

Lars Arvestad

List of Publications by Year in descending order

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43
papers

3,036
citations

331670

21
h-index

289244

40
g-index

48
all docs

48
docs citations

48
times ranked

4935
citing authors

#	ARTICLE	IF	CITATIONS
1	The Norway spruce genome sequence and conifer genome evolution. <i>Nature</i> , 2013, 497, 579-584.	27.8	1,303
2	BESST - Efficient scaffolding of large fragmented assemblies. <i>BMC Bioinformatics</i> , 2014, 15, 281.	2.6	157
3	Evolution after gene duplication: models, mechanisms, sequences, systems, and organisms. <i>Journal of Experimental Zoology Part B: Molecular and Developmental Evolution</i> , 2007, 308B, 58-73.	1.3	148
4	Simultaneous Bayesian gene tree reconstruction and reconciliation analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 5714-5719.	7.1	140
5	Bayesian gene/species tree reconciliation and orthology analysis using MCMC. <i>Bioinformatics</i> , 2003, 19, i7-i15.	4.1	137
6	The genome sequence of black cottonwood (<i>Populus trichocarpa</i>) reveals 18 conserved cellulose synthase (CesA) genes. <i>Planta</i> , 2005, 221, 739-746.	3.2	121
7	Gene tree reconstruction and orthology analysis based on an integrated model for duplications and sequence evolution. , 2004, , .		82
8	MAP20, a Microtubule-Associated Protein in the Secondary Cell Walls of Hybrid Aspen, Is a Target of the Cellulose Synthesis Inhibitor 2,6-Dichlorobenzonitrile A. <i>Plant Physiology</i> , 2008, 148, 1283-1294.	4.8	76
9	GAM-NGS: genomic assemblies merger for next generation sequencing. <i>BMC Bioinformatics</i> , 2013, 14, S6.	2.6	76
10	Genome-Wide Survey for Biologically Functional Pseudogenes. <i>PLoS Computational Biology</i> , 2006, 2, e46.	3.2	75
11	A Bayesian Method for Analyzing Lateral Gene Transfer. <i>Systematic Biology</i> , 2014, 63, 409-420.	5.6	73
12	The gene evolution model and computing its associated probabilities. <i>Journal of the ACM</i> , 2009, 56, 1-44.	2.2	66
13	Classification of DNA sequences using Bloom filters. <i>Bioinformatics</i> , 2010, 26, 1595-1600.	4.1	57
14	mtDNA Tandem Repeats in Domestic Dogs and Wolves: Mutation Mechanism Studied by Analysis of the Sequence of Imperfect Repeats. <i>Molecular Biology and Evolution</i> , 2000, 17, 474-488.	8.9	42
15	Assembly scaffolding with PE-contaminated mate-pair libraries. <i>Bioinformatics</i> , 2016, 32, 1925-1932.	4.1	42
16	GenPhyloData: realistic simulation of gene family evolution. <i>BMC Bioinformatics</i> , 2013, 14, 209.	2.6	39
17	DLRS: gene tree evolution in light of a species tree. <i>Bioinformatics</i> , 2012, 28, 2994-2995.	4.1	36
18	The Mitogenome of Norway Spruce and a Reappraisal of Mitochondrial Recombination in Plants. <i>Genome Biology and Evolution</i> , 2020, 12, 3586-3598.	2.5	35

#	ARTICLE	IF	CITATIONS
19	Quantitative synteny scoring improves homology inference and partitioning of gene families. <i>BMC Bioinformatics</i> , 2013, 14, S12.	2.6	32
20	Identification of the cellulose synthase genes from the Oomycete <i>Saprolegnia monoica</i> and effect of cellulose synthesis inhibitors on gene expression and enzyme activity. <i>Fungal Genetics and Biology</i> , 2009, 46, 759-767.	2.1	27
21	Improved gap size estimation for scaffolding algorithms. <i>Bioinformatics</i> , 2012, 28, 2215-2222.	4.1	23
22	RecPhyloXML: a format for reconciled gene trees. <i>Bioinformatics</i> , 2018, 34, 3646-3652.	4.1	22
23	ESTs from brain and testis of White Leghorn and red junglefowl: annotation, bioinformatic classification of unknown transcripts and analysis of expression levels. <i>Cytogenetic and Genome Research</i> , 2005, 111, 79-87.	1.1	21
24	A Novel Method for Forensic DNA Investigations: Repeat-Type Sequence Analysis of Tandemly Repeated mtDNA in Domestic Dogs. <i>Journal of Forensic Sciences</i> , 2000, 45, 990-999.	1.6	21
25	primetv: a viewer for reconciled trees. <i>BMC Bioinformatics</i> , 2007, 8, 148.	2.6	20
26	VMCMC: a graphical and statistical analysis tool for Markov chain Monte Carlo traces. <i>BMC Bioinformatics</i> , 2017, 18, 97.	2.6	20
27	Estimation of Reversible Substitution Matrices from Multiple Pairs of Sequences. <i>Journal of Molecular Evolution</i> , 1997, 45, 696-703.	1.8	18
28	Fastphylo: Fast tools for phylogenetics. <i>BMC Bioinformatics</i> , 2013, 14, 334.	2.6	18
29	Assessment of Protein Distance Measures and Tree-Building Methods for Phylogenetic Tree Reconstruction. <i>Molecular Biology and Evolution</i> , 2005, 22, 2257-2264.	8.9	16
30	GenFamClust: an accurate, synteny-aware and reliable homology inference algorithm. <i>BMC Evolutionary Biology</i> , 2016, 16, 120.	3.2	14
31	Diversity and evolution of chitin synthases in oomycetes (Straminipila: Oomycota). <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106558.	2.7	14
32	Efficient Methods for Estimating Amino Acid Replacement Rates. <i>Journal of Molecular Evolution</i> , 2006, 62, 663-673.	1.8	13
33	Expressed sequence tags from the midgut and an epithelial cell line of <i>Chironomus tentans</i> : annotation, bioinformatic classification of unknown transcripts and analysis of expression levels. <i>Insect Molecular Biology</i> , 2005, 14, 689-695.	2.0	9
34	Evolution of a domain conserved in microtubule-associated proteins of eukaryotes. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2008, 1, 51.	2.6	6
35	Evolution and human tissue expression of the <i>Cres/Testatin</i> subgroup genes, a reproductive tissue specific subgroup of the type 2 cystatins. <i>Evolution & Development</i> , 2010, 12, 329-342.	2.0	6
36	Gene-pseudogene evolution: a probabilistic approach. <i>BMC Genomics</i> , 2015, 16, S12.	2.8	6

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37	Probabilistic inference of lateral gene transfer events. BMC Bioinformatics, 2016, 17, 431.	2.6	5
38	Forensic Informativity of ~3000Åbp of Coding Sequence of Domestic Dog mt<scp>DNA</scp>. Journal of Forensic Sciences, 2014, 59, 898-908.	1.6	4
39	Aligning coding DNA in the presence of frame-shift errors. Lecture Notes in Computer Science, 1997, , 180-190.	1.3	4
40	Structural Variation Detection with Read Pair Information: An Improved Null Hypothesis Reduces Bias. Journal of Computational Biology, 2017, 24, 581-589.	1.6	3
41	alv: a console-based viewer for molecular sequence alignments. Journal of Open Source Software, 2018, 3, 955.	4.6	3
42	Excav: Maximization of Haplotypic Diversity of Linked Markers. PLoS ONE, 2013, 8, e79012.	2.5	0
43	Structural Variation Detection with Read Pair Informationâ€™ An Improved Null-Hypothesis Reduces Bias. Lecture Notes in Computer Science, 2016, , 176-188.	1.3	0