

# Ari LÃ¤jytnoja

## List of Publications by Year in descending order

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Version: 2024-02-01

36  
papers

8,646  
citations

331670

21  
h-index

361022

35  
g-index

52  
all docs

52  
docs citations

52  
times ranked

15484  
citing authors

#	ARTICLE	IF	CITATIONS
1	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. <i>Nature</i> , 2007, 447, 799-816.	27.8	4,709
2	From The Cover: An algorithm for progressive multiple alignment of sequences with insertions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 10557-10562.	7.1	871
3	Phylogeny-Aware Gap Placement Prevents Errors in Sequence Alignment and Evolutionary Analysis. <i>Science</i> , 2008, 320, 1632-1635.	12.6	737
4	Phylogeny-aware alignment with PRANK. <i>Methods in Molecular Biology</i> , 2014, 1079, 155-170.	0.9	558
5	webPRANK: a phylogeny-aware multiple sequence aligner with interactive alignment browser. <i>BMC Bioinformatics</i> , 2010, 11, 579.	2.6	418
6	Analyses of deep mammalian sequence alignments and constraint predictions for 1% of the human genome. <i>Genome Research</i> , 2007, 17, 760-774.	5.5	184
7	A hidden Markov model for progressive multiple alignment. <i>Bioinformatics</i> , 2003, 19, 1505-1513.	4.1	157
8	Matrilinear phylogeography of Atlantic salmon ( <i>Salmo salar</i> L.) in Europe and postglacial colonization of the Baltic Sea area. <i>Molecular Ecology</i> , 2001, 10, 89-102.	3.9	145
9	Accurate extension of multiple sequence alignments using a phylogeny-aware graph algorithm. <i>Bioinformatics</i> , 2012, 28, 1684-1691.	4.1	126
10	An inducible genome editing system for plants. <i>Nature Plants</i> , 2020, 6, 766-772.	9.3	77
11	Mechanistic insights into the evolution of DUF26-containing proteins in land plants. <i>Communications Biology</i> , 2019, 2, 56.	4.4	75
12	Wasabi: An Integrated Platform for Evolutionary Sequence Analysis and Data Visualization. <i>Molecular Biology and Evolution</i> , 2016, 33, 1126-1130.	8.9	55
13	A high-quality assembly of the nine-spined stickleback ( <i>Pungitius pungitius</i> ) genome. <i>Genome Biology and Evolution</i> , 2019, 11, 3291-3308.	2.5	54
14	A model of evolution and structure for multiple sequence alignment. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2008, 363, 3913-3919.	4.0	44
15	Genome content of uncultivated marine <i>Roseobacters</i> in the surface ocean. <i>Environmental Microbiology</i> , 2012, 14, 41-51.	3.8	42
16	Genetic population structure constrains local adaptation in sticklebacks. <i>Molecular Ecology</i> , 2021, 30, 1946-1961.	3.9	33
17	A recurrent copy number variation of the NEB triplicate region: only revealed by the targeted nemaline myopathy CGH array. <i>European Journal of Human Genetics</i> , 2016, 24, 574-580.	2.8	32
18	Molecular phylogenetic analyses of the mitochondrial ADP-ATP carriers: The Plantae/Fungi/Metazoa trichotomy revisited. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 10202-10207.	7.1	31

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19	Short template switch events explain mutation clusters in the human genome. <i>Genome Research</i> , 2017, 27, 1039-1049.	5.5	31
20	Cleavage of the <i>Drosophila</i> screw prodomain is critical for a dynamic BMP morphogen gradient in embryogenesis. <i>Developmental Biology</i> , 2014, 389, 149-159.	2.0	26
21	Uniting Alignments and Trees. <i>Science</i> , 2009, 324, 1528-1529.	12.6	24
22	Bracketing phenogenotypic limits of mammalian hybridization. <i>Royal Society Open Science</i> , 2018, 5, 180903.	2.4	24
23	Determination and validation of principal gene products. <i>Bioinformatics</i> , 2008, 24, 11-17.	4.1	23
24	MATLIGN: a motif clustering, comparison and matching tool. <i>BMC Bioinformatics</i> , 2007, 8, 189.	2.6	21
25	Automated improvement of stickleback reference genome assemblies with <code>LepAnchor</code> software. <i>Molecular Ecology Resources</i> , 2021, 21, 2166-2176.	4.8	21
26	Simple chained guide trees give poorer multiple sequence alignments than inferred trees in simulation and phylogenetic benchmarks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E99-100.	7.1	18
27	Alignment Methods: Strategies, Challenges, Benchmarking, and Comparative Overview. <i>Methods in Molecular Biology</i> , 2012, 855, 203-235.	0.9	17
28	Phylogeny-Aware Alignment with PRANK and PAGAN. <i>Methods in Molecular Biology</i> , 2021, 2231, 17-37.	0.9	15
29	Tracking year-to-year changes in intestinal nematode communities of rufous mouse lemurs ( <i>Microcebus rufus</i> ). <i>Parasitology</i> , 2015, 142, 1095-1107.	1.5	14
30	Effects of marker type and filtering criteria on <code>QST</code> - <code>FST</code> comparisons. <i>Royal Society Open Science</i> , 2019, 6, 190666.	2.4	12
31	Analysis of CACTA transposases reveals intron loss as major factor influencing their exon/intron structure in monocotyledonous and eudicotyledonous hosts. <i>Mobile DNA</i> , 2014, 5, 24.	3.6	10
32	<code>ance</code> : reference-based phylogenetic analysis for 18S rRNA studies. <i>BMC Evolutionary Biology</i> , 2014, 14, 235.	3.2	8
33	Metabarcoding Gastrointestinal Nematodes in Sympatric Endemic and Nonendemic Species in Ranomafana National Park, Madagascar. <i>International Journal of Primatology</i> , 2018, 39, 49-64.	1.9	6
34	Template switching in DNA replication can create and maintain RNA hairpins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	3
35	Thousands of human mutation clusters are explained by short-range template switching. <i>Genome Research</i> , 0, , gr.276478.121.	5.5	3
36	Evolutionary Sequence Analysis and Visualization with Wasabi. <i>Methods in Molecular Biology</i> , 2021, 2231, 225-240.	0.9	0