

Arndt von Haeseler

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

96 papers	26,788 citations	50 h-index	106 g-index
106 ext. papers	42,845 ext. citations	12.2 avg, IF	7.81 L-index

#	Paper	IF	Citations
96	IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. <i>Molecular Biology and Evolution</i> , 2015 , 32, 268-74	8.3	8116
95	ModelFinder: fast model selection for accurate phylogenetic estimates. <i>Nature Methods</i> , 2017 , 14, 587-596	22.6	3957
94	UFBoot2: Improving the Ultrafast Bootstrap Approximation. <i>Molecular Biology and Evolution</i> , 2018 , 35, 518-522	8.3	2342
93	Ultrafast approximation for phylogenetic bootstrap. <i>Molecular Biology and Evolution</i> , 2013 , 30, 1188-95	8.3	1669
92	W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. <i>Nucleic Acids Research</i> , 2016 , 44, W232-5	20.1	1497
91	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	8.3	1466
90	Terrace Aware Data Structure for Phylogenomic Inference from Supermatrices. <i>Systematic Biology</i> , 2016 , 65, 997-1008	8.4	704
89	Accurate detection of complex structural variations using single-molecule sequencing. <i>Nature Methods</i> , 2018 , 15, 461-468	21.6	585
88	Unexpected complexity of the Wnt gene family in a sea anemone. <i>Nature</i> , 2005 , 433, 156-60	50.4	435
87	A view of Neandertal genetic diversity. <i>Nature Genetics</i> , 2000 , 26, 144-6	36.3	277
86	A phylogenomic approach to resolve the arthropod tree of life. <i>Molecular Biology and Evolution</i> , 2010 , 27, 2451-64	8.3	265
85	Updating benchtop sequencing performance comparison. <i>Nature Biotechnology</i> , 2013 , 31, 294-6	44.5	255
84	The performance of phylogenetic algorithms in estimating haplotype genealogies with migration. <i>Molecular Ecology</i> , 2011 , 20, 1952-63	5.7	251
83	NextGenMap: fast and accurate read mapping in highly polymorphic genomes. <i>Bioinformatics</i> , 2013 , 29, 2790-1	7.2	246
82	Genome-wide RNAi screen identifies genes involved in intestinal pathogenic bacterial infection. <i>Science</i> , 2009 , 325, 340-3	33.3	244
81	Thiol-linked alkylation of RNA to assess expression dynamics. <i>Nature Methods</i> , 2017 , 14, 1198-1204	21.6	204
80	DNA sequence variation in a non-coding region of low recombination on the human X chromosome. <i>Nature Genetics</i> , 1999 , 22, 78-81	36.3	202

79	A nuclear fossil of the mitochondrial D-loop and the origin of modern humans. <i>Nature</i> , 1995 , 378, 489-92	30.4	190
78	A stochastic model for the evolution of autocorrelated DNA sequences. <i>Molecular Phylogenetics and Evolution</i> , 1994 , 3, 240-7	4.1	184
77	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	9.7	182
76	Pattern of nucleotide substitution and rate heterogeneity in the hypervariable regions I and II of human mtDNA. <i>Genetics</i> , 1999 , 152, 1103-10	4	182
75	Central control of fever and female body temperature by RANKL/RANK. <i>Nature</i> , 2009 , 462, 505-9	50.4	173
74	Next-generation sequencing diagnostics of bacteremia in septic patients. <i>Genome Medicine</i> , 2016 , 8, 73	14.4	164
73	SLAM-seq defines direct gene-regulatory functions of the BRD4-MYC axis. <i>Science</i> , 2018 , 360, 800-805	33.3	147
72	Unifying the global phylogeny and environmental distribution of ammonia-oxidising archaea based on amoA genes. <i>Nature Communications</i> , 2018 , 9, 1517	17.4	131
71	A-type lamins bind both hetero- and euchromatin, the latter being regulated by lamina-associated polypeptide 2 alpha. <i>Genome Research</i> , 2016 , 26, 462-73	9.7	119
70	IQPNNI: moving fast through tree space and stopping in time. <i>Molecular Biology and Evolution</i> , 2004 , 21, 1565-71	8.3	116
69	Inference of population history using a likelihood approach. <i>Genetics</i> , 1998 , 149, 1539-46	4	113
68	The mitochondrial genome of a monotreme--the platypus (<i>Ornithorhynchus anatinus</i>). <i>Journal of Molecular Evolution</i> , 1996 , 42, 153-9	3.1	109
67	A consistent phylogenetic backbone for the fungi. <i>Molecular Biology and Evolution</i> , 2012 , 29, 1319-34	8.3	104
66	Decisive data sets in phylogenomics: lessons from studies on the phylogenetic relationships of primarily wingless insects. <i>Molecular Biology and Evolution</i> , 2014 , 31, 239-49	8.3	100
65	Mapping human genetic ancestry. <i>Molecular Biology and Evolution</i> , 2007 , 24, 2266-76	8.3	99
64	The genetical archaeology of the human genome. <i>Nature Genetics</i> , 1996 , 14, 135-40	36.3	88
63	Distribution and phylogeny of light-oxygen-voltage-blue-light-signaling proteins in the three kingdoms of life. <i>Journal of Bacteriology</i> , 2009 , 191, 7234-42	3.5	79
62	EST sequencing of Onychophora and phylogenomic analysis of Metazoa. <i>Molecular Phylogenetics and Evolution</i> , 2007 , 45, 942-51	4.1	76

61	Simultaneous statistical multiple alignment and phylogeny reconstruction. <i>Systematic Biology</i> , 2005 , 54, 548-61	8.4	76
60	Conserved pore-forming regions in polypeptide-transporting proteins. <i>FEBS Journal</i> , 2005 , 272, 1367-78	5.7	74
59	Functional and phylogenetic properties of the pore-forming beta-barrel transporters of the Omp85 family. <i>Journal of Biological Chemistry</i> , 2007 , 282, 1882-90	5.4	73
58	Adenosine deaminases that act on RNA induce reproducible changes in abundance and sequence of embryonic miRNAs. <i>Genome Research</i> , 2012 , 22, 1468-76	9.7	71
57	The evolution of the ribosome biogenesis pathway from a yeast perspective. <i>Nucleic Acids Research</i> , 2014 , 42, 1509-23	20.1	69
56	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, 2745-55	5.4	68
55	A coalescent approach to study linkage disequilibrium between single-nucleotide polymorphisms. <i>American Journal of Human Genetics</i> , 2000 , 66, 615-28	11	66
54	MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. <i>BMC Evolutionary Biology</i> , 2018 , 18, 11	3	65
53	The genomic basis of circadian and circalunar timing adaptations in a midge. <i>Nature</i> , 2016 , 540, 69-73	50.4	64
52	Cooperation of multiple chromatin modifications can generate unanticipated stability of epigenetic States in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2010 , 22, 34-47	11.6	63
51	A phylogenomic approach to resolve the basal pterygote divergence. <i>Molecular Biology and Evolution</i> , 2009 , 26, 2719-30	8.3	60
50	piQPNNI: parallel reconstruction of large maximum likelihood phylogenies. <i>Bioinformatics</i> , 2005 , 21, 3794-6	7.2	60
49	Quartet-mapping, a generalization of the likelihood-mapping procedure. <i>Molecular Biology and Evolution</i> , 2001 , 18, 1204-19	8.3	55
48	Split diversity in constrained conservation prioritization using integer linear programming. <i>Methods in Ecology and Evolution</i> , 2015 , 6, 83-91	7.7	51
47	The tetratricopeptide repeats of receptors involved in protein translocation across membranes. <i>Molecular Biology and Evolution</i> , 2007 , 24, 2763-74	8.3	51
46	NGC: lossless and lossy compression of aligned high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2013 , 41, e27	20.1	43
45	Modeling the polymerase chain reaction. <i>Journal of Computational Biology</i> , 1995 , 2, 49-61	1.7	41
44	GHOST: Recovering Historical Signal from Heterotachously Evolved Sequence Alignments. <i>Systematic Biology</i> , 2020 , 69, 249-264	8.4	38

43	ADAR2 induces reproducible changes in sequence and abundance of mature microRNAs in the mouse brain. <i>Nucleic Acids Research</i> , 2014 , 42, 12155-68	20.1	38
42	Quantification of experimentally induced nucleotide conversions in high-throughput sequencing datasets. <i>BMC Bioinformatics</i> , 2019 , 20, 258	3.6	36
41	A human tissue screen identifies a regulator of ER secretion as a brain-size determinant. <i>Science</i> , 2020 , 370, 935-941	33.3	36
40	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	8.4	35
39	Network models for sequence evolution. <i>Journal of Molecular Evolution</i> , 1993 , 37, 77-85	3.1	35
38	Reversible polymorphism-aware phylogenetic models and their application to tree inference. <i>Journal of Theoretical Biology</i> , 2016 , 407, 362-370	2.3	34
37	The Candida albicans Histone Acetyltransferase Hat1 Regulates Stress Resistance and Virulence via Distinct Chromatin Assembly Pathways. <i>PLoS Pathogens</i> , 2015 , 11, e1005218	7.6	33
36	Recent origin and cultural reversion of a hunter-gatherer group. <i>PLoS Biology</i> , 2005 , 3, e71	9.7	32
35	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, 347-55	6.6	31
34	Phylogenetic diversity within seconds. <i>Systematic Biology</i> , 2006 , 55, 769-73	8.4	31
33	Identifying site-specific substitution rates. <i>Molecular Biology and Evolution</i> , 2003 , 20, 182-9	8.3	28
32	Innate immune response to Streptococcus pyogenes depends on the combined activation of TLR13 and TLR2. <i>PLoS ONE</i> , 2015 , 10, e0119727	3.7	27
31	Combined transcriptome and proteome profiling reveals specific molecular brain signatures for sex, maturation and circalunar clock phase. <i>ELife</i> , 2019 , 8,	8.9	26
30	Towards integration of multiple alignment and phylogenetic tree construction. <i>Journal of Computational Biology</i> , 1997 , 4, 23-34	1.7	25
29	Teaser: Individualized benchmarking and optimization of read mapping results for NGS data. <i>Genome Biology</i> , 2015 , 16, 235	18.3	21
28	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	11.6	17
27	In vivo insertion pool sequencing identifies virulence factors in a complex fungal-host interaction. <i>PLoS Biology</i> , 2018 , 16, e2005129	9.7	16
26	Do we still need supertrees?. <i>BMC Biology</i> , 2012 , 10, 13	7.3	14

25	Sequencing of the Arabidopsis NOR2 reveals its distinct organization and tissue-specific rRNA ribosomal variants. <i>Nature Communications</i> , 2021 , 12, 387	17.4	14
24	TRUmiCount: correctly counting absolute numbers of molecules using unique molecular identifiers. <i>Bioinformatics</i> , 2018 , 34, 3137-3144	7.2	12
23	The Evolutionary Traceability of a Protein. <i>Genome Biology and Evolution</i> , 2019 , 11, 531-545	3.9	12
22	Polymorphism-Aware Species Trees with Advanced Mutation Models, Bootstrap, and Rate Heterogeneity. <i>Molecular Biology and Evolution</i> , 2019 , 36, 1294-1301	8.3	11
21	HvrBase++: a phylogenetic database for primate species. <i>Nucleic Acids Research</i> , 2006 , 34, D700-4	20.1	11
20	Genetic distances and nucleotide substitution models111-141		10
19	A-to-I RNA Editing Uncovers Hidden Signals of Adaptive Genome Evolution in Animals. <i>Genome Biology and Evolution</i> , 2020 , 12, 345-357	3.9	9
18	Germline Variants in the POT1-Gene in High-Risk Melanoma Patients in Austria. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 1475-1480	3.2	7
17	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	8.4	6
16	Distinguishing Felsenstein Zone from Farris Zone Using Neural Networks. <i>Molecular Biology and Evolution</i> , 2020 , 37, 3632-3641	8.3	4
15	Exploring the sampling universe of RNA-seq. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2013 , 12, 175-88	1.2	4
14	Decreased expression of endogenous feline leukemia virus in cat lymphomas: a case control study. <i>BMC Veterinary Research</i> , 2015 , 11, 90	2.7	3
13	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	17.4	3
12	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	8.3	3
11	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. <i>PLoS Biology</i> , 2021 , 19, e3001012	9.7	3
10	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	6.2	1
9	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	1.7	1
8	Computational Molecular Evolution Ziheng Yang. 2006. Oxford University Press, Oxford. 376 pp. ISBN 978-0-19-856699-1 (ISBN-10 0-19-856699-9) £60 \$115 (hardback). ISBN 978-0-19-856702-8 (ISBN-10 0-19-856702-2) £27.50 \$52.50 (paperback).. <i>Systematic Biology</i> , 2007 , 56, 1024-1026	8.4	

7 Structure of the space of taboo-free sequences. *Journal of Mathematical Biology*, **2020**, 81, 1029-1057 2

6 TMT-Opsins differentially modulate medaka brain function in a context-dependent manner **2021**, 19, e3001012

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1 TMT-Opsins differentially modulate medaka brain function in a context-dependent manner **2021**, 19, e3001012