Reports</i> , 2015, 5, 11826.   | 3.3  | 61        |

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|-----|---|------|-----------|
| 109 | The Evolutionary Origin and Genetic Makeup of Domestic Horses. <i>Genetics</i> , 2016, 204, 423-434.  | 2.9  | 61        |
| 110 | Detecting taxonomic and phylogenetic signals in equid cheek teeth: towards new palaeontological and archaeological proxies. <i>Royal Society Open Science</i> , 2017, 4, 160997.                      | 2.4  | 61        |
| 111 | Joint Estimates of Heterozygosity and Runs of Homozygosity for Modern and Ancient Samples. <i>Genetics</i> , 2019, 212, 587-614.  | 2.9  | 61        |
| 112 | A new genus of horse from Pleistocene North America. <i>ELife</i> , 2017, 6, .  | 6.0  | 61        |
| 113 | Ancient DNA sequences point to a large loss of mitochondrial genetic diversity in the saiga antelope ( <i>Saiga tatarica</i> ) since the Pleistocene. <i>Molecular Ecology</i> , 2010, 19, 4863-4875. | 3.9  | 59        |
| 114 | Regulatory mutations in <i>TBX3</i> disrupt asymmetric hair pigmentation that underlies Dun camouflage color in horses. <i>Nature Genetics</i> , 2016, 48, 152-158.                                   | 21.4 | 59        |
| 115 | Paleogenomics: reconstruction of plant evolutionary trajectories from modern and ancient DNA. <i>Genome Biology</i> , 2019, 20, 29.   | 8.8  | 58        |
| 116 | Horse Y chromosome assembly displays unique evolutionary features and putative stallion fertility genes. <i>Nature Communications</i> , 2018, 9, 2945.  | 12.8 | 56        |
| 117 | Shotgun microbial profiling of fossil remains. <i>Molecular Ecology</i> , 2014, 23, 1780-1798.  | 3.9  | 55        |
| 118 | Fast, Accurate and Automatic Ancient Nucleosome and Methylation Maps with epiPALEOMIX. <i>Molecular Biology and Evolution</i> , 2016, 33, 3284-3298.  | 8.9  | 53        |
| 119 | Human evolution: a tale from ancient genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20150484.  | 4.0  | 51        |
| 120 | Genome-wide Ancestry and Demographic History of African-Descendant Maroon Communities from French Guiana and Suriname. <i>American Journal of Human Genetics</i> , 2017, 101, 725-736.                | 6.2  | 50        |
| 121 | Evidence for early dispersal of domestic sheep into Central Asia. <i>Nature Human Behaviour</i> , 2021, 5, 1169-1179.   | 12.0 | 50        |
| 122 | Grey wolf genomic history reveals a dual ancestry of dogs. <i>Nature</i> , 2022, 607, 313-320.  | 27.8 | 48        |
| 123 | Improved de novo genomic assembly for the domestic donkey. <i>Science Advances</i> , 2018, 4, eaaq0392.   | 10.3 | 46        |
| 124 | Early pastoral economies along the Ancient Silk Road: Biomolecular evidence from the Alay Valley, Kyrgyzstan. <i>PLoS ONE</i> , 2018, 13, e0205646.   | 2.5  | 46        |
| 125 | Population Demography and Genetic Diversity in the Pleistocene Cave Lion. <i>Open Quaternary</i> , 2015, 1, 4.  | 1.0  | 44        |
| 126 | Zonkey: A simple, accurate and sensitive pipeline to genetically identify equine F1-hybrids in archaeological assemblages. <i>Journal of Archaeological Science</i> , 2017, 78, 147-157.              | 2.4  | 44        |



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|-----|---|------|-----------|
| 127 | New insights on single-stranded versus double-stranded DNA library preparation for ancient DNA. <i>BioTechniques</i> , 2015, 59, 368-371.   | 1.8  | 43        |
| 128 | Ancient DNA Clarifies the Evolutionary History of American Late Pleistocene Equids. <i>Journal of Molecular Evolution</i> , 2008, 66, 533-538.  | 1.8  | 42        |
| 129 | An epigenetic window into the past?. <i>Science</i> , 2014, 345, 511-512.   | 12.6 | 41        |
| 130 | DNA from extinct giant lemurs links archaeolemurids to extant indriids. <i>BMC Evolutionary Biology</i> , 2008, 8, 121.   | 3.2  | 40        |
| 131 | Statistical Guidelines for Detecting Past Population Shifts Using Ancient DNA. <i>Molecular Biology and Evolution</i> , 2012, 29, 2241-2251.  | 8.9  | 40        |
| 132 | Mitogenomic phylogeny, diversification, and biogeography of South American spiny rats. <i>Molecular Biology and Evolution</i> , 2017, 34, msw261.   | 8.9  | 40        |
| 133 | Next-generation sequencing offers new insights into DNA degradation. <i>Trends in Biotechnology</i> , 2012, 30, 364-368.  | 9.3  | 39        |
| 134 | Using Classical Population Genetics Tools with Heterochroneous Data: Time Matters!. <i>PLoS ONE</i> , 2009, 4, e5541.   | 2.5  | 37        |
| 135 | Major transitions in human evolution revisited: A tribute to ancient DNA. <i>Journal of Human Evolution</i> , 2015, 79, 4-20.   | 2.6  | 37        |
| 136 | Mitochondrial genomes reveal the extinct <i>Hippidion</i> as an outgroup to all living equids. <i>Biology Letters</i> , 2015, 11, 20141058.   | 2.3  | 36        |
| 137 | Planktonic foraminifera-derived environmental DNA extracted from abyssal sediments preserves patterns of plankton macroecology. <i>Biogeosciences</i> , 2017, 14, 2741-2754.                        | 3.3  | 36        |
| 138 | Improving the performance of true single molecule sequencing for ancient DNA. <i>BMC Genomics</i> , 2012, 13, 177.  | 2.8  | 35        |
| 139 | The first aurochs genome reveals the breeding history of British and European cattle. <i>Genome Biology</i> , 2015, 16, 225.  | 8.8  | 35        |
| 140 | metaBIT, an integrative and automated metagenomic pipeline for analysing microbial profiles from high-throughput sequencing shotgun data. <i>Molecular Ecology Resources</i> , 2016, 16, 1415-1427. | 4.8  | 35        |
| 141 | Museomics identifies genetic erosion in two butterfly species across the 20th century in Finland. <i>Molecular Ecology Resources</i> , 2020, 20, 1191-1205.   | 4.8  | 34        |
| 142 | Out of the Pacific and Back Again: Insights into the Matrilineal History of Pacific Killer Whale Ecotypes. <i>PLoS ONE</i> , 2011, 6, e24980.   | 2.5  | 33        |
| 143 | A southern African origin and cryptic structure in the highly mobile plains zebra. <i>Nature Ecology and Evolution</i> , 2018, 2, 491-498.  | 7.8  | 32        |
| 144 | Late Quaternary horses in Eurasia in the face of climate and vegetation change. <i>Science Advances</i> , 2018, 4, eaar5589.  | 10.3 | 32        |

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|-----|---|------|-----------|
| 145 | The Microcephalin Ancestral Allele in a Neanderthal Individual. PLoS ONE, 2010, 5, e10648.  | 2.5  | 31        |
| 146 | Spotted phenotypes in horses lost attractiveness in the Middle Ages. Scientific Reports, 2016, 6, 38548.  | 3.3  | 31        |
| 147 | Origin and Evolution of Deleterious Mutations in Horses. Genes, 2019, 10, 649.  | 2.4  | 31        |
| 148 | Ancient Genomes Reveal Unexpected Horse Domestication and Management Dynamics. BioEssays, 2020, 42, e1900164.   | 2.5  | 31        |
| 149 | Ancient horse genomes reveal the timing and extent of dispersals across the Bering Land Bridge. Molecular Ecology, 2021, 30, 6144-6161.   | 3.9  | 30        |
| 150 | Annotation of the Protein Coding Regions of the Equine Genome. PLoS ONE, 2015, 10, e0124375.  | 2.5  | 29        |
| 151 | Decline of genetic diversity in ancient domestic stallions in Europe. Science Advances, 2018, 4, eaap9691.  | 10.3 | 29        |
| 152 | Unveiling the Ecological Applications of Ancient DNA From Mollusk Shells. Frontiers in Ecology and Evolution, 2020, 8, .  | 2.2  | 29        |
| 153 | Conceptual bases for quantifying the role of the environment on gene evolution: the participation of positive selection and neutral evolution. Biological Reviews, 2007, 82, 551-572. | 10.4 | 28        |
| 154 | Assessing DNA Sequence Alignment Methods for Characterizing Ancient Genomes and Methylomes. Frontiers in Ecology and Evolution, 2020, 8, .  | 2.2  | 27        |
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