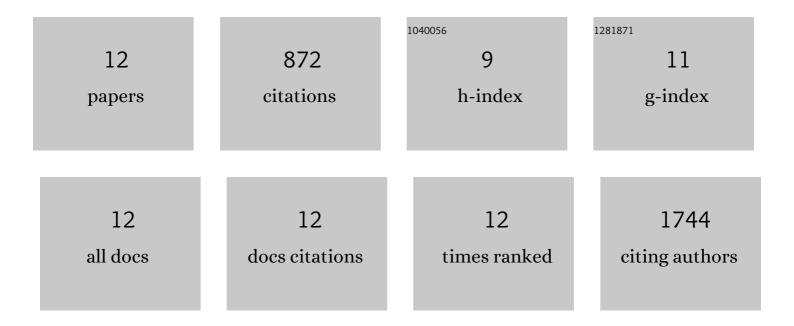
## MiklÃ<sup>3</sup>s Csűrös

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/10101357/publications.pdf Version: 2024-02-01



Μικι Δ3ς CsÅ+ρΔης

#	Article	IF	CITATIONS
1	Count: evolutionary analysis of phylogenetic profiles with parsimony and likelihood. Bioinformatics, 2010, 26, 1910-1912.	4.1	393
2	A Detailed History of Intron-rich Eukaryotic Ancestors Inferred from a Global Survey of 100 Complete Genomes. PLoS Computational Biology, 2011, 7, e1002150.	3.2	160
3	Streamlining and Large Ancestral Genomes in Archaea Inferred with a Phylogenetic Birth-and-Death Model. Molecular Biology and Evolution, 2009, 26, 2087-2095.	8.9	114
4	Extremely Intron-Rich Genes in the Alveolate Ancestors Inferred with a Flexible Maximum-Likelihood Approach. Molecular Biology and Evolution, 2008, 25, 903-911.	8.9	55
5	Malin: maximum likelihood analysis of intron evolution in eukaryotes. Bioinformatics, 2008, 24, 1538-1539.	4.1	47
6	Reconsidering the significance of genomic word frequencies. Trends in Genetics, 2007, 23, 543-546.	6.7	31
7	In search of lost introns. Bioinformatics, 2007, 23, i87-i96.	4.1	27
8	Rapid Homology Search with Neighbor Seeds. Algorithmica, 2007, 48, 187-202.	1.3	14
9	Splice Sites Seldom Slide: Intron Evolution in Oomycetes. Genome Biology and Evolution, 2016, 8, 2340-2350.	2.5	14
10	Non-identifiability of identity coefficients at biallelic loci. Theoretical Population Biology, 2014, 92, 22-29.	1.1	9
11	Statistical Alignment of Retropseudogenes and Their Functional Paralogs. Molecular Biology and Evolution, 2005, 22, 2457-2471.	8.9	8
12	Gain-loss-duplication models for copy number evolution on a phylogeny: Exact algorithms for computing the likelihood and its gradient. Theoretical Population Biology, 2022, 145, 80-94.	1.1	0