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	Insights from the rescue and breeding management of Cuvierâ€™s gazelle (Gazella cuvieri) through wholeâ€genome sequencing. Evolutionary Applications, 2022, 15, 351-364.	1.5	2
2	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
3	The era of reference genomes in conservation genomics. Trends in Ecology and Evolution, 2022, 37, 197-202.	4.2	138
4	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
5	Initiation of the Primate Genome Project. Zoological Research, 2022, 43, 147-149.	0.9	7
6	A high-quality, long-read genome assembly of the endangered ring-tailed lemur (Lemur catta). GigaScience, 2022, 11, .	3.3	1
7	Recovering the genomes hidden in museum wet collections. Molecular Ecology Resources, 2022, , .	2.2	4
8	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
9	Population dynamics and genetic connectivity in recent chimpanzee history. Cell Genomics, 2022, 2, 100133.	3.0	18
10	Maximizing the acquisition of unique reads in noninvasive capture sequencing experiments. Molecular Ecology Resources, 2021, 21, 745-761.	2.2	18
11	The Diversity of Primates: From Biomedicine to Conservation Genomics. Annual Review of Animal Biosciences, 2021, 9, 103-124.	3.6	8
12	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
13	Variation in predicted COVIDâ€19 risk among lemurs and lorises. American Journal of Primatology, 2021, 83, e23255.	0.8	7
14	Copy number variation underlies complex phenotypes in domestic dog breeds and other canids. Genome Research, 2021, 31, 762-774.	2.4	12
15	Towards complete and error-free genome assemblies of all vertebrate species. Nature, 2021, 592, 737-746.	13.7	1,139
16	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
17	HuConTest: Testing Human Contamination in Great Ape Samples. Genome Biology and Evolution, 2021, 13, .	1.1	6
18	A genomic exploration of the early evolution of extant cats and their sabre-toothed relatives. Open Research Europe, 2021, 1, 25.	2.0	2

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19	Assessment of the gene mosaicism burden in blood and its implications for immune disorders. Scientific Reports, 2021, 11, 12940.	1.6	5
20	Historical population declines prompted significant genomic erosion in the northern and southern white rhinoceros (Ceratotherium simum). Molecular Ecology, 2021, 30, 6355-6369.	2.0	39
21	Salmonella enterica from a soldier from the 1652 siege of Barcelona (Spain) supports historical transatlantic epidemic contacts. IScience, 2021, 24, 103021.	1.9	2
22	Ancient and modern genomes unravel the evolutionary history of the rhinoceros family. Cell, 2021, 184, 4874-4885.e16.	13.5	49
23	Ancient DNA of the pygmy marmoset type specimen Cebuella pygmaea (Spix, 1823) resolves a taxonomic conundrum. Zoological Research, 2021, 42, 761-771.	0.9	6
24	The genetic impact of an Ebola outbreak on a wild gorilla population. BMC Genomics, 2021, 22, 735.	1.2	2
25	Genomic Analysis of 18th-Century Kazakh Individuals and Their Oral Microbiome. Biology, 2021, 10, 1324.	1.3	2
26	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
27	Plasmodium vivax Malaria Viewed through the Lens of an Eradicated European Strain. Molecular Biology and Evolution, 2020, 37, 773-785.	3.5	38
28	Evolutionary History, Genomic Adaptation to Toxic Diet, and Extinction of the Carolina Parakeet. Current Biology, 2020, 30, 108-114.e5.	1.8	24
29	Genomic Adaptations and Evolutionary History of the Extinct Scimitar-Toothed Cat, Homotherium latidens. Current Biology, 2020, 30, 5018-5025.e5.	1.8	34
30	Circular DNA intermediates in the generation of large human segmental duplications. BMC Genomics, 2020, 21, 593.	1.2	3
31	Targeted conservation genetics of the endangered chimpanzee. Heredity, 2020, 125, 15-27.	1.2	11
32	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
33	Extreme differences between human germline and tumor mutation densities are driven by ancestral human-specific deviations. Nature Communications, 2020, 11, 2512.	5.8	9
34	Copy number variantsÂand fixed duplications among 198 rhesus macaques (Macaca mulatta). PLoS Genetics, 2020, 16, e1008742.	1.5	10
35	Inference of natural selection from ancient DNA. Evolution Letters, 2020, 4, 94-108.	1.6	58
36	The dental proteome of Homo antecessor. Nature, 2020, 580, 235-238.	13.7	100

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37	Differential DNA methylation of vocal and facial anatomy genes in modern humans. Nature Communications, 2020, 11, 1189.	5.8	69
38	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
39	Arctic-adapted dogs emerged at the Pleistoceneâ€“Holocene transition. Science, 2020, 368, 1495-1499.	6.0	60
40	Branching out: what omics can tell us about primate evolution. Current Opinion in Genetics and Development, 2020, 62, 65-71.	1.5	9
41	A comparison of gene expression and DNA methylation patterns across tissues and species. Genome Research, 2020, 30, 250-262.	2.4	91
42	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
43	Pan-cancer analysis of whole genomes. Nature, 2020, 578, 82-93.	13.7	1,966
44	Genetic diagnosis of autoinflammatory disease patients using clinical exome sequencing. European Journal of Medical Genetics, 2020, 63, 103920.	0.7	15
45	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	0.8	5
46	Characterization of nuclear mitochondrial insertions in the whole genomes of primates. NAR Genomics and Bioinformatics, 2020, 2, lqaa089.	1.5	14
47	Gene Fusions Derived by Transcriptional Readthrough are Driven by Segmental Duplication in Human. Genome Biology and Evolution, 2019, 11, 2678-2690.	1.1	7
48	Admixture in Mammals and How to Understand Its Functional Implications. BioEssays, 2019, 41, e1900123.	1.2	24
49	Reconstructing Denisovan Anatomy Using DNA Methylation Maps. Cell, 2019, 179, 180-192.e10.	13.5	51
50	Direct estimation of mutations in great apes reconciles phylogenetic dating. Nature Ecology and Evolution, 2019, 3, 286-292.	3.4	122
51	The comparative genomics and complex population history of Papio baboons. Science Advances, 2019, 5, eaau6947.	4.7	115
52	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
53	Ancient admixture from an extinct ape lineage into bonobos. Nature Ecology and Evolution, 2019, 3, 957-965.	3.4	59
54	Tracking Five Millennia of Horse Management with Extensive Ancient Genome Time Series. Cell, 2019, 177, 1419-1435.e31.	13.5	195

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55	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
56	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
57	Dog10K: an international sequencing effort to advance studies of canine domestication, phenotypes and health. National Science Review, 2019, 6, 810-824.	4.6	65
58	The impact of genetic adaptation on chimpanzee subspecies differentiation. PLoS Genetics, 2019, 15, e1008485.	1.5	15
59	Enamel proteome shows that Gigantopithecus was an early diverging pongine. Nature, 2019, 576, 262-265.	13.7	82
60	Historical Genomes Reveal the Genomic Consequences of Recent Population Decline in Eastern Gorillas. Current Biology, 2019, 29, 165-170.e6.	1.8	126
61	Selective single molecule sequencing and assembly of a human Y chromosome of African origin. Nature Communications, 2019, 10, 4.	5.8	90
62	The Genomic Footprints of the Fall and Recovery of the Crested Ibis. Current Biology, 2019, 29, 340-349.e7.	1.8	94
63	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
64	Giant tortoise genomes provide insights into longevity and age-related disease. Nature Ecology and Evolution, 2019, 3, 87-95.	3.4	79
65	Flow Sorting Enrichment and Nanopore Sequencing of Chromosome 1 From a Chinese Individual. Frontiers in Genetics, 2019, 10, 1315.	1.1	5
66	The impact of genetic adaptation on chimpanzee subspecies differentiation. , 2019, 15, e1008485.		0
67	The impact of genetic adaptation on chimpanzee subspecies differentiation. , 2019, 15, e1008485.		0
68	The impact of genetic adaptation on chimpanzee subspecies differentiation. , 2019, 15, e1008485.		0
69	Selection in the Introgressed Regions of the Chimpanzee Genome. Genome Biology and Evolution, 2018, 10, 1132-1138.	1.1	13
70	Clonal polymorphism and high heterozygosity in the celibate genome of the Amazon molly. Nature Ecology and Evolution, 2018, 2, 669-679.	3.4	117
71	The impact of endogenous content, replicates and pooling on genome capture from faecal samples. Molecular Ecology Resources, 2018, 18, 319-333.	2.2	33
72	Genomes reveal marked differences in the adaptive evolution between orangutan species. Genome Biology, 2018, 19, 193.	3.8	18

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73	Spatiotemporal transcriptomic divergence across human and macaque brain development. Science, 2018, 362, .	6.0	279
74	Interspecific Gene Flow Shaped the Evolution of the Genus Canis. Current Biology, 2018, 28, 3441-3449.e5.	1.8	110
75	On the path to extinction: Inbreeding and admixture in a declining grey wolf population. Molecular Ecology, 2018, 27, 3599-3612.	2.0	46
76	Evaluating the Genetics of Common Variable Immunodeficiency: Monogenetic Model and Beyond. Frontiers in Immunology, 2018, 9, 636.	2.2	142
77	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
78	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
79	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
80	Ancient genomic changes associated with domestication of the horse. Science, 2017, 356, 442-445.	6.0	185
81	MHC class I diversity in chimpanzees and bonobos. Immunogenetics, 2017, 69, 661-676.	1.2	25
82	An evolutionary medicine perspective on Neandertal extinction. Journal of Human Evolution, 2017, 108, 62-71.	1.3	16
83	Morphometric, Behavioral, and Genomic Evidence for a New Orangutan Species. Current Biology, 2017, 27, 3487-3498.e10.	1.8	192
84	FOXP2 variation in great ape populations offers insight into the evolution of communication skills. Scientific Reports, 2017, 7, 16866.	1.6	27
85	Molecular and cellular reorganization of neural circuits in the human lineage. Science, 2017, 358, 1027-1032.	6.0	192
86	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
87	The wolf reference genome sequence (Canis lupus lupus) and its implications for Canis spp. population genomics. BMC Genomics, 2017, 18, 495.	1.2	73
88	Comparative performance of the BGISEQ-500 vs Illumina HiSeq2500 sequencing platforms for palaeogenomic sequencing. GigaScience, 2017, 6, 1-13.	3.3	137
89	The Novel Evolution of the Sperm Whale Genome. Genome Biology and Evolution, 2017, 9, 3260-3264.	1.1	33
90	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

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91	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
92	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
93	Human Oocyte-Derived Methylation Differences Persist in the Placenta Revealing Widespread Transient Imprinting. PLoS Genetics, 2016, 12, e1006427.	1.5	94
94	Whole mitochondrial genomes illuminate ancient intercontinental dispersals of grey wolves (Canis lupus). Journal of Biogeography, 2016, 43, 1728-1738.	1.4	57
95	Extreme genomic erosion after recurrent demographic bottlenecks in the highly endangered Iberian lynx. Genome Biology, 2016, 17, 251.	3.8	131
96	Genetic Load of Loss-of-Function Polymorphic Variants in Great Apes. Genome Biology and Evolution, 2016, 8, 871-877.	1.1	22
97	Evolution and demography of the great apes. Current Opinion in Genetics and Development, 2016, 41, 124-129.	1.5	27
98	Demographic History of the GenusPanInferred from Whole Mitochondrial Genome Reconstructions. Genome Biology and Evolution, 2016, 8, 2020-2030.	1.1	19
99	Chimpanzee genomic diversity reveals ancient admixture with bonobos. Science, 2016, 354, 477-481.	6.0	230
100	Natural Selection in the Great Apes. Molecular Biology and Evolution, 2016, 33, 3268-3283.	3.5	70
101	Worldwide patterns of genomic variation and admixture in gray wolves. Genome Research, 2016, 26, 163-173.	2.4	160
102	Ancient gene flow from early modern humans into Eastern Neanderthals. Nature, 2016, 530, 429-433.	13.7	392
103	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
104	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. PLoS Genetics, 2016, 12, e1005851.	1.5	77
105	Functional Implications of Human-Specific Changes in Great Ape microRNAs. PLoS ONE, 2016, 11, e0154194.	1.1	12
106	DNA Methylation: Insights into Human Evolution. PLoS Genetics, 2015, 11, e1005661.	1.5	90
107	A panel of induced pluripotent stem cells from chimpanzees: a resource for comparative functional genomics. ELife, 2015, 4, e07103.	2.8	114
108	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

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109	Genomic legacy of the African cheetah, Acinonyx jubatus. Genome Biology, 2015, 16, 277.	3.8	167
110	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
111	Mountain gorilla genomes reveal the impact of long-term population decline and inbreeding. Science, 2015, 348, 242-245.	6.0	326
112	The interplay between DNA methylation and sequence divergence in recent human evolution. Nucleic Acids Research, 2015, 43, 8204-8214.	6.5	67
113	Evolutionary Genomics and Conservation of the Endangered Przewalskiâ€™s Horse. Current Biology, 2015, 25, 2577-2583.	1.8	161
114	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
115	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
116	Limiting replication stress during somatic cell reprogramming reduces genomic instability in induced pluripotent stem cells. Nature Communications, 2015, 6, 8036.	5.8	84
117	The genome of the vervet (Chlorocebus aethiops sabaeus). Genome Research, 2015, 25, 1921-1933.	2.4	114
118	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
119	Genomic analysis of the blood attributed to Louis XVI (1754â€“1793), king of France. Scientific Reports, 2015, 4, 4666.	1.6	16
120	Origins of De Novo Genes in Human and Chimpanzee. PLoS Genetics, 2015, 11, e1005721.	1.5	123
121	Genome Sequencing Highlights the Dynamic Early History of Dogs. PLoS Genetics, 2014, 10, e1004016.	1.5	481
122	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
123	Elephant shark genome provides unique insights into gnathostome evolution. Nature, 2014, 505, 174-179.	13.7	689
124	Derived immune and ancestral pigmentation alleles in a 7,000-year-old Mesolithic European. Nature, 2014, 507, 225-228.	13.7	328
125	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
126	The common marmoset genome provides insight into primate biology and evolution. Nature Genetics, 2014, 46, 850-857.	9.4	225

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127	Analysis of structural diversity in wolf-like canids reveals post-domestication variants. BMC Genomics, 2014, 15, 465.	1.2	16
128	Annotated features of domestic cat â€“ Felis catus genome. GigaScience, 2014, 3, 13.	3.3	30
129	Gibbon genome and the fast karyotype evolution of small apes. Nature, 2014, 513, 195-201.	13.7	320
130	The Genetics of Microdeletion and Microduplication Syndromes: An Update. Annual Review of Genomics and Human Genetics, 2014, 15, 215-244.	2.5	145
131	Accelerated exon evolution within primate segmental duplications. Genome Biology, 2013, 14, R9.	13.9	19
132	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. BMC Genomics, 2013, 14, 363.	1.2	48
133	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
134	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	13.7	768
135	Late-replicating CNVs as a source of new genes. Biology Open, 2013, 2, 1402-1411.	0.6	9
136	Dynamics of DNA Methylation in Recent Human and Great Ape Evolution. PLoS Genetics, 2013, 9, e1003763.	1.5	118
137	Evolution and diversity of copy number variation in the great ape lineage. Genome Research, 2013, 23, 1373-1382.	2.4	161
138	Evolutionary dynamism of the primate LRRC37 gene family. Genome Research, 2013, 23, 46-59.	2.4	29
139	DNA methylation contributes to natural human variation. Genome Research, 2013, 23, 1363-1372.	2.4	353
140	The evolution of African great ape subtelomeric heterochromatin and the fusion of human chromosome 2. Genome Research, 2012, 22, 1036-1049.	2.4	28
141	The bonobo genome compared with the chimpanzee and human genomes. Nature, 2012, 486, 527-531.	13.7	445
142	The genome of melon (Cucumis melo L.). Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11872-11877.	3.3	654
143	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	13.7	663
144	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	13.7	541

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145	Lineage-specific evolution of the vertebrate Otopetringene family revealed by comparative genomic analyses. BMC Evolutionary Biology, 2011, 11, 23.	3.2	16
146	Copy number variation analysis in the great apes reveals species-specific patterns of structural variation. Genome Research, 2011, 21, 1626-1639.	2.4	66
147	Gorilla genome structural variation reveals evolutionary parallelisms with chimpanzee. Genome Research, 2011, 21, 1640-1649.	2.4	65
148	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	6.0	3,588
149	Temporal and spatial expression of CCN genes in zebrafish. Developmental Dynamics, 2010, 239, 1755-1767.	0.8	20
150	Genetic history of an archaic hominin group from Denisova Cave in Siberia. Nature, 2010, 468, 1053-1060.	13.7	1,537
151	A large and complex structural polymorphism at 16p12.1 underlies microdeletion disease risk. Nature Genetics, 2010, 42, 745-750.	9.4	89
152	Selection upon Genome Architecture: Conservation of Functional Neighborhoods with Changing Genes. PLoS Computational Biology, 2010, 6, e1000953.	1.5	53
153	Sequencing humanâ€“gibbon breakpoints of synteny reveals mosaic new insertions at rearrangement sites. Genome Research, 2009, 19, 178-190.	2.4	29
154	Human pseudogenes of the ABO family show a complex evolutionary dynamics and loss of function. Glycobiology, 2009, 19, 583-591.	1.3	12
155	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
156	Characterization of six human disease-associated inversion polymorphisms. Human Molecular Genetics, 2009, 18, 2555-2566.	1.4	118
157	Death and Resurrection of the Human IRGM Gene. PLoS Genetics, 2009, 5, e1000403.	1.5	93
158	The origins and impact of primate segmental duplications. Trends in Genetics, 2009, 25, 443-454.	2.9	137
159	A burst of segmental duplications in the genome of the African great ape ancestor. Nature, 2009, 457, 877-881.	13.7	222
160	Personalized copy number and segmental duplication maps using next-generation sequencing. Nature Genetics, 2009, 41, 1061-1067.	9.4	656
161	Sequencing Primate Genomes: What Have We Learned?. Annual Review of Genomics and Human Genetics, 2009, 10, 355-386.	2.5	54
162	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

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163	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
164	Copy number variation and evolution in humans and chimpanzees. Genome Research, 2008, 18, 1698-1710.	2.4	215
165	Balancing Selection Is the Main Force Shaping the Evolution of Innate Immunity Genes. Journal of Immunology, 2008, 181, 1315-1322.	0.4	173
166	Patterns and rates of intron divergence between humans and chimpanzees. Genome Biology, 2007, 8, R21.	13.9	81
167	On the association between chromosomal rearrangements and genic evolution in humans and chimpanzees. Genome Biology, 2007, 8, R230.	13.9	24
168	Ancestral reconstruction of segmental duplications reveals punctuated cores of human genome evolution. Nature Genetics, 2007, 39, 1361-1368.	9.4	192
169	Frequent appearance of novel protein-coding sequences by frameshift translation. Genomics, 2006, 88, 690-697.	1.3	47
170	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
171	The prion protein gene in humans revisited: Lessons from a worldwide resequencing study. Genome Research, 2005, 16, 231-239.	2.4	29
172	Association Cluster Detector: a tool for heuristic detection of significance clusters in whole-genome scans. Bioinformatics, 2005, 21, ii180-ii181.	1.8	6
173	Chromosomal rearrangements are associated with higher rates of molecular evolution in mammals. Gene, 2005, 353, 147-154.	1.0	22
174	Murine segmental duplications are hot spots for chromosome and gene evolution. Genomics, 2005, 86, 692-700.	1.3	28
175	Chromosomal rearrangements and the genomic distribution of gene-expression divergence in humans and chimpanzees. Trends in Genetics, 2004, 20, 524-529.	2.9	66
176	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
177	Rivers as possible landmarks in the orientation flight of Miniopterus schreibersii. Acta Theriologica, 2000, 45, 347-352.	1.1	36
178	A genomic exploration of the early evolution of extant cats and their sabre-toothed relatives. Open Research Europe, 0, 1, 25.	2.0	1