

ANGSD: Analysis of Next Generation Sequencing Data

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Reassessing the Evolutionary History of the 17q21 Inversion Polymorphism. <i>Genome Biology and Evolution</i> , 2015, 7, 3239-3248.	2.5	11
2	Evolutionary history inferred from the de novo assembly of a nonmodel organism, the blue-eyed black lemur. <i>Molecular Ecology</i> , 2015, 24, 4392-4405.	3.9	25
3	Amphibian molecular ecology and how it has informed conservation. <i>Molecular Ecology</i> , 2015, 24, 5084-5109.	3.9	45
4	NgsRelate: a software tool for estimating pairwise relatedness from next-generation sequencing data. <i>Bioinformatics</i> , 2015, 31, 4009-4011.	4.1	109
5	Reticulate Speciation and Barriers to Introgression in the <i>Anopheles gambiae</i> Species Complex. <i>Genome Biology and Evolution</i> , 2015, 7, 3116-3131.	2.5	32
6	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015, 522, 167-172.	27.8	1,166
7	Linked selection and recombination rate variation drive the evolution of the genomic landscape of differentiation across the speciation continuum of <i>Ficedula</i> flycatchers. <i>Genome Research</i> , 2015, 25, 1656-1665.	5.5	385
8	Yak whole-genome resequencing reveals domestication signatures and prehistoric population expansions. <i>Nature Communications</i> , 2015, 6, 10283.	12.8	214
9	Uncovering the Genetic History of the Present-Day Greenlandic Population. <i>American Journal of Human Genetics</i> , 2015, 96, 54-69.	6.2	85
10	Exome and Transcriptome Sequencing of <i>Aedes aegypti</i> Identifies a Locus That Confers Resistance to <i>Brugia malayi</i> and Alters the Immune Response. <i>PLoS Pathogens</i> , 2015, 11, e1004765.	4.7	37
11	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	12.6	449
12	Schmutzi: estimation of contamination and endogenous mitochondrial consensus calling for ancient DNA. <i>Genome Biology</i> , 2015, 16, 224.	8.8	307
13	Genotype-Frequency Estimation from High-Throughput Sequencing Data. <i>Genetics</i> , 2015, 201, 473-486.	2.9	39
14	Ancient Ethiopian genome reveals extensive Eurasian admixture in Eastern Africa. <i>Science</i> , 2015, 350, 820-822.	12.6	277
15	Museum samples reveal rapid evolution by wild honey bees exposed to a novel parasite. <i>Nature Communications</i> , 2015, 6, 7991.	12.8	81
16	Greenlandic Inuit show genetic signatures of diet and climate adaptation. <i>Science</i> , 2015, 349, 1343-1347.	12.6	397
17	Genome-wide patterns of selection in 230 ancient Eurasians. <i>Nature</i> , 2015, 528, 499-503.	27.8	1,160
18	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

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19	Methods and models for unravelling human evolutionary history. <i>Nature Reviews Genetics</i> , 2015, 16, 727-740.	16.3	166
20	Redefining Androgen Receptor Function: Clinical Implications in Understanding Prostate Cancer Progression and Therapeutic Resistance. , 0, , .		0
21	The Use of Genomics in Conservation Management of the Endangered Visayan Warty Pig (<i>Sus</i>) Tj ETQq0 0 0 rgBT/Overlock 10 Tf 50	1.6	12
22	Selection on Coding and Regulatory Variation Maintains Individuality in Major Urinary Protein Scent Marks in Wild Mice. <i>PLoS Genetics</i> , 2016, 12, e1005891.	3.5	46
23	Joint Estimation of Contamination, Error and Demography for Nuclear DNA from Ancient Humans. <i>PLoS Genetics</i> , 2016, 12, e1005972.	3.5	52
24	Genotyping-by-Sequencing SNP Identification for Crops without a Reference Genome: Using Transcriptome Based Mapping as an Alternative Strategy. <i>Frontiers in Plant Science</i> , 2016, 7, 777.	3.6	21
25	Next-Generation Sequencing “ An Overview of the History, Tools, and “Omic” Applications. , 0, , .		94
26	Whole-Genome Sequencing of Native Sheep Provides Insights into Rapid Adaptations to Extreme Environments. <i>Molecular Biology and Evolution</i> , 2016, 33, 2576-2592.	8.9	271
27	Phylogenetics support an ancient common origin of two scientific icons: Devils Hole and Devils Hole pupfish. <i>Molecular Ecology</i> , 2016, 25, 3962-3973.	3.9	24
28	Evolution of <i>GOUNDRY</i> , a cryptic subgroup of <i>Anopheles gambiae</i> s.l., and its impact on susceptibility to <i>Plasmodium</i> infection. <i>Molecular Ecology</i> , 2016, 25, 1494-1510.	3.9	18
29	Evolutionary Patterns and Processes: Lessons from Ancient DNA. <i>Systematic Biology</i> , 2017, 66, syw059.	5.6	73
30	Selective Landscapes in newt Immune Genes Inferred from Patterns of Nucleotide Variation. <i>Genome Biology and Evolution</i> , 2016, 8, 3417-3432.	2.5	13
31	The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild fish. <i>Science</i> , 2016, 354, 1305-1308.	12.6	348
32	A whole mitochondria analysis of the Tyrolean Iceman’s leather provides insights into the animal sources of Copper Age clothing. <i>Scientific Reports</i> , 2016, 6, 31279.	3.3	95
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35	Variation in Linked Selection and Recombination Drive Genomic Divergence during Allopatric Speciation of European and American Aspens. <i>Molecular Biology and Evolution</i> , 2016, 33, 1754-1767.	8.9	83
36	The genetic history of Ice Age Europe. <i>Nature</i> , 2016, 534, 200-205.	27.8	729

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38	The Power of Inbreeding: NGS-Based GWAS of Rice Reveals Convergent Evolution during Rice Domestication. <i>Molecular Plant</i> , 2016, 9, 975-985.	8.3	102
39	<sc>angsd</sc>â€ wrapper: utilities for analysing nextâ€ generation sequencing data. <i>Molecular Ecology Resources</i> , 2016, 16, 1449-1454.	4.8	18
40	Genome-wide SNP data suggest complex ancestry of sympatric North Pacific killer whale ecotypes. <i>Heredity</i> , 2016, 117, 316-325.	2.6	35
41	Domestication history and geographical adaptation inferred from a SNP map of African rice. <i>Nature Genetics</i> , 2016, 48, 1083-1088.	21.4	158
42	Hidden histories of gene flow in highland birds revealed with genomic markers. <i>Molecular Ecology</i> , 2016, 25, 5144-5157.	3.9	64
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46	Genome biogeography reveals the intraspecific spread of adaptive mutations for a complex trait. <i>Molecular Ecology</i> , 2016, 25, 6107-6123.	3.9	51
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48	Genomic insights into the origin of farming in the ancient Near East. <i>Nature</i> , 2016, 536, 419-424.	27.8	733
49	Early Neolithic genomes from the eastern Fertile Crescent. <i>Science</i> , 2016, 353, 499-503.	12.6	230
50	Genome-Wide Divergence in the West-African Malaria Vector <i>Anopheles melas</i> . <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2867-2879.	1.8	10
51	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016, 7, 11693.	12.8	222
52	Feralisation targets different genomic loci to domestication in the chicken. <i>Nature Communications</i> , 2016, 7, 12950.	12.8	60
53	Whole-genome sequence analysis shows that two endemic species of North American wolf are admixtures of the coyote and gray wolf. <i>Science Advances</i> , 2016, 2, e1501714.	10.3	150
54	Full circumpolar migration ensures evolutionary unity in the Emperor penguin. <i>Nature Communications</i> , 2016, 7, 11842.	12.8	43

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56	Possible introgression of the VRTN mutation increasing vertebral number, carcass length and teat number from Chinese pigs into European pigs. <i>Scientific Reports</i> , 2016, 6, 19240.	3.3	58
57	Genomic study of the Ket: a Paleo-Eskimo-related ethnic group with significant ancient North Eurasian ancestry. <i>Scientific Reports</i> , 2016, 6, 20768.	3.3	48
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60	The genetics of an early Neolithic pastoralist from the Zagros, Iran. <i>Scientific Reports</i> , 2016, 6, 31326.	3.3	61
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63	Early farmers from across Europe directly descended from Neolithic Aegeans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 6886-6891.	7.1	376
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70	Evolutionary signals of selection on cognition from the great tit genome and methylome. <i>Nature Communications</i> , 2016, 7, 10474.	12.8	172
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74	Natural Selection and Recombination Rate Variation Shape Nucleotide Polymorphism Across the Genomes of Three Related <i>Populus</i> Species. <i>Genetics</i> , 2016, 202, 1185-1200.	2.9	93
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76	From the field to the laboratory: Controlling DNA contamination in human ancient DNA research in the high-throughput sequencing era. <i>Science and Technology of Archaeological Research</i> , 2017, 3, 1-14.	2.4	126
77	Characterizing restriction enzyme-associated loci in historic ragweed (<i>Ambrosia artemisiifolia</i>) voucher specimens using custom-designed <i>scRNA</i> probes. <i>Molecular Ecology Resources</i> , 2017, 17, 209-220.	4.8	31
78	Deleterious variants in Asian rice and the potential cost of domestication. <i>Molecular Biology and Evolution</i> , 2017, 34, msw296.	8.9	68
79	Population genomics reveals that an anthropophilic population of <i>Aedes aegypti</i> mosquitoes in West Africa recently gave rise to American and Asian populations of this major disease vector. <i>BMC Biology</i> , 2017, 15, 16.	3.8	96
80	Genome-wide data from two early Neolithic East Asian individuals dating to 7700 years ago. <i>Science Advances</i> , 2017, 3, e1601877.	10.3	100
81	Correlated patterns of genetic diversity and differentiation across an avian family. <i>Molecular Ecology</i> , 2017, 26, 3982-3997.	3.9	81
82	Diverse origin of mitochondrial lineages in Iron Age Black Sea Scythians. <i>Scientific Reports</i> , 2017, 7, 43950.	3.3	24
83	Nucleotide diversity in the two co-resident genomes of allopolyploid cotton. <i>Plant Systematics and Evolution</i> , 2017, 303, 1021-1042.	0.9	4
84	Pollutants and Insecticides Drive Local Adaptation in African Malaria Mosquitoes. <i>Molecular Biology and Evolution</i> , 2017, 34, 1261-1275.	8.9	50
85	The evolutionary history of bears is characterized by gene flow across species. <i>Scientific Reports</i> , 2017, 7, 46487.	3.3	176
86	Genome sequencing and population genomic analyses provide insights into the adaptive landscape of silver birch. <i>Nature Genetics</i> , 2017, 49, 904-912.	21.4	221
87	Congruent population structure across paralogous and nonparalogous loci in Salish Sea chum salmon (<i>Oncorhynchus keta</i>). <i>Molecular Ecology</i> , 2017, 26, 4131-4144.	3.9	9
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89	Ancient genomic changes associated with domestication of the horse. <i>Science</i> , 2017, 356, 442-445.	12.6	185
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93	Repeated divergent selection on pigmentation genes in a rapid finch radiation. <i>Science Advances</i> , 2017, 3, e1602404.	10.3	148
94	Extremely low-coverage whole genome sequencing in South Asians captures population genomics information. <i>BMC Genomics</i> , 2017, 18, 396.	2.8	26
95	Paleogenomic Evidence for Multi-generational Mixing between Neolithic Farmers and Mesolithic Hunter-Gatherers in the Lower Danube Basin. <i>Current Biology</i> , 2017, 27, 1801-1810.e10.	3.9	110
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104	Mosaic genome evolution in a recent and rapid avian radiation. <i>Nature Ecology and Evolution</i> , 2017, 1, 1912-1922.	7.8	93
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106	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	12.6	263
107	Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago. <i>Science</i> , 2017, 358, 652-655.	12.6	351
108	Genetic Ancestry of Rapanui before and after European Contact. <i>Current Biology</i> , 2017, 27, 3209-3215.e6.	3.9	25

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109	40,000-Year-Old Individual from Asia Provides Insight into Early Population Structure in Eurasia. <i>Current Biology</i> , 2017, 27, 3202-3208.e9.	3.9	191
110	Evolutionary genomics of grape (<i>Vitis vinifera</i> ssp. <i>vinifera</i>) domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 11715-11720.	7.1	236
111	Ecological plant epigenetics: Evidence from model and non-model species, and the way forward. <i>Ecology Letters</i> , 2017, 20, 1576-1590.	6.4	279
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115	The evolutionary basis of premature migration in Pacific salmon highlights the utility of genomics for informing conservation. <i>Science Advances</i> , 2017, 3, e1603198.	10.3	188
116	Genomic and proteomic identification of Late Holocene remains: Setting baselines for Black Sea odontocetes. <i>Journal of Archaeological Science: Reports</i> , 2017, 15, 262-271.	0.5	6
117	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017, 3, e1700299.	10.3	142
118	Inferring Demographic History Using Genomic Data. <i>Population Genomics</i> , 2017, , 511-537.	0.5	16
119	Extensive Farming in Estonia Started through a Sex-Biased Migration from the Steppe. <i>Current Biology</i> , 2017, 27, 2185-2193.e6.	3.9	111
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123	Continuity and Admixture in the Last Five Millennia of Levantine History from Ancient Canaanite and Present-Day Lebanese Genome Sequences. <i>American Journal of Human Genetics</i> , 2017, 101, 274-282.	6.2	102
124	Whole-genome sequencing approaches for conservation biology: Advantages, limitations and practical recommendations. <i>Molecular Ecology</i> , 2017, 26, 5369-5406.	3.9	249
125	Whole-Genome Sequencing and Concordance Between Antimicrobial Susceptibility Genotypes and Phenotypes of Bacterial Isolates Associated with Bovine Respiratory Disease. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3059-3071.	1.8	19
126	Genetic origins of the Minoans and Mycenaeans. <i>Nature</i> , 2017, 548, 214-218.	27.8	203

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128	Structural variants in genes associated with human Williams-Beuren syndrome underlie stereotypical hypersociability in domestic dogs. <i>Science Advances</i> , 2017, 3, e1700398.	10.3	139
129	Genomic Analysis Reveals Genetic Distinctiveness of the Paiute Cutthroat Trout <i>Oncorhynchus clarkii seleniris</i>. <i>Transactions of the American Fisheries Society</i> , 2017, 146, 1291-1302.	1.4	8
130	Heterogeneous Patterns of Genetic Diversity and Differentiation in European and Siberian Chiffchaff (<i>Phylloscopus collybita abietinus</i>/<i>P. tristis</i>). <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3983-3998.	1.8	4
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132	Archaeogenomic analysis of the first steps of Neolithization in Anatolia and the Aegean. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20172064.	2.6	26
133	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	12.8	105
134	Parallel palaeogenomic transects reveal complex genetic history of early European farmers. <i>Nature</i> , 2017, 551, 368-372.	27.8	306
135	Reproductive isolation and environmental adaptation shape the phylogeography of mountain pine beetle (<i>Dendroctonus ponderosae</i>). <i>Molecular Ecology</i> , 2017, 26, 6071-6084.	3.9	31
136	Genome-Wide Analysis of Colonization History and Concomitant Selection in <i>Arabidopsis lyrata</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 2665-2677.	8.9	31
137	Mining Metagenomic Data Sets for Ancient DNA: Recommended Protocols for Authentication. <i>Trends in Genetics</i> , 2017, 33, 508-520.	6.7	90
138	Estimating genomic diversity and population differentiation “an empirical comparison of microsatellite and SNP variation in <i>Arabidopsis halleri</i> . <i>BMC Genomics</i> , 2017, 18, 69.	2.8	216
139	Genomic history of the origin and domestication of common bean unveils its closest sister species. <i>Genome Biology</i> , 2017, 18, 60.	8.8	142
140	Bioinformatic processing of RAD-seq data dramatically impacts downstream population genetic inference. <i>Methods in Ecology and Evolution</i> , 2017, 8, 907-917.	5.2	253
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142	Inferring Heterozygosity from Ancient and Low Coverage Genomes. <i>Genetics</i> , 2017, 205, 317-332.	2.9	39
143	Investigating kinship of Neolithic post-LBK human remains from Krusza Zamkowa, Poland using ancient DNA. <i>Forensic Science International: Genetics</i> , 2017, 26, 30-39.	3.1	26
144	Practical low-coverage genomewide sequencing of hundreds of individually barcoded samples for population and evolutionary genomics in nonmodel species. <i>Molecular Ecology Resources</i> , 2017, 17, 194-208.	4.8	104

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145	Genomic diversity in <i>Onchocerca volvulus</i> and its <i>Wolbachia</i> endosymbiont. <i>Nature Microbiology</i> , 2017, 2, 16207.	13.3	53
146	Continental-level population differentiation and environmental adaptation in the mushroom <i>Suillus brevipes</i> . <i>Molecular Ecology</i> , 2017, 26, 2063-2076.	3.9	55
147	Discovery and preliminary multi-species evaluation of single nucleotide polymorphism resources for genus <i>Buteo</i> developed from restriction site-associated DNA paired-end data. <i>Conservation Genetics Resources</i> , 2017, 9, 151-156.	0.8	0
148	Sequence and Structural Diversity of Mouse Y Chromosomes. <i>Molecular Biology and Evolution</i> , 2017, 34, 3186-3204.	8.9	54
149	Genomic data reveal a loss of diversity in two species of tuco-tucos (genus <i>Ctenomys</i>) following a volcanic eruption. <i>Scientific Reports</i> , 2017, 7, 16227.	3.3	8
150	The Landscape of Extreme Genomic Variation in the Highly Adaptable Atlantic Killifish. <i>Genome Biology and Evolution</i> , 2017, 9, 659-676.	2.5	43
151	Exome Sequencing Provides Evidence of Polygenic Adaptation to a Fat-Rich Animal Diet in Indigenous Siberian Populations. <i>Molecular Biology and Evolution</i> , 2017, 34, 2913-2926.	8.9	31
152	Genome Analysis Identified Novel Candidate Genes for <i>Ascochyta</i> Blight Resistance in Chickpea Using Whole Genome Re-sequencing Data. <i>Frontiers in Plant Science</i> , 2017, 8, 359.	3.6	53
153	The Role of Alternative Splicing and Differential Gene Expression in Cichlid Adaptive Radiation. <i>Genome Biology and Evolution</i> , 2017, 9, 2764-2781.	2.5	63
154	Genomics clarifies taxonomic boundaries in a difficult species complex. <i>PLoS ONE</i> , 2017, 12, e0189417.	2.5	17
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1435	Museum Genomics of an Agricultural Super-Pest, the Colorado Potato Beetle, <i>Leptinotarsa decemlineata</i> (Chrysomelidae), Provides Evidence of Adaptation from Standing Variation. <i>Integrative and Comparative Biology</i> , 2022, 62, 1827-1837.	2.0	6
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1451	From common gardens to candidate genes: exploring local adaptation to climate in red spruce. <i>New Phytologist</i> , 2023, 237, 1590-1605.	7.3	18
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1466	Advances in coral immunity â€”omics in response to disease outbreaks. <i>Frontiers in Marine Science</i> , 0, 9, .	2.5	5
1467	Chromosome-level genome assembly for the Aldabra giant tortoise enables insights into the genetic health of a threatened population. <i>GigaScience</i> , 2022, 11, .	6.4	5
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1470	Genome report: chromosome-level draft assemblies of the snow leopard, African leopard, and tiger (<i>Panthera uncia</i> , <i>Panthera pardus pardus</i> , and <i>Panthera tigris</i>). <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	1.8	5
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1488	Environmental response in gene expression and DNA methylation reveals factors influencing the adaptive potential of <i>Arabidopsis lyrata</i> . <i>ELife</i> , 0, 11, .	6.0	4
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1520	The demographic history of house mice (<i>Mus musculus domesticus</i>) in eastern North America. <i>G3: Genes, Genomes, Genetics</i> , 2023, 13, .	1.8	8
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1625	Genomics reveals broad hybridization in deeply divergent Palearctic grass and water snakes (<i>Natrix</i>) Tj ETQq1 1 0.784314 rgBT /Overl	2.7	3
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1641	Population Genomics Provide Insights into the Evolution and Adaptation of the Asia Corn Borer. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	5
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1644	Multigenic resistance to <i>Xylella fastidiosa</i> in wild grapes (<i>Vitis</i> spp.) and its implications within a changing climate. <i>Communications Biology</i> , 2023, 6, .	4.4	6
1645	A method to generate capture baits for targeted sequencing. <i>Nucleic Acids Research</i> , 2023, 51, e69-e69.	14.5	1
1646	Next-Generation Sequencing Data-Based Association Testing of a Group of Genetic Markers for Complex Responses Using a Generalized Linear Model Framework. <i>Mathematics</i> , 2023, 11, 2560.	2.2	0
1647	A near-complete genome assembly of the allotetraploid <i>Cenchrus fungigraminus</i> (JUJUNCAO) provides insights into its evolution and C4 photosynthesis. <i>Plant Communications</i> , 2023, 4, 100633.	7.7	5
1649	Emergence of Rice Blast AVR-Pi9 Resistance Breaking Haplotypes in Yunnan Province, China. <i>Life</i> , 2023, 13, 1320.	2.4	1
1651	HaploCart: Human mtDNA haplogroup classification using a pangenomic reference graph. <i>PLoS Computational Biology</i> , 2023, 19, e1011148.	3.2	1
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1655	Genomic signatures of local adaptation in recent invasive <i>Aedes aegypti</i> populations in California. <i>BMC Genomics</i> , 2023, 24, .	2.8	1
1658	North African fox genomes show signatures of repeated introgression and adaptation to life in deserts. <i>Nature Ecology and Evolution</i> , 2023, 7, 1267-1286.	7.8	8
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1662	Migration of Eastern North American monarch butterflies via the South-east and the Atlantic: evidence from stable isotopes, thin layer chromatography, DNA and phenotype. <i>Biological Journal of the Linnean Society</i> , 2023, 139, 294-325.	1.6	1
1663	Historical DNA reveals climate adaptation in an endangered songbird. <i>Nature Climate Change</i> , 2023, 13, 735-741.	18.8	3
1664	Genomic conservation of crop wild relatives: A case study of citrus. <i>PLoS Genetics</i> , 2023, 19, e1010811.	3.5	2
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1668	Iron age genomic data from Althiburos “ Tunisia renew the debate on the origins of African taurine cattle. <i>IScience</i> , 2023, 26, 107196.	4.1	6
1670	Searching for intralocus sexual conflicts in the three-spined stickleback (<i>Gasterosteus</i>) Tj ETQq1 1 0.784314 rgBT./Overlock 10 Tf 50 2.3		
1672	Genomics reveal the origins and current structure of a genetically depauperate freshwater species in its introduced Alaskan range. <i>Evolutionary Applications</i> , 2023, 16, 1119-1134.	3.1	1
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1674	Whole genome sequencing reveals regulatory and low pleiotropy variants underlie local adaptation to environmental variability in purple sea urchins. <i>American Naturalist</i> , 0, , .	2.1	1
1675	Museomics and phylogenomics of lovebirds (Psittaciformes, Psittaculidae, Agapornis) using low-coverage whole-genome sequencing. <i>Molecular Phylogenetics and Evolution</i> , 2023, 185, 107822.	2.7	3
1678	Comparative genomics reveals the hybrid origin of a macaque group. <i>Science Advances</i> , 2023, 9, .	10.3	8
1680	Admixture and introgression obscure evolutionary patterns in lesser whitethroat complex (<i>Curruca</i> <i>curruca</i> ; Passeriformes; Aves). <i>Journal of Avian Biology</i> , 2023, 2023, .	1.2	0
1681	Trans-Acting Genotypes Associated with mRNA Expression Affect Metabolic and Thermal Tolerance Traits. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	2
1684	Estimating admixture pedigrees of recent hybrids without a contiguous reference genome. <i>Molecular Ecology Resources</i> , 2023, 23, 1604-1619.	4.8	1
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1686	Whole-genome Analyses Reveal Past Population Fluctuations and Low Genetic Diversities of the North Pacific Albatrosses. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	2
1687	A review of genomics methods and bioinformatics tools for the analysis of close-kin mark-recapture. <i>Frontiers in Marine Science</i> , 0, 10, .	2.5	2
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1691	The extinct Sicilian wolf shows a complex history of isolation and admixture with ancient dogs. <i>IScience</i> , 2023, 26, 107307.	4.1	2

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1693	Chromosome-level genome assembly and population genomic analysis reveal evolution and local adaptation in common hairfin anchovy (<i>Setipinna tenuifilis</i>). <i>Molecular Ecology</i> , 0, , .	3.9	0
1694	ngsJulia: population genetic analysis of next-generation DNA sequencing data with Julia language. <i>F1000Research</i> , 0, 11, 126.	1.6	0
1695	Sampling affects population genetic inference: a case study of the Allen's (<i>Selasphorus sasin</i>) and rufous hummingbird (<i>Selasphorus rufus</i>). <i>Journal of Heredity</i> , 0, , .	2.4	0
1699	Characterising a genetic stronghold amidst pervasive admixture: Morelet's crocodiles (<i>Crocodylus</i>) Tj ETQq0 0 0 rgBT /Overlock 10 T	1.5	0
1702	Bioarchaeological and paleogenomic profiling of the unusual Neolithic burial from Grotta di Pietra Sant'Angelo (Calabria, Italy). <i>Scientific Reports</i> , 2023, 13, .	3.3	0
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1705	Ancient cattle DNA provides novel insight into the subsistence mode transition from the late Neolithic to Bronze Age in the Nenjiang River Basin. <i>Journal of Archaeological Science: Reports</i> , 2023, 51, 104136.	0.5	1
1707	A multidisciplinary study on the social customs of the Tang Empire in the Medieval Ages. <i>PLoS ONE</i> , 2023, 18, e0288128.	2.5	0
1708	Extensive pedigrees reveal the social organization of a Neolithic community. <i>Nature</i> , 2023, 620, 600-606.	27.8	16
1709	Insights into the genetic histories and lifeways of Machu Picchu's occupants. <i>Science Advances</i> , 2023, 9, .	10.3	4
1710	Ecological differences among hydrothermal vent symbioses may drive contrasting patterns of symbiont population differentiation. <i>MSystems</i> , 0, , .	3.8	2
1712	Ancient dolphin genomes reveal rapid repeated adaptation to coastal waters. <i>Nature Communications</i> , 2023, 14, .	12.8	0
1714	Genomic history of coastal societies from eastern South America. <i>Nature Ecology and Evolution</i> , 2023, 7, 1315-1330.	7.8	3
1716	Mid-Pleistocene Transitions Forced Himalayan ibex to Evolve Independently after Split into an Allopatric Refugium. <i>Biology</i> , 2023, 12, 1097.	2.8	0
1717	Seasonal variation in defense behavior in European and scutellata-hybrid honey bees (<i>Apis mellifera</i>) in Southern California. <i>Scientific Reports</i> , 2023, 13, .	3.3	2
1718	Historic Sampling of a Vanishing Beast: Population Structure and Diversity in the Black Rhinoceros. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	3
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1722	Genetic continuity, isolation, and gene flow in Stone Age Central and Eastern Europe. <i>Communications Biology</i> , 2023, 6, .	4.4	5
1725	High-coverage genome of the Tyrolean Iceman reveals unusually high Anatolian farmer ancestry. <i>Cell Genomics</i> , 2023, 3, 100377.	6.5	4
1729	Geographic Variation in Genomic Signals of Admixture Between Two Closely Related European Sepsid Fly Species. <i>Evolutionary Biology</i> , 0, , .	1.1	0
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1735	<i>De novo</i> mutation rates in sticklebacks. <i>Molecular Biology and Evolution</i> , 0, , .	8.9	0
1737	Ancient DNA reveals genetic admixture in China during tiger evolution. <i>Nature Ecology and Evolution</i> , 2023, 7, 1914-1929.	7.8	3
1738	Ploidy Variation and Its Implications for Reproduction and Population Dynamics in Two Sympatric Hawaiian Coral Species. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	2
1739	Don't mind if I do: Arctic humpback whales respond to winter foraging opportunities before migration. <i>Royal Society Open Science</i> , 2023, 10, .	2.4	1
1740	Ancient <i>Yersinia pestis</i> genomes lack the virulence-associated Ypf prophage present in modern pandemic strains. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2023, 290, .	2.6	1
1741	Uncovering the genetic architecture of parallel evolution. <i>Molecular Ecology</i> , 2023, 32, 5575-5589.	3.9	0
1742	Whole genome assessment of a declining game bird reveals cryptic genetic structure and insights for population management. <i>Molecular Ecology</i> , 2023, 32, 5498-5513.	3.9	1
1743	Holocene deglaciation drove rapid genetic diversification of Atlantic walrus. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2023, 290, .	2.6	0
1744	Fine-scale sampling uncovers the complexity of migrations in 5th–6th century Pannonia. <i>Current Biology</i> , 2023, 33, 3951-3961.e11.	3.9	2
1745	Genome-wide DNA methylation patterns in bumble bee (<i>Bombus vosnesenskii</i>) populations from spatial-environmental range extremes. <i>Scientific Reports</i> , 2023, 13, .	3.3	3
1747	Genomic Variation, Population History, and Long-Term Genetic Adaptation to High Altitudes in Tibetan Partridge (<i>Perdix hodgsoniae</i>). <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	0

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1749	Allele surfing causes maladaptation in a Pacific salmon of conservation concern. <i>PLoS Genetics</i> , 2023, 19, e1010918.	3.5	0
1750	Patterns of phylogenetic diversification in the Dollarbird (<i>Eurystomus orientalis</i>) and Azure Roller (<i>Eurystomus azureus</i>) complex. <i>Molecular Phylogenetics and Evolution</i> , 2023, 189, 107909.	2.7	0
1751	Uncovering neutral and adaptive genomic differentiation among European perch with brackish water and freshwater origin in the western Baltic Sea region. <i>Fisheries Research</i> , 2023, 268, 106846.	1.7	0
1752	Contrasting genomic consequences of anthropogenic reintroduction and natural recolonization in highâ€arctic wild reindeer. <i>Evolutionary Applications</i> , 2023, 16, 1531-1548.	3.1	2
1753	Population evolution of seagrasses returning to the ocean. <i>Heliyon</i> , 2023, 9, e20231.	3.2	0
1754	Can demographic histories explain longâ€term isolation and recent pulses of asymmetric gene flow between highly divergent grey fox lineages?. <i>Molecular Ecology</i> , 2023, 32, 5323-5337.	3.9	2
1756	Patrilocal and hunter-gatherer-related ancestry of populations in East-Central Europe during the Middle Bronze Age. <i>Nature Communications</i> , 2023, 14, .	12.8	3
1757	<i>Porites astreoides</i> coral populations demonstrate high clonality and connectivity in southeast Florida. <i>Coral Reefs</i> , 2023, 42, 1131-1145.	2.2	2
1758	Genomic signatures of disease resistance in endangered staghorn corals. <i>Science</i> , 2023, 381, 1451-1454.	12.6	4
1759	First genome-wide data from Italian European beech (<i>Fagus sylvatica</i> L.): Strong and ancient differentiation between Alps and Apennines. <i>PLoS ONE</i> , 2023, 18, e0288986.	2.5	0
1760	Practical application of the linkage disequilibrium method for estimating contemporary effective population size: A review. <i>Molecular Ecology Resources</i> , 2024, 24, .	4.8	2
1761	Implementation of different relationship estimate methodologies in breeding value prediction in kiwiberry (<i>Actinidia arguta</i>). <i>Molecular Breeding</i> , 2023, 43, .	2.1	0
1762	Genome-wide association studies of human and rat BMI converge on synapse, epigenome, and hormone signaling networks. <i>Cell Reports</i> , 2023, 42, 112873.	6.4	4
1763	Contrasting whole-genome and reduced representation sequencing for population demographic and adaptive inference: an alpine mammal case study. <i>Heredity</i> , 2023, 131, 273-281.	2.6	2
1765	Dense residential areas promote gene flow in dengue vector mosquito <i>Aedes albopictus</i> . <i>IScience</i> , 2023, 26, 107577.	4.1	0
1766	Marine heatwaves threaten cryptic coral diversity and erode associations among coevolving partners. <i>Science Advances</i> , 2023, 9, .	10.3	4
1768	Descent, marriage, and residence practices of a 3,800-year-old pastoral community in Central Eurasia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2023, 120, .	7.1	4

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1772	Pangolin Genomes Offer Key Insights and Resources for the World’s Most Trafficked Wild Mammals. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	1
1774	Fine-scale environmentally associated spatial structure of lumpfish (<i>Cyclopterus lumpus</i>) across the Northwest Atlantic. <i>Evolutionary Applications</i> , 2023, 16, 1619-1636.	3.1	0
1776	Genetic identification of members of the prominent Břithory aristocratic family. <i>IScience</i> , 2023, 26, 107911.	4.1	1
1780	Analysis of population structure and genetic diversity in low-variance Saimaa ringed seals using low-coverage whole-genome sequence data. <i>STAR Protocols</i> , 2023, 4, 102567.	1.2	0
1782	Candidate gene polymorphisms are linked to dispersive and migratory behaviour: Searching for a mechanism behind the ‘paradox of the great speciators’ <i>Journal of Evolutionary Biology</i> , 2023, 36, 1503-1516.	1.7	2
1783	Community-wide genome sequencing reveals 30 years of Darwin’s finch evolution. <i>Science</i> , 2023, 381, .	12.6	6
1784	Adulis and the transshipment of baboons during classical antiquity. <i>ELife</i> , 0, 12, .	6.0	0
1785	On Roth’s ‘human fossil’ from Baradero, Buenos Aires Province, Argentina: morphological and genetic analysis. <i>Swiss Journal of Palaeontology</i> , 2023, 142, .	1.7	4
1789	Review: Computational analysis of human skeletal remains in ancient DNA and forensic genetics. <i>IScience</i> , 2023, 26, 108066.	4.1	0
1790	Hybridization of Atlantic puffins in the Arctic coincides with 20th-century climate change. <i>Science Advances</i> , 2023, 9, .	10.3	0
1791	Rivers have shaped the phylogeography of a narrowly distributed cycad lineage in Southwest China. <i>Conservation Genetics</i> , 0, , .	1.5	0
1794	Ancestry testing of ‘Old Tom,’ a killer whale central to mutualistic interactions with human whalers. <i>Journal of Heredity</i> , 0, , .	2.4	0
1795	Genomic analysis reveals limited hybridization among three giraffe species in Kenya. <i>BMC Biology</i> , 2023, 21, .	3.8	2
1797	Conservation implications of diverse demographic histories: the case study of green peafowl (<i>Pavo</i>) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	1.5	0
1798	Combining genomic and field analyses to reveal migratory status in a burrowing owl population. <i>Conservation Genetics</i> , 2024, 25, 427-437.	1.5	0
1799	Range-wide and temporal genomic analyses reveal the consequences of near-extinction in Swedish moose. <i>Communications Biology</i> , 2023, 6, .	4.4	0
1800	Reduction of genetic diversity in ‘Alalā (Hawaiian crow; <i>Corvus hawaiiensis</i>) between the late 1800s and the late 1900s. <i>Journal of Heredity</i> , 0, , .	2.4	0

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1804	Concurrent invasions of European starlings in Australia and North America reveal population-specific differentiation in shared genomic regions. <i>Molecular Ecology</i> , 0, , .	3.9	0
1805	Biological and substitute parents in Beaker period adult-child graves. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
1806	Estimating microhaplotype allele frequencies from low-coverage or pooled sequencing data. <i>BMC Bioinformatics</i> , 2023, 24, .	2.6	1
1807	Panmixia in the American eel extends to its tropical range of distribution: Biological implications and policymaking challenges. <i>Evolutionary Applications</i> , 2023, 16, 1872-1888.	3.1	0
1808	Population genomics of the muskox' resilience in the near absence of genetic variation. <i>Molecular Ecology</i> , 2024, 33, .	3.9	1
1809	Determinants of genetic diversity in Neotropical salamanders (Plethodontidae: Bolitoglossini). <i>Ecology and Evolution</i> , 2023, 13, .	1.9	0
1810	Ancient DNA sheds light on the origin and migration patterns of the Xianbei confederation. <i>Archaeological and Anthropological Sciences</i> , 2023, 15, .	1.8	0
1811	Genetic continuity and change among the Indigenous peoples of California. <i>Nature</i> , 2023, 624, 122-129.	27.8	1
1812	Deleterious and Adaptive Mutations in Plant Germplasm Conserved Ex Situ. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	0
1814	Limited historical admixture between European wildcats and domestic cats. <i>Current Biology</i> , 2023, 33, 4751-4760.e14.	3.9	2
1817	Relationships of Late Pleistocene giant deer as revealed by <i>Sinomegaceros</i> mitogenomes from East Asia. <i>IScience</i> , 2023, 26, 108406.	4.1	0
1818	Impact of Holocene environmental change on the evolutionary ecology of an Arctic top predator. <i>Science Advances</i> , 2023, 9, .	10.3	0
1819	Redefining the Evolutionary History of the Rock Dove, <i>Columba livia</i> , Using Whole Genome Sequences. <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	0
1820	Ancient Wheat Genomes Illuminate Domestication, Dispersal, and Diversity. <i>Compendium of Plant Genomes</i> , 2024, , 113-134.	0.5	0
1825	Extensive Phylogenomic Discordance and the Complex Evolutionary History of the Neotropical Cat Genus <i>Leopardus</i> . <i>Molecular Biology and Evolution</i> , 2023, 40, .	8.9	1
1827	Genome-wide analysis of the harbour porpoise (<i>Phocoena phocoena</i>) indicates isolation-by-distance across the North Atlantic and potential local adaptation in adjacent waters. <i>Conservation Genetics</i> , 0, , .	1.5	0
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1831	Identifying risk variants for embryo aneuploidy using ultra-low coverage whole-genome sequencing from preimplantation genetic testing. <i>American Journal of Human Genetics</i> , 2023, 110, 2092-2102.	6.2	0
1836	Ancient genome analyses shed light on the origin and kinship among humans of a cliff tomb from southwestern China. <i>Journal of Archaeological Science: Reports</i> , 2024, 53, 104333.	0.5	0
1837	A genetic history of the Balkans from Roman frontier to Slavic migrations. <i>Cell</i> , 2023, 186, 5472-5485.e9.	28.9	0
1838	Overcoming barriers to reef restoration: field-based method for approximate genotyping of <i>Acropora cervicornis</i> . <i>Restoration Ecology</i> , 2024, 32, .	2.9	0
1839	Genomic insights into the Montseny brook newt (<i>Calotriton arnoldi</i>), a Critically Endangered glacial relict. <i>IScience</i> , 2024, 27, 108665.	4.1	0
1841	Widespread deviant patterns of heterozygosity in whole-genome sequencing due to autopolyploidy, repeated elements, and duplication. <i>Genome Biology and Evolution</i> , 0, , .	2.5	0
1842	How Veeries vary: Whole genome sequencing resolves genetic structure in a long-distance migratory bird. <i>Auk</i> , 0, , .	1.4	1
1843	A genomic region associated with iteroparous spawning phenology is linked with age-at-maturity in female steelhead trout. <i>Evolutionary Applications</i> , 2024, 17, .	3.1	0
1844	Phylogenomic species delimitation of the twisted-winged parasite genus <i>Stylops</i> (<i>Strepsiptera</i>). <i>Systematic Entomology</i> , 2024, 49, 294-313.	3.9	0
1845	Two teosintes made modern maize. <i>Science</i> , 2023, 382, .	12.6	8
1846	Genomic analysis of wolves from Pakistan clarifies boundaries among three divergent wolf lineages. <i>Journal of Heredity</i> , 0, , .	2.4	0
1848	The history of Coast Salish "woolly dogs" revealed by ancient genomics and Indigenous Knowledge. <i>Science</i> , 2023, 382, 1303-1308.	12.6	1
1849	Ancient dog DNA reveals the human livelihood mode transitions during the late Neolithic in Northeastern China. <i>Journal of Archaeological Science: Reports</i> , 2024, 53, 104349.	0.5	0
1851	Identification and high-throughput genotyping of single nucleotide polymorphism markers in a non-model conifer (<i>Abies nordmanniana</i> (Steven) Spach). <i>Scientific Reports</i> , 2023, 13, .	3.3	0
1852	An individual with Sarmatian-related ancestry in Roman Britain. <i>Current Biology</i> , 2023, , .	3.9	0
1854	Genealogical Analyses of 3 Cultivated and 1 Wild Specimen of <i>Vitis vinifera</i> from Greece. <i>Genome Biology and Evolution</i> , 2023, 15, .	2.5	0
1856	Genomic portrait and relatedness patterns of the Iron Age Log Coffin culture in northwestern Thailand. <i>Nature Communications</i> , 2023, 14, .	12.8	1
1857	Genomic analysis supports Cape Lion population connectivity prior to colonial eradication and extinction. <i>Journal of Heredity</i> , 2024, 115, 155-165.	2.4	0

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1858	Ancient genomes reveal the origin and kinship burial patterns of human remains during the 11th to 13th centuries in northern China. <i>International Journal of Osteoarchaeology</i> , 2024, 34, .	1.2	0
1859	Whole-genome sequencing provides novel insights into the evolutionary history and genetic adaptation of reindeer populations in northern Eurasia. <i>Scientific Reports</i> , 2023, 13, .	3.3	0
1860	Population genomic data reveal low genetic diversity, divergence and local adaptation among threatened Reeves's Pheasant (<i>Syrnaticus reevesii</i>). <i>Avian Research</i> , 2024, 15, 100156.	1.2	0
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