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List of Publications by Year
in descending order

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40 papers	15,475 citations	236925 25 h-index	302126 39 g-index
55 all docs	55 docs citations	55 times ranked	31289 citing authors

#	Article	IF	Citations
1	Near-optimal probabilistic RNA-seq quantification. Nature Biotechnology, 2016, 34, 525-527.	17.5	7,322
2	Mash: fast genome and metagenome distance estimation using MinHash. Genome Biology, 2016, 17, 132.	8.8	2,099
3	Differential analysis of RNA-seq incorporating quantification uncertainty. Nature Methods, 2017, 14, 687-690.	19.0	1,296
4	Spread of SARS-CoV-2 in the Icelandic Population. New England Journal of Medicine, 2020, 382, 2302-2315.	27.0	1,093
5	Humoral Immune Response to SARS-CoV-2 in Iceland. New England Journal of Medicine, 2020, 383, 1724-1734.	27.0	845
6	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	21.4	340
7	Modular, efficient and constant-memory single-cell RNA-seq preprocessing. Nature Biotechnology, 2021, 39, 813-818.	17.5	252
8	Efficient counting of k-mers in DNA sequences using a bloom filter. BMC Bioinformatics, 2011, 12, 333.	2.6	222
9	Graphtyper enables population-scale genotyping using pangenome graphs. Nature Genetics, 2017, 49, 1654-1660.	21.4	189
10	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. Genome Research, 2012, 22, 602-610.	5.5	145
11	Genomic-scale capture and sequencing of endogenous DNA from feces. Molecular Ecology, 2010, 19, 5332-5344.	3.9	127
12	A discriminative learning approach to differential expression analysis for single-cell RNA-seq. Nature Methods, 2019, 16, 163-166.	19.0	123
13	The barcode, UMI, set format and BUStools. Bioinformatics, 2019, 35, 4472-4473.	4.1	117
14	GraphTyper2 enables population-scale genotyping of structural variation using pangenome graphs. Nature Communications, 2019, 10, 5402.	12.8	96
15	Insights into imprinting from parent-of-origin phased methylomes and transcriptomes. Nature Genetics, 2018, 50, 1542-1552.	21.4	94
16	Bifrost: highly parallel construction and indexing of colored and compacted de Bruijn graphs. Genome Biology, 2020, 21, 249.	8.8	92
17	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. Nature, 2020, 584, 619-623.	27.8	81
18	Diversity in non-repetitive human sequences not found in the reference genome. Nature Genetics, 2017, 49, 588-593.	21.4	70

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19	A Genome Sequence Resource for the Aye-Aye (Daubentonia madagascariensis), a Nocturnal Lemur from Madagascar. Genome Biology and Evolution, 2012, 4, 126-135.	2.5	59
20	KmerStream: streaming algorithms for k -mer abundance estimation. Bioinformatics, 2014, 30, 3541-3547.	4.1	56
21	Looking into the past â€“ the reaction of three grouse species to climate change over the last million years using whole genome sequences. Molecular Ecology, 2016, 25, 570-580.	3.9	49
22	Coding variants in RPL3L and MYZAP increase risk of atrial fibrillation. Communications Biology, 2018, 1, 68.	4.4	42
23	Maximum matchings in random bipartite graphs and the space utilization of Cuckoo Hash tables. Random Structures and Algorithms, 2012, 41, 334-364.	1.1	34
24	PopIns: population-scale detection of novel sequence insertions. Bioinformatics, 2016, 32, 961-967.	4.1	33
25	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. Communications Biology, 2021, 4, 706.	4.4	30
26	An Analysis of Random-Walk Cuckoo Hashing. Lecture Notes in Computer Science, 2009, , 490-503.	1.3	19
27	An Analysis of Random-Walk Cuckoo Hashing. SIAM Journal on Computing, 2011, 40, 291-308.	1.0	17
28	Loss-of-Function Variants in the Tumor-Suppressor Gene PTPN14 Confer Increased Cancer Risk. Cancer Research, 2021, 81, 1954-1964.	0.9	15
29	The Lair: a resource for exploratory analysis of published RNA-Seq data. BMC Bioinformatics, 2016, 17, 490.	2.6	13
30	Lifelong Reduction in LDL (Low-Density Lipoprotein) Cholesterol due to a Gain-of-Function Mutation in LDLR. Circulation Genomic and Precision Medicine, 2021, 14, e003029.	3.6	12
31	Reconstruction of a large-scale outbreak of SARS-CoV-2 infection in Iceland informs vaccination strategies. Clinical Microbiology and Infection, 2022, 28, 852-858.	6.0	11
32	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. Nature Communications, 2019, 10, 1777.	12.8	7
33	Genetic variants associated with platelet count are predictive of human disease and physiological markers. Communications Biology, 2021, 4, 1132.	4.4	7
34	Randomly coloring simple hypergraphs. Information Processing Letters, 2011, 111, 848-853.	0.6	6
35	Molecular benchmarks of a SARS-CoV-2 epidemic. Nature Communications, 2021, 12, 3633.	12.8	3
36	BamHash: a checksum program for verifying the integrity of sequence data. Bioinformatics, 2016, 32, 140-141.	4.1	2

#	Article	IF	Citations
37	Average-Case Analyses of Vickrey Costs. Lecture Notes in Computer Science, 2009, , 434-447.	1.3	2
38	Finding a Maximum Matching in a Sparse Random Graph in O(n) Expected Time. Lecture Notes in Computer Science, 2008, , 161-172.	1.3	1
39	chopBAI: BAM index reduction solves I/O bottlenecks in the joint analysis of large sequencing cohorts. Bioinformatics, 2016, 32, 2202-2204.	4.1	0
40	Algorithm 1005. ACM Transactions on Mathematical Software, 2020, 46, 1-20.	2.9	0