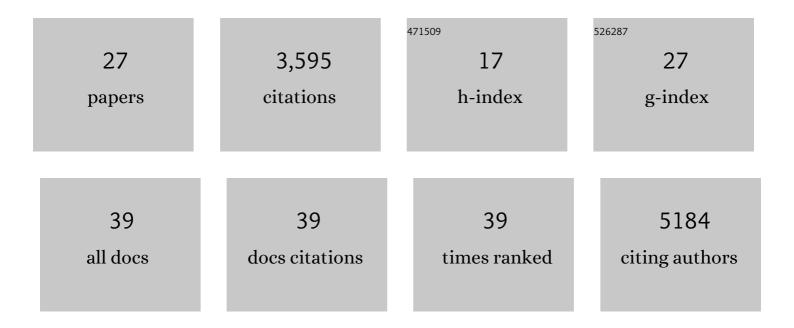
Adam M Novak

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/396302/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Toil enables reproducible, open source, big biomedical data analyses. Nature Biotechnology, 2017, 35, 314-316.	17.5	873
2	Variation graph toolkit improves read mapping by representing genetic variation in the reference. Nature Biotechnology, 2018, 36, 875-879.	17.5	435
3	Human-Specific NOTCH2NL Genes Affect Notch Signaling and Cortical Neurogenesis. Cell, 2018, 173, 1356-1369.e22.	28.9	366
4	Genome graphs and the evolution of genome inference. Genome Research, 2017, 27, 665-676.	5.5	264
5	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. Nature, 2020, 587, 246-251.	27.8	256
6	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	6.5	207
7	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	27.8	192
8	Genotyping structural variants in pangenome graphs using the vg toolkit. Genome Biology, 2020, 21, 35.	8.8	150
9	Pangenome Graphs. Annual Review of Genomics and Human Genetics, 2020, 21, 139-162.	6.2	148
10	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	12.6	132
11	TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. Cancer Research, 2017, 77, e111-e114.	0.9	59
12	A graph-based approach to diploid genome assembly. Bioinformatics, 2018, 34, i105-i114.	4.1	59
13	Haplotype-aware graph indexes. Bioinformatics, 2020, 36, 400-407.	4.1	59
14	Superbubbles, Ultrabubbles, and Cacti. Journal of Computational Biology, 2018, 25, 649-663.	1.6	46
15	A graph extension of the positional Burrows–Wheeler transform and its applications. Algorithms for Molecular Biology, 2017, 12, 18.	1.2	33
16	The NIH BD2K center for big data in translational genomics. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1143-1147.	4.4	30
17	Sequence tube maps: making graph genomes intuitive to commuters. Bioinformatics, 2019, 35, 5318-5320.	4.1	28
18	Efficient dynamic variation graphs. Bioinformatics, 2021, 36, 5139-5144.	4.1	18

Αδαμ Μ Νονακ

#	Article	IF	CITATIONS
19	Modeling the Role of Negative Cooperativity in Metabolic Regulation and Homeostasis. PLoS ONE, 2012, 7, e48920.	2.5	17
20	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	14
21	Distance indexing and seed clustering in sequence graphs. Bioinformatics, 2020, 36, i146-i153.	4.1	10
22	A Graph Extension of the Positional Burrows-Wheeler Transform and Its Applications. Lecture Notes in Computer Science, 2016, , 246-256.	1.3	9
23	Superbubbles, Ultrabubbles and Cacti. Lecture Notes in Computer Science, 2017, , 173-189.	1.3	7
24	Canonical, stable, general mapping using context schemes. Bioinformatics, 2015, 31, btv435.	4.1	5
25	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	5
26	A Flow Procedure for Linearization of Genome Sequence Graphs. Journal of Computational Biology, 2018, 25, 664-676.	1.6	3
27	A Flow Procedure for the Linearization of Genome Sequence Graphs. Lecture Notes in Computer Science, 2017, , 34-49.	1.3	2