

# Adam M Novak

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/396302/publications.pdf>

Version: 2024-02-01

27  
papers

3,595  
citations

471509

17  
h-index

526287

27  
g-index

39  
all docs

39  
docs citations

39  
times ranked

5184  
citing authors

#	ARTICLE	IF	CITATIONS
1	Toil enables reproducible, open source, big biomedical data analyses. <i>Nature Biotechnology</i> , 2017, 35, 314-316.	17.5	873
2	Variation graph toolkit improves read mapping by representing genetic variation in the reference. <i>Nature Biotechnology</i> , 2018, 36, 875-879.	17.5	435
3	Human-Specific NOTCH2NL Genes Affect Notch Signaling and Cortical Neurogenesis. <i>Cell</i> , 2018, 173, 1356-1369.e22.	28.9	366
4	Genome graphs and the evolution of genome inference. <i>Genome Research</i> , 2017, 27, 665-676.	5.5	264
5	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. <i>Nature</i> , 2020, 587, 246-251.	27.8	256
6	Computational pan-genomics: status, promises and challenges. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw089.	6.5	207
7	The Human Pangenome Project: a global resource to map genomic diversity. <i>Nature</i> , 2022, 604, 437-446.	27.8	192
8	Genotyping structural variants in pangenome graphs using the vg toolkit. <i>Genome Biology</i> , 2020, 21, 35.	8.8	150
9	Pangenome Graphs. <i>Annual Review of Genomics and Human Genetics</i> , 2020, 21, 139-162.	6.2	148
10	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. <i>Science</i> , 2021, 374, abg8871.	12.6	132
11	TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. <i>Cancer Research</i> , 2017, 77, e1111-e1114.	0.9	59
12	A graph-based approach to diploid genome assembly. <i>Bioinformatics</i> , 2018, 34, i105-i114.	4.1	59
13	Haplotype-aware graph indexes. <i>Bioinformatics</i> , 2020, 36, 400-407.	4.1	59
14	Superbubbles, Ultrabubbles, and Cacti. <i>Journal of Computational Biology</i> , 2018, 25, 649-663.	1.6	46
15	A graph extension of the positional Burrows-Wheeler transform and its applications. <i>Algorithms for Molecular Biology</i> , 2017, 12, 18.	1.2	33
16	The NIH BD2K center for big data in translational genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1143-1147.	4.4	30
17	Sequence tube maps: making graph genomes intuitive to commuters. <i>Bioinformatics</i> , 2019, 35, 5318-5320.	4.1	28
18	Efficient dynamic variation graphs. <i>Bioinformatics</i> , 2021, 36, 5139-5144.	4.1	18

#	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