

# Axel Janke

## List of Publications by Year in descending order

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98  
papers

7,376  
citations

46918

47  
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56606

83  
g-index

103  
all docs

103  
docs citations

103  
times ranked

6805  
citing authors

#	ARTICLE	IF	CITATIONS
1	Mammalian mitogenomic relationships and the root of the eutherian tree. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 8151-8156.	3.3	356
2	Implementing and testing the multispecies coalescent model: A valuable paradigm for phylogenomics. Molecular Phylogenetics and Evolution, 2016, 94, 447-462.	1.2	321
3	Phylogenetic relationships among eutherian orders estimated from inferred sequences of mitochondrial proteins: Instability of a tree based on a single gene. Journal of Molecular Evolution, 1994, 39, 519-27.	0.8	239
4	The complete mitochondrial genome of the wallaroo ( <i>Macropus robustus</i> ) and the phylogenetic relationship among Monotremata, Marsupialia, and Eutheria. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 1276-1281.	3.3	239
5	Nuclear Genomic Sequences Reveal that Polar Bears Are an Old and Distinct Bear Lineage. Science, 2012, 336, 344-347.	6.0	238
6	Pinniped phylogeny and a new hypothesis for their origin and dispersal. Molecular Phylogenetics and Evolution, 2006, 41, 345-354.	1.2	222
7	Molecular analysis of wild and domestic sheep questions current nomenclature and provides evidence for domestication from two different subspecies. Proceedings of the Royal Society B: Biological Sciences, 2002, 269, 893-904.	1.2	210
8	Conflict Among Individual Mitochondrial Proteins in Resolving the Phylogeny of Eutherian Orders. Journal of Molecular Evolution, 1998, 47, 307-322.	0.8	208
9	Marsupial relationships and a timeline for marsupial radiation in South Gondwana. Gene, 2004, 340, 189-196.	1.0	191
10	Networks: expanding evolutionary thinking. Trends in Genetics, 2013, 29, 439-441.	2.9	176
11	The evolutionary history of bears is characterized by gene flow across species. Scientific Reports, 2017, 7, 46487.	1.6	176
12	Multi-locus Analyses Reveal Four Giraffe Species Instead of One. Current Biology, 2016, 26, 2543-2549.	1.8	175
13	The complete mitochondrial genome of <i>Alligator mississippiensis</i> and the separation between recent archosauria (birds and crocodiles). Molecular Biology and Evolution, 1997, 14, 1266-1272.	3.5	162
14	The Complete Mitochondrial DNA Sequence of the Domestic Sheep ( <i>Ovis aries</i> ) and Comparison with the Other Major Ovine Haplotype. Journal of Molecular Evolution, 1998, 47, 441-448.	0.8	161
15	Bears in a Forest of Gene Trees: Phylogenetic Inference Is Complicated by Incomplete Lineage Sorting and Gene Flow. Molecular Biology and Evolution, 2014, 31, 2004-2017.	3.5	148
16	Editing of a tRNA anticodon in marsupial mitochondria changes its codon recognition. Nucleic Acids Research, 1993, 21, 1523-1525.	6.5	144
17	Mitogenomic relationships of placental mammals and molecular estimates of their divergences. Gene, 2008, 421, 37-51.	1.0	144
18	Molecular Timing of Primate Divergences as Estimated by Two Nonprimate Calibration Points. Journal of Molecular Evolution, 1998, 47, 718-727.	0.8	138

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19	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
20	Mitogenomic analyses provide new insights into cetacean origin and evolution. <i>Gene</i> , 2004, 333, 27-34.	1.0	136
21	Mammalian Evolution May not Be Strictly Bifurcating. <i>Molecular Biology and Evolution</i> , 2010, 27, 2804-2816.	3.5	131
22	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
23	Mitogenomic analyses of caniform relationships. <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 863-874.	1.2	125
24	The Earth BioGenome Project 2020: Starting the clock. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	124
25	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
26	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
27	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
28	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
29	Whole-genome sequencing of the blue whale and other rorquals finds signatures for introgressive gene flow. <i>Science Advances</i> , 2018, 4, eaap9873.	4.7	112
30	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
31	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
32	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
33	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
34	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
35	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
36	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

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37	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
38	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
39	Mitogenomic analyses of eutherian relationships. <i>Cytogenetic and Genome Research</i> , 2002, 96, 20-32.	0.6	74
40	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
41	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
42	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
43	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
44	Molecular phylogenetics of gnathostomous (jawed) fishes: old bones, new cartilage. <i>Zoologica Scripta</i> , 2001, 30, 249-255.	0.7	58
45	Mitogenomic analyses of deep gnathostome divergences: a fish is a fish. <i>Gene</i> , 2004, 333, 61-70.	1.0	53
46	The mitochondrial genome of the pufferfish, <i>Fugu rubripes</i> , and ordinal teleostean relationships. <i>Gene</i> , 2002, 295, 163-172.	1.0	52
47	Whole-genome analysis of giraffe supports four distinct species. <i>Current Biology</i> , 2021, 31, 2929-2938.e5.	1.8	49
48	Housekeeping Genes for Phylogenetic Analysis of Eutherian Relationships. <i>Molecular Biology and Evolution</i> , 2006, 23, 1493-1503.	3.5	48
49	Gnathostome Phylogenomics Utilizing Lungfish EST Sequences. <i>Molecular Biology and Evolution</i> , 2009, 26, 463-471.	3.5	45
50	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
51	Coalescent-Based Genome Analyses Resolve the Early Branches of the Euarchontoglires. <i>PLoS ONE</i> , 2013, 8, e60019.	1.1	43
52	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
53	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> ). <i>Tj ETQq1 1 0.7843141rgBT /Overlock 10</i>	1.1	41
54	Limited introgression supports division of giraffe into four species. <i>Ecology and Evolution</i> , 2018, 8, 10156-10165.	0.8	40

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55	Revisiting the Glires conceptâ€”phylogenetic analysis of nuclear sequences. <i>Molecular Phylogenetics and Evolution</i> , 2003, 28, 320-327.	1.2	38
56	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
57	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
58	SambaR: An R package for fast, easy and reproducible populationâ€”genetic analyses of biallelic SNP data sets. <i>Molecular Ecology Resources</i> , 2021, 21, 1369-1379.	2.2	37
59	A Genomic Approach to Examine the Complex Evolution of Laurasiatherian Mammals. <i>PLoS ONE</i> , 2011, 6, e28199.	1.1	32
60	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
61	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
62	A mitogenomic study on the phylogenetic position of snakes. <i>Zoologica Scripta</i> , 2006, 35, 545-558.	0.7	26
63	Speciation Generates Mosaic Genomes in Kangaroos. <i>Genome Biology and Evolution</i> , 2018, 10, 33-44.	1.1	26
64	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
65	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
66	Gene losses in the common vampire bat illuminate molecular adaptations to blood feeding. <i>Science Advances</i> , 2022, 8, eabm6494.	4.7	24
67	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
68	Mitochondrial DNA analyses show that Zambia's South Luangwa Valley giraffe ( <i>Giraffa camelopardalis</i> ) Tj ETQq0 0 0 rgBT /Overlock 10 T	0.4	22
69	Genetic signatures of adaptation revealed from transcriptome sequencing of Arctic and red foxes. <i>BMC Genomics</i> , 2015, 16, 585.	1.2	22
70	Phylogenetic analysis of 1.5Â”Mb 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
71	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
72	Two high-quality <i>de novo</i> genomes from single ethanol-preserved specimens of tiny metazoans ( <i>Collembola</i> ). <i>GigaScience</i> , 2021, 10, .	3.3	17

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73	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
74	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
75	Response to "How many species of giraffe are there?" <i>Current Biology</i> , 2017, 27, R137-R138.	1.8	13
76	The impact of fossil calibrations, codon positions and relaxed clocks on the divergence time estimates of the native Australian rodents (Conilurini). <i>Gene</i> , 2010, 455, 22-31.	1.0	12
77	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
78	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
79	Expansion of CORE-SINEs in the genome of the Tasmanian devil. <i>BMC Genomics</i> , 2012, 13, 172.	1.2	10
80	Cloning and characterization of the platypus mitochondrial genome. <i>Journal of Molecular Evolution</i> , 1994, 39, 200-205.	0.8	10
81	Genomic Impact of Whaling in North Atlantic Fin Whales. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	10
82	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
83	Matrilineal population structure and distribution of the Angolan giraffe in the Namib desert and beyond. <i>Ecological Genetics and Genomics</i> , 2018, 7-8, 1-5.	0.3	9
84	Education in the genomics era: Generating high-quality genome assemblies in university courses. <i>GigaScience</i> , 2020, 9, .	3.3	9
85	Expressed Sequence Tags as a Tool for Phylogenetic Analysis of Placental Mammal Evolution. <i>PLoS ONE</i> , 2007, 2, e775.	1.1	7
86	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
87	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
88	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
89	Species assignment and conservation genetics of giraffe in the Republic of Malawi. <i>Conservation Genetics</i> , 2019, 20, 665-670.	0.8	5
90	Genomic resources and genetic diversity of captive lesser kudu ( <i>Tragelaphus imberbis</i> ). <i>Zoo Biology</i> , 2014, 33, 440-445.	0.5	4

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91	Conservation Genomics of Two Threatened Subspecies of Northern Giraffe: The West African and the Kordofan Giraffe. <i>Genes</i> , 2022, 13, 221.	1.0	4
92	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
93	A Chromosome-Scale Genome Assembly of the Okapi ( <i>Okapia johnstoni</i> ). <i>Journal of Heredity</i> , 2022, 113, 568-576.	1.0	2
94	The importance of data sampling and analysis in resolving crocodylian relationships. <i>Molecular Phylogenetics and Evolution</i> , 2008, 49, 407-408.	1.2	1
95	Divergence with Genetic Exchange. M. L. Arnold. <i>Systematic Biology</i> , 2016, 65, 941-942.	2.7	1
96	Speciation and population divergence in a mutualistic seed dispersing bird. <i>Communications Biology</i> , 2022, 5, 429.	2.0	1
97	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
98	Systematics, Evolution, and Genetics of Bears. , 2020, , 3-20.		0