

# 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	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
2	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
3	Probabilistic Models of k-mer Frequencies (Extended Abstract). <i>Lecture Notes in Computer Science</i> , 2021, , 227-236.	1.3	0
4	Nanopore base calling on the edge. <i>Bioinformatics</i> , 2021, 37, 4661-4667.	4.1	20
5	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
6	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
7	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
8	Dynamic Pooling Improves Nanopore Base Calling Accuracy. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, PP, 1-1.	3.0	1
9	Mosaicism in old trees and its patterns. <i>Trees - Structure and Function</i> , 2020, 34, 357-370.	1.9	17
10	DeepNano-blitz: a fast base caller for MinION nanopore sequencers. <i>Bioinformatics</i> , 2020, 36, 4191-4192.	4.1	21
11	A draft genome sequence of the elusive giant squid, <i>Architeuthis dux</i> . <i>GigaScience</i> , 2020, 9, .	6.4	37
12	The comparative genomics and complex population history of <i>Papio</i> baboons. <i>Science Advances</i> , 2019, 5, eaau6947.	10.3	115
13	Genome Sequence of Flavor-Producing Yeast <i>Saprochaete suaveolens</i> NRRL Y-17571. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
14	Genome Sequence of an Arthroconidial Yeast, <i>Saprochaete fungicola</i> CBS 625.85. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
15	Genome Sequence of the Yeast <i>Saprochaete ingens</i> CBS 517.90. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	1
16	Genome sequence of the opportunistic human pathogen <i>Magnusiomyces capitatus</i> . <i>Current Genetics</i> , 2019, 65, 539-560.	1.7	14
17	Isometric gene tree reconciliation revisited. <i>Algorithms for Molecular Biology</i> , 2017, 12, 17.	1.2	1
18	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

#	ARTICLE	IF	CITATIONS
19	Papio Baboon Species Indicative Alu Elements. <i>Genome Biology and Evolution</i> , 2017, 9, 1788-1796.	2.5	12
20	Alu Insertion Polymorphisms as Evidence for Population Structure in Baboons. <i>Genome Biology and Evolution</i> , 2017, 9, 2418-2427.	2.5	13
21	DeepNano: Deep recurrent neural networks for base calling in MinION nanopore reads. <i>PLoS ONE</i> , 2017, 12, e0178751.	2.5	186
22	RNA motif search with data-driven element ordering. <i>BMC Bioinformatics</i> , 2016, 17, 216.	2.6	6
23	Genome-culture coevolution promotes rapid divergence of killer whale ecotypes. <i>Nature Communications</i> , 2016, 7, 11693.	12.8	222
24	Isometric Gene Tree Reconciliation Revisited. <i>Lecture Notes in Computer Science</i> , 2016, , 40-51.	1.3	0
25	GAML: genome assembly by maximum likelihood. <i>Algorithms for Molecular Biology</i> , 2015, 10, 18.	1.2	6
26	Convergent evolution of the genomes of marine mammals. <i>Nature Genetics</i> , 2015, 47, 272-275.	21.4	392
27	Sequence annotation with HMMs: New problems and their complexity. <i>Information Processing Letters</i> , 2015, 115, 635-639.	0.6	0
28	Fishing in Read Collections: Memory Efficient Indexing for Sequence Assembly. <i>Lecture Notes in Computer Science</i> , 2015, , 188-198.	1.3	0
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	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
31	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
32	The common marmoset genome provides insight into primate biology and evolution. <i>Nature Genetics</i> , 2014, 46, 850-857.	21.4	225
33	Probabilistic approaches to alignment with tandem repeats. <i>Algorithms for Molecular Biology</i> , 2014, 9, 3.	1.2	4
34	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
35	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
36	The genome of the hydatid tapeworm <i>Echinococcus granulosus</i> . <i>Nature Genetics</i> , 2013, 45, 1168-1175.	21.4	260

#	ARTICLE	IF	CITATIONS
37	Efficient routing in carrier-based mobile networks. <i>Theoretical Computer Science</i> , 2013, 509, 113-121.	0.9	3
38	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
39	Probabilistic Approaches to Alignment with Tandem Repeats. <i>Lecture Notes in Computer Science</i> , 2013, , 287-299.	1.3	0
40	Sequencing the genome of <i>Marssonina brunnea</i> reveals fungus-poplar co-evolution. <i>BMC Genomics</i> , 2012, 13, 382.	2.8	61
41	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
42	Fast Computation of a String Duplication History under No-Breakpoint-Reuse. <i>Lecture Notes in Computer Science</i> , 2011, , 144-155.	1.3	0
43	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011, 469, 529-533.	27.8	541
44	Evolution of linear chromosomes and multipartite genomes in yeast mitochondria. <i>Nucleic Acids Research</i> , 2011, 39, 4202-4219.	14.5	69
45	Routing in Carrier-Based Mobile Networks. <i>Lecture Notes in Computer Science</i> , 2011, , 222-233.	1.3	3
46	A Practical Algorithm for Ancestral Rearrangement Reconstruction. <i>Lecture Notes in Computer Science</i> , 2011, , 163-174.	1.3	7
47	Automated Segmentation of DNA Sequences with Complex Evolutionary Histories. <i>Lecture Notes in Computer Science</i> , 2011, , 1-13.	1.3	0
48	Positive selection on apoptosis related genes. <i>FEBS Letters</i> , 2010, 584, 469-476.	2.8	38
49	The sequence and de novo assembly of the giant panda genome. <i>Nature</i> , 2010, 463, 311-317.	27.8	1,058
50	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. <i>Journal of Computational Biology</i> , 2010, 17, 1267-1279.	1.6	8
51	CAGE: Combinatorial Analysis of Gene-Cluster Evolution. <i>Journal of Computational Biology</i> , 2010, 17, 1227-1242.	1.6	10
52	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
53	Evolutionary History Reconstruction for Mammalian Complex Gene Clusters. <i>Journal of Computational Biology</i> , 2009, 16, 1051-1070.	1.6	7
54	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

#	ARTICLE	IF	CITATIONS
55	The Schistosoma japonicum genome reveals features of host-parasite interplay. Nature, 2009, 460, 345-351.	27.8	635
56	Predicting Gene Structures from Multiple RT-PCR Tests. Lecture Notes in Computer Science, 2009, , 181-193.	1.3	2
57	Inferring the Recent Duplication History of a Gene Cluster. Lecture Notes in Computer Science, 2009, , 111-125.	1.3	1
58	Reconstructing Histories of Complex Gene Clusters on a Phylogeny. Lecture Notes in Computer Science, 2009, , 150-163.	1.3	2
59	nGASP - the nematode genome annotation assessment project. BMC Bioinformatics, 2008, 9, 549.	2.6	61
60	Patterns of Positive Selection in Six Mammalian Genomes. PLoS Genetics, 2008, 4, e1000144.	3.5	529
61	Reconstructing the Evolutionary History of Complex Human Gene Clusters. , 2008, , 29-49.		9
62	Homology search for genes. Bioinformatics, 2007, 23, i97-i103.	4.1	13
63	Advances in Hidden Markov Models for Sequence Annotation. , 2007, , 55-91.		6
64	Evolutionary and Biomedical Insights from the Rhesus Macaque Genome. Science, 2007, 316, 222-234.	12.6	1,283
65	The most probable annotation problem in HMMs and its application to bioinformatics. Journal of Computer and System Sciences, 2007, 73, 1060-1077.	1.2	13
66	On-Line Viterbi Algorithm for Analysis of Long Biological Sequences. Lecture Notes in Computer Science, 2007, , 240-251.	1.3	8
67	Vector seeds: An extension to spaced seeds. Journal of Computer and System Sciences, 2005, 70, 364-380.	1.2	42
68	ExonHunter: a comprehensive approach to gene finding. Bioinformatics, 2005, 21, i57-i65.	4.1	45
69	Sharper Upper and Lower Bounds for an Approximation Scheme for Consensus-Pattern. Lecture Notes in Computer Science, 2005, , 1-10.	1.3	4
70	The Most Probable Labeling Problem in HMMs and Its Application to Bioinformatics. Lecture Notes in Computer Science, 2004, , 426-437.	1.3	0
71	OPTIMAL SPACED SEEDS FOR HOMOLOGOUS CODING REGIONS. Journal of Bioinformatics and Computational Biology, 2004, 01, 595-610.	0.8	48
72	Finding hidden independent sets in interval graphs. Theoretical Computer Science, 2004, 310, 287-307.	0.9	8

#	ARTICLE	IF	CITATIONS
73	Palindrome recognition using a multidimensional tape. Theoretical Computer Science, 2003, 302, 475-480.	0.9	8
74	Vector Seeds: An Extension to Spaced Seeds Allows Substantial Improvements in Sensitivity and Specificity. Lecture Notes in Computer Science, 2003, , 39-54.	1.3	22
75	Optimal DNA Signal Recognition Models with a Fixed Amount of Intrasignal Dependency. Lecture Notes in Computer Science, 2003, , 78-94.	1.3	2
76	Optimal Spaced Seeds for Hidden Markov Models, with Application to Homologous Coding Regions. Lecture Notes in Computer Science, 2003, , 42-54.	1.3	16
77	A Better Method for Length Distribution Modeling in HMMs and Its Application to Gene Finding. Lecture Notes in Computer Science, 2002, , 190-202.	1.3	2
78	Simplifying Flow Networks. Lecture Notes in Computer Science, 2000, , 192-201.	1.3	10