

Great ape genetic diversity and population history

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Comparative Species Divergence across Eight Triplets of Spiny Lizards (Sceloporus) Using Genomic Sequence Data. <i>Genome Biology and Evolution</i> , 2013, 5, 2410-2419.	1.1	30
2	Cortical Evolution: Judge the Brain by Its Cover. <i>Neuron</i> , 2013, 80, 633-647.	3.8	444
3	Rates and patterns of great ape retrotransposition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13457-13462.	3.3	57
4	Dynamics of DNA Methylation in Recent Human and Great Ape Evolution. <i>PLoS Genetics</i> , 2013, 9, e1003763.	1.5	118
5	Improving Genome Assemblies and Annotations for Nonhuman Primates. <i>ILAR Journal</i> , 2013, 54, 144-153.	1.8	23
6	Great Ape Genomics. <i>ILAR Journal</i> , 2013, 54, 82-90.	1.8	16
7	Evolution and diversity of copy number variation in the great ape lineage. <i>Genome Research</i> , 2013, 23, 1373-1382.	2.4	161
8	Great ape skeletal collections: Making the most of scarce and irreplaceable resources in the digital age. <i>American Journal of Physical Anthropology</i> , 2013, 152, 2-32.	2.1	33
9	Extracting population genetics information from a diploid genome sequence. <i>Frontiers in Ecology and Evolution</i> , 0, 2, .	1.1	4
10	Sequence differences at orthologous microsatellites inflate estimates of human-chimpanzee differentiation. <i>BMC Genomics</i> , 2014, 15, 990.	1.2	5
11	Pseudogenization of testis-specific Lfg5 predates human/Neanderthal divergence. <i>Journal of Human Genetics</i> , 2014, 59, 288-291.	1.1	7
12	Genome-Wide Inference of Ancestral Recombination Graphs. <i>PLoS Genetics</i> , 2014, 10, e1004342.	1.5	323
13	Reduced Representation Genome Sequencing Suggests Low Diversity on the Sex Chromosomes of Tonkean Macaque Monkeys. <i>Molecular Biology and Evolution</i> , 2014, 31, 2425-2440.	3.5	16
14	A Homogenizing Process of Selection Has Maintained an "Ultra-Slow" Acetylation & NAT2 Variant in Humans. <i>Human Biology</i> , 2014, 86, 185.	0.4	19
15	Emerging Technologies: Smarter ways to fight wildlife crime. <i>Environmental Development</i> , 2014, 12, 62-72.	1.8	1
16	Unraveling recombination rate evolution using ancestral recombination maps. <i>BioEssays</i> , 2014, 36, 892-900.	1.2	5
17	On the tool use behavior of the bonobo-chimpanzee last common ancestor, and the origins of hominine stone tool use. <i>American Journal of Primatology</i> , 2014, 76, 910-918.	0.8	20
18	Lineage Sorting in Apes. <i>Annual Review of Genetics</i> , 2014, 48, 519-535.	3.2	48

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19	Brief Communication: Quantitative and molecular genetic differentiation in humans and chimpanzees: Implications for the evolutionary processes underlying cranial diversification. <i>American Journal of Physical Anthropology</i> , 2014, 154, 615-620.	2.1	8
20	Khoisan hunter-gatherers have been the largest population throughout most of modern-human demographic history. <i>Nature Communications</i> , 2014, 5, 5692.	5.8	65
21	<scp>ABC</scp> inference of multi-population divergence with admixture from unphased population genomic data. <i>Molecular Ecology</i> , 2014, 23, 4458-4471.	2.0	49
22	Multispecies Coalescent Analysis of the Early Diversification of Neotropical Primates: Phylogenetic Inference under Strong Gene Trees/Species Tree Conflict. <i>Genome Biology and Evolution</i> , 2014, 6, 3105-3114.	1.1	15
23	Bayesian Inference of Shared Recombination Hotspots Between Humans and Chimpanzees. <i>Genetics</i> , 2014, 198, 1621-1628.	1.2	8
24	Generation of SNP datasets for orangutan population genomics using improved reduced-representation sequencing and direct comparisons of SNP calling algorithms. <i>BMC Genomics</i> , 2014, 15, 16.	1.2	72
25	Comparative primate genomics: emerging patterns of genome content and dynamics. <i>Nature Reviews Genetics</i> , 2014, 15, 347-359.	7.7	234
26	The Human Condition—A Molecular Approach. <i>Cell</i> , 2014, 157, 216-226.	13.5	175
27	Resequencing studies of nonmodel organisms using closely related reference genomes: optimal experimental designs and bioinformatics approaches for population genomics. <i>Molecular Ecology</i> , 2014, 23, 1764-1779.	2.0	45
28	DNA-based approaches for evaluating historical demography in terrestrial vertebrates. <i>Biological Journal of the Linnean Society</i> , 2014, 112, 367-386.	0.7	17
29	Stability and phylogenetic correlation in gut microbiota: lessons from ants and apes. <i>Molecular Ecology</i> , 2014, 23, 1268-1283.	2.0	276
30	Why primate models matter. <i>American Journal of Primatology</i> , 2014, 76, 801-827.	0.8	451
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32	Whole-genome sequencing of the snub-nosed monkey provides insights into folivory and evolutionary history. <i>Nature Genetics</i> , 2014, 46, 1303-1310.	9.4	174
33	Recent divergences and size decreases of eastern gorilla populations. <i>Biology Letters</i> , 2014, 10, 20140811.	1.0	64
34	African Great Apes Are Naturally Infected with Roseoloviruses Closely Related to Human Herpesvirus 7. <i>Journal of Virology</i> , 2014, 88, 13212-13220.	1.5	14
35	Primate evolution of the recombination regulator PRDM9. <i>Nature Communications</i> , 2014, 5, 4370.	5.8	72
36	Genetic and developmental basis for parallel evolution and its significance for hominoid evolution. <i>Evolutionary Anthropology</i> , 2014, 23, 188-200.	1.7	43

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37	Identification of species-specific nuclear insertions of mitochondrial DNA (numts) in gorillas and their potential as population genetic markers. <i>Molecular Phylogenetics and Evolution</i> , 2014, 81, 61-70.	1.2	12
38	Lethal aggression in Pan is better explained by adaptive strategies than human impacts. <i>Nature</i> , 2014, 513, 414-417.	13.7	375
39	Using Pseudogene Database to Identify Lineage-Specific Genes and Pseudogenes in Humans and Chimpanzees. <i>Journal of Heredity</i> , 2014, 105, 436-443.	1.0	4
40	All models are wrong. <i>Molecular Ecology</i> , 2014, 23, 2887-2889.	2.0	7
41	Complete Mitochondrial Genome Sequence of the Eastern Gorilla (<i>Gorilla beringei</i>) and Implications for African Ape Biogeography. <i>Journal of Heredity</i> , 2014, 105, 846-855.	1.0	14
42	How and why should we implement genomics into conservation?. <i>Evolutionary Applications</i> , 2014, 7, 999-1007.	1.5	152
43	Killer Whale Nuclear Genome and mtDNA Reveal Widespread Population Bottleneck during the Last Glacial Maximum. <i>Molecular Biology and Evolution</i> , 2014, 31, 1121-1131.	3.5	61
44	Mouse models of human evolution. <i>Current Opinion in Genetics and Development</i> , 2014, 29, 75-80.	1.5	15
45	MHC polymorphism in Caribbean African green monkeys. <i>Immunogenetics</i> , 2014, 66, 353-360.	1.2	4
46	Evidence for Increased Levels of Positive and Negative Selection on the X Chromosome versus Autosomes in Humans. <i>Molecular Biology and Evolution</i> , 2014, 31, 2267-2282.	3.5	59
47	No Positive Selection for G Allele in a p53 Response Element in Europeans. <i>Cell</i> , 2014, 157, 1497-1499.	13.5	2
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49	Further evidence for phenotypic signatures of hybridization in descendant baboon populations. <i>Journal of Human Evolution</i> , 2014, 76, 54-62.	1.3	30
50	Universal Grammar and Biological Variation: An EvoDevo Agenda for Comparative Biolinguistics. <i>Biological Theory</i> , 2014, 9, 122-134.	0.8	30
51	The Genetics of Microdeletion and Microduplication Syndromes: An Update. <i>Annual Review of Genomics and Human Genetics</i> , 2014, 15, 215-244.	2.5	145
52	A fine-scale recombination map of the human-chimpanzee ancestor reveals faster change in humans than in chimpanzees and a strong impact of GC-biased gene conversion. <i>Genome Research</i> , 2014, 24, 467-474.	2.4	37
53	The limiting distribution of the effective population size of the ancestor of humans and chimpanzees. <i>Journal of Theoretical Biology</i> , 2014, 357, 55-61.	0.8	5
54	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

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55	Tempo and mode of genomic mutations unveil human evolutionary history. <i>Genes and Genetic Systems</i> , 2015, 90, 123-131.	0.2	0
56	Genetic diversity in humans and non-human primates and its evolutionary consequences. <i>Genes and Genetic Systems</i> , 2015, 90, 133-145.	0.2	27
58	Identification of Diagnostic Mitochondrial DNA Single Nucleotide Polymorphisms Specific to Sumatran Orangutan (<i>Pongo abelii</i>) Populations. <i>HAYATI Journal of Biosciences</i> , 2015, 22, 149-156.	0.1	2
59	Unique human orbital morphology compared with that of apes. <i>Scientific Reports</i> , 2015, 5, 11528.	1.6	9
60	Human rather than ape-like orbital morphology allows much greater lateral visual field expansion with eye abduction. <i>Scientific Reports</i> , 2015, 5, 12437.	1.6	5
62	The geographic distribution of genetic diversity within gorillas. <i>American Journal of Primatology</i> , 2015, 77, 974-985.	0.8	12
63	Anthropological Genetics and Social Media. <i>American Anthropologist</i> , 2015, 117, 744-749.	0.7	1
64	Coevolution of MHC class I and variable NK cell receptors in placental mammals. <i>Immunological Reviews</i> , 2015, 267, 259-282.	2.8	80
65	Characterization of MHC class II B polymorphism in multiple populations of wild gorillas using non-invasive samples and next-generation sequencing. <i>American Journal of Primatology</i> , 2015, 77, 1193-1206.	0.8	11
66	Engaging Native Americans in Genomics Research. <i>American Anthropologist</i> , 2015, 117, 743-744.	0.7	20
67	Positive selection underlies the species-specific binding of <i>Plasmodium falciparum</i> RH5 to human basigin. <i>Molecular Ecology</i> , 2015, 24, 4711-4722.	2.0	12
68	An Introduction to Genome Annotation. <i>Current Protocols in Bioinformatics</i> , 2015, 52, 4.1.1-4.1.17.	25.8	4
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70	Comparative Genomic Analyses of the Human NPHP1 Locus Reveal Complex Genomic Architecture and Its Regional Evolution in Primates. <i>PLoS Genetics</i> , 2015, 11, e1005686.	1.5	21
71	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6413-6418.	3.3	75
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73	Oxytocin receptor gene sequences in owl monkeys and other primates show remarkable interspecific regulatory and protein coding variation. <i>Molecular Phylogenetics and Evolution</i> , 2015, 91, 160-177.	1.2	11
74	PoMo: An Allele Frequency-Based Approach for Species Tree Estimation. <i>Systematic Biology</i> , 2015, 64, 1018-1031.	2.7	66

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76	Leveraging Distant Relatedness to Quantify Human Mutation and Gene-Conversion Rates. <i>American Journal of Human Genetics</i> , 2015, 97, 775-789.	2.6	77
77	Natural Selection at the Brush-Border: Adaptations to Carbohydrate Diets in Humans and Other Mammals. <i>Genome Biology and Evolution</i> , 2015, 7, 2569-2584.	1.1	16
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79	Long-Term Balancing Selection in LAD1 Maintains a Missense Trans-Species Polymorphism in Humans, Chimpanzees, and Bonobos. <i>Molecular Biology and Evolution</i> , 2015, 32, 1186-1196.	3.5	70
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82	Evolution of the indoor biome. <i>Trends in Ecology and Evolution</i> , 2015, 30, 223-232.	4.2	75
83	Origin of the HIV-1 group O epidemic in western lowland gorillas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1343-52.	3.3	136
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88	Balancing immunity and tolerance: genetic footprint of natural selection in the transcriptional regulatory region of HLA-G. <i>Genes and Immunity</i> , 2015, 16, 57-70.	2.2	24
89	Whole-Genome Sequencing of Six Mauritian <i>Cynomolgus</i> Macaques (<i>Macaca fascicularis</i>) Reveals a Genome-Wide Pattern of Polymorphisms under Extreme Population Bottleneck. <i>Genome Biology and Evolution</i> , 2015, 7, 821-830.	1.1	37
90	Inference of Purifying and Positive Selection in Three Subspecies of Chimpanzees (<i>Pan troglodytes</i>) from Exome Sequencing. <i>Genome Biology and Evolution</i> , 2015, 7, 1122-1132.	1.1	33
91	Multiple Cross-Species Transmission Events of Human Adenoviruses (HAdV) during Hominine Evolution. <i>Molecular Biology and Evolution</i> , 2015, 32, 2072-2084.	3.5	54
92	Going the whole orang: Darwin, Wallace and the natural history of orangutans. <i>Studies in History and Philosophy of Science Part C: Studies in History and Philosophy of Biological and Biomedical Sciences</i> , 2015, 51, 53-63.	0.8	11

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96	Diversity of malaria parasites in great apes in Gabon. <i>Malaria Journal</i> , 2015, 14, 111.	0.8	42
97	Maternal ancestry and population history from whole mitochondrial genomes. <i>Investigative Genetics</i> , 2015, 6, 3.	3.3	94
98	Admixture Between Historically Isolated Mitochondrial Lineages in Captive Western Gorillas: Recommendations for Future Management. <i>Journal of Heredity</i> , 2015, 106, 310-314.	1.0	5
99	Ancestral population genomics using coalescence hidden Markov models and heuristic optimisation algorithms. <i>Computational Biology and Chemistry</i> , 2015, 57, 80-92.	1.1	3
100	Examining Phylogenetic Relationships Among Gibbon Genera Using Whole Genome Sequence Data Using an Approximate Bayesian Computation Approach. <i>Genetics</i> , 2015, 200, 295-308.	1.2	44
101	Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. <i>Science</i> , 2015, 348, 242-245.	6.0	326
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110	Progressive alignment of genomic signals by multiple dynamic time warping. <i>Journal of Theoretical Biology</i> , 2015, 385, 20-30.	0.8	24

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112	Reconstructing the demographic history of orangâ€utans using Approximate <sc>B</sc> Bayesian Computation. <i>Molecular Ecology</i> , 2015, 24, 310-327.	2.0	32
113	Demographic inferences using shortâ€read genomic data in an approximate Bayesian computation framework: in silico evaluation of power, biases and proof of concept in Atlantic walrus. <i>Molecular Ecology</i> , 2015, 24, 328-345.	2.0	54
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117	The sampling scheme matters: <i>Pan troglodytes troglodytes</i> and <i>P. t.</i> <i>schweinfurthii</i> are characterized by clinal genetic variation rather than a strong subspecies break. <i>American Journal of Physical Anthropology</i> , 2015, 156, 181-191.	2.1	24
118	Sixteen kiwi (<i>Apteryx</i> spp) transcriptomes provide a wealth of genetic markers and insight into sex chromosome evolution in birds. <i>BMC Genomics</i> , 2016, 17, 410.	1.2	16
119	Human Germline Mutation and the Erratic Evolutionary Clock. <i>PLoS Biology</i> , 2016, 14, e2000744.	2.6	70
120	A Single Nucleotide Polymorphism in Human APOBEC3C Enhances Restriction of Lentiviruses. <i>PLoS Pathogens</i> , 2016, 12, e1005865.	2.1	50
121	Y-Chromosome Structural Diversity in the Bonobo and Chimpanzee Lineages. <i>Genome Biology and Evolution</i> , 2016, 8, 2231-2240.	1.1	19
122	Genomic analysis of snub-nosed monkeys (<i>Rhinopithecus</i>) identifies genes and processes related to high-altitude adaptation. <i>Nature Genetics</i> , 2016, 48, 947-952.	9.4	109
123	Effects of Linked Selective Sweeps on Demographic Inference and Model Selection. <i>Genetics</i> , 2016, 204, 1207-1223.	1.2	144
124	Bonobo personality traits are heritable and associated with vasopressin receptor gene 1a variation. <i>Scientific Reports</i> , 2016, 6, 38193.	1.6	47
125	The evolutionary history of genes involved in spoken and written language: beyond FOXP2. <i>Scientific Reports</i> , 2016, 6, 22157.	1.6	55
126	Genomes of cryptic chimpanzee <i>Plasmodium</i> species reveal key evolutionary events leading to human malaria. <i>Nature Communications</i> , 2016, 7, 11078.	5.8	122
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128	Purifying selection shapes the coincident SNP distribution of primate coding sequences. <i>Scientific Reports</i> , 2016, 6, 27272.	1.6	5

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130	Genetic Load of Loss-of-Function Polymorphic Variants in Great Apes. <i>Genome Biology and Evolution</i> , 2016, 8, 871-877.	1.1	22
131	Genome sequencing of <i>Metrosideros polymorpha</i> (Myrtaceae), a dominant species in various habitats in the Hawaiian Islands with remarkable phenotypic variations. <i>Journal of Plant Research</i> , 2016, 129, 727-736.	1.2	18
132	Genomic signatures of sex-biased demography: progress and prospects. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 62-71.	1.5	34
133	Incomplete Lineage Sorting in Mammalian Phylogenomics. <i>Systematic Biology</i> , 2017, 66, syw082.	2.7	88
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135	Reversible polymorphism-aware phylogenetic models and their application to tree inference. <i>Journal of Theoretical Biology</i> , 2016, 407, 362-370.	0.8	70
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137	Evolution and demography of the great apes. <i>Current Opinion in Genetics and Development</i> , 2016, 41, 124-129.	1.5	27
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144	The conservation genetics juggling act: integrating genetics and ecology, science and policy. <i>Evolutionary Applications</i> , 2016, 9, 181-195.	1.5	38
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150	Assessing Host-Virus Codivergence for Close Relatives of Merkel Cell Polyomavirus Infecting African Great Apes. Journal of Virology, 2016, 90, 8531-8541.	1.5	21
151	Genomic diversity and geographical structure of the Pyrenean desman. Conservation Genetics, 2016, 17, 1333-1344.	0.8	15
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154	Inter-variational structural variation in grapevine genomes. Plant Journal, 2016, 88, 648-661.	2.8	45
155	The population genomics of rhesus macaques (<i>Macaca mulatta</i>) based on whole-genome sequences. Genome Research, 2016, 26, 1651-1662.	2.4	101
156	Elastic Properties of Chimpanzee Craniofacial Cortical Bone. Anatomical Record, 2016, 299, 1718-1733.	0.8	7
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158	The Molecular Basis of Human Brain Evolution. Current Biology, 2016, 26, R1109-R1117.	1.8	47
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162	A Comparison Between Bonobos and Chimpanzees: A Review and Update. Evolutionary Anthropology, 2016, 25, 239-252.	1.7	123
163	Variable Autosomal and X Divergence Near and Far from Genes Affects Estimates of Male Mutation Bias in Great Apes. Genome Biology and Evolution, 2016, 8, 3393-3405.	1.1	4
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167	Geographic variation in gorilla limb bones. <i>Journal of Human Evolution</i> , 2016, 95, 68-79.	1.3	10
168	Genomewide ancestry and divergence patterns from low-coverage sequencing data reveal a complex history of admixture in wild baboons. <i>Molecular Ecology</i> , 2016, 25, 3469-3483.	2.0	73
169	Structural Insights into HIV-1 Vif-APOBEC3F Interaction. <i>Journal of Virology</i> , 2016, 90, 1034-1047.	1.5	53
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171	No Distinction of Orthology/Paralogy between Human and Chimpanzee Rh Blood Group Genes. <i>Genome Biology and Evolution</i> , 2016, 8, 519-527.	1.1	4
172	An Evolutionary View of the Arms Race between Protein Kinase R and Large DNA Viruses. <i>Journal of Virology</i> , 2016, 90, 3280-3283.	1.5	6
173	Ancient gene flow from early modern humans into Eastern Neanderthals. <i>Nature</i> , 2016, 530, 429-433.	13.7	392
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175	The Uromodulin Gene Locus Shows Evidence of Pathogen Adaptation through Human Evolution. <i>Journal of the American Society of Nephrology: JASN</i> , 2016, 27, 2983-2996.	3.0	37
176	DNA Editing of LTR Retrotransposons Reveals the Impact of APOBECs on Vertebrate Genomes. <i>Molecular Biology and Evolution</i> , 2016, 33, 554-567.	3.5	29
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181	Population Structure Shapes Copy Number Variation in Malaria Parasites. <i>Molecular Biology and Evolution</i> , 2016, 33, 603-620.	3.5	45
182	The complete mitochondrial genome of the central chimpanzee, <i>Pan troglodytes troglodytes</i> . <i>Mitochondrial DNA Part A: DNA Mapping, Sequencing, and Analysis</i> , 2016, 27, 2775-2776.	0.7	0
183	Intragroup Lethal Aggression in West African Chimpanzees (<i>Pan troglodytes verus</i>): Inferred Killing of a Former Alpha Male at Fongoli, Senegal. <i>International Journal of Primatology</i> , 2017, 38, 31-57.	0.9	40

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185	Modeling Human Population Separation History Using Physically Phased Genomes. <i>Genetics</i> , 2017, 205, 385-395.	1.2	46
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187	The principles and practice of human evolution research: Are we asking questions that can be answered?. <i>Comptes Rendus - Palevol</i> , 2017, 16, 670-679.	0.1	12
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189	Sensitivity analysis of effective population size to demographic parameters in house sparrow populations. <i>Molecular Ecology</i> , 2017, 26, 2449-2465.	2.0	14
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197	Combining Genetic and Developmental Methods to Study Musculoskeletal Evolution in Primates. , 2017, , 175-204.		1
198	MHC class I diversity in chimpanzees and bonobos. <i>Immunogenetics</i> , 2017, 69, 661-676.	1.2	25
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200	An evolutionary medicine perspective on Neandertal extinction. <i>Journal of Human Evolution</i> , 2017, 108, 62-71.	1.3	16
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203	<i>GARLIC</i>: Genomic Autozygosity Regions Likelihood-based Inference and Classification. <i>Bioinformatics</i> , 2017, 33, 2059-2062.	1.8	22
204	Mapping Region of Human Restriction Factor APOBEC3H Critical for Interaction with HIV-1 Vif. <i>Journal of Molecular Biology</i> , 2017, 429, 1262-1276.	2.0	18
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213	The evolution of hominoid cranial diversity: A quantitative genetic approach. <i>Evolution; International Journal of Organic Evolution</i> , 2017, 71, 2634-2649.	1.1	29
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217	Whole mitochondrial genome capture from faecal samples and museumâ€špreserved specimens. <i>Molecular Ecology Resources</i> , 2017, 17, e111-e121.	2.2	32
218	The Critically Endangered western chimpanzee declines by 80%. <i>American Journal of Primatology</i> , 2017, 79, e22681.	0.8	69
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221	Distinct selective forces and Neanderthal introgression shaped genetic diversity at genes involved in neurodevelopmental disorders. <i>Scientific Reports</i> , 2017, 7, 6116.	1.6	16
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232	The evolution of vertebral formulae in Hominoidea. <i>Journal of Human Evolution</i> , 2017, 110, 18-36.	1.3	20
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234	Patterns of MHC-dependent mate selection in humans and nonhuman primates: a meta-analysis. <i>Molecular Ecology</i> , 2017, 26, 668-688.	2.0	89
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245	Weighted likelihood inference of genomic autozygosity patterns in dense genotype data. <i>BMC Genomics</i> , 2017, 18, 928.	1.2	9
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247	Genetic Diversity on the Sex Chromosomes. <i>Genome Biology and Evolution</i> , 2018, 10, 1064-1078.	1.1	96
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256	Quantifying Temporal Genomic Erosion in Endangered Species. <i>Trends in Ecology and Evolution</i> , 2018, 33, 176-185.	4.2	162

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263	Genetic analyses in a bonobo (<i>Pan paniscus</i>) with arrhythmogenic right ventricular cardiomyopathy. <i>Scientific Reports</i> , 2018, 8, 4350.	1.6	3
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271	Comparative demography elucidates the longevity of parasitic and symbiotic relationships. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2018, 285, 20181032.	1.2	14
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287	Loss of CXCR6 coreceptor usage characterizes pathogenic lentiviruses. <i>PLoS Pathogens</i> , 2018, 14, e1007003.	2.1	12
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296	Whole-Genome Shotgun Sequence CNV Detection Using Read Depth. <i>Methods in Molecular Biology</i> , 2018, 1833, 61-72.	0.4	4
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319	Island area, body size and demographic history shape genomic diversity in Darwin's finches and related tanagers. <i>Molecular Ecology</i> , 2019, 28, 4914-4925.	2.0	22
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324	Biological relevance of computationally predicted pathogenicity of noncoding variants. <i>Nature Communications</i> , 2019, 10, 330.	5.8	44
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335	Biological Resources for Genomic Investigation in the Vervet Monkey (<i>Chlorocebus</i>). , 2019, , 16-28.		3
336	Savanna Monkey Taxonomy. , 2019, , 31-54.		2
337	The Promise of Vervet Genomics. , 2019, , 55-59.		0
338	African Green Monkeys as a Natural Host of SIV. , 2019, , 60-70.		0
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347	Life History of Savanna Monkeys. , 2019, , 163-198.		1
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