Arndt von Haeseler

List of Publications by Year in Descending Order

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	It Is Just a Matter of Time: Balancing Homologous Recombination and Non-homologous End Joining at the rDNA Locus During Meiosis. *Frontiers in Plant Science*, **2021**, 12, 773052	6.2	1
95	Complex Evolution of Light-Dependent Protochlorophyllide Oxidoreductases in Aerobic Anoxygenic Phototrophs: Origin, Phylogeny, and Function. *Molecular Biology and Evolution*, **2021**, 38, 819-837	8.3	3
94	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. *PLoS Biology*, **2021**, 19, e3001012	9.7	3
93	ATM controls meiotic DNA double-strand break formation and recombination and affects synaptonemal complex organization in plants. *Plant Cell*, **2021**, 33, 1633-1656	11.6	17
92	Sequencing of the Arabidopsis NOR2 reveals its distinct organization and tissue-specific rRNA ribosomal variants. *Nature Communications*, **2021**, 12, 387	17.4	14
91	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner **2021**, 19, e3001012		
90	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner **2021**, 19, e3001012		
89	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner **2021**, 19, e3001012		
88	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner **2021**, 19, e3001012		
87	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner **2021**, 19, e3001012		
86	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner **2021**, 19, e3001012		
85	A-to-I RNA Editing Uncovers Hidden Signals of Adaptive Genome Evolution in Animals. *Genome Biology and Evolution*, **2020**, 12, 345-357	3.9	9
84	Distinguishing Felsenstein Zone from Farris Zone Using Neural Networks. *Molecular Biology and Evolution*, **2020**, 37, 3632-3641	8.3	4
83	GHOST: Recovering Historical Signal from Heterotachously Evolved Sequence Alignments. *Systematic Biology*, **2020**, 69, 249-264	8.4	38
82	IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. *Molecular Biology and Evolution*, **2020**, 37, 1530-1534	8.3	1466
81	Poly(ADP-ribose) glycohydrolase coordinates meiotic DNA double-strand break induction and repair independent of its catalytic activity. *Nature Communications*, **2020**, 11, 4869	17.4	3
80	Structure of the space of taboo-free sequences. *Journal of Mathematical Biology*, **2020**, 81, 1029-1057	2	

79	A human tissue screen identifies a regulator of ER secretion as a brain-size determinant. *Science*, **2020**, 370, 935-941	33.3	36
78	Quantification of experimentally induced nucleotide conversions in high-throughput sequencing datasets. *BMC Bioinformatics*, **2019**, 20, 258	3.6	36
77	Polymorphism-Aware Species Trees with Advanced Mutation Models, Bootstrap, and Rate Heterogeneity. *Molecular Biology and Evolution*, **2019**, 36, 1294-1301	8.3	11
76	Combined transcriptome and proteome profiling reveals specific molecular brain signatures for sex, maturation and circalunar clock phase. *ELife*, **2019**, 8,	8.9	26
75	The Evolutionary Traceability of a Protein. *Genome Biology and Evolution*, **2019**, 11, 531-545	3.9	12
74	Unifying the global phylogeny and environmental distribution of ammonia-oxidising archaea based on amoA genes. *Nature Communications*, **2018**, 9, 1517	17.4	131
73	TRUmiCount: correctly counting absolute numbers of molecules using unique molecular identifiers. *Bioinformatics*, **2018**, 34, 3137-3144	7.2	12
72	SLAM-seq defines direct gene-regulatory functions of the BRD4-MYC axis. *Science*, **2018**, 360, 800-805	33.3	147
71	Complex Models of Sequence Evolution Require Accurate Estimators as Exemplified with the Invariable Site Plus Gamma Model. *Systematic Biology*, **2018**, 67, 552-558	8.4	6
70	Accurate detection of complex structural variations using single-molecule sequencing. *Nature Methods*, **2018**, 15, 461-468	21.6	585
69	Germline Variants in the POT1-Gene in High-Risk Melanoma Patients in Austria. *G3: Genes, Genomes, Genetics*, **2018**, 8, 1475-1480	3.2	7
68	UFBoot2: Improving the Ultrafast Bootstrap Approximation. *Molecular Biology and Evolution*, **2018**, 35, 518-522	8.3	2342
67	In vivo insertion pool sequencing identifies virulence factors in a complex fungal-host interaction. *PLoS Biology*, **2018**, 16, e2005129	9.7	16
66	MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. *BMC Evolutionary Biology*, **2018**, 18, 11	3	65
65	ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods*, **2017**, 14, 587-589	21.6	3957
64	Thiol-linked alkylation of RNA to assess expression dynamics. *Nature Methods*, **2017**, 14, 1198-1204	21.6	204
63	An Enumerative Combinatorics Model for Fragmentation Patterns in RNA Sequencing Provides Insights into Nonuniformity of the Expected Fragment Starting-Point and Coverage Profile. *Journal of Computational Biology*, **2017**, 24, 200-212	1.7	1
62	The genomic basis of circadian and circalunar timing adaptations in a midge. *Nature*, **2016**, 540, 69-73	50.4	64

61	Next-generation sequencing diagnostics of bacteremia in septic patients. *Genome Medicine*, **2016**, 8, 73	14.4	164
60	W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. *Nucleic Acids Research*, **2016**, 44, W232-5	20.1	1497
59	Terrace Aware Data Structure for Phylogenomic Inference from Supermatrices. *Systematic Biology*, **2016**, 65, 997-1008	8.4	704
58	A-type lamins bind both hetero- and euchromatin, the latter being regulated by lamina-associated polypeptide 2 alpha. *Genome Research*, **2016**, 26, 462-73	9.7	119
57	Reversible polymorphism-aware phylogenetic models and their application to tree inference. *Journal of Theoretical Biology*, **2016**, 407, 362-370	2.3	34
56	IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Molecular Biology and Evolution*, **2015**, 32, 268-74	8.3	8116
55	Split diversity in constrained conservation prioritization using integer linear programming. *Methods in Ecology and Evolution*, **2015**, 6, 83-91	7.7	51
54	Innate immune response to Streptococcus pyogenes depends on the combined activation of TLR13 and TLR2. *PLoS ONE*, **2015**, 10, e0119727	3.7	27
53	The Candida albicans Histone Acetyltransferase Hat1 Regulates Stress Resistance and Virulence via Distinct Chromatin Assembly Pathways. *PLoS Pathogens*, **2015**, 11, e1005218	7.6	33
52	Decreased expression of endogenous feline leukemia virus in cat lymphomas: a case control study. *BMC Veterinary Research*, **2015**, 11, 90	2.7	3
51	Teaser: Individualized benchmarking and optimization of read mapping results for NGS data. *Genome Biology*, **2015**, 16, 235	18.3	21
50	Decisive data sets in phylogenomics: lessons from studies on the phylogenetic relationships of primarily wingless insects. *Molecular Biology and Evolution*, **2014**, 31, 239-49	8.3	100
49	The first myriapod genome sequence reveals conservative arthropod gene content and genome organisation in the centipede Strigamia maritima. *PLoS Biology*, **2014**, 12, e1002005	9.7	182
48	The evolution of the ribosome biogenesis pathway from a yeast perspective. *Nucleic Acids Research*, **2014**, 42, 1509-23	20.1	69
47	ADAR2 induces reproducible changes in sequence and abundance of mature microRNAs in the mouse brain. *Nucleic Acids Research*, **2014**, 42, 12155-68	20.1	38
46	NextGenMap: fast and accurate read mapping in highly polymorphic genomes. *Bioinformatics*, **2013**, 29, 2790-1	7.2	246
45	Exploring the sampling universe of RNA-seq. *Statistical Applications in Genetics and Molecular Biology*, **2013**, 12, 175-88	1.2	4
44	Updating benchtop sequencing performance comparison. *Nature Biotechnology*, **2013**, 31, 294-6	44.5	255

43	Ultrafast approximation for phylogenetic bootstrap. *Molecular Biology and Evolution*, **2013**, 30, 1188-95	8.3	1669
42	NGC: lossless and lossy compression of aligned high-throughput sequencing data. *Nucleic Acids Research*, **2013**, 41, e27	20.1	43
41	Do we still need supertrees?. *BMC Biology*, **2012**, 10, 13	7.3	14
40	Adenosine deaminases that act on RNA induce reproducible changes in abundance and sequence of embryonic miRNAs. *Genome Research*, **2012**, 22, 1468-76	9.7	71
39	A consistent phylogenetic backbone for the fungi. *Molecular Biology and Evolution*, **2012**, 29, 1319-34	8.3	104
38	The performance of phylogenetic algorithms in estimating haplotype genealogies with migration. *Molecular Ecology*, **2011**, 20, 1952-63	5.7	251
37	Cooperation of multiple chromatin modifications can generate unanticipated stability of epigenetic States in Arabidopsis. *Plant Cell*, **2010**, 22, 34-47	11.6	63
36	A phylogenomic approach to resolve the arthropod tree of life. *Molecular Biology and Evolution*, **2010**, 27, 2451-64	8.3	265
35	Genome-wide RNAi screen identifies genes involved in intestinal pathogenic bacterial infection. *Science*, **2009**, 325, 340-3	33.3	244
34	Distribution and phylogeny of light-oxygen-voltage-blue-light-signaling proteins in the three kingdoms of life. *Journal of Bacteriology*, **2009**, 191, 7234-42	3.5	79
33	A phylogenomic approach to resolve the basal pterygote divergence. *Molecular Biology and Evolution*, **2009**, 26, 2719-30	8.3	60
32	Central control of fever and female body temperature by RANKL/RANK. *Nature*, **2009**, 462, 505-9	50.4	173
31	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. *Haematologica*, **2008**, 93, 347-55	6.6	31
30	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).. *Systematic Biology*, **2007**, 56, 1024-1026	8.4	
29	EST sequencing of Onychophora and phylogenomic analysis of Metazoa. *Molecular Phylogenetics and Evolution*, **2007**, 45, 942-51	4.1	76
28	Mapping human genetic ancestry. *Molecular Biology and Evolution*, **2007**, 24, 2266-76	8.3	99
27	The tetratricopeptide repeats of receptors involved in protein translocation across membranes. *Molecular Biology and Evolution*, **2007**, 24, 2763-74	8.3	51
26	Functional and phylogenetic properties of the pore-forming beta-barrel transporters of the Omp85 family. *Journal of Biological Chemistry*, **2007**, 282, 1882-90	5.4	73

25	HvrBase++: a phylogenetic database for primate species. *Nucleic Acids Research*, **2006**, 34, D700-4	20.1	11
24	Phylogenetic diversity within seconds. *Systematic Biology*, **2006**, 55, 769-73	8.4	31
23	Unexpected complexity of the Wnt gene family in a sea anemone. *Nature*, **2005**, 433, 156-60	50.4	435
22	Conserved pore-forming regions in polypeptide-transporting proteins. *FEBS Journal*, **2005**, 272, 1367-78	5.7	74
21	Recent origin and cultural reversion of a hunter-gatherer group. *PLoS Biology*, **2005**, 3, e71	9.7	32
20	pIQPNNI: parallel reconstruction of large maximum likelihood phylogenies. *Bioinformatics*, **2005**, 21, 3794-6	7.2	60
19	Simultaneous statistical multiple alignment and phylogeny reconstruction. *Systematic Biology*, **2005**, 54, 548-61	8.4	76
18	IQPNNI: moving fast through tree space and stopping in time. *Molecular Biology and Evolution*, **2004**, 21, 1565-71	8.3	116
17	Identifying site-specific substitution rates. *Molecular Biology and Evolution*, **2003**, 20, 182-9	8.3	28
16	Quartet-mapping, a generalization of the likelihood-mapping procedure. *Molecular Biology and Evolution*, **2001**, 18, 1204-19	8.3	55
15	A view of Neandertal genetic diversity. *Nature Genetics*, **2000**, 26, 144-6	36.3	277
14	A developmentally regulated aconitase related to iron-regulatory protein-1 is localized in the cytoplasm and in the mitochondrion of Trypanosoma brucei. *Journal of Biological Chemistry*, **2000**, 275, 2745-55	5.4	68
13	A coalescent approach to study linkage disequilibrium between single-nucleotide polymorphisms. *American Journal of Human Genetics*, **2000**, 66, 615-28	11	66
12	DNA sequence variation in a non-coding region of low recombination on the human X chromosome. *Nature Genetics*, **1999**, 22, 78-81	36.3	202
11	Pattern of nucleotide substitution and rate heterogeneity in the hypervariable regions I and II of human mtDNA. *Genetics*, **1999**, 152, 1103-10	4	182
10	Inference of population history using a likelihood approach. *Genetics*, **1998**, 149, 1539-46	4	113
9	Towards integration of multiple alignment and phylogenetic tree construction. *Journal of Computational Biology*, **1997**, 4, 23-34	1.7	25
8	The mitochondrial genome of a monotreme--the platypus (Ornithorhynchus anatinus). *Journal of Molecular Evolution*, **1996**, 42, 153-9	3.1	109

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7	The genetical archaeology of the human genome. *Nature Genetics*, **1996**, 14, 135-40	36.3	88
6	A nuclear ⑥ossil⑥of the mitochondrial D-loop and the origin of modern humans. *Nature*, **1995**, 378, 489-92	30.4	190
5	Performance of the Maximum Likelihood, Neighbor Joining, and Maximum Parsimony Methods When Sequence Sites are Not Independent. *Systematic Biology*, **1995**, 44, 533-547	8.4	35
4	Modeling the polymerase chain reaction. *Journal of Computational Biology*, **1995**, 2, 49-61	1.7	41
3	A stochastic model for the evolution of autocorrelated DNA sequences. *Molecular Phylogenetics and Evolution*, **1994**, 3, 240-7	4.1	184
2	Network models for sequence evolution. *Journal of Molecular Evolution*, **1993**, 37, 77-85	3.1	35
1	Genetic distances and nucleotide substitution models111-141		10