Adam M Novak

List of Publications by Year
in descending order

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	The Human Pangenome Project: a global resource to map genomic diversity. Nature, 2022, 604, 437-446.	27.8	192
2	Efficient dynamic variation graphs. Bioinformatics, 2021, 36, 5139-5144.	4.1	18
3	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. Science, 2021, 374, abg8871.	12.6	132
4	Haplotype-aware graph indexes. Bioinformatics, 2020, 36, 400-407.	4.1	59
5	Distance indexing and seed clustering in sequence graphs. Bioinformatics, 2020, 36, i146-i153.	4.1	10
6	Progressive Cactus is a multiple-genome aligner for the thousand-genome era. Nature, 2020, 587, 246-251.	27.8	256
7	Pangenome Graphs. Annual Review of Genomics and Human Genetics, 2020, 21, 139-162.	6.2	148
8	Genotyping structural variants in pangenome graphs using the vg toolkit. Genome Biology, 2020, 21, 35.	8.8	150
9	Sequence tube maps: making graph genomes intuitive to commuters. Bioinformatics, 2019, 35, 5318-5320.	4.1	28
10	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	5
11	A strategy for building and using a human reference pangenome. F1000Research, 2019, 8, 1751.	1.6	14
12	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	6.5	207
13	Superbubbles, Ultrabubbles, and Cacti. Journal of Computational Biology, 2018, 25, 649-663.	1.6	46
14	Human-Specific NOTCH2NL Genes Affect Notch Signaling and Cortical Neurogenesis. Cell, 2018, 173, 1356-1369.e22.	28.9	366
15	A Flow Procedure for Linearization of Genome Sequence Graphs. Journal of Computational Biology, 2018, 25, 664-676.	1.6	3
16	A graph-based approach to diploid genome assembly. Bioinformatics, 2018, 34, i105-i114.	4.1	59
17	Variation graph toolkit improves read mapping by representing genetic variation in the reference. Nature Biotechnology, 2018, 36, 875-879.	17.5	435
18	Toil enables reproducible, open source, big biomedical data analyses. Nature Biotechnology, 2017, 35, 314-316.	17.5	873

#	Article	IF	Citations
19	Genome graphs and the evolution of genome inference. Genome Research, 2017, 27, 665-676.	5.5	264
20	TumorMap: Exploring the Molecular Similarities of Cancer Samples in an Interactive Portal. Cancer Research, 2017, 77, e111-e114.	0.9	59
21	A graph extension of the positional Burrowsâ€"Wheeler transform and its applications. Algorithms for Molecular Biology, 2017, 12, 18.	1.2	33
22	Superbubbles, Ultrabubbles and Cacti. Lecture Notes in Computer Science, 2017, , 173-189.	1.3	7
23	A Flow Procedure for the Linearization of Genome Sequence Graphs. Lecture Notes in Computer Science, 2017, , 34-49.	1.3	2
24	A Graph Extension of the Positional Burrows-Wheeler Transform and Its Applications. Lecture Notes in Computer Science, 2016, , 246-256.	1.3	9
25	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
26	Canonical, stable, general mapping using context schemes. Bioinformatics, 2015, 31, btv435.	4.1	5
27	Modeling the Role of Negative Cooperativity in Metabolic Regulation and Homeostasis. PLoS ONE, 2012, 7, e48920.	2.5	17