

Arndt von Haeseler

List of Publications by Year in descending order

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Version: 2024-02-01

97
papers

55,472
citations

31902

53
h-index

46693

89
g-index

106
all docs

106
docs citations

106
times ranked

43134
citing authors

#	ARTICLE	IF	CITATIONS
1	IQ-TREE: A Fast and Effective Stochastic Algorithm for Estimating Maximum-Likelihood Phylogenies. <i>Molecular Biology and Evolution</i> , 2015, 32, 268-274.	3.5	16,610
2	ModelFinder: fast model selection for accurate phylogenetic estimates. <i>Nature Methods</i> , 2017, 14, 587-589.	9.0	9,486
3	IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. <i>Molecular Biology and Evolution</i> , 2020, 37, 1530-1534.	3.5	5,960
4	UFBoot2: Improving the Ultrafast Bootstrap Approximation. <i>Molecular Biology and Evolution</i> , 2018, 35, 518-522.	3.5	5,798
5	Ultrafast Approximation for Phylogenetic Bootstrap. <i>Molecular Biology and Evolution</i> , 2013, 30, 1188-1195.	3.5	3,123
6	W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. <i>Nucleic Acids Research</i> , 2016, 44, W232-W235.	6.5	3,039
7	Terrace Aware Data Structure for Phylogenomic Inference from Supermatrices. <i>Systematic Biology</i> , 2016, 65, 997-1008.	2.7	1,453
8	Accurate detection of complex structural variations using single-molecule sequencing. <i>Nature Methods</i> , 2018, 15, 461-468.	9.0	1,175
9	Unexpected complexity of the Wnt gene family in a sea anemone. <i>Nature</i> , 2005, 433, 156-160.	13.7	516
10	Updating benchtop sequencing performance comparison. <i>Nature Biotechnology</i> , 2013, 31, 294-296.	9.4	423
11	Thiol-linked alkylation of RNA to assess expression dynamics. <i>Nature Methods</i> , 2017, 14, 1198-1204.	9.0	411
12	NextGenMap: fast and accurate read mapping in highly polymorphic genomes. <i>Bioinformatics</i> , 2013, 29, 2790-2791.	1.8	408
13	A view of Neandertal genetic diversity. <i>Nature Genetics</i> , 2000, 26, 144-146.	9.4	330
14	The performance of phylogenetic algorithms in estimating haplotype genealogies with migration. <i>Molecular Ecology</i> , 2011, 20, 1952-1963.	2.0	316
15	A Phylogenomic Approach to Resolve the Arthropod Tree of Life. <i>Molecular Biology and Evolution</i> , 2010, 27, 2451-2464.	3.5	308
16	SLAM-seq defines direct gene-regulatory functions of the BRD4-MYC axis. <i>Science</i> , 2018, 360, 800-805.	6.0	284
17	Genome-Wide RNAi Screen Identifies Genes Involved in Intestinal Pathogenic Bacterial Infection. <i>Science</i> , 2009, 325, 340-343.	6.0	277
18	Next-generation sequencing diagnostics of bacteremia in septic patients. <i>Genome Medicine</i> , 2016, 8, 73.	3.6	265

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19	Unifying the global phylogeny and environmental distribution of ammonia-oxidising archaea based on amoA genes. <i>Nature Communications</i> , 2018, 9, 1517.	5.8	256
20	DNA sequence variation in a non-coding region of low recombination on the human X chromosome. <i>Nature Genetics</i> , 1999, 22, 78-81.	9.4	237
21	Pattern of Nucleotide Substitution and Rate Heterogeneity in the Hypervariable Regions I and II of Human mtDNA. <i>Genetics</i> , 1999, 152, 1103-1110.	1.2	232
22	A Stochastic Model for the Evolution of Autocorrelated DNA Sequences. <i>Molecular Phylogenetics and Evolution</i> , 1994, 3, 240-247.	1.2	224
23	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede <i>Strigamia maritima</i> . <i>PLoS Biology</i> , 2014, 12, e1002005.	2.6	221
24	A nuclear 'fossil' of the mitochondrial D-loop and the origin of modern humans. <i>Nature</i> , 1995, 378, 489-492.	13.7	217
25	Central control of fever and female body temperature by RANKL/RANK. <i>Nature</i> , 2009, 462, 505-509.	13.7	212
26	A-type lamins bind both hetero- and euchromatin, the latter being regulated by lamina-associated polypeptide 2 alpha. <i>Genome Research</i> , 2016, 26, 462-473.	2.4	157
27	IQPNNI: Moving Fast Through Tree Space and Stopping in Time. <i>Molecular Biology and Evolution</i> , 2004, 21, 1565-1571.	3.5	146
28	Inference of Population History Using a Likelihood Approach. <i>Genetics</i> , 1998, 149, 1539-1546.	1.2	141
29	A Consistent Phylogenetic Backbone for the Fungi. <i>Molecular Biology and Evolution</i> , 2012, 29, 1319-1334.	3.5	129
30	MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. <i>BMC Evolutionary Biology</i> , 2018, 18, 11.	3.2	129
31	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
32	Decisive Data Sets in Phylogenomics: Lessons from Studies on the Phylogenetic Relationships of Primarily Wingless Insects. <i>Molecular Biology and Evolution</i> , 2014, 31, 239-249.	3.5	127
33	Mapping Human Genetic Ancestry. <i>Molecular Biology and Evolution</i> , 2007, 24, 2266-2276.	3.5	117
34	Simultaneous Statistical Multiple Alignment and Phylogeny Reconstruction. <i>Systematic Biology</i> , 2005, 54, 548-561.	2.7	114
35	The genetical archaeology of the human genome. <i>Nature Genetics</i> , 1996, 14, 135-140.	9.4	105
36	A human tissue screen identifies a regulator of ER secretion as a brain-size determinant. <i>Science</i> , 2020, 370, 935-941.	6.0	101

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37	The genomic basis of circadian and circalunar timing adaptations in a midge. <i>Nature</i> , 2016, 540, 69-73.	13.7	96
38	Distribution and Phylogeny of Light-Oxygen-Voltage-Blue-Light-Signaling Proteins in the Three Kingdoms of Life. <i>Journal of Bacteriology</i> , 2009, 191, 7234-7242.	1.0	95
39	EST sequencing of Onychophora and phylogenomic analysis of Metazoa. <i>Molecular Phylogenetics and Evolution</i> , 2007, 45, 942-951.	1.2	92
40	The evolution of the ribosome biogenesis pathway from a yeast perspective. <i>Nucleic Acids Research</i> , 2014, 42, 1509-1523.	6.5	87
41	Quantification of experimentally induced nucleotide conversions in high-throughput sequencing datasets. <i>BMC Bioinformatics</i> , 2019, 20, 258.	1.2	86
42	A Developmentally Regulated Aconitase Related to Iron-regulatory Protein-1 Is Localized in the Cytoplasm and in the Mitochondrion of <i>Trypanosoma brucei</i> . <i>Journal of Biological Chemistry</i> , 2000, 275, 2745-2755.	1.6	82
43	Cooperation of Multiple Chromatin Modifications Can Generate Unanticipated Stability of Epigenetic States in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2010, 22, 34-47.	3.1	82
44	Adenosine deaminases that act on RNA induce reproducible changes in abundance and sequence of embryonic miRNAs. <i>Genome Research</i> , 2012, 22, 1468-1476.	2.4	80
45	A Coalescent Approach to Study Linkage Disequilibrium between Single-Nucleotide Polymorphisms. <i>American Journal of Human Genetics</i> , 2000, 66, 615-628.	2.6	77
46	Split diversity in constrained conservation prioritization using integer linear programming. <i>Methods in Ecology and Evolution</i> , 2015, 6, 83-91.	2.2	75
47	GHOST: Recovering Historical Signal from Heterotachously Evolved Sequence Alignments. <i>Systematic Biology</i> , 2020, 69, 249-264.	2.7	75
48	Conserved pore-forming regions in polypeptide-transporting proteins. <i>FEBS Journal</i> , 2005, 272, 1367-1378.	2.2	74
49	Functional and Phylogenetic Properties of the Pore-forming β -Barrel Transporters of the Omp85 Family. <i>Journal of Biological Chemistry</i> , 2007, 282, 1882-1890.	1.6	74
50	Reversible polymorphism-aware phylogenetic models and their application to tree inference. <i>Journal of Theoretical Biology</i> , 2016, 407, 362-370.	0.8	70
51	pIQPNNI: parallel reconstruction of large maximum likelihood phylogenies. <i>Bioinformatics</i> , 2005, 21, 3794-3796.	1.8	69
52	A Phylogenomic Approach to Resolve the Basal Pterygote Divergence. <i>Molecular Biology and Evolution</i> , 2009, 26, 2719-2730.	3.5	66
53	Quartet-Mapping, a Generalization of the Likelihood-Mapping Procedure. <i>Molecular Biology and Evolution</i> , 2001, 18, 1204-1219.	3.5	63
54	NGC: lossless and lossy compression of aligned high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2013, 41, e27-e27.	6.5	57

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55	The Tetratricopeptide Repeats of Receptors Involved in Protein Translocation across Membranes. <i>Molecular Biology and Evolution</i> , 2007, 24, 2763-2774.	3.5	56
56	Combined transcriptome and proteome profiling reveals specific molecular brain signatures for sex, maturation and circalunar clock phase. <i>ELife</i> , 2019, 8, .	2.8	51
57	The <i>Candida albicans</i> Histone Acetyltransferase Hat1 Regulates Stress Resistance and Virulence via Distinct Chromatin Assembly Pathways. <i>PLoS Pathogens</i> , 2015, 11, e1005218.	2.1	48
58	Recent Origin and Cultural Reversion of a Hunter-Gatherer Group. <i>PLoS Biology</i> , 2005, 3, e71.	2.6	47
59	Modeling the Polymerase Chain Reaction. <i>Journal of Computational Biology</i> , 1995, 2, 49-61.	0.8	46
60	ADAR2 induces reproducible changes in sequence and abundance of mature microRNAs in the mouse brain. <i>Nucleic Acids Research</i> , 2014, 42, 12155-12168.	6.5	42
61	Network models for sequence evolution. <i>Journal of Molecular Evolution</i> , 1993, 37, 77-85.	0.8	39
62	Pegylated granulocyte colony-stimulating factor mobilizes CD34+ cells with different stem and progenitor subsets and distinct functional properties in comparison with unconjugated granulocyte colony-stimulating factor. <i>Haematologica</i> , 2008, 93, 347-355.	1.7	39
63	Performance of the Maximum Likelihood, Neighbor Joining, and Maximum Parsimony Methods When Sequence Sites are Not Independent. <i>Systematic Biology</i> , 1995, 44, 533-547.	2.7	37
64	Phylogenetic Diversity within Seconds. <i>Systematic Biology</i> , 2006, 55, 769-773.	2.7	37
65	Innate Immune Response to <i>Streptococcus pyogenes</i> Depends on the Combined Activation of TLR13 and TLR2. <i>PLoS ONE</i> , 2015, 10, e0119727.	1.1	37
66	Towards Integration of Multiple Alignment and Phylogenetic Tree Construction. <i>Journal of Computational Biology</i> , 1997, 4, 23-34.	0.8	35
67	ATM controls meiotic DNA double-strand break formation and recombination and affects synaptonemal complex organization in plants. <i>Plant Cell</i> , 2021, 33, 1633-1656.	3.1	33
68	Sequencing of the <i>Arabidopsis</i> NOR2 reveals its distinct organization and tissue-specific rRNA ribosomal variants. <i>Nature Communications</i> , 2021, 12, 387.	5.8	32
69	Identifying Site-Specific Substitution Rates. <i>Molecular Biology and Evolution</i> , 2003, 20, 182-189.	3.5	29
70	Polymorphism-Aware Species Trees with Advanced Mutation Models, Bootstrap, and Rate Heterogeneity. <i>Molecular Biology and Evolution</i> , 2019, 36, 1294-1301.	3.5	27
71	Teaser: Individualized benchmarking and optimization of read mapping results for NGS data. <i>Genome Biology</i> , 2015, 16, 235.	3.8	25
72	TRUmiCount: correctly counting absolute numbers of molecules using unique molecular identifiers. <i>Bioinformatics</i> , 2018, 34, 3137-3144.	1.8	25

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73	The Evolutionary Traceability of a Protein. <i>Genome Biology and Evolution</i> , 2019, 11, 531-545.	1.1	23
74	Genetic distances and nucleotide substitution models. , 2009, , 111-141.		20
75	In vivo insertion pool sequencing identifies virulence factors in a complex fungalâ€“host interaction. <i>PLoS Biology</i> , 2018, 16, e2005129.	2.6	20
76	Do we still need supertrees?. <i>BMC Biology</i> , 2012, 10, 13.	1.7	19
77	A-to-I RNA Editing Uncovers Hidden Signals of Adaptive Genome Evolution in Animals. <i>Genome Biology and Evolution</i> , 2020, 12, 345-357.	1.1	17
78	Poly(ADP-ribose) glycohydrolase coordinates meiotic DNA double-strand break induction and repair independent of its catalytic activity. <i>Nature Communications</i> , 2020, 11, 4869.	5.8	16
79	Distinguishing Felsenstein Zone from Farris Zone Using Neural Networks. <i>Molecular Biology and Evolution</i> , 2020, 37, 3632-3641.	3.5	16
80	HvrBase++: a phylogenetic database for primate species. <i>Nucleic Acids Research</i> , 2006, 34, D700-D704.	6.5	15
81	Germline Variants in the POT1-Gene in High-Risk Melanoma Patients in Austria. <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 1475-1480.	0.8	12
82	Complex Models of Sequence Evolution Require Accurate Estimators as Exemplified with the Invariable Site Plus Gamma Model. <i>Systematic Biology</i> , 2018, 67, 552-558.	2.7	11
83	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. <i>PLoS Biology</i> , 2021, 19, e3001012.	2.6	9
84	Decreased expression of endogenous feline leukemia virus in cat lymphomas: a case control study. <i>BMC Veterinary Research</i> , 2015, 11, 90.	0.7	8
85	Complex Evolution of Light-Dependent Protochlorophyllide Oxidoreductases in Aerobic Anoxygenic Phototrophs: Origin, Phylogeny, and Function. <i>Molecular Biology and Evolution</i> , 2021, 38, 819-837.	3.5	6
86	Exploring the sampling universe of RNA-seq. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013, 12, 175-88.	0.2	5
87	It Is Just a Matter of Time: Balancing Homologous Recombination and Non-homologous End Joining at the rDNA Locus During Meiosis. <i>Frontiers in Plant Science</i> , 2021, 12, 773052.	1.7	3
88	An Enumerative Combinatorics Model for Fragmentation Patterns in RNA Sequencing Provides Insights into Nonuniformity of the Expected Fragment Starting-Point and Coverage Profile. <i>Journal of Computational Biology</i> , 2017, 24, 200-212.	0.8	2
89	Computational Molecular Evolutionâ€“Ziheng Yang. 2006. Oxford University Press, Oxford. 376 pp. ISBN 978-0-19-856699-1 (ISBN-10 0-19-856699-9) Â£60 \$115 (hardback). ISBN 978-0-19-856702-8 (ISBN-10 0-19-856702-2) Â£27.50 \$52.50 (paperback).. <i>Systematic Biology</i> , 2007, 56, 1024-1026.		1
90	VARIFlâ€“Web-Based Automatic Variant Identification, Filtering and Annotation of Amplicon Sequencing Data. <i>Journal of Personalized Medicine</i> , 2019, 9, 10.	1.1	1

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91	Structure of the space of taboo-free sequences. <i>Journal of Mathematical Biology</i> , 2020, 81, 1029-1057.	0.8	0
92	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. , 2021, 19, e3001012.		0
93	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. , 2021, 19, e3001012.		0
94	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. , 2021, 19, e3001012.		0
95	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. , 2021, 19, e3001012.		0
96	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. , 2021, 19, e3001012.		0
97	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. , 2021, 19, e3001012.		0