

Pulling out the 1%: Whole-Genome Capture for the Targeted Sequencing Libraries

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Population Genomic Analysis of Ancient and Modern Genomes Yields New Insights into the Genetic Ancestry of the Tyrolean Iceman and the Genetic Structure of Europe. <i>PLoS Genetics</i> , 2014, 10, e1004353.	1.5	86
2	Shotgun microbial profiling of fossil remains. <i>Molecular Ecology</i> , 2014, 23, 1780-1798.	2.0	55
3	How Much DNA Is Lost? Measuring DNA Loss of Short-Tandem-Repeat Length Fragments Targeted by the PowerPlex 16 ^Å System Using the Qiagen MinElute Purification Kit. <i>Human Biology</i> , 2014, 86, 313.	0.4	41
4	Sequencing ancient DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 2401-2401.	3.3	3
5	Prevention, diagnosis and treatment of high-throughput sequencing data pathologies. <i>Molecular Ecology</i> , 2014, 23, 1679-1700.	2.0	24
6	Selective enrichment of damaged DNA molecules for ancient genome sequencing. <i>Genome Research</i> , 2014, 24, 1543-1549.	2.4	93
7	Toward a new history and geography of human genes informed by ancient DNA. <i>Trends in Genetics</i> , 2014, 30, 377-389.	2.9	227
8	A 400,000-year-old mitochondrial genome questions phylogenetic relationships amongst archaic hominins. <i>BioEssays</i> , 2014, 36, 598-605.	1.2	9
9	Ancient Whole Genome Enrichment Using Baits Built from Modern DNA. <i>Molecular Biology and Evolution</i> , 2014, 31, 1292-1294.	3.5	141
10	Population Genomics of Marine Fishes: Next-Generation Prospects and Challenges. <i>Biological Bulletin</i> , 2014, 227, 117-132.	0.7	61
12	Pros and cons of methylation-based enrichment methods for ancient DNA. <i>Scientific Reports</i> , 2015, 5, 11826.	1.6	61
13	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. <i>Scientific Reports</i> , 2015, 5, 13201.	1.6	34
14	Selective enrichment of STRs for applications in forensic human identification. <i>Electrophoresis</i> , 2015, 36, 1768-1774.	1.3	0
15	A method for positive forensic identification of samples from extremely low-coverage sequence data. <i>BMC Genomics</i> , 2015, 16, 1034.	1.2	18
16	Comparative performance of two whole-genome capture methodologies on ancient DNA Illumina libraries. <i>Methods in Ecology and Evolution</i> , 2015, 6, 725-734.	2.2	43
17	Tracing the origin of our species through palaeogenomics. <i>BIO Web of Conferences</i> , 2015, 4, 00005.	0.1	1
18	Reducing microbial and human contamination in DNA extractions from ancient bones and teeth. <i>BioTechniques</i> , 2015, 59, 87-93.	0.8	210
19	Affected Kindred Analysis of Human X Chromosome Exomes to Identify Novel X-Linked Intellectual Disability Genes. <i>PLoS ONE</i> , 2015, 10, e0116454.	1.1	49

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20	Using targeted enrichment of nuclear genes to increase phylogenetic resolution in the neotropical rain forest genus <i>Inga</i> (Leguminosae: Mimosoideae). <i>Frontiers in Plant Science</i> , 2015, 6, 710.	1.7	147
21	New insights on single-stranded versus double-stranded DNA library preparation for ancient DNA. <i>BioTechniques</i> , 2015, 59, 368-371.	0.8	43
22	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015, 522, 167-172.	13.7	1,166
23	Reconstructing ancient genomes and epigenomes. <i>Nature Reviews Genetics</i> , 2015, 16, 395-408.	7.7	197
24	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.	3.3	110
25	Ancient human genomics: the methodology behind reconstructing evolutionary pathways. <i>Journal of Human Evolution</i> , 2015, 79, 21-34.	1.3	22
26	Ancient genomics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130387.	1.8	142
27	The use of museum specimens with high-throughput DNA sequencers. <i>Journal of Human Evolution</i> , 2015, 79, 35-44.	1.3	163
28	Impacts of low coverage depths and post-mortem DNA damage on variant calling: a simulation study. <i>BMC Genomics</i> , 2015, 16, 19.	1.2	26
29	Improving access to endogenous DNA in ancient bones and teeth. <i>Scientific Reports</i> , 2015, 5, 11184.	1.6	182
30	Impacts of degraded <sc>DNA</sc> on restriction enzyme associated <sc>DNA</sc> sequencing (<sc>RADS</sc>eq). <i>Molecular Ecology Resources</i> , 2015, 15, 1304-1315.	2.2	114
31	A Common Genetic Origin for Early Farmers from Mediterranean Cardial and Central European LBK Cultures. <i>Molecular Biology and Evolution</i> , 2015, 32, msv181.	3.5	155
32	Phylogenomics of Horned Lizards (Genus: <i>Phrynosoma</i>) Using Targeted Sequence Capture Data. <i>Copeia</i> , 2015, 103, 586-594.	1.4	22
33	Genomic Repeat Abundances Contain Phylogenetic Signal. <i>Systematic Biology</i> , 2015, 64, 112-126.	2.7	126
34	Major transitions in human evolution revisited: A tribute to ancient DNA. <i>Journal of Human Evolution</i> , 2015, 79, 4-20.	1.3	37
35	Ancient population genomics and the study of evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130381.	1.8	18
36	Partial uracilâ€“DNAâ€“glycosylase treatment for screening of ancient DNA. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130624.	1.8	381
37	Almost 20 years of Neanderthal palaeogenetics: adaptation, admixture, diversity, demography and extinction. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2015, 370, 20130374.	1.8	42

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38	Ancient <scp>DNA</scp> from the <scp>S</scp>child site in <scp>I</scp>llinois: Implications for the <scp>M</scp>ississippian transition in the <scp>L</scp>ower <scp>I</scp>llinois <scp>R</scp>iver <scp>V</scp>alley. American Journal of Physical Anthropology, 2015, 156, 434-448.	2.1	6
39	The future of ancient DNA: Technical advances and conceptual shifts. BioEssays, 2015, 37, 284-293.	1.2	209
40	Hunting for Pathogens. , 2016, , 81-100.		5
41	Mammoth Population Dynamics in Late Pleistocene North America: Divergence, Phylogeography, and Introgression. Frontiers in Ecology and Evolution, 2016, 4, .	1.1	56
42	Comparing the performance of three ancient <scp>DNA</scp> extraction methods for high-throughput sequencing. Molecular Ecology Resources, 2016, 16, 459-469.	2.2	127
43	Crossing disciplinary lines: reconciling social and genomic perspectives on the histories and legacies of the transatlantic trade in enslaved Africans. New Genetics and Society, 2016, 35, 149-185.	0.7	10
44	Evolutionary Patterns and Processes: Lessons from Ancient DNA. Systematic Biology, 2017, 66, syw059.	2.7	73
45	The early colonial atlantic world: New insights on the African Diaspora from isotopic and ancient <scp>DNA</scp> analyses of a multiethnic 15th-17th century burial population from the Canary Islands, Spain. American Journal of Physical Anthropology, 2016, 159, 300-312.	2.1	22
46	The efficacy of high-throughput sequencing and target enrichment on charred archaeobotanical remains. Scientific Reports, 2016, 6, 37347.	1.6	40
47	Natural history collections as windows on evolutionary processes. Molecular Ecology, 2016, 25, 864-881.	2.0	199
48	Targeted capture in evolutionary and ecological genomics. Molecular Ecology, 2016, 25, 185-202.	2.0	295
49	The historical ecology of Pacific herring: Tracing Alaska Native use of a forage fish. Journal of Archaeological Science: Reports, 2016, 8, 504-512.	0.2	12
50	Advances in DNA typing in the agro-food supply chain. Trends in Food Science and Technology, 2016, 52, 80-89.	7.8	25
51	Sequence capture by hybridization to explore modern and ancient genomic diversity in model and nonmodel organisms. Nucleic Acids Research, 2016, 44, 4504-4518.	6.5	69
52	The Evolutionary Origin and Genetic Makeup of Domestic Horses. Genetics, 2016, 204, 423-434.	1.2	61
53	Native American Genomics and Population Histories. Annual Review of Anthropology, 2016, 45, 319-340.	0.4	49
54	Ancient DNA: the next generation—Chapter and verse. Biological Journal of the Linnean Society, 2016, 117, 150-160.	0.7	30
55	Impact of enrichment conditions on cross-species capture of fresh and degraded <scp>DNA</scp>. Molecular Ecology Resources, 2016, 16, 42-55.	2.2	70

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56	Massively Parallel Mitochondrial DNA Sequencing in Forensic Genetics: Principles and Opportunities. Security Science and Technology, 2016, , 293-335.	0.5	2
57	Efficient Genome-Wide Sequencing and Low-Coverage Pedigree Analysis from Noninvasively Collected Samples. Genetics, 2016, 203, 699-714.	1.2	76
58	Field Guidelines for Genetic Experimental Designs in High-Throughput Sequencing. , 2016, , .		6
59	Targeted DNA Region Re-sequencing. , 2016, , 43-68.		9
60	Ancient mtDNA sequences from the First Australians revisited. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 6892-6897.	3.3	26
61	The limits and potential of paleogenomic techniques for reconstructing grapevine domestication. Journal of Archaeological Science, 2016, 72, 57-70.	1.2	43
62	DNA Sequencing in Cultural Heritage. Topics in Current Chemistry, 2016, 374, 8.	3.0	4
63	Using ancient DNA and coalescent-based methods to infer extinction. Biology Letters, 2016, 12, 20150822.	1.0	12
64	Harnessing the power of RADseq for ecological and evolutionary genomics. Nature Reviews Genetics, 2016, 17, 81-92.	7.7	1,169
65	Combined hybridization capture and shotgun sequencing for ancient <scp>DNA</scp> analysis of extinct wild and domestic dromedary camel. Molecular Ecology Resources, 2017, 17, 300-313.	2.2	25
66	From the field to the laboratory: Controlling DNA contamination in human ancient DNA research in the high-throughput sequencing era. Science and Technology of Archaeological Research, 2017, 3, 1-14.	2.4	126
67	Characterizing restriction enzyme-associated loci in historic ragweed (<i>Ambrosia artemisiifolia</i>) voucher specimens using custom-designed <scp>RNA</scp> probes. Molecular Ecology Resources, 2017, 17, 209-220.	2.2	31
69	A paleogenetic perspective on the early population history of the high altitude Andes. Quaternary International, 2017, 461, 25-33.	0.7	12
70	Neandertal and Denisovan DNA from Pleistocene sediments. Science, 2017, 356, 605-608.	6.0	329
71	Genetic studies of the peopling of the Americas: What insights do diachronic mitochondrial genome datasets provide?. Quaternary International, 2017, 444, 26-35.	0.7	29
72	Comprehensive analysis of microorganisms accompanying human archaeological remains. GigaScience, 2017, 6, 1-13.	3.3	15
73	Hy<scp>RAD</scp>-EX, a versatile method combining exome capture and <scp>RAD</scp> sequencing to extract genomic information from ancient <scp>DNA</scp>. Methods in Ecology and Evolution, 2017, 8, 1374-1388.	2.2	52
74	A phylogenetic approach for haplotype analysis of sequence data from complex mitochondrial mixtures. Forensic Science International: Genetics, 2017, 30, 93-105.	1.6	39

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75	Phylogenomics. , 2017, , .		47
76	Determining the population affinity of an unprovenienced human skull for repatriation. <i>Journal of Archaeological Science: Reports</i> , 2017, 12, 384-394.	0.2	12
77	Human evolution: a tale from ancient genomes. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20150484.	1.8	51
78	Performance evaluation of a mitogenome capture and Illumina sequencing protocol using non-probative, case-type skeletal samples: Implications for the use of a positive control in a next-generation sequencing procedure. <i>Forensic Science International: Genetics</i> , 2017, 31, 198-206.	1.6	63
79	Harnessing ancient genomes to study the history of human adaptation. <i>Nature Reviews Genetics</i> , 2017, 18, 659-674.	7.7	165
80	Whole mitochondrial genome capture from faecal samples and museumâ€preserved specimens. <i>Molecular Ecology Resources</i> , 2017, 17, e111-e121.	2.2	32
81	Ancient DNA reveals the Arctic origin of Viking Age cod from Haithabu, Germany. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9152-9157.	3.3	66
82	A mitogenomic timetree for Darwinâ€™s enigmatic South American mammal <i>Macrauchenia patachonica</i> . <i>Nature Communications</i> , 2017, 8, 15951.	5.8	71
83	A massively parallel strategy for STR marker development, capture, and genotyping. <i>Nucleic Acids Research</i> , 2017, 45, e142-e142.	6.5	8
84	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. <i>GigaScience</i> , 2017, 6, 1-13.	3.3	137
85	Taming the Past: Ancient DNA and the Study of Animal Domestication. <i>Annual Review of Animal Biosciences</i> , 2017, 5, 329-351.	3.6	120
86	Combining bleach and mild predigestion improves ancient <sc>DNA</sc> recovery from bones. <i>Molecular Ecology Resources</i> , 2017, 17, 742-751.	2.2	77
87	Experimental conditions improving inâ€solution target enrichment for ancient <sc>DNA</sc>. <i>Molecular Ecology Resources</i> , 2017, 17, 508-522.	2.2	67
88	Reduction of the contaminant fraction of DNA obtained from an ancient giant panda bone. <i>BMC Research Notes</i> , 2017, 10, 754.	0.6	26
89	Novel Substrates as Sources of Ancient DNA: Prospects and Hurdles. <i>Genes</i> , 2017, 8, 180.	1.0	44
90	Comparison of two ancient DNA extraction protocols for skeletal remains from tropical environments. <i>American Journal of Physical Anthropology</i> , 2018, 166, 824-836.	2.1	16
91	Target capture enrichment of nuclear SNP markers for massively parallel sequencing of degraded and mixed samples. <i>Forensic Science International: Genetics</i> , 2018, 34, 186-196.	1.6	45
92	Paleogenomics: Genome-Scale Analysis of Ancient DNA and Population and Evolutionary Genomic Inferences. <i>Population Genomics</i> , 2018, , 323-360.	0.2	4

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93	Methylation-based enrichment facilitates low-cost, noninvasive genomic scale sequencing of populations from feces. <i>Scientific Reports</i> , 2018, 8, 1975.	1.6	58
94	A multi-faceted anthropological and genomic approach to framing <i>Plasmodium falciparum</i> malaria in Imperial period central-southern Italy (1st–4th c. CE). <i>Journal of Anthropological Archaeology</i> , 2018, 49, 210-224.	0.7	13
95	Complete mitogenomes of ancient Caribbean Guinea pigs (<i>Cavia porcellus</i>). <i>Journal of Archaeological Science: Reports</i> , 2018, 17, 678-688.	0.2	15
96	Ancient Biomolecules and Evolutionary Inference. <i>Annual Review of Biochemistry</i> , 2018, 87, 1029-1060.	5.0	76
97	Ancient Epigenomics. <i>Population Genomics</i> , 2018, , 75-111.	0.2	11
98	Whole-genome sequencing of Atacama skeleton shows novel mutations linked with dysplasia. <i>Genome Research</i> , 2018, 28, 423-431.	2.4	19
99	Neolithic animal domestication as seen from ancient DNA. <i>Quaternary International</i> , 2018, 496, 102-107.	0.7	14
100	The value of space–time substitution for studying fine-scale microevolutionary processes. <i>Ecography</i> , 2018, 41, 1456-1468.	2.1	40
101	Anchored hybrid enrichment provides new insights into the phylogeny and evolution of longhorned beetles (<i>Cerambycidae</i>). <i>Systematic Entomology</i> , 2018, 43, 68-89.	1.7	73
102	A preliminary molecular phylogeny of shield-bearer moths (Lepidoptera: Adeloidea: Heliozelidae) highlights rich undescribed diversity. <i>Molecular Phylogenetics and Evolution</i> , 2018, 120, 129-143.	1.2	13
105	Hybrid Capture-Based Next Generation Sequencing and Its Application to Human Infectious Diseases. <i>Frontiers in Microbiology</i> , 2018, 9, 2924.	1.5	68
106	Ancient Pathogens Through Human History: A Paleogenomic Perspective. <i>Population Genomics</i> , 2018, , 115-138.	0.2	5
107	Paleogenomics of Animal Domestication. <i>Population Genomics</i> , 2018, , 225-272.	0.2	14
108	Genetic analyses of Scandinavian desiccated, charred and waterlogged remains of barley (<i>Hordeum</i>) Tj ETQq1 1 0.784314 rgBT /Overlo 0.2	0.2	3
109	Technical Advances and Challenges in Genome-Scale Analysis of Ancient DNA. <i>Population Genomics</i> , 2018, , 3-29.	0.2	2
110	The use and domestication of <i>Theobroma cacao</i> during the mid-Holocene in the upper Amazon. <i>Nature Ecology and Evolution</i> , 2018, 2, 1879-1888.	3.4	105
111	Ancient genome-wide analyses infer kinship structure in an Early Medieval Alemannic graveyard. <i>Science Advances</i> , 2018, 4, eaao1262.	4.7	28
112	Advances in Using Non-invasive, Archival, and Environmental Samples for Population Genomic Studies. <i>Population Genomics</i> , 2018, , 63-99.	0.2	24

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113	An Ancient DNA Perspective on Horse Evolution. <i>Population Genomics</i> , 2018, , 325-351.	0.2	6
114	The prehistoric peopling of Southeast Asia. <i>Science</i> , 2018, 361, 88-92.	6.0	291
115	Ancient DNA from latrines in Northern Europe and the Middle East (500 BCâ€“1700 AD) reveals past parasites and diet. <i>PLoS ONE</i> , 2018, 13, e0195481.	1.1	63
116	Mitochondrial genomes reveal an east to west cline of steppe ancestry in Corded Ware populations. <i>Scientific Reports</i> , 2018, 8, 11603.	1.6	30
117	Genome Sequencing of Ancient Plant Remains: Findings, Uses and Potential Applications for the Study and Improvement of Modern Crops. <i>Frontiers in Plant Science</i> , 2018, 9, 441.	1.7	19
118	A new targeted capture method using bacterial artificial chromosome (BAC) libraries as baits for sequencing relatively large genes. <i>PLoS ONE</i> , 2018, 13, e0200170.	1.1	2
119	An environmental <scp>DNA</scp> sampling method for ayeâ€“eyes from their feeding traces. <i>Ecology and Evolution</i> , 2018, 8, 9229-9240.	0.8	24
120	Applications of Probe Capture Enrichment Next Generation Sequencing for Whole Mitochondrial Genome and 426 Nuclear SNPs for Forensically Challenging Samples. <i>Genes</i> , 2018, 9, 49.	1.0	42
121	Targeted resequencing of coding <scp>DNA</scp> sequences for <scp>SNP</scp> discovery in nonmodel species. <i>Molecular Ecology Resources</i> , 2018, 18, 1356-1373.	2.2	19
122	Capture enrichment of aquatic environmental DNA: A first proof of concept. <i>Molecular Ecology Resources</i> , 2018, 18, 1392-1401.	2.2	42
123	Invoking adaptation to decipher the genetic legacy of past climate change. <i>Ecology</i> , 2018, 99, 1530-1546.	1.5	72
125	In-solution Y-chromosome capture-enrichment on ancient DNA libraries. <i>BMC Genomics</i> , 2018, 19, 608.	1.2	20
126	Ancient genomes from North Africa evidence prehistoric migrations to the Maghreb from both the Levant and Europe. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 6774-6779.	3.3	131
127	One future of clinical metagenomic sequencing for infectious diseases. <i>Expert Review of Molecular Diagnostics</i> , 2019, 19, 849-851.	1.5	6
129	Unlocking the potential of ancient fish DNA in the genomic era. <i>Evolutionary Applications</i> , 2019, 12, 1513-1522.	1.5	30
130	MitoIMP: A Computational Framework for Imputation of Missing Data in Low-Coverage Human Mitochondrial Genome. <i>Bioinformatics and Biology Insights</i> , 2019, 13, 117793221987388.	1.0	5
131	Ancient DNA in the Study of Ancient Disease. , 2019, , 183-210.		14
132	Approaching sheep herds origins and the emergence of the wool economy in continental Europe during the Bronze Age. <i>Archaeological and Anthropological Sciences</i> , 2019, 11, 4909-4925.	0.7	28

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133	Goth migration induced changes in the matrilineal genetic structure of the central-east European population. <i>Scientific Reports</i> , 2019, 9, 6737.	1.6	15
134	Mitogenomes illuminate the origin and migration patterns of the indigenous people of the Canary Islands. <i>PLoS ONE</i> , 2019, 14, e0209125.	1.1	54
135	Generating RNA Baits for Capture-Based Enrichment. <i>Methods in Molecular Biology</i> , 2019, 1963, 107-120.	0.4	1
136	Whole-Genome Capture of Ancient DNA Using Homemade Baits. <i>Methods in Molecular Biology</i> , 2019, 1963, 93-105.	0.4	15
137	Beyond Biodiversity: Can Environmental DNA (eDNA) Cut It as a Population Genetics Tool?. <i>Genes</i> , 2019, 10, 192.	1.0	160
138	Digging for the spiny rat and hutia phylogeny using a gene capture approach, with the description of a new mammal subfamily. <i>Molecular Phylogenetics and Evolution</i> , 2019, 136, 241-253.	1.2	32
140	Assembly of Ancient Mitochondrial Genomes Without a Closely Related Reference Sequence. <i>Methods in Molecular Biology</i> , 2019, 1963, 195-213.	0.4	1
141	Hybridization Capture of Ancient DNA Using RNA Baits. <i>Methods in Molecular Biology</i> , 2019, 1963, 121-128.	0.4	5
142	Towards population genomics in non-model species with large genomes: a case study of the marine zooplankton <i>Calanus finmarchicus</i> . <i>Royal Society Open Science</i> , 2019, 6, 180608.	1.1	34
143	Paleogenomics: reconstruction of plant evolutionary trajectories from modern and ancient DNA. <i>Genome Biology</i> , 2019, 20, 29.	3.8	58
144	Mitogenomic diversity in Sacred Ibis Mummies sheds light on early Egyptian practices. <i>PLoS ONE</i> , 2019, 14, e0223964.	1.1	14
145	Ancient DNA. , 2019, , 13-34.		0
146	The efficacy of whole human genome capture on ancient dental calculus and dentin. <i>American Journal of Physical Anthropology</i> , 2019, 168, 496-509.	2.1	24
147	Evaluating the Efficiency of Primer Extension Capture as a Method to Enrich DNA Extractions,. <i>Journal of Forensic Sciences</i> , 2019, 64, 1145-1151.	0.9	1
148	A roadmap for high-throughput sequencing studies of wild animal populations using noninvasive samples and hybridization capture. <i>Molecular Ecology Resources</i> , 2019, 19, 609-622.	2.2	24
149	Ancient <i>scp</i> DNA reveals the timing and persistence of organellar genetic bottlenecks over 3,000 years of sunflower domestication and improvement. <i>Evolutionary Applications</i> , 2019, 12, 38-53.	1.5	27
150	Ancient DNA Reconstructs the Genetic Legacies of Precontact Puerto Rico Communities. <i>Molecular Biology and Evolution</i> , 2020, 37, 611-626.	3.5	31
151	Select methods for microbial forensic nucleic acid analysis of trace and uncultivable specimens. , 2020, , 195-205.		2

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152	The Recovery, Interpretation and Use of Ancient Pathogen Genomes. <i>Current Biology</i> , 2020, 30, R1215-R1231.	1.8	33
153	Ancient genomes reveal tropical bovid species in the Tibetan Plateau contributed to the prevalence of hunting game until the late Neolithic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 28150-28159.	3.3	28
154	Analysis of Low Copy Number DNA and Degraded DNA. , 2020, , 1-20.		0
155	Targeted analysis of polymorphic loci from low-coverage shotgun sequence data allows accurate genotyping of HLA genes in historical human populations. <i>Scientific Reports</i> , 2020, 10, 7339.	1.6	6
156	Palaeomicrobiology: Application of Ancient DNA Sequencing to Better Understand Bacterial Genome Evolution and Adaptation. <i>Frontiers in Ecology and Evolution</i> , 2020, 8, .	1.1	19
157	Leveraging eDNA to expand the study of hybrid zones. <i>Molecular Ecology</i> , 2020, 29, 2768-2776.	2.0	9
158	Ancient DNA analysis of food remains in human dental calculus from the Edo period, Japan. <i>PLoS ONE</i> , 2020, 15, e0226654.	1.1	24
159	Chimpanzee (<i>Pan troglodytes schweinfurthii</i>) Population Spans Multiple Protected Areas in the Albertine Rift. <i>Folia Primatologica</i> , 2020, 91, 595-609.	0.3	2
160	Advantages of an easy-to-use DNA extraction method for minimal-destructive analysis of collection specimens. <i>PLoS ONE</i> , 2020, 15, e0235222.	1.1	15
161	Advances and prospects of environmental DNA in neotropical rainforests. <i>Advances in Ecological Research</i> , 2020, , 331-373.	1.4	27
162	Beyond broad strokes: sociocultural insights from the study of ancient genomes. <i>Nature Reviews Genetics</i> , 2020, 21, 355-366.	7.7	50
163	Dramatic HIV DNA degradation associated with spontaneous HIV suppression and disease-free outcome in a young seropositive woman following her infection. <i>Scientific Reports</i> , 2020, 10, 2548.	1.6	3
164	Separating the signal from the noise in metagenomic cell-free DNA sequencing. <i>Microbiome</i> , 2020, 8, 18.	4.9	31
165	Minimally invasive bone biopsies of fully wrapped mummies guided by computed tomography and fibre-optic endoscopy: Methods and suggested guidelines. <i>Journal of Archaeological Science: Reports</i> , 2020, 31, 102363.	0.2	1
166	Mitochondrial genomes from Bronze Age Poland reveal genetic continuity from the Late Neolithic and additional genetic affinities with the steppe populations. <i>American Journal of Physical Anthropology</i> , 2020, 172, 176-188.	2.1	12
167	Metagenomic analysis of historical herbarium specimens reveals a postmortem microbial community. <i>Molecular Ecology Resources</i> , 2020, 20, 1206-1219.	2.2	23
168	History of Ancient DNA Analysis in Mummy Research. , 2021, , 1-14.		0
169	Genome-scale target capture of mitochondrial and nuclear environmental DNA from water samples. <i>Molecular Ecology Resources</i> , 2021, 21, 690-702.	2.2	29

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170	Maximizing the acquisition of unique reads in noninvasive capture sequencing experiments. <i>Molecular Ecology Resources</i> , 2021, 21, 745-761.	2.2	18
171	Hybridization capture of larch (<i>Larix</i> Mill.) chloroplast genomes from sedimentary ancient DNA reveals past changes of Siberian forest. <i>Molecular Ecology Resources</i> , 2021, 21, 801-815.	2.2	26
172	Tracking the history of grapevine cultivation in Georgia by combining geometric morphometrics and ancient DNA. <i>Vegetation History and Archaeobotany</i> , 2021, 30, 63-76.	1.0	29
173	Optimizing extraction and targeted capture of ancient environmental DNA for reconstructing past environments using the PalaeoChip Arctic-1.0 bait-set. <i>Quaternary Research</i> , 2021, 99, 305-328.	1.0	46
176	Environmental DNA captures the genetic diversity of bowhead whales (<i>Balaena mysticetus</i>) in West Greenland. <i>Environmental DNA</i> , 2021, 3, 248-260.	3.1	31
177	A minimally destructive protocol for DNA extraction from ancient teeth. <i>Genome Research</i> , 2021, 31, 472-483.	2.4	31
178	Ancient DNA analysis. <i>Nature Reviews Methods Primers</i> , 2021, 1, .	11.8	133
179	Ancient DNA studies: Use of ethnonyms and collaborative research in South America. <i>Journal of Anthropological Archaeology</i> , 2021, 61, 101265.	0.7	6
180	Paleogenomics illuminates the evolutionary history of the extinct Holocene "horned" crocodile of Madagascar, <i>Voay robustus</i> . <i>Communications Biology</i> , 2021, 4, 505.	2.0	16
181	HyRAD-X Exome Capture Museomics Unravels Giant Ground Beetle Evolution. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	13
182	The genomes of ancient date palms germinated from 2,000 y old seeds. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	13
183	New Data from Old Specimens. <i>Ichthyology and Herpetology</i> , 2021, 109, .	0.3	5
184	Investigative genetic genealogy: Current methods, knowledge and practice. <i>Forensic Science International: Genetics</i> , 2021, 52, 102474.	1.6	73
185	The Phylogenetics and Biogeography of the Central Asian Hawkmoths, <i>Hyles hippophaes</i> and <i>H. chamyla</i> : Can Mitogenomics and Machine Learning Bring Clarity?. <i>Diversity</i> , 2021, 13, 213.	0.7	0
187	Ancient DNA analysis of rare genetic bone disorders. <i>International Journal of Paleopathology</i> , 2021, 33, 182-187.	0.8	2
188	A method for the temperature-controlled extraction of DNA from ancient bones. <i>BioTechniques</i> , 2021, 71, 382-386.	0.8	6
189	Maternal genetic origin of the late and final Neolithic human populations from present-day Poland. <i>American Journal of Physical Anthropology</i> , 2021, 176, 223-236.	2.1	3
190	Capture enrichment and massively parallel sequencing for human identification. <i>Forensic Science International: Genetics</i> , 2021, 53, 102496.	1.6	19

#	ARTICLE	IF	CITATIONS
191	A Genetic Perspective on Cetacean Evolution. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 2021, 52, 131-151.	3.8	8
192	Uncovering the genomic and metagenomic research potential in old ethanol-preserved snakes. <i>PLoS ONE</i> , 2021, 16, e0256353.	1.1	6
193	Ancient genomes reveal long-range influence of the pre-Columbian culture and site of Tiwanaku. <i>Science Advances</i> , 2021, 7, eabg7261.	4.7	8
194	Performance and automation of ancient DNA capture with RNA hyRAD probes. <i>Molecular Ecology Resources</i> , 2022, 22, 891-907.	2.2	11
195	A 3,000-year-old, basal <i>S. enterica</i> lineage from Bronze Age Xinjiang suggests spread along the Proto-Silk Road. <i>PLoS Pathogens</i> , 2021, 17, e1009886.	2.1	7
196	Molecular advances in archaeological and biological research on Atlantic walrus. , 2021, , 215-249.		2
197	Anthropological genetics perspectives on the transatlantic slave trade. <i>Human Molecular Genetics</i> , 2021, 30, R79-R87.	1.4	18
198	The past, present and future of ancient bacterial DNA. <i>Microbial Genomics</i> , 2020, 6, .	1.0	12
211	Targeted Sequencing of Large Genomic Regions with CATCH-Seq. <i>PLoS ONE</i> , 2014, 9, e111756.	1.1	16
212	Successful Recovery of Nuclear Protein-Coding Genes from Small Insects in Museums Using Illumina Sequencing. <i>PLoS ONE</i> , 2015, 10, e0143929.	1.1	55
213	DNA Metabarcoding of Amazonian Ichthyoplankton Swarms. <i>PLoS ONE</i> , 2017, 12, e0170009.	1.1	23
214	Validation of a Non-Targeted LC-MS Approach for Identifying Ancient Proteins: Method Development on Bone to Improve Artifact Residue Analysis. <i>Ethnobiology Letters</i> , 2015, 6, 162-174.	0.5	20
215	Genomics and metagenomics technologies to recover ribosomal DNA and single-copy genes from old fruit-body and ectomycorrhiza specimens. <i>MycKeys</i> , 0, 13, 1-20.	0.8	21
216	From promise to practice: pairing non-invasive sampling with genomics in conservation. <i>PeerJ</i> , 2015, 3, e1106.	0.9	158
218	Sequencing Strategies. , 2017, , 61-80.		0
226	Emerging palaeoecological frameworks for elucidating plant dynamics in response to fire and other disturbance. <i>Global Ecology and Biogeography</i> , 2022, 31, 138-154.	2.7	13
228	History of Ancient DNA Analysis in Mummy Research. , 2021, , 271-284.		0
229	Genotyping-in-Thousands by sequencing of archival fish scales reveals maintenance of genetic variation following a severe demographic contraction in kokanee salmon. <i>Scientific Reports</i> , 2021, 11, 22798.	1.6	3

#	ARTICLE	IF	CITATIONS
230	Analysis of Low Copy Number DNA and Degraded DNA. , 2021, , 351-370.		0
231	Improved DNA Extraction and Illumina Sequencing of DNA Recovered from Aged Rootless Hair Shafts Found in Relics Associated with the Romanov Family. <i>Genes</i> , 2022, 13, 202.	1.0	7
234	Detection of Low-Copy Human Virus DNA upon Prolonged Formalin Fixation. <i>Viruses</i> , 2022, 14, 133.	1.5	4
235	Conservation genomics and systematics of a near-extinct island radiation. <i>Molecular Ecology</i> , 2022, 31, 1995-2012.	2.0	4
236	Ancient mitochondrial genomes recovered from small vertebrate bones through minimally destructive DNA extraction: Phylogeography of the New Zealand gecko genus <i>Hoplodactylus</i> . <i>Molecular Ecology</i> , 2023, 32, 2964-2984.	2.0	7
237	Quantifying and reducing cross-contamination in single- and multiplex hybridization capture of ancient DNA. <i>Molecular Ecology Resources</i> , 2022, 22, 2196-2207.	2.2	9
238	The untapped potential of macrofossils in ancient plant DNA research. <i>New Phytologist</i> , 2022, 235, 391-401.	3.5	7
239	Assessing the impact of USER-treatment on hyRAD capture applied to ancient DNA. <i>Molecular Ecology Resources</i> , 2022, 22, 2262-2274.	2.2	2
241	A review of the spread and habitat of the genus <i>Homo</i> . <i>Anthropological Science</i> , 2022, , .	0.2	0
242	Exploring the Emergence and Evolution of Plant Pathogenic Microbes Using Historical and Paleontological Sources. <i>Annual Review of Phytopathology</i> , 2022, 60, 187-209.	3.5	8
245	High-throughput method for the hybridisation-based targeted enrichment of long genomic fragments for PacBio third-generation sequencing. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	1.5	7
246	Simultaneously collecting coding and non-coding phylogenomic data using homemade full-length cDNA probes, tested by resolving the high-level relationships of Colubridae. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	1
247	MTaxi: A comparative tool for taxon identification of ultra low coverage ancient genomes. <i>Open Research Europe</i> , 0, 2, 100.	2.0	1
248	Ancient DNA reveals phenological diversity of Coast Salish herring harvests over multiple centuries. <i>Scientific Reports</i> , 2022, 12, .	1.6	0
249	Adenine imprinted beads as a novel selective extracellular DNA extraction method reveals underestimated prevalence of extracellular antibiotic resistance genes in various environments. <i>Science of the Total Environment</i> , 2022, 852, 158570.	3.9	1
250	Assessing the performance of historical skins and bones for museomics using wolf specimens as a case study. <i>Frontiers in Ecology and Evolution</i> , 0, 10, .	1.1	4
251	Insect Landscape Genomics. <i>Population Genomics</i> , 2022, , .	0.2	1
252	Three assays for in-solution enrichment of ancient human DNA at more than a million SNPs. <i>Genome Research</i> , 2022, 32, 2068-2078.	2.4	27

#	ARTICLE	IF	CITATIONS
253	Mitochondrial genomes reveal mid-Pleistocene population divergence, and post-glacial expansion, in Australasian snapper (<i>Chrysophrys auratus</i>). <i>Heredity</i> , 0, , .	1.2	0
254	Methodological Changes in the Field of Paleogenetics. <i>Genes</i> , 2023, 14, 234.	1.0	2
255	Genetic Impoverishment in the Anthropocene: A Tale from Bats. <i>Fascinating Life Sciences</i> , 2022, , 19-31.	0.5	0
256	Ancient genomes reveal the origin and evolutionary history of Chinese populations. <i>Frontiers in Earth Science</i> , 0, 10, .	0.8	0
257	Mitochondrial DNA and its use in the forensic analysis of skeletal material. , 2023, , 213-230.		0
258	Advancements and Challenges in Ancient DNA Research: Bridging the Global Northâ€“South Divide. <i>Genes</i> , 2023, 14, 479.	1.0	0
259	Shallow sequencing can mislead when evaluating hybridization capture methods. <i>Conservation Genetics Resources</i> , 0, , .	0.4	0
265	DNA Fragment Enrichment for High-Throughput Sequencing. <i>Molecular Biology</i> , 2023, 57, 424-439.	0.4	1
278	Terrestrial Fauna and Hominin DNA from Sedimentary Archives. <i>Developments in Paleoenvironmental Research</i> , 2023, , 299-378.	7.5	0
281	Unwrapping the palimpsest of animal domestication through ancient nuclear genomes. , 2024, , .		0