

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.	1.1	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.	2.0	25
3	Amphibian molecular ecology and how it has informed conservation. <i>Molecular Ecology</i> , 2015, 24, 5084-5109.	2.0	45
4	NgsRelate: a software tool for estimating pairwise relatedness from next-generation sequencing data. <i>Bioinformatics</i> , 2015, 31, 4009-4011.	1.8	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.	1.1	32
6	Population genomics of Bronze Age Eurasia. <i>Nature</i> , 2015, 522, 167-172.	13.7	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.	2.4	385
8	Yak whole-genome resequencing reveals domestication signatures and prehistoric population expansions. <i>Nature Communications</i> , 2015, 6, 10283.	5.8	214
9	Uncovering the Genetic History of the Present-Day Greenlandic Population. <i>American Journal of Human Genetics</i> , 2015, 96, 54-69.	2.6	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.	2.1	37
11	Genomic evidence for the Pleistocene and recent population history of Native Americans. <i>Science</i> , 2015, 349, aab3884.	6.0	449
12	Schmutzi: estimation of contamination and endogenous mitochondrial consensus calling for ancient DNA. <i>Genome Biology</i> , 2015, 16, 224.	3.8	307
13	Genotype-Frequency Estimation from High-Throughput Sequencing Data. <i>Genetics</i> , 2015, 201, 473-486.	1.2	39
14	Ancient Ethiopian genome reveals extensive Eurasian admixture in Eastern Africa. <i>Science</i> , 2015, 350, 820-822.	6.0	277
15	Museum samples reveal rapid evolution by wild honey bees exposed to a novel parasite. <i>Nature Communications</i> , 2015, 6, 7991.	5.8	81
16	Greenlandic Inuit show genetic signatures of diet and climate adaptation. <i>Science</i> , 2015, 349, 1343-1347.	6.0	397
17	Genome-wide patterns of selection in 230 ancient Eurasians. <i>Nature</i> , 2015, 528, 499-503.	13.7	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.	3.3	139

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19	Methods and models for unravelling human evolutionary history. <i>Nature Reviews Genetics</i> , 2015, 16, 727-740.	7.7	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	0.8	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.	1.5	46
23	Joint Estimation of Contamination, Error and Demography for Nuclear DNA from Ancient Humans. <i>PLoS Genetics</i> , 2016, 12, e1005972.	1.5	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.	1.7	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.	3.5	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.	2.0	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.	2.0	18
29	Evolutionary Patterns and Processes: Lessons from Ancient DNA. <i>Systematic Biology</i> , 2017, 66, syw059.	2.7	73
30	Selective Landscapes in newt Immune Genes Inferred from Patterns of Nucleotide Variation. <i>Genome Biology and Evolution</i> , 2016, 8, 3417-3432.	1.1	13
31	The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild fish. <i>Science</i> , 2016, 354, 1305-1308.	6.0	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.	1.6	95
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34	Population genomics of the filarial nematode parasite <i>Wuchereria bancrofti</i> from mosquitoes. <i>Molecular Ecology</i> , 2016, 25, 1465-1477.	2.0	38
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.	3.5	83
36	The genetic history of Ice Age Europe. <i>Nature</i> , 2016, 534, 200-205.	13.7	729

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37	Estimating IBD tracts from low coverage NGS data. <i>Bioinformatics</i> , 2016, 32, 2096-2102.	1.8	36
38	The Power of Inbreeding: NGS-Based GWAS of Rice Reveals Convergent Evolution during Rice Domestication. <i>Molecular Plant</i> , 2016, 9, 975-985.	3.9	102
39	<sc>angsd</sc>â€ wrapper: utilities for analysing nextâ€ generation sequencing data. <i>Molecular Ecology Resources</i> , 2016, 16, 1449-1454.	2.2	18
40	Genome-wide SNP data suggest complex ancestry of sympatric North Pacific killer whale ecotypes. <i>Heredity</i> , 2016, 117, 316-325.	1.2	35
41	Domestication history and geographical adaptation inferred from a SNP map of African rice. <i>Nature Genetics</i> , 2016, 48, 1083-1088.	9.4	158
42	Hidden histories of gene flow in highland birds revealed with genomic markers. <i>Molecular Ecology</i> , 2016, 25, 5144-5157.	2.0	64
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44	Genomic Methods Take the Plunge: Recent Advances in High-Throughput Sequencing of Marine Mammals. <i>Journal of Heredity</i> , 2016, 107, 481-495.	1.0	50
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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.	2.0	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.	13.7	733
49	Early Neolithic genomes from the eastern Fertile Crescent. <i>Science</i> , 2016, 353, 499-503.	6.0	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.	0.8	10
51	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016, 7, 11693.	5.8	222
52	Feralisation targets different genomic loci to domestication in the chicken. <i>Nature Communications</i> , 2016, 7, 12950.	5.8	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.	4.7	150
54	Full circumpolar migration ensures evolutionary unity in the Emperor penguin. <i>Nature Communications</i> , 2016, 7, 11842.	5.8	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.	1.6	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.	1.6	48
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60	The genetics of an early Neolithic pastoralist from the Zagros, Iran. <i>Scientific Reports</i> , 2016, 6, 31326.	1.6	61
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62	MODEM: multi-omics data envelopment and mining in maize. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw117.	1.4	39
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.	3.3	376
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67	Maintenance of Species Boundaries Despite Ongoing Gene Flow in Ragworts. <i>Genome Biology and Evolution</i> , 2016, 8, 1038-1047.	1.1	18
68	Conservation genomics of natural and managed populations: building a conceptual and practical framework. <i>Molecular Ecology</i> , 2016, 25, 2967-2977.	2.0	141
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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.	5.8	172
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72	RAD Capture (Rapture): Flexible and Efficient Sequence-Based Genotyping. <i>Genetics</i> , 2016, 202, 389-400.	1.2	366

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73	Genomic signals of migration and continuity in Britain before the Anglo-Saxons. <i>Nature Communications</i> , 2016, 7, 10326.	5.8	100
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.	1.2	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 RNA probes. <i>Molecular Ecology Resources</i> , 2017, 17, 209-220.	2.2	31
78	Deleterious variants in Asian rice and the potential cost of domestication. <i>Molecular Biology and Evolution</i> , 2017, 34, msw296.	3.5	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.	1.7	96
80	Genome-wide data from two early Neolithic East Asian individuals dating to 7700 years ago. <i>Science Advances</i> , 2017, 3, e1601877.	4.7	100
81	Correlated patterns of genetic diversity and differentiation across an avian family. <i>Molecular Ecology</i> , 2017, 26, 3982-3997.	2.0	81
82	Diverse origin of mitochondrial lineages in Iron Age Black Sea Scythians. <i>Scientific Reports</i> , 2017, 7, 43950.	1.6	24
83	Nucleotide diversity in the two co-resident genomes of allopolyploid cotton. <i>Plant Systematics and Evolution</i> , 2017, 303, 1021-1042.	0.3	4
84	Pollutants and Insecticides Drive Local Adaptation in African Malaria Mosquitoes. <i>Molecular Biology and Evolution</i> , 2017, 34, 1261-1275.	3.5	50
85	The evolutionary history of bears is characterized by gene flow across species. <i>Scientific Reports</i> , 2017, 7, 46487.	1.6	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.	9.4	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.	2.0	9
88	Genetic diversity is largely unpredictable but scales with museum occurrences in a species-rich clade of Australian lizards. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2017, 284, 20162588.	1.2	18
89	Ancient genomic changes associated with domestication of the horse. <i>Science</i> , 2017, 356, 442-445.	6.0	185
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93	Repeated divergent selection on pigmentation genes in a rapid finch radiation. <i>Science Advances</i> , 2017, 3, e1602404.	4.7	148
94	Extremely low-coverage whole genome sequencing in South Asians captures population genomics information. <i>BMC Genomics</i> , 2017, 18, 396.	1.2	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.	1.8	110
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97	Young inversion with multiple linked QTLs under selection in a hybrid zone. <i>Nature Ecology and Evolution</i> , 2017, 1, 119.	3.4	94
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99	Molecular Population Genetics. <i>Genetics</i> , 2017, 205, 1003-1035.	1.2	100
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101	Late Danubian mitochondrial genomes shed light into the Neolithisation of Central Europe in the 5th millennium BC. <i>BMC Evolutionary Biology</i> , 2017, 17, 80.	3.2	13
102	Genotype Calling from Population-Genomic Sequencing Data. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 1393-1404.	0.8	84
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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.	3.4	93
105	Natural Selection on Genes Related to Cardiovascular Health in High-Altitude Adapted Andeans. <i>American Journal of Human Genetics</i> , 2017, 101, 752-767.	2.6	99
106	Ancient genomes show social and reproductive behavior of early Upper Paleolithic foragers. <i>Science</i> , 2017, 358, 659-662.	6.0	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.	6.0	351
108	Genetic Ancestry of Rapanui before and after European Contact. <i>Current Biology</i> , 2017, 27, 3209-3215.e6.	1.8	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.	1.8	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.	3.3	236
111	Ecological plant epigenetics: Evidence from model and non-model species, and the way forward. <i>Ecology Letters</i> , 2017, 20, 1576-1590.	3.0	279
112	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.	3.3	140
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114	Chromosome arm-specific patterns of polymorphism associated with chromosomal inversions in the major African malaria vector, <i>Anopheles funestus</i> . <i>Molecular Ecology</i> , 2017, 26, 5552-5566.	2.0	9
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.	4.7	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.	0.2	6
117	Genome-wide signatures of complex introgression and adaptive evolution in the big cats. <i>Science Advances</i> , 2017, 3, e1700299.	4.7	142
118	Inferring Demographic History Using Genomic Data. <i>Population Genomics</i> , 2017, , 511-537.	0.2	16
119	Extensive Farming in Estonia Started through a Sex-Biased Migration from the Steppe. <i>Current Biology</i> , 2017, 27, 2185-2193.e6.	1.8	111
120	Evaluating hybridization capture with <i>scp</i> RAD probes as a tool for museum genomics with historical bird specimens. <i>Ecology and Evolution</i> , 2017, 7, 4755-4767.	0.8	34
121	The Discovery of Wild Date Palms in Oman Reveals a Complex Domestication History Involving Centers in the Middle East and Africa. <i>Current Biology</i> , 2017, 27, 2211-2218.e8.	1.8	63
122	Range instability leads to cytonuclear discordance in a morphologically cryptic ground squirrel species complex. <i>Molecular Ecology</i> , 2017, 26, 4743-4755.	2.0	23
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.	2.6	102
124	Whole-genome sequencing approaches for conservation biology: Advantages, limitations and practical recommendations. <i>Molecular Ecology</i> , 2017, 26, 5369-5406.	2.0	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.	0.8	19
126	Genetic origins of the Minoans and Mycenaeans. <i>Nature</i> , 2017, 548, 214-218.	13.7	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.	4.7	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.	0.6	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.	0.8	4
131	Computational prediction of the phenotypic effects of genetic variants: basic concepts and some application examples in <i>Drosophila</i> nervous system genes. <i>Journal of Neurogenetics</i> , 2017, 31, 307-319.	0.6	2
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.	1.2	26
133	The effect of artificial selection on phenotypic plasticity in maize. <i>Nature Communications</i> , 2017, 8, 1348.	5.8	105
134	Parallel palaeogenomic transects reveal complex genetic history of early European farmers. <i>Nature</i> , 2017, 551, 368-372.	13.7	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.	2.0	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.	3.5	31
137	Mining Metagenomic Data Sets for Ancient DNA: Recommended Protocols for Authentication. <i>Trends in Genetics</i> , 2017, 33, 508-520.	2.9	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.	1.2	216
139	Genomic history of the origin and domestication of common bean unveils its closest sister species. <i>Genome Biology</i> , 2017, 18, 60.	3.8	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.	2.2	253
141	Partitioning the effects of isolation by distance, environment, and physical barriers on genomic divergence between parapatric threespine stickleback. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 342-356.	1.1	32
142	Inferring Heterozygosity from Ancient and Low Coverage Genomes. <i>Genetics</i> , 2017, 205, 317-332.	1.2	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.	1.6	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.	2.2	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.	5.9	53
146	Continental-level population differentiation and environmental adaptation in the mushroom <i>Ustilago violacea</i> . <i>Molecular Ecology</i> , 2017, 26, 2063-2076.	2.0	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.	0.4	0
148	Sequence and Structural Diversity of Mouse Y Chromosomes. <i>Molecular Biology and Evolution</i> , 2017, 34, 3186-3204.	3.5	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.	1.6	8
150	The Landscape of Extreme Genomic Variation in the Highly Adaptable Atlantic Killifish. <i>Genome Biology and Evolution</i> , 2017, 9, 659-676.	1.1	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.	3.5	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.	1.7	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.	1.1	63
154	Genomics clarifies taxonomic boundaries in a difficult species complex. <i>PLoS ONE</i> , 2017, 12, e0189417.	1.1	17
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268	Adaptive introgression underlies polymorphic seasonal camouflage in snowshoe hares. <i>Science</i> , 2018, 360, 1355-1358. doi:10.1126/science.1258000	6.0	234
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300	Stacks 2: Analytical methods for paired-end sequencing improve RADseq-based population genomics. <i>Molecular Ecology</i> , 2019, 28, 4737-4754.	2.0	648
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1222	A unified genealogy of modern and ancient genomes. <i>Science</i> , 2022, 375, eabi8264.	6.0	59
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1233	Population structure in Neotropical plants: Integrating pollination biology, topography and climatic niches. <i>Molecular Ecology</i> , 2022, 31, 2264-2280.	2.0	10
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1242	Low-coverage reduced representation sequencing reveals subtle within-island genetic structure in Aldabra giant tortoises. <i>Ecology and Evolution</i> , 2022, 12, e8739.	0.8	4
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1282	Genomic changes underlying repeated niche shifts in an adaptive radiation. <i>Evolution; International Journal of Organic Evolution</i> , 2022, 76, 1301-1319.	1.1	3
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1285	The genomic prehistory of the Indigenous peoples of Uruguay. , 2022, 1, .		7
1286	High genomic diversity in the endangered East Greenland Svalbard Barents Sea stock of bowhead whales (<i>Balaena mysticetus</i>). <i>Scientific Reports</i> , 2022, 12, 6118.	1.6	2
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1329	Ancient mitochondrial and modern whole genomes unravel massive genetic diversity loss during near extinction of Alpine ibex. <i>Molecular Ecology</i> , 2022, 31, 3548-3565.	2.0	9
1330	Genomic insights into recent species divergence in <i>Nicotiana benthamiana</i> and natural variation in <i>Rdr1</i> gene controlling viral susceptibility. <i>Plant Journal</i> , 2022, 111, 7-18.	2.8	9
1331	The flying spider-monkey tree fern genome provides insights into fern evolution and arborescence. <i>Nature Plants</i> , 2022, 8, 500-512.	4.7	42
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1350	Bioarchaeological and palaeogenomic portrait of two Pompeians that died during the eruption of Vesuvius in 79 AD. <i>Scientific Reports</i> , 2022, 12, .	1.6	6
1351	Polygenic discrimination of migratory phenotypes in an estuarine forage fish. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
1352	The genetic origin of Huns, Avars, and conquering Hungarians. <i>Current Biology</i> , 2022, 32, 2858-2870.e7.	1.8	18
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1355	Potential millennial-scale avian declines by humans in southern China. <i>Global Change Biology</i> , 2022, 28, 5505-5513.	4.2	5
1356	Genomic status of yellow-breasted bunting following recent rapid population decline. <i>IScience</i> , 2022, 25, 104501.	1.9	1
1357	A guide to avian museomics: Insights gained from resequencing hundreds of avian study skins. <i>Molecular Ecology Resources</i> , 2022, 22, 2672-2684.	2.2	19
1358	distAngsd: Fast and Accurate Inference of Genetic Distances for Next-Generation Sequencing Data. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	1
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1362	Travel Tales of a Worldwide Weed: Genomic Signatures of <i>Plantago major</i> L. Reveal Distinct Genotypic Groups With Links to Colonial Trade Routes. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	4
1363	Genomics facilitates evaluation and monitoring of McCloud River Redband Trout (<i>Oncorhynchus</i>) Tj ETQq1 1 0.784314 rgBT /Overloc	0.8	0
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1371	Moment estimators of relatedness from low-depth whole-genome sequencing data. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
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1374	The genomic signature of wild-to-crop introgression during the domestication of scarlet runner bean (<i>Phaseolus coccineus</i> L.). <i>Evolution Letters</i> , 2022, 6, 295-307.	1.6	1
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1390	Revised Species Delimitation in the Giant Water Lily Genus <i>Victoria</i> (Nymphaeaceae) Confirms a New Species and Has Implications for Its Conservation. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	9
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1397	Phylogenomics of the world's otters. <i>Current Biology</i> , 2022, 32, 3650-3658.e4.	1.8	14
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1402	A chromosomal inversion contributes to divergence in multiple traits between deer mouse ecotypes. <i>Science</i> , 2022, 377, 399-405.	6.0	47
1403	An extinct and deeply divergent tiger lineage from northeastern China recognized through palaeogenomics. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2022, 289, .	1.2	4
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1405	A need for standardized reporting of introgression: Insights from studies across eukaryotes. <i>Evolution Letters</i> , 2022, 6, 344-357.	1.6	14
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1407	Genome Sequencing of up to 6,000-Year-Old <i>Citrullus</i> Seeds Reveals Use of a Bitter-Fleshed Species Prior to Watermelon Domestication. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
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1414	Repeated genetic adaptation to altitude in two tropical butterflies. <i>Nature Communications</i> , 2022, 13, .	5.8	17
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1421	Genetic confirmation of a hybrid between two highly divergent cardinalid species: A rose-breasted grosbeak (<i>Pheucticus ludovicianus</i>) and a scarlet tanager (<i>Piranga olivacea</i>). <i>Ecology and Evolution</i> , 2022, 12, .	0.8	0
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1425	The genetic history of the Southern Arc: A bridge between West Asia and Europe. <i>Science</i> , 2022, 377, .	6.0	31
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1434	Genomic Data Reveals Profound Genetic Structure and Multiple Glacial Refugia in <i>Lonicera oblata</i> (Caprifoliaceae), a Threatened Montane Shrub Endemic to North China. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	5
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.	0.9	6
1436	A mechanism for red coloration in vertebrates. <i>Current Biology</i> , 2022, 32, 4201-4214.e12.	1.8	20
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1441	Transcriptomic heterochrony and completely cleistogamous flower development in the mycoheterotrophic orchid <i>Gastrodia</i> . <i>New Phytologist</i> , 2023, 237, 323-338.	3.5	7

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1459	Genomic basis of insularity and ecological divergence in barn owls (<i>Tyto alba</i>) of the Canary Islands. <i>Heredity</i> , 2022, 129, 281-294.	1.2	3
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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, .	3.3	5
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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, .	0.8	8
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1543	Exposure to global change and microplastics elicits an immune response in an endangered coral. <i>Frontiers in Marine Science</i> , 0, 9, .	1.2	4
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1591	Weak reproductive isolation and extensive gene flow between <i>Mimulus glaucescens</i> and <i>M. guttatus</i> in northern California. <i>Evolution; International Journal of Organic Evolution</i> , 2023, 77, 1245-1261.	1.1	5
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1594	The multifaceted genomic history of Ashaninka from Amazonian Peru. <i>Current Biology</i> , 2023, , .	1.8	1

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