Tomas Marques-Bonet

List of Publications by Year
in descending order

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178

papers

25,321

citations

14644

66

h-index

9334

143

g-index

212

all docs

212

docs citations

212

times ranked

29516

citing authors

#	ARTICLE	IF	CITATIONS
1	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	6.0	3,588
2	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
3	Genetic history of an archaic hominin group from Denisova Cave in Siberia. Nature, 2010, 468, 1053-1060.	13.7	1,537
4	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
5	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	13.7	768
6	Elephant shark genome provides unique insights into gnathostome evolution. Nature, 2014, 505, 174-179.	13.7	689
7	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	13.7	663
8	Personalized copy number and segmental duplication maps using next-generation sequencing. Nature Genetics, 2009, 41, 1061-1067.	9.4	656
9	The genome of melon (<i>Cucumis melo</i> L.). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11872-11877.	3.3	654
10	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	13.7	541
11	Genome Sequencing Highlights the Dynamic Early History of Dogs. PLoS Genetics, 2014, 10, e1004016.	1.5	481
12	The bonobo genome compared with the chimpanzee and human genomes. Nature, 2012, 486, 527-531.	13.7	445
13	Ancient gene flow from early modern humans into Eastern Neanderthals. Nature, 2016, 530, 429-433.	13.7	392
14	DNA methylation contributes to natural human variation. Genome Research, 2013, 23, 1363-1372.	2.4	353
15	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. Nature, 2014, 507, 225-228.	13.7	328
16	Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. Science, 2015, 348, 242-245.	6.0	326
17	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	13.7	320
18	Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17230-17235.	3.3	281

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19	Spatiotemporal transcriptomic divergence across human and macaque brain development. Science, 2018, 362, .	6.0	279
20	Bottlenecks and selective sweeps during domestication have increased deleterious genetic variation in dogs. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 152-157.	3.3	265
21	Prehistoric genomes reveal the genetic foundation and cost of horse domestication. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5661-9.	3.3	260
22	Chimpanzee genomic diversity reveals ancient admixture with bonobos. Science, 2016, 354, 477-481.	6.0	230
23	The common marmoset genome provides insight into primate biology and evolution. Nature Genetics, 2014, 46, 850-857.	9.4	225
24	A burst of segmental duplications in the genome of the African great ape ancestor. Nature, 2009, 457, 877-881.	13.7	222
25	Copy number variation and evolution in humans and chimpanzees. Genome Research, 2008, 18, 1698-1710.	2.4	215
26	Tracking Five Millennia of Horse Management with Extensive Ancient Genome Time Series. Cell, 2019, 177, 1419-1435.e31.	13.5	195
27	Ancestral reconstruction of segmental duplications reveals punctuated cores of human genome evolution. Nature Genetics, 2007, 39, 1361-1368.	9.4	192
28	Morphometric, Behavioral, and Genomic Evidence for a New Orangutan Species. Current Biology, 2017, 27, 3487-3498.e10.	1.8	192
29	Molecular and cellular reorganization of neural circuits in the human lineage. Science, 2017, 358, 1027-1032.	6.0	192
30	Ancient genomic changes associated with domestication of the horse. Science, 2017, 356, 442-445.	6.0	185
31	Balancing Selection Is the Main Force Shaping the Evolution of Innate Immunity Genes. Journal of Immunology, 2008, 181, 1315-1322.	0.4	173
32	Genomic legacy of the African cheetah, Acinonyx jubatus. Genome Biology, 2015, 16, 277.	3.8	167
33	Evolution and diversity of copy number variation in the great ape lineage. Genome Research, 2013, 23, 1373-1382.	2.4	161
34	Evolutionary Genomics and Conservation of the Endangered Przewalskiâ€™s Horse. Current Biology, 2015, 25, 2577-2583.	1.8	161
35	Worldwide patterns of genomic variation and admixture in gray wolves. Genome Research, 2016, 26, 163-173.	2.4	160
36	A Common Genetic Origin for Early Farmers from Mediterranean Cardial and Central European LBK Cultures. Molecular Biology and Evolution, 2015, 32, msv181.	3.5	155

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37	The Genetics of Microdeletion and Microduplication Syndromes: An Update. Annual Review of Genomics and Human Genetics, 2014, 15, 215-244.	2.5	145
38	Evaluating the Genetics of Common Variable Immunodeficiency: Monogenetic Model and Beyond. Frontiers in Immunology, 2018, 9, 636.	2.2	142
39	Tracking the origins of Yakutian horses and the genetic basis for their fast adaptation to subarctic environments. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E6889-97.	3.3	139
40	The era of reference genomes in conservation genomics. Trends in Ecology and Evolution, 2022, 37, 197-202.	4.2	138
41	The origins and impact of primate segmental duplications. Trends in Genetics, 2009, 25, 443-454.	2.9	137
42	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. GigaScience, 2017, 6, 1-13.	3.3	137
43	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	3.8	131
44	Historical Genomes Reveal the Genomic Consequences of Recent Population Decline in Eastern Gorillas. Current Biology, 2019, 29, 165-170.e6.	1.8	126
45	The Earth BioGenome Project 2020: Starting the clock. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	124
46	Origins of De Novo Genes in Human and Chimpanzee. PLoS Genetics, 2015, 11, e1005721.	1.5	123
47	Direct estimation of mutations in great apes reconciles phylogenetic dating. Nature Ecology and Evolution, 2019, 3, 286-292.	3.4	122
48	Characterization of six human disease-associated inversion polymorphisms. Human Molecular Genetics, 2009, 18, 2555-2566.	1.4	118
49	Dynamics of DNA Methylation in Recent Human and Great Ape Evolution. PLoS Genetics, 2013, 9, e1003763.	1.5	118
50	Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. Nature Ecology and Evolution, 2018, 2, 669-679.	3.4	117
51	The comparative genomics and complex population history of <i>Papio</i> baboons. Science Advances, 2019, 5, eaau6947.	4.7	115
52	A panel of induced pluripotent stem cells from chimpanzees: a resource for comparative functional genomics. ELife, 2015, 4, e07103.	2.8	114
53	The genome of the vervet (<i>Chlorocebus aethiops sabaeus</i>). Genome Research, 2015, 25, 1921-1933.	2.4	114
54	Interspecific Gene Flow Shaped the Evolution of the Genus Canis. Current Biology, 2018, 28, 3441-3449.e5.	1.8	110

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55	The dental proteome of Homo antecessor. Nature, 2020, 580, 235-238.	13.7	100
56	Human Oocyte-Derived Methylation Differences Persist in the Placenta Revealing Widespread Transient Imprinting. PLoS Genetics, 2016, 12, e1006427.	1.5	94
57	The Genomic Footprints of the Fall and Recovery of the Crested Ibis. Current Biology, 2019, 29, 340-349.e7.	1.8	94
58	Death and Resurrection of the Human IRGM Gene. PLoS Genetics, 2009, 5, e1000403.	1.5	93
59	A comparison of gene expression and DNA methylation patterns across tissues and species. Genome Research, 2020, 30, 250-262.	2.4	91
60	DNA Methylation: Insights into Human Evolution. PLoS Genetics, 2015, 11, e1005661.	1.5	90
61	Selective single molecule sequencing and assembly of a human Y chromosome of African origin. Nature Communications, 2019, 10, 4.	5.8	90
62	A large and complex structural polymorphism at 16p12.1 underlies microdeletion disease risk. Nature Genetics, 2010, 42, 745-750.	9.4	89
63	Limiting replication stress during somatic cell reprogramming reduces genomic instability in induced pluripotent stem cells. Nature Communications, 2015, 6, 8036.	5.8	84
64	Enamel proteome shows that Gigantopithecus was an early diverging pongine. Nature, 2019, 576, 262-265.	13.7	82
65	Patterns and rates of intron divergence between humans and chimpanzees. Genome Biology, 2007, 8, R21.	13.9	81
66	Giant tortoise genomes provide insights into longevity and age-related disease. Nature Ecology and Evolution, 2019, 3, 87-95.	3.4	79
67	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. PLoS Genetics, 2016, 12, e1005851.	1.5	77
68	Extreme selective sweeps independently targeted the X chromosomes of the great apes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6413-6418.	3.3	75
69	Return to the Sea, Get Huge, Beat Cancer: An Analysis of Cetacean Genomes Including an Assembly for the Humpback Whale (Megaptera novaeangliae). Molecular Biology and Evolution, 2019, 36, 1746-1763.	3.5	75
70	The wolf reference genome sequence (Canis lupus lupus) and its implications for Canis spp. population genomics. BMC Genomics, 2017, 18, 495.	1.2	73
71	The Evolution of Human Segmental Duplications and the Core Duplicon Hypothesis. Cold Spring Harbor Symposia on Quantitative Biology, 2009, 74, 355-362.	2.0	70
72	Natural Selection in the Great Apes. Molecular Biology and Evolution, 2016, 33, 3268-3283.	3.5	70

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73	The evolutionary history of extinct and living lions. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10927-10934.	3.3	70
74	Tandem repeat variation in human and great ape populations and its impact on gene expression divergence. Genome Research, 2015, 25, 1591-1599.	2.4	69
75	Differential DNA methylation of vocal and facial anatomy genes in modern humans. Nature Communications, 2020, 11, 1189.	5.8	69
76	The interplay between DNA methylation and sequence divergence in recent human evolution. Nucleic Acids Research, 2015, 43, 8204-8214.	6.5	67
77	Chromosomal rearrangements and the genomic distribution of gene-expression divergence in humans and chimpanzees. Trends in Genetics, 2004, 20, 524-529.	2.9	66
78	Molecular dating of caprines using ancient DNA sequences of Myotragus balearicus, an extinct endemic Balearic mammal. BMC Evolutionary Biology, 2005, 5, 70.	3.2	66
79	Copy number variation analysis in the great apes reveals species-specific patterns of structural variation. Genome Research, 2011, 21, 1626-1639.	2.4	66
80	Gorilla genome structural variation reveals evolutionary parallelisms with chimpanzee. Genome Research, 2011, 21, 1640-1649.	2.4	65
81	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. National Science Review, 2019, 6, 810-824.	4.6	65
82	Arctic-adapted dogs emerged at the Pleistoceneâ€"Holocene transition. Science, 2020, 368, 1495-1499.	6.0	60
83	Ancient admixture from an extinct ape lineage into bonobos. Nature Ecology and Evolution, 2019, 3, 957-965.	3.4	59
84	Inference of natural selection from ancient DNA. Evolution Letters, 2020, 4, 94-108.	1.6	58
85	Rates and patterns of great ape retrotransposition. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13457-13462.	3.3	57
86	Whole mitochondrial genomes illuminate ancient intercontinental dispersals of grey wolves (<i>Canis lupus</i>). Journal of Biogeography, 2016, 43, 1728-1738.	1.4	57
87	Sequencing Primate Genomes: What Have We Learned?. Annual Review of Genomics and Human Genetics, 2009, 10, 355-386.	2.5	54
88	Selection upon Genome Architecture: Conservation of Functional Neighborhoods with Changing Genes. PLoS Computational Biology, 2010, 6, e1000953.	1.5	53
89	Reconstructing Denisovan Anatomy Using DNA Methylation Maps. Cell, 2019, 179, 180-192.e10.	13.5	51
90	Whole-genome sequence analysis of a Pan African set of samples reveals archaic gene flow from an extinct basal population of modern humans into sub-Saharan populations. Genome Biology, 2019, 20, 77.	3.8	50

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91	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. Cell, 2021, 184, 4874-4885.e16.	13.5	49
92	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. BMC Genomics, 2013, 14, 363.	1.2	48
93	Frequent appearance of novel protein-coding sequences by frameshift translation. Genomics, 2006, 88, 690-697.	1.3	47
94	On the path to extinction: Inbreeding and admixture in a declining grey wolf population. Molecular Ecology, 2018, 27, 3599-3612.	2.0	46
95	Examining Phylogenetic Relationships Among Gibbon Genera Using Whole Genome Sequence Data Using an Approximate Bayesian Computation Approach. Genetics, 2015, 200, 295-308.	1.2	44
96	Evidence that the rate of strong selective sweeps increases with population size in the great apes. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 1613-1618.	3.3	40
97	Historical population declines prompted significant genomic erosion in the northern and southern white rhinoceros (<i>Ceratotherium simum</i>). Molecular Ecology, 2021, 30, 6355-6369.	2.0	39
98	Plasmodium vivax Malaria Viewed through the Lens of an Eradicated European Strain. Molecular Biology and Evolution, 2020, 37, 773-785.	3.5	38
99	Rivers as possible landmarks in the orientation flight of Miniopterus schreibersii. Acta Theriologica, 2000, 45, 347-352.	1.1	36
100	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, Homotherium latidens. Current Biology, 2020, 30, 5018-5025.e5.	1.8	34
101	The genomics of ecological flexibility, large brains, and long lives in capuchin monkeys revealed with fecalFACS. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	34
102	The Novel Evolution of the Sperm Whale Genome. Genome Biology and Evolution, 2017, 9, 3260-3264.	1.1	33
103	The impact of endogenous content, replicates and pooling on genome capture from faecal samples. Molecular Ecology Resources, 2018, 18, 319-333.	2.2	33
104	Standards recommendations for the Earth BioGenome Project. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	33
105	Stably expressed APOBEC3H forms a barrier for cross-species transmission of simian immunodeficiency virus of chimpanzee to humans. PLoS Pathogens, 2017, 13, e1006746.	2.1	32
106	Annotated features of domestic cat â€“ Felis catus genome. GigaScience, 2014, 3, 13.	3.3	30
107	The prion protein gene in humans revisited: Lessons from a worldwide resequencing study. Genome Research, 2005, 16, 231-239.	2.4	29
108	Sequencing humanâ€“gibbon breakpoints of synteny reveals mosaic new insertions at rearrangement sites. Genome Research, 2009, 19, 178-190.	2.4	29

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109	Evolutionary dynamism of the primate <i>LRRC37</i> gene family. Genome Research, 2013, 23, 46-59.	2.4	29
110	Murine segmental duplications are hot spots for chromosome and gene evolution. Genomics, 2005, 86, 692-700.	1.3	28
111	The evolution of African great ape subtelomeric heterochromatin and the fusion of human chromosome 2. Genome Research, 2012, 22, 1036-1049.	2.4	28
112	Evolution and demography of the great apes. Current Opinion in Genetics and Development, 2016, 41, 124-129.	1.5	27
113	FOXP2 variation in great ape populations offers insight into the evolution of communication skills. Scientific Reports, 2017, 7, 16866.	1.6	27
114	MHC class I diversity in chimpanzees and bonobos. Immunogenetics, 2017, 69, 661-676.	1.2	25
115	On the association between chromosomal rearrangements and genic evolution in humans and chimpanzees. Genome Biology, 2007, 8, R230.	13.9	24
116	Similar genomic proportions of copy number variation within gray wolves and modern dog breeds inferred from whole genome sequencing. BMC Genomics, 2017, 18, 977.	1.2	24
117	Admixture in Mammals and How to Understand Its Functional Implications. BioEssays, 2019, 41, e1900123.	1.2	24
118	A roadmap for highâ€throughput sequencing studies of wild animal populations using noninvasive samples and hybridization capture. Molecular Ecology Resources, 2019, 19, 609-622.	2.2	24
119	Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet. Current Biology, 2020, 30, 108-114.e5.	1.8	24
120	Chromosomal rearrangements are associated with higher rates of molecular evolution in mammals. Gene, 2005, 353, 147-154.	1.0	22
121	Genetic Load of Loss-of-Function Polymorphic Variants in Great Apes. Genome Biology and Evolution, 2016, 8, 871-877.	1.1	22
122	Interrogating 11 Fast-Evolving Genes for Signatures of Recent Positive Selection in Worldwide Human Populations. Molecular Biology and Evolution, 2009, 26, 2285-2297.	3.5	20
123	Temporal and spatial expression of CCN genes in zebrafish. Developmental Dynamics, 2010, 239, 1755-1767.	0.8	20
124	Accelerated exon evolution within primate segmental duplications. Genome Biology, 2013, 14, R9.	13.9	19
125	Demographic History of the Genus<i>Pan</i>Inferred from Whole Mitochondrial Genome Reconstructions. Genome Biology and Evolution, 2016, 8, 2020-2030.	1.1	19
126	Epigenomic profiling of primate lymphoblastoid cell lines reveals the evolutionary patterns of epigenetic activities in gene regulatory architectures. Nature Communications, 2021, 12, 3116.	5.8	19

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127	Genomes reveal marked differences in the adaptive evolution between orangutan species. Genome Biology, 2018, 19, 193.	3.8	18
128	Maximizing the acquisition of unique reads in noninvasive capture sequencing experiments. Molecular Ecology Resources, 2021, 21, 745-761.	2.2	18
129	Population dynamics and genetic connectivity in recent chimpanzee history. Cell Genomics, 2022, 2, 100133.	3.0	18
130	A 3-way hybrid approach to generate a new high-quality chimpanzee reference genome (Pan_tro_3.0). GigaScience, 2017, 6, 1-6.	3.3	17
131	Lineage-specific evolution of the vertebrate Otopetringene family revealed by comparative genomic analyses. BMC Evolutionary Biology, 2011, 11, 23.	3.2	16
132	Analysis of structural diversity in wolf-like canids reveals post-domestication variants. BMC Genomics, 2014, 15, 465.	1.2	16
133	Genomic analysis of the blood attributed to Louis XVI (1754â€“1793), king of France. Scientific Reports, 2015, 4, 4666.	1.6	16
134	An evolutionary medicine perspective on Neandertal extinction. Journal of Human Evolution, 2017, 108, 62-71.	1.3	16
135	Genetic Variation in Pan Species Is Shaped by Demographic History and Harbors Lineage-Specific Functions. Genome Biology and Evolution, 2019, 11, 1178-1191.	1.1	15
136	The impact of genetic adaptation on chimpanzee subspecies differentiation. PLoS Genetics, 2019, 15, e1008485.	1.5	15
137	Genetic diagnosis of autoinflammatory disease patients using clinical exome sequencing. European Journal of Medical Genetics, 2020, 63, 103920.	0.7	15
138	Multiple Genomic Events Altering Hominin SIGLEC Biology and Innate Immunity Predated the Common Ancestor of Humans and Archaic Hominins. Genome Biology and Evolution, 2020, 12, 1040-1050.	1.1	14
139	Characterization of nuclear mitochondrial insertions in the whole genomes of primates. NAR Genomics and Bioinformatics, 2020, 2, lqaa089.	1.5	14
140	Selection in the Introgressed Regions of the Chimpanzee Genome. Genome Biology and Evolution, 2018, 10, 1132-1138.	1.1	13
141	Human pseudogenes of the ABO family show a complex evolutionary dynamics and loss of function. Glycobiology, 2009, 19, 583-591.	1.3	12
142	Copy number variation underlies complex phenotypes in domestic dog breeds and other canids. Genome Research, 2021, 31, 762-774.	2.4	12
143	Functional Implications of Human-Specific Changes in Great Ape microRNAs. PLoS ONE, 2016, 11, e0154194.	1.1	12
144	Targeted conservation genetics of the endangered chimpanzee. Heredity, 2020, 125, 15-27.	1.2	11

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145	Differential Gene Expression in the Human Brain Is Associated with Conserved, but Not Accelerated, Noncoding Sequences. Molecular Biology and Evolution, 2017, 34, 1217-1229.	3.5	10
146	Copy number variantsÂand fixed duplications among 198 rhesus macaques (Macaca mulatta). PLoS Genetics, 2020, 16, e1008742.	1.5	10
147	Two hundred and five newly assembled mitogenomes provide mixed evidence for rivers as drivers of speciation for Amazonian primates. Molecular Ecology, 2022, 31, 3888-3902.	2.0	10
148	Late-replicating CNVs as a source of new genes. Biology Open, 2013, 2, 1402-1411.	0.6	9
149	Extreme differences between human germline and tumor mutation densities are driven by ancestral human-specific deviations. Nature Communications, 2020, 11, 2512.	5.8	9
150	Branching out: what omics can tell us about primate evolution. Current Opinion in Genetics and Development, 2020, 62, 65-71.	1.5	9
151	The Diversity of Primates: From Biomedicine to Conservation Genomics. Annual Review of Animal Biosciences, 2021, 9, 103-124.	3.6	8
152	Gene Fusions Derived by Transcriptional Readthrough are Driven by Segmental Duplication in Human. Genome Biology and Evolution, 2019, 11, 2678-2690.	1.1	7
153	Variation in predicted COVIDâ€‘19 risk among lemurs and lorises. American Journal of Primatology, 2021, 83, e23255.	0.8	7
154	Initiation of the Primate Genome Project. Zoological Research, 2022, 43, 147-149.	0.9	7
155	Association Cluster Detector: a tool for heuristic detection of significance clusters in whole-genome scans. Bioinformatics, 2005, 21, ii180-ii181.	1.8	6
156	The genomic distribution of intraspecific and interspecific sequence divergence of human segmental duplications relative to human/chimpanzee chromosomal rearrangements. BMC Genomics, 2008, 9, 384.	1.2	6
157	Potential damaging mutation in LRP5 from genome sequencing of the first reported chimpanzee with the Chiari malformation. Scientific Reports, 2017, 7, 15224.	1.6	6
158	HuConTest: Testing Human Contamination in Great Ape Samples. Genome Biology and Evolution, 2021, 13, .	1.1	6
159	Ancient DNA of the pygmy marmoset type specimen <i>Cebuella pygmaea</i> (Spix, 1823) resolves a taxonomic conundrum. Zoological Research, 2021, 42, 761-771.	0.9	6
160	Flow Sorting Enrichment and Nanopore Sequencing of Chromosome 1 From a Chinese Individual. Frontiers in Genetics, 2019, 10, 1315.	1.1	5
161	Assessment of the gene mosaicism burden in blood and its implications for immune disorders. Scientific Reports, 2021, 11, 12940.	1.6	5
162	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	0.8	5

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163	Genetic data from the extinct giant rat from Tenerife (Canary Islands) points to a recent divergence from mainland relatives. Biology Letters, 2021, 17, 20210533.	1.0	5
164	Whole genome sequencing in the search for genes associated with the control of SIV infection in the Mauritian macaque model. Scientific Reports, 2018, 8, 7131.	1.6	4
165	Recovering the genomes hidden in museum wet collections. Molecular Ecology Resources, 2022, , .	2.2	4
166	Circular DNA intermediates in the generation of large human segmental duplications. BMC Genomics, 2020, 21, 593.	1.2	3
167	ECOLOGICAL SEGREGATION BETWEEN RANA PYRENAICA AND RANA TEMPORARIA, AND DIFFERENTIAL PREDATION OF EUPROCTUS ASPER ON THEIR TADPOLES. Animal Biology, 2000, 50, 65-73.	0.4	3
168	Metagenomic analysis of a blood stain from the French revolutionary Jean-Paul Marat (1743â€“1793). Infection, Genetics and Evolution, 2020, 80, 104209.	1.0	2
169	A genomic exploration of the early evolution of extant cats and their sabre-toothed relatives. Open Research Europe, 2021, 1, 25.	2.0	2
170	Salmonella enterica from a soldier from the 1652 siege of Barcelona (Spain) supports historical transatlantic epidemic contacts. IScience, 2021, 24, 103021.	1.9	2
171	The genetic impact of an Ebola outbreak on a wild gorilla population. BMC Genomics, 2021, 22, 735.	1.2	2
172	Insights from the rescue and breeding management of Cuvierâ€™s gazelle (<i>Gazella cuvieri</i>) through wholeâ€genome sequencing. Evolutionary Applications, 2022, 15, 351-364.	1.5	2
173	Genomic Analysis of 18th-Century Kazakh Individuals and Their Oral Microbiome. Biology, 2021, 10, 1324.	1.3	2
174	A genomic exploration of the early evolution of extant cats and their sabre-toothed relatives. Open Research Europe, 0, 1, 25.	2.0	1
175	A high-quality, long-read genome assembly of the endangered ring-tailed lemur (<i>Lemur catta</i>). GigaScience, 2022, 11, .	3.3	1
176	The impact of genetic adaptation on chimpanzee subspecies differentiation. , 2019, 15, e1008485.		0
177	The impact of genetic adaptation on chimpanzee subspecies differentiation. , 2019, 15, e1008485.		0
178	The impact of genetic adaptation on chimpanzee subspecies differentiation. , 2019, 15, e1008485.		0