Can Alkan

List of Publications by Year
in descending order

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107 papers	56,415 citations	28242 55 h-index	29127 104 g-index
120 all docs	120 docs citations	120 times ranked	71889 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
3	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
4	A Hexanucleotide Repeat Expansion in C9ORF72 Is the Cause of Chromosome 9p21-Linked ALS-FTD. Neuron, 2011, 72, 257-268.	3.8	3,833
5	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	6.0	3,588
6	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
7	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. Science, 2012, 338, 222-226.	6.0	1,695
8	Genetic history of an archaic hominin group from Denisova Cave in Siberia. Nature, 2010, 468, 1053-1060.	13.7	1,537
9	Genome structural variation discovery and genotyping. Nature Reviews Genetics, 2011, 12, 363-376.	7.7	1,240
10	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991
11	Mapping and sequencing of structural variation from eight human genomes. Nature, 2008, 453, 56-64.	13.7	983
12	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	13.7	768
13	Limitations of next-generation genome sequence assembly. Nature Methods, 2011, 8, 61-65.	9.0	685
14	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	13.7	663
15	Personalized copy number and segmental duplication maps using next-generation sequencing. Nature Genetics, 2009, 41, 1061-1067.	9.4	656
16	Diversity of Human Copy Number Variation and Multicopy Genes. Science, 2010, 330, 641-646.	6.0	609
17	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	13.7	541
18	Genome Sequencing Highlights the Dynamic Early History of Dogs. PLoS Genetics, 2014, 10, e1004016.	1.5	481

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19	Sequence and structural variation in a human genome uncovered by short-read, massively parallel ligation sequencing using two-base encoding. Genome Research, 2009, 19, 1527-1541.	2.4	448
20	The bonobo genome compared with the chimpanzee and human genomes. Nature, 2012, 486, 527-531.	13.7	445
21	Complete Khoisan and Bantu genomes from southern Africa. Nature, 2010, 463, 943-947.	13.7	400
22	Activating mutations of STAT5B and STAT3 in lymphomas derived from Î³Î´-T or NK cells. Nature Communications, 2015, 6, 6025.	5.8	334
23	Comparative analysis of the domestic cat genome reveals genetic signatures underlying feline biology and domestication. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17230-17235.	3.3	281
24	Refinement and Discovery of New Hotspots of Copy-Number Variation Associated with Autism Spectrum Disorder. American Journal of Human Genetics, 2013, 92, 221-237.	2.6	279
25	Combinatorial algorithms for structural variation detection in high-throughput sequenced genomes. Genome Research, 2009, 19, 1270-1278.	2.4	266
26	Copy number variation of individual cattle genomes using next-generation sequencing. Genome Research, 2012, 22, 778-790.	2.4	259
27	mrsFAST: a cache-oblivious algorithm for short-read mapping. Nature Methods, 2010, 7, 576-577.	9.0	248
28	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	9.4	233
29	A burst of segmental duplications in the genome of the African great ape ancestor. Nature, 2009, 457, 877-881.	13.7	222
30	Reconstructing complex regions of genomes using long-read sequencing technology. Genome Research, 2014, 24, 688-696.	2.4	222
31	Haplotype-resolved genome sequencing of a Gujarati Indian individual. Nature Biotechnology, 2011, 29, 59-63.	9.4	216
32	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	3.2	207
33	Next-generation VariationHunter: combinatorial algorithms for transposon insertion discovery. Bioinformatics, 2010, 26, i350-i357.	1.8	190
34	The structure and evolution of centromeric transition regions within the human genome. Nature, 2004, 430, 857-864.	13.7	179
35	Characterization of missing human genome sequences and copy-number polymorphic insertions. Nature Methods, 2010, 7, 365-371.	9.0	138
36	Nanopore sequencing technology and tools for genome assembly: computational analysis of the current state, bottlenecks and future directions. Briefings in Bioinformatics, 2019, 20, 1542-1559.	3.2	137

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37	SCALCE: boosting sequence compression algorithms using locally consistent encoding. Bioinformatics, 2012, 28, 3051-3057.	1.8	129
38	Analysis of Primate Genomic Variation Reveals a Repeat-Driven Expansion of the Human Genome. Genome Research, 2003, 13, 358-368.	2.4	127
39	MoDIL: detecting small indels from clone-end sequencing with mixtures of distributions. Nature Methods, 2009, 6, 473-474.	9.0	115
40	Detection of structural variants and indels within exome data. Nature Methods, 2012, 9, 176-178.	9.0	109
41	RNAâ€“RNA Interaction Prediction and Antisense RNA Target Search. Journal of Computational Biology, 2006, 13, 267-282.	0.8	106
42	Realizing the potential of blockchain technologies in genomics. Genome Research, 2018, 28, 1255-1263.	2.4	101
43	Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. Bioinformatics, 2010, 26, 1277-1283.	1.8	98
44	Alu repeat discovery and characterization within human genomes. Genome Research, 2011, 21, 840-849.	2.4	94
45	Death and Resurrection of the Human IRGM Gene. PLoS Genetics, 2009, 5, e1000403.	1.5	93
46	GRIM-Filter: Fast seed location filtering in DNA read mapping using processing-in-memory technologies. BMC Genomics, 2018, 19, 89.	1.2	92
47	A large and complex structural polymorphism at 16p12.1 underlies microdeletion disease risk. Nature Genetics, 2010, 42, 745-750.	9.4	89
48	Organization and Evolution of Primate Centromeric DNA from Whole-Genome Shotgun Sequence Data. PLoS Computational Biology, 2007, 3, e181.	1.5	80
49	Identification and validation of a novel mature microRNA encoded by the Merkel cell polyomavirus in human Merkel cell carcinomas. Journal of Clinical Virology, 2011, 52, 272-275.	1.6	80
50	Accelerating read mapping with FastHASH. BMC Genomics, 2013, 14, S13.	1.2	79
51	Genome-wide characterization of centromeric satellites from multiple mammalian genomes. Genome Research, 2011, 21, 137-145.	2.4	78
52	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. PLoS Genetics, 2016, 12, e1005851.	1.5	77
53	Extreme selective sweeps independently targeted the X chromosomes of the great apes. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 6413-6418.	3.3	75
54	Comparative analysis of Alu repeats in primate genomes. Genome Research, 2009, 19, 876-885.	2.4	71

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55	GateKeeper: a new hardware architecture for accelerating pre-alignment in DNA short read mapping. Bioinformatics, 2017, 33, 3355-3363.	1.8	67
56	Gorilla genome structural variation reveals evolutionary parallelisms with chimpanzee. Genome Research, 2011, 21, 1640-1649.	2.4	65
57	Rates and patterns of great ape retrotransposition. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 13457-13462.	3.3	57
58	Fast characterization of segmental duplications in genome assemblies. Bioinformatics, 2018, 34, i706-i714.	1.8	55
59	mrsFAST-Ultra: a compact, SNP-aware mapper for high performance sequencing applications. Nucleic Acids Research, 2014, 42, W494-W500.	6.5	54
60	Shifted Hamming distance: a fast and accurate SIMD-friendly filter to accelerate alignment verification in read mapping. Bioinformatics, 2015, 31, 1553-1560.	1.8	54
61	Technology dictates algorithms: recent developments in read alignment. Genome Biology, 2021, 22, 249.	3.8	51
62	Targeting PLK1 overcomes T-DM1 resistance via CDK1-dependent phosphorylation and inactivation of Bcl-2/xL in HER2-positive breast cancer. Oncogene, 2018, 37, 2251-2269.	2.6	49
63	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. BMC Genomics, 2013, 14, 363.	1.2	48
64	Whole genome sequencing of Turkish genomes reveals functional private alleles and impact of genetic interactions with Europe, Asia and Africa. BMC Genomics, 2014, 15, 963.	1.2	46
65	New Insights into Centromere Organization and Evolution from the White-Cheeked Gibbon and Marmoset. Molecular Biology and Evolution, 2009, 26, 1889-1900.	3.5	45
66	Interâ€varietal structural variation in grapevine genomes. Plant Journal, 2016, 88, 648-661.	2.8	45
67	Shouji: a fast and efficient pre-alignment filter for sequence alignment. Bioinformatics, 2019, 35, 4255-4263.	1.8	44
68	Early postzygotic mutations contribute to de novo variation in a healthy monozygotic twin pair. Journal of Medical Genetics, 2014, 51, 455-459.	1.5	42
69	Accelerating Genome Analysis: A Primer on an Ongoing Journey. IEEE Micro, 2020, 40, 65-75.	1.8	41
70	GenASM: A High-Performance, Low-Power Approximate String Matching Acceleration Framework for Genome Sequence Analysis. , 2020, , .		37
71	On genomic repeats and reproducibility. Bioinformatics, 2016, 32, 2243-2247.	1.8	33
72	Annotated features of domestic cat â€“ Felis catus genome. GigaScience, 2014, 3, 13.	3.3	30

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73	Discovery and genotyping of novel sequence insertions in many sequenced individuals. Bioinformatics, 2017, 33, i161-i169.	1.8	29
74	Discovery of tandem and interspersed segmental duplications using high-throughput sequencing. Bioinformatics, 2019, 35, 3923-3930.	1.8	29
75	Toolkit for automated and rapid discovery of structural variants. Methods, 2017, 129, 3-7.	1.9	28
76	Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm. Bioinformatics, 2020, 36, 3669-3679.	1.8	26
77	Divergent Origins and Concerted Expansion of Two Segmental Duplications on Chromosome 16. Journal of Heredity, 2001, 92, 462-468.	1.0	25
78	Optimal design of oligonucleotide microarrays for measurement of DNA copy-number. Human Molecular Genetics, 2007, 16, 2770-2779.	1.4	25
79	Hercules: a profile HMM-based hybrid error correction algorithm for long reads. Nucleic Acids Research, 2018, 46, e125.	6.5	23
80	Optimal seed solver: optimizing seed selection in read mapping. Bioinformatics, 2016, 32, 1632-1642.	1.8	21
81	The Role of Unequal Crossover in Alpha-Satellite DNA Evolution: A Computational Analysis. Journal of Computational Biology, 2004, 11, 933-944.	0.8	20
82	SneakySnake: a fast and accurate universal genome pre-alignment filter for CPUs, GPUs and FPGAs. Bioinformatics, 2021, 36, 5282-5290.	1.8	19
83	Clcn4-2 genomic structure differs between the X locus in Mus spretus and the autosomal locus in Mus musculus: AT motif enrichment on the X. Genome Research, 2011, 21, 402-409.	2.4	18
84	Discovery of large genomic inversions using long range information. BMC Genomics, 2017, 18, 65.	1.2	18
85	Determining the origin of synchronous multifocal bladder cancer by exome sequencing. BMC Cancer, 2015, 15, 871.	1.1	17
86	Sensitive and fast mapping of di-base encoded reads. Bioinformatics, 2011, 27, 1915-1921.	1.8	16
87	VALOR2: characterization of large-scale structural variants using linked-reads. Genome Biology, 2020, 21, 72.	3.8	15
88	taveRNA: a web suite for RNA algorithms and applications. Nucleic Acids Research, 2007, 35, W325-W329.	6.5	14
89	Fast characterization of segmental duplication structure in multiple genome assemblies. Algorithms for Molecular Biology, 2022, 17, 4.	0.3	10
90	RNA Secondary Structure Prediction Via Energy Density Minimization. Lecture Notes in Computer Science, 2006, , 130-142.	1.0	9

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91	Building and Improving Reference Genome Assemblies. Proceedings of the IEEE, 2017, , 1-14.	16.4	6
92	Manipulating multiple sequence alignments via MaM and WebMaM. Nucleic Acids Research, 2005, 33, W295-W298.	6.5	5
93	Fast and accurate mapping of Complete Genomics reads. Methods, 2015, 79-80, 3-10.	1.9	5
94	GateKeeper-GPU: Fast and Accurate Pre-Alignment Filtering in Short Read Mapping. , 2021, , .		5
95	Polishing copy number variant calls on exome sequencing data via deep learning. Genome Research, 2022, 32, 1170-1182.	2.4	5
96	Whole-Genome Shotgun Sequence CNV Detection Using Read Depth. Methods in Molecular Biology, 2018, 1833, 61-72.	0.4	4
97	An algorithmic analysis of the role of unequal crossover in alpha-satellite DNA evolution. Genome Informatics, 2002, 13, 93-102.	0.4	4
98	Robustness of Massively Parallel Sequencing Platforms. PLoS ONE, 2015, 10, e0138259.	1.1	3
99	Combinatorial Algorithms for Structural Variation Detection in High Throughput Sequenced Genomes. Lecture Notes in Computer Science, 2009, , 218-219.	1.0	3
100	Automatic characterization of copy number polymorphism using high throughput sequencing. Turkish Journal of Electrical Engineering and Computer Sciences, 2020, 28, 253-261.	0.9	2
101	Characterizing microsatellite polymorphisms using assembly-based and mapping-based tools. Turkish Journal of Biology, 2019, 43, 264-273.	2.1	1
102	Frequent Activating Mutations Of JAK-STAT Pathway Genes In Natural Killer Cell Lymphomas. Blood, 2013, 122, 812-812.	0.6	1
103	Can you Really Anonymize the Donors of Genomic Data in Todayâ€™s Digital World?. Lecture Notes in Computer Science, 2016, , 237-244.	1.0	1
104	Genomics technologies to study structural variations in the grapevine genome. BIO Web of Conferences, 2016, 7, 01016.	0.1	0
105	Evaluation of genome scaffolding tools using pooled clone sequencing. Turkish Journal of Biology, 2018, 42, 471-476.	2.1	0
106	PERSONAL GENOMICS â€“ Session Introduction. , 2009, , 302-304.		0
107	Abstract 2848: Identifying and targeting competing endogenous RNA (ceRNAs) networks to inhibit lung metastasis in triple negative breast cancer. , 2017, , .		0