

Can Alkan

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

106
papers

42,205
citations

53
h-index

120
g-index

120
ext. papers

51,220
ext. citations

15.9
avg, IF

6.68
L-index

#	Paper	IF	Citations
106	A global reference for human genetic variation. <i>Nature</i> , 2015 , 526, 68-74	50.4	8599
105	A map of human genome variation from population-scale sequencing. <i>Nature</i> , 2010 , 467, 1061-73	50.4	6142
104	An integrated map of genetic variation from 1,092 human genomes. <i>Nature</i> , 2012 , 491, 56-65	50.4	6049
103	A hexanucleotide repeat expansion in C9ORF72 is the cause of chromosome 9p21-linked ALS-FTD. <i>Neuron</i> , 2011 , 72, 257-68	13.9	3018
102	A draft sequence of the Neandertal genome. <i>Science</i> , 2010 , 328, 710-722	33.3	2599
101	An integrated map of structural variation in 2,504 human genomes. <i>Nature</i> , 2015 , 526, 75-81	50.4	1368
100	A high-coverage genome sequence from an archaic Denisovan individual. <i>Science</i> , 2012 , 338, 222-6	33.3	1276
99	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010 , 468, 1053-60	50.4	1169
98	Genome structural variation discovery and genotyping. <i>Nature Reviews Genetics</i> , 2011 , 12, 363-76	30.1	947
97	Mapping and sequencing of structural variation from eight human genomes. <i>Nature</i> , 2008 , 453, 56-64	50.4	878
96	Mapping copy number variation by population-scale genome sequencing. <i>Nature</i> , 2011 , 470, 59-65	50.4	833
95	Great ape genetic diversity and population history. <i>Nature</i> , 2013 , 499, 471-5	50.4	574
94	Personalized copy number and segmental duplication maps using next-generation sequencing. <i>Nature Genetics</i> , 2009 , 41, 1061-7	36.3	543
93	Insights into hominid evolution from the gorilla genome sequence. <i>Nature</i> , 2012 , 483, 169-75	50.4	517
92	Limitations of next-generation genome sequence assembly. <i>Nature Methods</i> , 2011 , 8, 61-5	21.6	503
91	Diversity of human copy number variation and multicopy genes. <i>Science</i> , 2010 , 330, 641-6	33.3	491
90	Comparative and demographic analysis of orang-utan genomes. <i>Nature</i> , 2011 , 469, 529-33	50.4	431

89	Sequence and structural variation in a human genome uncovered by short-read, massively parallel ligation sequencing using two-base encoding. <i>Genome Research</i> , 2009 , 19, 1527-41	9.7	401
88	Genome sequencing highlights the dynamic early history of dogs. <i>PLoS Genetics</i> , 2014 , 10, e1004016	6	372
87	The bonobo genome compared with the chimpanzee and human genomes. <i>Nature</i> , 2012 , 486, 527-31	50.4	350
86	Complete Khoisan and Bantu genomes from southern Africa. <i>Nature</i> , 2010 , 463, 943-7	50.4	342
85	Activating mutations of STAT5B and STAT3 in lymphomas derived from T or NK cells. <i>Nature Communications</i> , 2015 , 6, 6025	17.4	261
84	Combinatorial algorithms for structural variation detection in high-throughput sequenced genomes. <i>Genome Research</i> , 2009 , 19, 1270-8	9.7	230
83	mrsFAST: a cache-oblivious algorithm for short-read mapping. <i>Nature Methods</i> , 2010 , 7, 576-7	21.6	216
82	Refinement and discovery of new hotspots of copy-number variation associated with autism spectrum disorder. <i>American Journal of Human Genetics</i> , 2013 , 92, 221-37	11	214
81	Copy number variation of individual cattle genomes using next-generation sequencing. <i>Genome Research</i> , 2012 , 22, 778-90	9.7	204
80	Haplotype-resolved genome sequencing of a Gujarati Indian individual. <i>Nature Biotechnology</i> , 2011 , 29, 59-63	44.5	194
79	Reconstructing complex regions of genomes using long-read sequencing technology. <i>Genome Research</i> , 2014 , 24, 688-96	9.7	188
78	Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17230-5	11.5	184
77	A burst of segmental duplications in the genome of the African great ape ancestor. <i>Nature</i> , 2009 , 457, 877-81	50.4	179
76	Next-generation VariationHunter: combinatorial algorithms for transposon insertion discovery. <i>Bioinformatics</i> , 2010 , 26, i350-7	7.2	161
75	The structure and evolution of centromeric transition regions within the human genome. <i>Nature</i> , 2004 , 430, 857-64	50.4	160
74	Computational pan-genomics: status, promises and challenges. <i>Briefings in Bioinformatics</i> , 2018 , 19, 118-134	13.4	130
73	Characterization of missing human genome sequences and copy-number polymorphic insertions. <i>Nature Methods</i> , 2010 , 7, 365-71	21.6	114
72	MoDIL: detecting small indels from clone-end sequencing with mixtures of distributions. <i>Nature Methods</i> , 2009 , 6, 473-4	21.6	103

71	Analysis of primate genomic variation reveals a repeat-driven expansion of the human genome. <i>Genome Research</i> , 2003 , 13, 358-68	9.7	101
70	A robust benchmark for detection of germline large deletions and insertions. <i>Nature Biotechnology</i> , 2020 , 38, 1347-1355	44.5	98
69	Detection of structural variants and indels within exome data. <i>Nature Methods</i> , 2011 , 9, 176-8	21.6	93
68	RNA-RNA interaction prediction and antisense RNA target search. <i>Journal of Computational Biology</i> , 2006 , 13, 267-82	1.7	93
67	SCALCE: boosting sequence compression algorithms using locally consistent encoding. <i>Bioinformatics</i> , 2012 , 28, 3051-7	7.2	89
66	Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. <i>Bioinformatics</i> , 2010 , 26, 1277-83	7.2	84
65	Alu repeat discovery and characterization within human genomes. <i>Genome Research</i> , 2011 , 21, 840-9	9.7	84
64	Nanopore sequencing technology and tools for genome assembly: computational analysis of the current state, bottlenecks and future directions. <i>Briefings in Bioinformatics</i> , 2019 , 20, 1542-1559	13.4	83
63	A large and complex structural polymorphism at 16p12.1 underlies microdeletion disease risk. <i>Nature Genetics</i> , 2010 , 42, 745-50	36.3	81
62	Death and resurrection of the human IRGM gene. <i>PLoS Genetics</i> , 2009 , 5, e1000403	6	75
61	Identification and validation of a novel mature microRNA encoded by the Merkel cell polyomavirus in human Merkel cell carcinomas. <i>Journal of Clinical Virology</i> , 2011 , 52, 272-5	14.5	67
60	Organization and evolution of primate centromeric DNA from whole-genome shotgun sequence data. <i>PLoS Computational Biology</i> , 2007 , 3, 1807-18	5	66
59	Realizing the potential of blockchain technologies in genomics. <i>Genome Research</i> , 2018 , 28, 1255-1263	9.7	63
58	Genome-wide characterization of centromeric satellites from multiple mammalian genomes. <i>Genome Research</i> , 2011 , 21, 137-45	9.7	59
57	Gorilla genome structural variation reveals evolutionary parallelisms with chimpanzee. <i>Genome Research</i> , 2011 , 21, 1640-9	9.7	56
56	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. <i>PLoS Genetics</i> , 2016 , 12, e1005851	6	56
55	GRIM-Filter: Fast seed location filtering in DNA read mapping using processing-in-memory technologies. <i>BMC Genomics</i> , 2018 , 19, 89	4.5	55
54	Comparative analysis of Alu repeats in primate genomes. <i>Genome Research</i> , 2009 , 19, 876-85	9.7	55

53	Accelerating read mapping with FastHASH. <i>BMC Genomics</i> , 2013 , 14 Suppl 1, S13	4.5	53
52	Extreme selective sweeps independently targeted the X chromosomes of the great apes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 6413-8	11.5	52
51	Rates and patterns of great ape retrotransposition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 13457-62	11.5	46
50	mrsFAST-Ultra: a compact, SNP-aware mapper for high performance sequencing applications. <i>Nucleic Acids Research</i> , 2014 , 42, W494-500	20.1	41
49	GateKeeper: a new hardware architecture for accelerating pre-alignment in DNA short read mapping. <i>Bioinformatics</i> , 2017 , 33, 3355-3363	7.2	39
48	New insights into centromere organization and evolution from the white-cheeked gibbon and marmoset. <i>Molecular Biology and Evolution</i> , 2009 , 26, 1889-900	8.3	37
47	Early postzygotic mutations contribute to de novo variation in a healthy monozygotic twin pair. <i>Journal of Medical Genetics</i> , 2014 , 51, 455-9	5.8	35
46	A robust benchmark for germline structural variant detection		34
45	Inter-varietal structural variation in grapevine genomes. <i>Plant Journal</i> , 2016 , 88, 648-661	6.9	33
44	Whole genome sequencing of Turkish genomes reveals functional private alleles and impact of genetic interactions with Europe, Asia and Africa. <i>BMC Genomics</i> , 2014 , 15, 963	4.5	33
43	Targeting PLK1 overcomes T-DM1 resistance via CDK1-dependent phosphorylation and inactivation of Bcl-2/xL in HER2-positive breast cancer. <i>Oncogene</i> , 2018 , 37, 2251-2269	9.2	30
42	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. <i>BMC Genomics</i> , 2013 , 14, 363	4.5	30
41	Shifted Hamming distance: a fast and accurate SIMD-friendly filter to accelerate alignment verification in read mapping. <i>Bioinformatics</i> , 2015 , 31, 1553-60	7.2	28
40	Annotated features of domestic cat - <i>Felis catus</i> genome. <i>GigaScience</i> , 2014 , 3, 13	7.6	26
39	Fast characterization of segmental duplications in genome assemblies. <i>Bioinformatics</i> , 2018 , 34, i706-i714	4.2	25
38	Optimal design of oligonucleotide microarrays for measurement of DNA copy-number. <i>Human Molecular Genetics</i> , 2007 , 16, 2770-9	5.6	23
37	On genomic repeats and reproducibility. <i>Bioinformatics</i> , 2016 , 32, 2243-7	7.2	22
36	Divergent origins and concerted expansion of two segmental duplications on chromosome 16. <i>Journal of Heredity</i> , 2001 , 92, 462-8	2.4	22

35	Shouji: a fast and efficient pre-alignment filter for sequence alignment. <i>Bioinformatics</i> , 2019 , 35, 4255-4263	7.2	20
34	Discovery of tandem and interspersed segmental duplications using high-throughput sequencing. <i>Bioinformatics</i> , 2019 , 35, 3923-3930	7.2	17
33	The role of unequal crossover in alpha-satellite DNA evolution: a computational analysis. <i>Journal of Computational Biology</i> , 2004 , 11, 933-44	1.7	17
32	Accelerating Genome Analysis: A Primer on an Ongoing Journey. <i>IEEE Micro</i> , 2020 , 40, 65-75	1.8	17
31	Toolkit for automated and rapid discovery of structural variants. <i>Methods</i> , 2017 , 129, 3-7	4.6	16
30	Discovery and genotyping of novel sequence insertions in many sequenced individuals. <i>Bioinformatics</i> , 2017 , 33, i161-i169	7.2	16
29	Sensitive and fast mapping of di-base encoded reads. <i>Bioinformatics</i> , 2011 , 27, 1915-21	7.2	16
28	Optimal seed solver: optimizing seed selection in read mapping. <i>Bioinformatics</i> , 2016 , 32, 1632-42	7.2	14
27	Discovery of large genomic inversions using long range information. <i>BMC Genomics</i> , 2017 , 18, 65	4.5	14
26	taveRNA: a web suite for RNA algorithms and applications. <i>Nucleic Acids Research</i> , 2007 , 35, W325-9	20.1	14
25	Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm. <i>Bioinformatics</i> , 2020 , 36, 3669-3679	7.2	13
24	GenASM: A High-Performance, Low-Power Approximate String Matching Acceleration Framework for Genome Sequence Analysis 2020 ,		13
23	Hercules: a profile HMM-based hybrid error correction algorithm for long reads. <i>Nucleic Acids Research</i> , 2018 , 46, e125	20.1	13
22	Determining the origin of synchronous multifocal bladder cancer by exome sequencing. <i>BMC Cancer</i> , 2015 , 15, 871	4.8	12
21	Clcn4-2 genomic structure differs between the X locus in <i>Mus spretus</i> and the autosomal locus in <i>Mus musculus</i> : AT motif enrichment on the X. <i>Genome Research</i> , 2011 , 21, 402-9	9.7	12
20	SneakySnake: A Fast and Accurate Universal Genome Pre-Alignment Filter for CPUs, GPUs, and FPGAs. <i>Bioinformatics</i> , 2020 ,	7.2	9
19	RNA Secondary Structure Prediction Via Energy Density Minimization. <i>Lecture Notes in Computer Science</i> , 2006 , 130-142	0.9	7
18	Technology dictates algorithms: recent developments in read alignment. <i>Genome Biology</i> , 2021 , 22, 249	18.3	7

17	Computational Pan-Genomics: Status, Promises and Challenges		6
16	Manipulating multiple sequence alignments via MaM and WebMaM. <i>Nucleic Acids Research</i> , 2005 , 33, W295-8	20.1	5
15	Building and Improving Reference Genome Assemblies. <i>Proceedings of the IEEE</i> , 2017 , 1-14	14.3	4
14	VALOR2: characterization of large-scale structural variants using linked-reads. <i>Genome Biology</i> , 2020 , 21, 72	18.3	4
13	Characterization of segmental duplications and large inversions using Linked-Reads		4
12	An algorithmic analysis of the role of unequal crossover in alpha-satellite DNA evolution. <i>Genome Informatics</i> , 2002 , 13, 93-102		4
11	Robustness of Massively Parallel Sequencing Platforms. <i>PLoS ONE</i> , 2015 , 10, e0138259	3.7	3
10	Fast and accurate mapping of Complete Genomics reads. <i>Methods</i> , 2015 , 79-80, 3-10	4.6	2
9	Whole-Genome Shotgun Sequence CNV Detection Using Read Depth. <i>Methods in Molecular Biology</i> , 2018 , 1833, 61-72	1.4	2
8	Characterizing microsatellite polymorphisms using assembly-based and mapping-based tools. <i>Turkish Journal of Biology</i> , 2019 , 43, 264-273	3.1	1
7	Discovery of tandem and interspersed segmental duplications using high throughput sequencing		1
6	LEAP: A Generalization of the Landau-Vishkin Algorithm with Custom Gap Penalties		1
5	Frequent Activating Mutations Of JAK-STAT Pathway Genes In Natural Killer Cell Lymphomas. <i>Blood</i> , 2013 , 122, 812-812	2.2	1
4	Fast characterization of segmental duplication structure in multiple genome assemblies.. <i>Algorithms for Molecular Biology</i> , 2022 , 17, 4	1.8	1
3	Can you Really Anonymize the Donors of Genomic Data in Today's Digital World?. <i>Lecture Notes in Computer Science</i> , 2016 , 237-244	0.9	
2	Genomics technologies to study structural variations in the grapevine genome. <i>BIO Web of Conferences</i> , 2016 , 7, 01016	0.4	
1	Evaluation of genome scaffolding tools using pooled clone sequencing. <i>Turkish Journal of Biology</i> , 2018 , 42, 471-476	3.1	