

# Tomas Vinar

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9047425/publications.pdf>

Version: 2024-02-01

78  
papers

6,732  
citations

257450

24  
h-index

91884

69  
g-index

89  
all docs

89  
docs citations

89  
times ranked

11159  
citing authors

#	ARTICLE	IF	CITATIONS
1	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. <i>Science</i> , 2007, 316, 222-234.	12.6	1,283
2	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	27.8	1,058
3	The <i>Schistosoma japonicum</i> genome reveals features of host-parasite interplay. <i>Nature</i> , 2009, 460, 345-351.	27.8	635
4	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	27.8	541
5	Patterns of Positive Selection in Six Mammalian Genomes. <i>PLoS Genetics</i> , 2008, 4, e1000144.	3.5	529
6	Convergent evolution of the genomes of marine mammals. <i>Nature Genetics</i> , 2015, 47, 272-275.	21.4	392
7	The western painted turtle genome, a model for the evolution of extreme physiological adaptations in a slowly evolving lineage. <i>Genome Biology</i> , 2013, 14, R28.	9.6	276
8	The genome of the hydatid tapeworm <i>Echinococcus granulosus</i> . <i>Nature Genetics</i> , 2013, 45, 1168-1175.	21.4	260
9	The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014, 46, 850-857.	21.4	225
10	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016, 7, 11693.	12.8	222
11	DeepNano: Deep recurrent neural networks for base calling in MinION nanopore reads. <i>PLoS ONE</i> , 2017, 12, e0178751.	2.5	186
12	The comparative genomics and complex population history of <i>Papio</i> baboons. <i>Science Advances</i> , 2019, 5, eaau6947.	10.3	115
13	Evolution of linear chromosomes and multipartite genomes in yeast mitochondria. <i>Nucleic Acids Research</i> , 2011, 39, 4202-4219.	14.5	69
14	Evolutionary genetics and implications of small size and twinning in callitrichine primates. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 1467-1472.	7.1	66
15	nCASP – the nematode genome annotation assessment project. <i>BMC Bioinformatics</i> , 2008, 9, 549.	2.6	61
16	Sequencing the genome of <i>Marssonina brunnea</i> reveals fungus-poplar co-evolution. <i>BMC Genomics</i> , 2012, 13, 382.	2.8	61
17	Massive programmed translational jumping in mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 5926-5931.	7.1	58
18	OPTIMAL SPACED SEEDS FOR HOMOLOGOUS CODING REGIONS. <i>Journal of Bioinformatics and Computational Biology</i> , 2004, 01, 595-610.	0.8	48

#	ARTICLE	IF	CITATIONS
19	ExonHunter: a comprehensive approach to gene finding. <i>Bioinformatics</i> , 2005, 21, i57-i65.	4.1	45
20	Vector seeds: An extension to spaced seeds. <i>Journal of Computer and System Sciences</i> , 2005, 70, 364-380.	1.2	42
21	Positive selection on apoptosis related genes. <i>FEBS Letters</i> , 2010, 584, 469-476.	2.8	38
22	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020, 9, .	6.4	37
23	A SARS-CoV-2 mutant from B.1.258 lineage with $\Delta$ H69/ $\Delta$ V70 deletion in the Spike protein circulating in Central Europe in the fall 2020. <i>Virus Genes</i> , 2021, 57, 556-560.	1.6	27
24	Surveillance of SARS-CoV-2 lineage B.1.1.7 in Slovakia using a novel, multiplexed RT-qPCR assay. <i>Scientific Reports</i> , 2021, 11, 20494.	3.3	24
25	Population Genomic Analysis Reveals a Rich Speciation and Demographic History of Orang-utans ( <i>Pongo pygmaeus</i> and <i>Pongo abelii</i> ). <i>PLoS ONE</i> , 2013, 8, e77175.	2.5	23
26	Vector Seeds: An Extension to Spaced Seeds Allows Substantial Improvements in Sensitivity and Specificity. <i>Lecture Notes in Computer Science</i> , 2003, , 39-54.	1.3	22
27	DeepNano-blitz: a fast base caller for MinION nanopore sequencers. <i>Bioinformatics</i> , 2020, 36, 4191-4192.	4.1	21
28	Nanopore base calling on the edge. <i>Bioinformatics</i> , 2021, 37, 4661-4667.	4.1	20
29	How Big is that Genome? Estimating Genome Size and Coverage from k-mer Abundance Spectra. <i>Lecture Notes in Computer Science</i> , 2015, , 199-209.	1.3	18
30	Mosaicism in old trees and its patterns. <i>Trees - Structure and Function</i> , 2020, 34, 357-370.	1.9	17
31	Optimal Spaced Seeds for Hidden Markov Models, with Application to Homologous Coding Regions. <i>Lecture Notes in Computer Science</i> , 2003, , 42-54.	1.3	16
32	Nanopore sequencing of SARS-CoV-2: Comparison of short and long PCR-tiling amplicon protocols. <i>PLoS ONE</i> , 2021, 16, e0259277.	2.5	16
33	Genome sequence of the opportunistic human pathogen <i>Magnusiomyces capitatus</i> . <i>Current Genetics</i> , 2019, 65, 539-560.	1.7	14
34	Monoclonal antibodies targeting two immunodominant epitopes on the Spike protein neutralize emerging SARS-CoV-2 variants of concern. <i>EBioMedicine</i> , 2022, 76, 103818.	6.1	14
35	Homology search for genes. <i>Bioinformatics</i> , 2007, 23, i97-i103.	4.1	13
36	The most probable annotation problem in HMMs and its application to bioinformatics. <i>Journal of Computer and System Sciences</i> , 2007, 73, 1060-1077.	1.2	13

#	ARTICLE	IF	CITATIONS
37	Finding genes in <i>Schistosoma japonicum</i> : annotating novel genomes with help of extrinsic evidence. <i>Nucleic Acids Research</i> , 2009, 37, e52-e52.	14.5	13
38	Alu Insertion Polymorphisms as Evidence for Population Structure in Baboons. <i>Genome Biology and Evolution</i> , 2017, 9, 2418-2427.	2.5	13
39	Papio Baboon Species Indicative Alu Elements. <i>Genome Biology and Evolution</i> , 2017, 9, 1788-1796.	2.5	12
40	CAGE: Combinatorial Analysis of Gene-Cluster Evolution. <i>Journal of Computational Biology</i> , 2010, 17, 1227-1242.	1.6	10
41	Simplifying Flow Networks. <i>Lecture Notes in Computer Science</i> , 2000, , 192-201.	1.3	10
42	Reconstructing the Evolutionary History of Complex Human Gene Clusters. , 2008, , 29-49.		9
43	Palindrome recognition using a multidimensional tape. <i>Theoretical Computer Science</i> , 2003, 302, 475-480.	0.9	8
44	Finding hidden independent sets in interval graphs. <i>Theoretical Computer Science</i> , 2004, 310, 287-307.	0.9	8
45	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. <i>Journal of Computational Biology</i> , 2010, 17, 1267-1279.	1.6	8
46	On-Line Viterbi Algorithm for Analysis of Long Biological Sequences. <i>Lecture Notes in Computer Science</i> , 2007, , 240-251.	1.3	8
47	Evolutionary History Reconstruction for Mammalian Complex Gene Clusters. <i>Journal of Computational Biology</i> , 2009, 16, 1051-1070.	1.6	7
48	A Practical Algorithm for Ancestral Rearrangement Reconstruction. <i>Lecture Notes in Computer Science</i> , 2011, , 163-174.	1.3	7
49	Advances in Hidden Markov Models for Sequence Annotation. , 2007, , 55-91.		6
50	GAML: genome assembly by maximum likelihood. <i>Algorithms for Molecular Biology</i> , 2015, 10, 18.	1.2	6
51	RNA motif search with data-driven element ordering. <i>BMC Bioinformatics</i> , 2016, 17, 216.	2.6	6
52	Probabilistic approaches to alignment with tandem repeats. <i>Algorithms for Molecular Biology</i> , 2014, 9, 3.	1.2	4
53	Discovery of RNA Motifs Using a Computational Pipeline that Allows Insertions in Paired Regions and Filtering of Candidate Sequences. <i>Methods in Molecular Biology</i> , 2012, 848, 145-158.	0.9	4
54	Sharper Upper and Lower Bounds for an Approximation Scheme for Consensus-Pattern. <i>Lecture Notes in Computer Science</i> , 2005, , 1-10.	1.3	4

#	ARTICLE	IF	CITATIONS
55	Efficient routing in carrier-based mobile networks. <i>Theoretical Computer Science</i> , 2013, 509, 113-121.	0.9	3
56	Routing in Carrier-Based Mobile Networks. <i>Lecture Notes in Computer Science</i> , 2011, , 222-233.	1.3	3
57	Optimal DNA Signal Recognition Models with a Fixed Amount of Intrasignal Dependency. <i>Lecture Notes in Computer Science</i> , 2003, , 78-94.	1.3	2
58	Fast computation of a string duplication history under no-breakpoint-reuse. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2014, 372, 20130133.	3.4	2
59	Draft Genome Sequence of an Obligate Psychrophilic Yeast, <i>Candida psychrophila</i> NRRL Y-17665 T. <i>Genome Announcements</i> , 2017, 5, .	0.8	2
60	Predicting Gene Structures from Multiple RT-PCR Tests. <i>Lecture Notes in Computer Science</i> , 2009, , 181-193.	1.3	2
61	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. <i>Lecture Notes in Computer Science</i> , 2009, , 150-163.	1.3	2
62	A Better Method for Length Distribution Modeling in HMMs and Its Application to Gene Finding. <i>Lecture Notes in Computer Science</i> , 2002, , 190-202.	1.3	2
63	Isometric gene tree reconciliation revisited. <i>Algorithms for Molecular Biology</i> , 2017, 12, 17.	1.2	1
64	Genome Sequence of Flavor-Producing Yeast <i>Saprochaete suaveolens</i> NRRL Y-17571. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
65	Genome Sequence of an Arthroconidial Yeast, <i>Saprochaete fungicola</i> CBS 625.85. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
66	Genome Sequence of the Yeast <i>Saprochaete ingens</i> CBS 517.90. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
67	Inferring the Recent Duplication History of a Gene Cluster. <i>Lecture Notes in Computer Science</i> , 2009, , 111-125.	1.3	1
68	The Highest Expected Reward Decoding for HMMs with Application to Recombination Detection. <i>Lecture Notes in Computer Science</i> , 2010, , 164-176.	1.3	1
69	Dynamic Pooling Improves Nanopore Base Calling Accuracy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	3.0	1
70	Transcriptome and proteome profiling reveals complex adaptations of <i>Candida parapsilosis</i> cells assimilating hydroxyaromatic carbon sources. <i>PLoS Genetics</i> , 2022, 18, e1009815.	3.5	1
71	The Most Probable Labeling Problem in HMMs and Its Application to Bioinformatics. <i>Lecture Notes in Computer Science</i> , 2004, , 426-437.	1.3	0
72	Fast Computation of a String Duplication History under No-Breakpoint-RReuse. <i>Lecture Notes in Computer Science</i> , 2011, , 144-155.	1.3	0

#	ARTICLE	IF	CITATIONS
73	Sequence annotation with HMMs: New problems and their complexity. Information Processing Letters, 2015, 115, 635-639.	0.6	0
74	Fishing in Read Collections: Memory Efficient Indexing for Sequence Assembly. Lecture Notes in Computer Science, 2015, , 188-198.	1.3	0
75	Isometric Gene Tree Reconciliation Revisited. Lecture Notes in Computer Science, 2016, , 40-51.	1.3	0
76	Probabilistic Models of k-mer Frequencies (Extended Abstract). Lecture Notes in Computer Science, 2021, , 227-236.	1.3	0
77	Automated Segmentation of DNA Sequences with Complex Evolutionary Histories. Lecture Notes in Computer Science, 2011, , 1-13.	1.3	0
78	Probabilistic Approaches to Alignment with Tandem Repeats. Lecture Notes in Computer Science, 2013, , 287-299.	1.3	0