PÃ¡ll Melsted

List of Publications by Year
in descending order

40 papers	15,475 citations	236912 25 h-index	302107 39 g-index
55 all docs	55 docs citations	55 times ranked	31289 citing authors

#	Article	IF	Citations
1	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
2	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
3	Loss-of-Function Variants in the Tumor-Suppressor Gene *PTPN14* Confer Increased Cancer Risk. Cancer Research, 2021, 81, 1954-1964.	0.9	15
4	Modular, efficient and constant-memory single-cell RNA-seq preprocessing. Nature Biotechnology, 2021, 39, 813-818.	17.5	252
5	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. Communications Biology, 2021, 4, 706.	4.4	30
6	Molecular benchmarks of a SARS-CoV-2 epidemic. Nature Communications, 2021, 12, 3633.	12.8	3
7	Genetic variants associated with platelet count are predictive of human disease and physiological markers. Communications Biology, 2021, 4, 1132.	4.4	7
8	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	21.4	340
9	Bifrost: highly parallel construction and indexing of colored and compacted de Bruijn graphs. Genome Biology, 2020, 21, 249.	8.8	92
10	Humoral Immune Response to SARS-CoV-2 in Iceland. New England Journal of Medicine, 2020, 383, 1724-1734.	27.0	845
11	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. Nature, 2020, 584, 619-623.	27.8	81
12	Spread of SARS-CoV-2 in the Icelandic Population. New England Journal of Medicine, 2020, 382, 2302-2315.	27.0	1,093
13	Algorithm 1005. ACM Transactions on Mathematical Software, 2020, 46, 1-20.	2.9	0
14	A discriminative learning approach to differential expression analysis for single-cell RNA-seq. Nature Methods, 2019, 16, 163-166.	19.0	123
15	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. Nature Communications, 2019, 10, 1777.	12.8	7
16	The barcode, UMI, set format and BUStools. Bioinformatics, 2019, 35, 4472-4473.	4.1	117
17	GraphTyper2 enables population-scale genotyping of structural variation using pangenome graphs. Nature Communications, 2019, 10, 5402.	12.8	96
18	Insights into imprinting from parent-of-origin phased methylomes and transcriptomes. Nature Genetics, 2018, 50, 1542-1552.	21.4	94

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19	Coding variants in RPL3L and MYZAP increase risk of atrial fibrillation. Communications Biology, 2018, 1, 68.	4.4	42
20	Diversity in non-repetitive human sequences not found in the reference genome. Nature Genetics, 2017, 49, 588-593.	21.4	70
21	Graphtyper enables population-scale genotyping using pangenome graphs. Nature Genetics, 2017, 49, 1654-1660.	21.4	189
22	Differential analysis of RNA-seq incorporating quantification uncertainty. Nature Methods, 2017, 14, 687-690.	19.0	1,296
23	BamHash: a checksum program for verifying the integrity of sequence data. Bioinformatics, 2016, 32, 140-141.	4.1	2
24	Mash: fast genome and metagenome distance estimation using MinHash. Genome Biology, 2016, 17, 132.	8.8	2,099
25	Looking into the past – 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
26	Near-optimal probabilistic RNA-seq quantification. Nature Biotechnology, 2016, 34, 525-527.	17.5	7,322
27	The Lair: a resource for exploratory analysis of published RNA-Seq data. BMC Bioinformatics, 2016, 17, 490.	2.6	13
28	chopBAI: BAM index reduction solves I/O bottlenecks in the joint analysis of large sequencing cohorts. Bioinformatics, 2016, 32, 2202-2204.	4.1	0
29	PopIns: population-scale detection of novel sequence insertions. Bioinformatics, 2016, 32, 961-967.	4.1	33
30	KmerStream: streaming algorithms for k-mer abundance estimation. Bioinformatics, 2014, 30, 3541-3547.	4.1	56
31	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
32	Comparative RNA sequencing reveals substantial genetic variation in endangered primates. Genome Research, 2012, 22, 602-610.	5.5	145
33	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
34	An Analysis of Random-Walk Cuckoo Hashing. SIAM Journal on Computing, 2011, 40, 291-308.	1.0	17
35	Efficient counting of k-mers in DNA sequences using a bloom filter. BMC Bioinformatics, 2011, 12, 333.	2.6	222
36	Randomly coloring simple hypergraphs. Information Processing Letters, 2011, 111, 848-853.	0.6	6

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37	Genomic-scale capture and sequencing of endogenous DNA from feces. Molecular Ecology, 2010, 19, 5332-5344.	3.9	127
38	Average-Case Analyses of Vickrey Costs. Lecture Notes in Computer Science, 2009, , 434-447.	1.3	2
39	An Analysis of Random-Walk Cuckoo Hashing. Lecture Notes in Computer Science, 2009, , 490-503.	1.3	19
40	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