Arndt von Haeseler

List of Publications by Year
in descending order

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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	Complex Evolution of Light-Dependent Protochlorophyllide Oxidoreductases in Aerobic Anoxygenic Phototrophs: Origin, Phylogeny, and Function. Molecular Biology and Evolution, 2021, 38, 819-837.	3.5	6
2	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. PLoS Biology, 2021, 19, e3001012.	2.6	9
3	ATM controls meiotic DNA double-strand break formation and recombination and affects synaptonemal complex organization in plants. Plant Cell, 2021, 33, 1633-1656.	3.1	33
4	Sequencing of the Arabidopsis NOR2 reveals its distinct organization and tissue-specific rRNA ribosomal variants. Nature Communications, 2021, 12, 387.	5.8	32
5	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.	1.7	3
6	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. , 2021, 19, e3001012.		0
7	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. , 2021, 19, e3001012.		0
8	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. , 2021, 19, e3001012.		0
9	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. , 2021, 19, e3001012.		0
10	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. , 2021, 19, e3001012.		0
11	TMT-Opsins differentially modulate medaka brain function in a context-dependent manner. , 2021, 19, e3001012.		0
12	GHOST: Recovering Historical Signal from Heterotachously Evolved Sequence Alignments. Systematic Biology, 2020, 69, 249-264.	2.7	75
13	Poly(ADP-ribose) glycohydrolase coordinates meiotic DNA double-strand break induction and repair independent of its catalytic activity. Nature Communications, 2020, 11, 4869.	5.8	16
14	Structure of the space of taboo-free sequences. Journal of Mathematical Biology, 2020, 81, 1029-1057.	0.8	0
15	A human tissue screen identifies a regulator of ER secretion as a brain-size determinant. Science, 2020, 370, 935-941.	6.0	101
16	A-to-I RNA Editing Uncovers Hidden Signals of Adaptive Genome Evolution in Animals. Genome Biology and Evolution, 2020, 12, 345-357.	1.1	17
17	Distinguishing Felsenstein Zone from Farris Zone Using Neural Networks. Molecular Biology and Evolution, 2020, 37, 3632-3641.	3.5	16
18	IQ-TREE 2: New Models and Efficient Methods for Phylogenetic Inference in the Genomic Era. Molecular Biology and Evolution, 2020, 37, 1530-1534.	3.5	5,960

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19	VARIFIâ€"Web-Based Automatic Variant Identification, Filtering and Annotation of Amplicon Sequencing Data. Journal of Personalized Medicine, 2019, 9, 10.	1.1	1
20	Quantification of experimentally induced nucleotide conversions in high-throughput sequencing datasets. BMC Bioinformatics, 2019, 20, 258.	1.2	86
21	Polymorphism-Aware Species Trees with Advanced Mutation Models, Bootstrap, and Rate Heterogeneity. Molecular Biology and Evolution, 2019, 36, 1294-1301.	3.5	27
22	The Evolutionary Traceability of a Protein. Genome Biology and Evolution, 2019, 11, 531-545.	1.1	23
23	Combined transcriptome and proteome profiling reveals specific molecular brain signatures for sex, maturation and circalunar clock phase. ELife, 2019, 8, .	2.8	51
24	Unifying the global phylogeny and environmental distribution of ammonia-oxidising archaea based on amoA genes. Nature Communications, 2018, 9, 1517.	5.8	256
25	TRUmiCount: correctly counting absolute numbers of molecules using unique molecular identifiers. Bioinformatics, 2018, 34, 3137-3144.	1.8	25
26	SLAM-seq defines direct gene-regulatory functions of the BRD4-MYC axis. Science, 2018, 360, 800-805.	6.0	284
27	Complex Models of Sequence Evolution Require Accurate Estimators as Exemplified with the Invariable Site Plus Gamma Model. Systematic Biology, 2018, 67, 552-558.	2.7	11
28	Accurate detection of complex structural variations using single-molecule sequencing. Nature Methods, 2018, 15, 461-468.	9.0	1,175
29	Germline Variants in the POT1-Gene in High-Risk Melanoma Patients in Austria. G3: Genes, Genomes, Genetics, 2018, 8, 1475-1480.	0.8	12
30	UFBoot2: Improving the Ultrafast Bootstrap Approximation. Molecular Biology and Evolution, 2018, 35, 518-522.	3.5	5,798
31	In vivo insertion pool sequencing identifies virulence factors in a complex fungalâ€"host interaction. PLoS Biology, 2018, 16, e2005129.	2.6	20
32	MPBoot: fast phylogenetic maximum parsimony tree inference and bootstrap approximation. BMC Evolutionary Biology, 2018, 18, 11.	3.2	129
33	ModelFinder: fast model selection for accurate phylogenetic estimates. Nature Methods, 2017, 14, 587-589.	9.0	9,486
34	Thiol-linked alkylation of RNA to assess expression dynamics. Nature Methods, 2017, 14, 1198-1204.	9.0	411
35	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.	0.8	2
36	Terrace Aware Data Structure for Phylogenomic Inference from Supermatrices. Systematic Biology, 2016, 65, 997-1008.	2.7	1,453

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37	A-type lamins bind both hetero- and euchromatin, the latter being regulated by lamina-associated polypeptide 2 alpha. Genome Research, 2016, 26, 462-473.	2.4	157
38	Reversible polymorphism-aware phylogenetic models and their application to tree inference. Journal of Theoretical Biology, 2016, 407, 362-370.	0.8	70
39	The genomic basis of circadian and circalunar timing adaptations in a midge. Nature, 2016, 540, 69-73.	13.7	96
40	Next-generation sequencing diagnostics of bacteremia in septic patients. Genome Medicine, 2016, 8, 73.	3.6	265
41	W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. Nucleic Acids Research, 2016, 44, W232-W235.	6.5	3,039
42	Split diversity in constrained conservation prioritization using integer linear programming. Methods in Ecology and Evolution, 2015, 6, 83-91.	2.2	75
43	Innate Immune Response to Streptococcus pyogenes Depends on the Combined Activation of TLR13 and TLR2. PLoS ONE, 2015, 10, e0119727.	1.1	37
44	The Candida albicans Histone Acetyltransferase Hat1 Regulates Stress Resistance and Virulence via Distinct Chromatin Assembly Pathways. PLoS Pathogens, 2015, 11, e1005218.	2.1	48
45	Decreased expression of endogenous feline leukemia virus in cat lymphomas: a case control study. BMC Veterinary Research, 2015, 11, 90.	0.7	8
46	Teaser: Individualized benchmarking and optimization of read mapping results for NGS data. Genome Biology, 2015, 16, 235.	3.8	25
47	IQ-TREE: A Fast and Effective Stochastic Algorithm for Estimating Maximum-Likelihood Phylogenies. Molecular Biology and Evolution, 2015, 32, 268-274.	3.5	16,610
48	The First Myriapod Genome Sequence Reveals Conservative Arthropod Gene Content and Genome Organisation in the Centipede Strigamia maritima. PLoS Biology, 2014, 12, e1002005.	2.6	221
49	The evolution of the ribosome biogenesis pathway from a yeast perspective. Nucleic Acids Research, 2014, 42, 1509-1523.	6.5	87
50	ADAR2 induces reproducible changes in sequence and abundance of mature microRNAs in the mouse brain. Nucleic Acids Research, 2014, 42, 12155-12168.	6.5	42
51	Decisive Data Sets in Phylogenomics: Lessons from Studies on the Phylogenetic Relationships of Primarily Wingless Insects. Molecular Biology and Evolution, 2014, 31, 239-249.	3.5	127
52	NextGenMap: fast and accurate read mapping in highly polymorphic genomes. Bioinformatics, 2013, 29, 2790-2791.	1.8	408
53	Exploring the sampling universe of RNA-seq. Statistical Applications in Genetics and Molecular Biology, 2013, 12, 175-88.	0.2	5
54	Updating benchtop sequencing performance comparison. Nature Biotechnology, 2013, 31, 294-296.	9.4	423

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55	Ultrafast Approximation for Phylogenetic Bootstrap. Molecular Biology and Evolution, 2013, 30, 1188-1195.	3.5	3,123
56	NGC: lossless and lossy compression of aligned high-throughput sequencing data. Nucleic Acids Research, 2013, 41, e27-e27.	6.5	57
57	Adenosine deaminases that act on RNA induce reproducible changes in abundance and sequence of embryonic miRNAs. Genome Research, 2012, 22, 1468-1476.	2.4	80
58	A Consistent Phylogenetic Backbone for the Fungi. Molecular Biology and Evolution, 2012, 29, 1319-1334.	3.5	129
59	Do we still need supertrees?. BMC Biology, 2012, 10, 13.	1.7	19
60	The performance of phylogenetic algorithms in estimating haplotype genealogies with migration. Molecular Ecology, 2011, 20, 1952-1963.	2.0	316
61	Cooperation of Multiple Chromatin Modifications Can Generate Unanticipated Stability of Epigenetic States in<i>Arabidopsis</i>Â Â Â. Plant Cell, 2010, 22, 34-47.	3.1	82
62	A Phylogenomic Approach to Resolve the Arthropod Tree of Life. Molecular Biology and Evolution, 2010, 27, 2451-2464.	3.5	308
63	Genetic distances and nucleotide substitution models. , 2009, , 111-141.		20
64	Genome-Wide RNAi Screen Identifies Genes Involved in Intestinal Pathogenic Bacterial Infection. Science, 2009, 325, 340-343.	6.0	277
65	Distribution and Phylogeny of Light-Oxygen-Voltage-Blue-Light-Signaling Proteins in the Three Kingdoms of Life. Journal of Bacteriology, 2009, 191, 7234-7242.	1.0	95
66	A Phylogenomic Approach to Resolve the Basal Pterygote Divergence. Molecular Biology and Evolution, 2009, 26, 2719-2730.	3.5	66
67	Central control of fever and female body temperature by RANKL/RANK. Nature, 2009, 462, 505-509.	13.7	212
68	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, 347-355.	1.7	39
69	Mapping Human Genetic Ancestry. Molecular Biology and Evolution, 2007, 24, 2266-2276.	3.5	117
70	The Tetratricopeptide Repeats of Receptors Involved in Protein Translocation across Membranes. Molecular Biology and Evolution, 2007, 24, 2763-2774.	3.5	56
71	Functional and Phylogenetic Properties of the Pore-forming Î²-Barrel Transporters of the Omp85 Family. Journal of Biological Chemistry, 2007, 282, 1882-1890.	1.6	74
72	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).. Systematic Biology, 2007, 56, 1024-1026.	2.7	1

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73	EST sequencing of Onychophora and phylogenomic analysis of Metazoa. Molecular Phylogenetics and Evolution, 2007, 45, 942-951.	1.2	92
74	HvrBase++: a phylogenetic database for primate species. Nucleic Acids Research, 2006, 34, D700-D704.	6.5	15
75	Phylogenetic Diversity within Seconds. Systematic Biology, 2006, 55, 769-773.	2.7	37
76	Conserved pore-forming regions in polypeptide- transporting proteins. FEBS Journal, 2005, 272, 1367-1378.	2.2	74
77	Recent Origin and Cultural Reversion of a Hunterâ€“Gatherer Group. PLoS Biology, 2005, 3, e71.	2.6	47
78	pIQPNNI: parallel reconstruction of large maximum likelihood phylogenies. Bioinformatics, 2005, 21, 3794-3796.	1.8	69
79	Simultaneous Statistical Multiple Alignment and Phylogeny Reconstruction. Systematic Biology, 2005, 54, 548-561.	2.7	114
80	Unexpected complexity of the Wnt gene family in a sea anemone. Nature, 2005, 433, 156-160.	13.7	516
81	IQPNNI: Moving Fast Through Tree Space and Stopping in Time. Molecular Biology and Evolution, 2004, 21, 1565-1571.	3.5	146
82	Identifying Site-Specific Substitution Rates. Molecular Biology and Evolution, 2003, 20, 182-189.	3.5	29
83	Quartet-Mapping, a Generalization of the Likelihood-Mapping Procedure. Molecular Biology and Evolution, 2001, 18, 1204-1219.	3.5	63
84	A view of Neandertal genetic diversity. Nature Genetics, 2000, 26, 144-146.	9.4	330
85	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, 2745-2755.	1.6	82
86	A Coalescent Approach to Study Linkage Disequilibrium between Single-Nucleotide Polymorphisms. American Journal of Human Genetics, 2000, 66, 615-628.	2.6	77
87	DNA sequence variation in a non-coding region of low recombination on the human X chromosome. Nature Genetics, 1999, 22, 78-81.	9.4	237
88	Pattern of Nucleotide Substitution and Rate Heterogeneity in the Hypervariable Regions I and II of Human mtDNA. Genetics, 1999, 152, 1103-1110.	1.2	232
89	Inference of Population History Using a Likelihood Approach. Genetics, 1998, 149, 1539-1546.	1.2	141
90	Towards Integration of Multiple Alignment and Phylogenetic Tree Construction. Journal of Computational Biology, 1997, 4, 23-34.	0.8	35

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91	The mitochondrial genome of a monotremeâ€”the platypus (Ornithrohynchus anatinus). Journal of Molecular Evolution, 1996, 42, 153-159.	0.8	127
92	The genetical archaeology of the human genome. Nature Genetics, 1996, 14, 135-140.	9.4	105
93	A nuclear 'fossil' of the mitochondrial D-loop and the origin of modern humans. Nature, 1995, 378, 489-492.	13.7	217
94	Performance of the Maximum Likelihood, Neighbor Joining, and Maximum Parsimony Methods When Sequence Sites are Not Independent. Systematic Biology, 1995, 44, 533-547.	2.7	37
95	Modeling the Polymerase Chain Reaction. Journal of Computational Biology, 1995, 2, 49-61.	0.8	46
96	A Stochastic Model for the Evolution of Autocorrelated DNA Sequences. Molecular Phylogenetics and Evolution, 1994, 3, 240-247.	1.2	224
97	Network models for sequence evolution. Journal of Molecular Evolution, 1993, 37, 77-85.	0.8	39