

Axel Janke

List of Publications by Year in descending order

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Version: 2024-02-01

98
papers

7,376
citations

46918

47
h-index

56606

83
g-index

103
all docs

103
docs citations

103
times ranked

6805
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Conservation Genomics of Two Threatened Subspecies of Northern Giraffe: The West African and the Kordofan Giraffe. Genes, 2022, 13, 221.	1.0	4
3	Gene losses in the common vampire bat illuminate molecular adaptations to blood feeding. Science Advances, 2022, 8, eabm6494.	4.7	24
4	Speciation and population divergence in a mutualistic seed dispersing bird. Communications Biology, 2022, 5, 429.	2.0	1
5	Genomic Impact of Whaling in North Atlantic Fin Whales. Molecular Biology and Evolution, 2022, 39, .	3.5	10
6	A Chromosome-Scale Genome Assembly of the Okapi (<i>Okapia johnstoni</i>). Journal of Heredity, 2022, 113, 568-576.	1.0	2
7	SambaR: An R package for fast, easy and reproducible population genetic analyses of biallelic SNP data sets. Molecular Ecology Resources, 2021, 21, 1369-1379.	2.2	37
8	Two high-quality <i>de novo</i> genomes from single ethanol-preserved specimens of tiny metazoans (Collembola). GigaScience, 2021, 10, .	3.3	17
9	Whole-genome analysis of giraffe supports four distinct species. Current Biology, 2021, 31, 2929-2938.e5.	1.8	49
10	Education in the genomics era: Generating high-quality genome assemblies in university courses. GigaScience, 2020, 9, .	3.3	9
11	Systematics, Evolution, and Genetics of Bears. , 2020, , 3-20.		0
12	Species assignment and conservation genetics of giraffe in the Republic of Malawi. Conservation Genetics, 2019, 20, 665-670.	0.8	5
13	Whole-genome sequencing of the blue whale and other rorquals finds signatures for introgressive gene flow. Science Advances, 2018, 4, eaap9873.	4.7	112
14	Speciation Generates Mosaic Genomes in Kangaroos. Genome Biology and Evolution, 2018, 10, 33-44.	1.1	26
15	Matrilineal population structure and distribution of the Angolan giraffe in the Namib desert and beyond. Ecological Genetics and Genomics, 2018, 7-8, 1-5.	0.3	9
16	Limited introgression supports division of giraffe into four species. Ecology and Evolution, 2018, 8, 10156-10165.	0.8	40
17	Response to "How many species of giraffe are there?". Current Biology, 2017, 27, R137-R138.	1.8	13
18	The evolutionary history of bears is characterized by gene flow across species. Scientific Reports, 2017, 7, 46487.	1.6	176

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19	Establishing species-specific sexing markers suitable for non-invasive samples of species lacking genomic resources: an example using the highly endangered common hamster <i>Cricetus cricetus</i> . <i>Conservation Genetics Resources</i> , 2017, 9, 253-255.	0.4	0
20	Phylogenetic Conflict in Bears Identified by Automated Discovery of Transposable Element Insertions in Low-Coverage Genomes. <i>Genome Biology and Evolution</i> , 2017, 9, 2862-2878.	1.1	14
21	Screening for the ancient polar bear mitochondrial genome reveals low integration of mitochondrial pseudogenes (<i>numts</i>) in bears. <i>Mitochondrial DNA Part B: Resources</i> , 2017, 2, 251-254.	0.2	5
22	Multi-locus Analyses Reveal Four Giraffe Species Instead of One. <i>Current Biology</i> , 2016, 26, 2543-2549.	1.8	175
23	Divergence with Genetic Exchange.â€”M. L. Arnold.. <i>Systematic Biology</i> , 2016, 65, 941-942.	2.7	1
24	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. <i>Molecular Phylogenetics and Evolution</i> , 2016, 94, 447-462.	1.2	321
25	Y chromosome haplotype distribution of brown bears (<i>Ursus arctos</i>) in Northern Europe provides insight into population history and recovery. <i>Molecular Ecology</i> , 2015, 24, 6041-6060.	2.0	12
26	Disentangling the Relationship of the Australian Marsupial Orders Using Retrotransposon and Evolutionary Network Analyses. <i>Genome Biology and Evolution</i> , 2015, 7, 985-992.	1.1	38
27	Genome-Wide Search Identifies 1.9 Mb from the Polar Bear Y Chromosome for Evolutionary Analyses. <i>Genome Biology and Evolution</i> , 2015, 7, 2010-2022.	1.1	37
28	Evolutionary Histories of Transposable Elements in the Genome of the Largest Living Marsupial Carnivore, the Tasmanian Devil. <i>Molecular Biology and Evolution</i> , 2015, 32, 1268-1283.	3.5	24
29	Y-chromosomal testing of brown bears (<i>Ursus arctos</i>): Validation of a multiplex PCR-approach for nine STRs suitable for fecal and hair samples. <i>Forensic Science International: Genetics</i> , 2015, 19, 197-204.	1.6	2
30	Genetic signatures of adaptation revealed from transcriptome sequencing of Arctic and red foxes. <i>BMC Genomics</i> , 2015, 16, 585.	1.2	22
31	Mitochondrial sequences reveal a clear separation between Angolan and South African giraffe along a cryptic rift valley. <i>BMC Evolutionary Biology</i> , 2014, 14, 219.	3.2	31
32	Brown and Polar Bear Y Chromosomes Reveal Extensive Male-Biased Gene Flow within Brother Lineages. <i>Molecular Biology and Evolution</i> , 2014, 31, 1353-1363.	3.5	90
33	Genomic resources and genetic diversity of captive lesser kudu (<i>Tragelaphus imberbis</i>). <i>Zoo Biology</i> , 2014, 33, 440-445.	0.5	4
34	Bears in a Forest of Gene Trees: Phylogenetic Inference Is Complicated by Incomplete Lineage Sorting and Gene Flow. <i>Molecular Biology and Evolution</i> , 2014, 31, 2004-2017.	3.5	148
35	A range-wide synthesis and timeline for phylogeographic events in the red fox (<i>Vulpes vulpes</i>). <i>BMC Evolutionary Biology</i> , 2013, 13, 114.	3.2	44
36	A sensitive and specific multiplex PCR approach for sex identification of ursine and tremarctine bears suitable for nonâ€invasive samples. <i>Molecular Ecology Resources</i> , 2013, 13, 362-368.	2.2	23

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37	Mitochondrial DNA analyses show that Zambia's South Luangwa Valley giraffe (<i>Giraffa camelopardalis</i>) Tj ETQq1 1 0.784314 1gBT /Over 0,4 22	0.4	22
38	Networks: expanding evolutionary thinking. <i>Trends in Genetics</i> , 2013, 29, 439-441.	2.9	176
39	Response to Comment on "Nuclear Genomic Sequences Reveal that Polar Bears Are an Old and Distinct Bear Lineage" <i>Science</i> , 2013, 339, 1522-1522.	6.0	12
40	Cryptic Population Structuring and the Role of the Isthmus of Tehuantepec as a Gene Flow Barrier in the Critically Endangered Central American River Turtle. <i>PLoS ONE</i> , 2013, 8, e71668.	1.1	9
41	Coalescent-Based Genome Analyses Resolve the Early Branches of the Euarchontoglires. <i>PLoS ONE</i> , 2013, 8, e60019.	1.1	43
42	Activity of Ancient RTE Retroposons during the Evolution of Cows, Spiral-Horned Antelopes, and Nilgais (<i>Bovinae</i>). <i>Molecular Biology and Evolution</i> , 2012, 29, 2885-2888.	3.5	17
43	Expansion of CORE-SINEs in the genome of the Tasmanian devil. <i>BMC Genomics</i> , 2012, 13, 172.	1.2	10
44	Nuclear Genomic Sequences Reveal that Polar Bears Are an Old and Distinct Bear Lineage. <i>Science</i> , 2012, 336, 344-347.	6.0	238
45	Identification and evaluation of novel di- and tetranucleotide microsatellite markers from the brown bear (<i>Ursus arctos</i>). <i>Conservation Genetics Resources</i> , 2012, 4, 737-741.	0.4	7
46	Impact of Carnivory on Human Development and Evolution Revealed by a New Unifying Model of Weaning in Mammals. <i>PLoS ONE</i> , 2012, 7, e32452.	1.1	24
47	A Genomic Approach to Examine the Complex Evolution of Laurasiatherian Mammals. <i>PLoS ONE</i> , 2011, 6, e28199.	1.1	32
48	Phylogenetic Analysis of Kindlins Suggests Subfunctionalization of an Ancestral Unduplicated Kindlin into Three Paralogs in Vertebrates. <i>Evolutionary Bioinformatics</i> , 2011, 7, EBO.S6179.	0.6	14
49	Mammalian Evolution May not Be Strictly Bifurcating. <i>Molecular Biology and Evolution</i> , 2010, 27, 2804-2816.	3.5	131
50	The impact of fossil calibrations, codon positions and relaxed clocks on the divergence time estimates of the native Australian rodents (<i>Conilurini</i>). <i>Gene</i> , 2010, 455, 22-31.	1.0	12
51	Gnathostome Phylogenomics Utilizing Lungfish EST Sequences. <i>Molecular Biology and Evolution</i> , 2009, 26, 463-471.	3.5	45
52	The importance of data sampling and analysis in resolving crocodylian relationships. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 407-408.	1.2	1
53	Phylogenetic analysis of 1.5ÅMbp and platypus EST data refute the Marsupionta hypothesis and unequivocally support Monotremata as sister group to Marsupialia/Placentalia. <i>Zoologica Scripta</i> , 2008, 37, 115-127.	0.7	18
54	Resolution among major placental mammal interordinal relationships with genome data imply that speciation influenced their earliest radiations. <i>BMC Evolutionary Biology</i> , 2008, 8, 162.	3.2	72

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55	Complete mitochondrial genomes of <i>Bos taurus</i> and <i>Bos indicus</i> ; provide new insights into intra-species variation, taxonomy and domestication. <i>Cytogenetic and Genome Research</i> , 2008, 120, 150-156.	0.6	106
56	Mitogenomic relationships of placental mammals and molecular estimates of their divergences. <i>Gene</i> , 2008, 421, 37-51.	1.0	144
57	Phylogenomic Data Analyses Provide Evidence that Xenarthra and Afrotheria Are Sister Groups. <i>Molecular Biology and Evolution</i> , 2007, 24, 2059-2068.	3.5	115
58	Expressed Sequence Tags as a Tool for Phylogenetic Analysis of Placental Mammal Evolution. <i>PLoS ONE</i> , 2007, 2, e775.	1.1	7
59	Extended mitogenomic phylogenetic analyses yield new insight into crocodylian evolution and their survival of the Cretaceous-Tertiary boundary. <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 663-673.	1.2	81
60	Mitogenomic analyses of caniform relationships. <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 863-874.	1.2	125
61	Housekeeping Genes for Phylogenetic Analysis of Eutherian Relationships. <i>Molecular Biology and Evolution</i> , 2006, 23, 1493-1503.	3.5	48
62	A mitogenomic study on the phylogenetic position of snakes. <i>Zoologica Scripta</i> , 2006, 35, 545-558.	0.7	26
63	Pinniped phylogeny and a new hypothesis for their origin and dispersal. <i>Molecular Phylogenetics and Evolution</i> , 2006, 41, 345-354.	1.2	222
64	Mitogenomic Analyses Place the Gharial (<i>Gavialis gangeticus</i>) on the Crocodile Tree and Provide Pre-K/T Divergence Times for Most Crocodylians. <i>Journal of Molecular Evolution</i> , 2005, 61, 620-626.	0.8	71
65	Mitogenomic analyses provide new insights into cetacean origin and evolution. <i>Gene</i> , 2004, 333, 27-34.	1.0	136
66	Mitogenomic analyses of deep gnathostome divergences: a fish is a fish. <i>Gene</i> , 2004, 333, 61-70.	1.0	53
67	Marsupial relationships and a timeline for marsupial radiation in South Gondwana. <i>Gene</i> , 2004, 340, 189-196.	1.0	191
68	Radiation of Extant Marsupials After the K/T Boundary: Evidence from Complete Mitochondrial Genomes. <i>Journal of Molecular Evolution</i> , 2003, 57, S3-S12.	0.8	81
69	Revisiting the Glires concept—phylogenetic analysis of nuclear sequences. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 320-327.	1.2	38
70	Two new avian mitochondrial genomes (penguin and goose) and a summary of bird and reptile mitogenomic features. <i>Gene</i> , 2003, 302, 43-52.	1.0	89
71	Molecular analysis of wild and domestic sheep questions current nomenclature and provides evidence for domestication from two different subspecies. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2002, 269, 893-904.	1.2	210
72	Mammalian mitogenomic relationships and the root of the eutherian tree. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 8151-8156.	3.3	356

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73	Mitogenomic analyses of eutherian relationships. <i>Cytogenetic and Genome Research</i> , 2002, 96, 20-32.	0.6	74
74	The mitochondrial genome of the pufferfish, <i>Fugu rubripes</i> , and ordinal teleostean relationships. <i>Gene</i> , 2002, 295, 163-172.	1.0	52
75	Phylogenetic Analysis of 18S rRNA and the Mitochondrial Genomes of the Wombat, <i>Vombatus ursinus</i> , and the Spiny Anteater, <i>Tachyglossus aculeatus</i> : Increased Support for the Marsupionta Hypothesis. <i>Journal of Molecular Evolution</i> , 2002, 54, 71-80.	0.8	71
76	Molecular phylogenetics of gnathostomous (jawed) fishes: old bones, new cartilage. <i>Zoologica Scripta</i> , 2001, 30, 249-255.	0.7	58
77	Molecular Evidence of an African Pliomorpha "South American Caviomorpha Clade and Support for Hystricognathi Based on the Complete Mitochondrial Genome of the Cane Rat (<i>Thryonomys</i>) Tj ETQq1 1 0.784314.rgBT /Overlock 10	1.0	107
78	The mitochondrial genomes of the iguana (<i>Iguana iguana</i>) and the caiman (<i>Caiman crocodylus</i>): implications for amniote phylogeny. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2001, 268, 623-631.	1.2	111
79	The Phylogenetic Position of the Talpidae Within Eutheria Based on Analysis of Complete Mitochondrial Sequences. <i>Molecular Biology and Evolution</i> , 2000, 17, 60-67.	3.5	114
80	Phylogenetic position of the Tenrecs (Mammalia: Tenrecidae) of Madagascar based on analysis of the complete mitochondrial genome sequence of <i>Echinops telfairi</i> . <i>Zoologica Scripta</i> , 2000, 29, 307-317.	0.7	42
81	The Mitochondrial Genome of the Sperm Whale and a New Molecular Reference for Estimating Eutherian Divergence Dates. <i>Journal of Molecular Evolution</i> , 2000, 50, 569-578.	0.8	122
82	The mitochondrial DNA molecule of the aardvark, <i>Orycteropus afer</i> , and the position of the Tubulidentata in the eutherian tree. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 1999, 266, 339-345.	1.2	28
83	Conflict Among Individual Mitochondrial Proteins in Resolving the Phylogeny of Eutherian Orders. <i>Journal of Molecular Evolution</i> , 1998, 47, 307-322.	0.8	208
84	The mitochondrial DNA molecule of the hagfish (<i>Myxine glutinosa</i>) and vertebrate phylogeny. <i>Journal of Molecular Evolution</i> , 1998, 46, 382-388.	0.8	69
85	The Complete Mitochondrial Genome of <i>Rhea americana</i> and Early Avian Divergences. <i>Journal of Molecular Evolution</i> , 1998, 46, 669-679.	0.8	84
86	The Complete Mitochondrial DNA Sequence of the Domestic Sheep (<i>Ovis aries</i>) and Comparison with the Other Major Ovine Haplotype. <i>Journal of Molecular Evolution</i> , 1998, 47, 441-448.	0.8	161
87	Molecular Timing of Primate Divergences as Estimated by Two Nonprimate Calibration Points. <i>Journal of Molecular Evolution</i> , 1998, 47, 718-727.	0.8	138
88	Phylogenetic analyses of mitochondrial DNA suggest a sister group relationship between Xenarthra (Edentata) and Ferungulates. <i>Molecular Biology and Evolution</i> , 1997, 14, 762-768.	3.5	79
89	The complete mitochondrial genome of <i>Alligator mississippiensis</i> and the separation between recent archosauria (birds and crocodiles). <i>Molecular Biology and Evolution</i> , 1997, 14, 1266-1272.	3.5	162
90	The mtDNA sequence of the ostrich and the divergence between paleognathous and neognathous birds. <i>Molecular Biology and Evolution</i> , 1997, 14, 754-761.	3.5	107

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91	The complete mitochondrial genome of the wallaroo (<i>Macropus robustus</i>) and the phylogenetic relationship among Monotremata, Marsupialia, and Eutheria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 1276-1281.	3.3	239
92	The complete mitochondrial DNA sequence of the greater Indian rhinoceros, <i>Rhinoceros unicornis</i> , and the Phylogenetic relationship among Carnivora, Perissodactyla, and Artiodactyla (+ Cetacea). <i>Molecular Biology and Evolution</i> , 1996, 13, 1167-1173.	3.5	113
93	The mitochondrial genome of a monotreme—the platypus (<i>Ornithorhynchus anatinus</i>). <i>Journal of Molecular Evolution</i> , 1996, 42, 153-159.	0.8	127
94	Pattern and timing of evolutionary divergences among hominoids based on analyses of complete mtDNAs. <i>Journal of Molecular Evolution</i> , 1996, 43, 650-661.	0.8	137
95	Phylogenetic relationships among eutherian orders estimated from inferred sequences of mitochondrial proteins: Instability of a tree based on a single gene. <i>Journal of Molecular Evolution</i> , 1994, 39, 519-27.	0.8	239
96	Cloning and characterization of the platypus mitochondrial genome. <i>Journal of Molecular Evolution</i> , 1994, 39, 200-205.	0.8	10
97	Editing of a tRNA anticodon in marsupial mitochondria changes its codon recognition. <i>Nucleic Acids Research</i> , 1993, 21, 1523-1525.	6.5	144
98	Chromosome-level genome assembly of a benthic associated Syngnathiformes species: the common dragonet, <i>Callionymus lyra</i> . <i>GigaByte</i> , 0, 2020, 1-10.	0.0	7