Can Alkan

List of Publications by Year
in descending order

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		32410	33145
107	56,415	55	104
papers	citations	h-index	g-index

120	120	120	79154
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Fast characterization of segmental duplication structure in multiple genome assemblies. Algorithms for Molecular Biology, 2022, 17, 4.	0.3	10
2	Polishing copy number variant calls on exome sequencing data via deep learning. Genome Research, 2022, 32, 1170-1182.	2.4	5
3	SneakySnake: a fast and accurate universal genome pre-alignment filter for CPUs, GPUs and FPGAs. Bioinformatics, 2021, 36, 5282-5290.	1.8	19
4	GateKeeper-GPU: Fast and Accurate Pre-Alignment Filtering in Short Read Mapping. , 2021, , .		5
5	Technology dictates algorithms: recent developments in read alignment. Genome Biology, 2021, 22, 249.	3.8	51
6	Accelerating Genome Analysis: A Primer on an Ongoing Journey. IEEE Micro, 2020, 40, 65-75.	1.8	41
7	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	9.4	233
8	Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm. Bioinformatics, 2020, 36, 3669-3679.	1.8	26
9	VALOR2: characterization of large-scale structural variants using linked-reads. Genome Biology, 2020, 21, 72.	3.8	15
10	GenASM: A High-Performance, Low-Power Approximate String Matching Acceleration Framework for Genome Sequence Analysis. , 2020, , .		37
11	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
12	Characterizing microsatellite polymorphisms using assembly-based and mapping-based tools. Turkish Journal of Biology, 2019, 43, 264-273.	2.1	1
13	Shouji: a fast and efficient pre-alignment filter for sequence alignment. Bioinformatics, 2019, 35, 4255-4263.	1.8	44
14	Discovery of tandem and interspersed segmental duplications using high-throughput sequencing. Bioinformatics, 2019, 35, 3923-3930.	1.8	29
15	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
16	Computational pan-genomics: status, promises and challenges. Briefings in Bioinformatics, 2018, 19, bbw089.	3.2	207
17	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
18	Evaluation of genome scaffolding tools using pooled clone sequencing. Turkish Journal of Biology, 2018, 42, 471-476.	2.1	0

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19	Fast characterization of segmental duplications in genome assemblies. Bioinformatics, 2018, 34, i706-i714.	1.8	55
20	Hercules: a profile HMM-based hybrid error correction algorithm for long reads. Nucleic Acids Research, 2018, 46, e125.	6.5	23
21	Realizing the potential of blockchain technologies in genomics. Genome Research, 2018, 28, 1255-1263.	2.4	101
22	Whole-Genome Shotgun Sequence CNV Detection Using Read Depth. Methods in Molecular Biology, 2018, 1833, 61-72.	0.4	4
23	GRIM-Filter: Fast seed location filtering in DNA read mapping using processing-in-memory technologies. BMC Genomics, 2018, 19, 89.	1.2	92
24	Building and Improving Reference Genome Assemblies. Proceedings of the IEEE, 2017, , 1-14.	16.4	6
25	Toolkit for automated and rapid discovery of structural variants. Methods, 2017, 129, 3-7.	1.9	28
26	GateKeeper: a new hardware architecture for accelerating pre-alignment in DNA short read mapping. Bioinformatics, 2017, 33, 3355-3363.	1.8	67
27	Discovery of large genomic inversions using long range information. BMC Genomics, 2017, 18, 65.	1.2	18
28	Discovery and genotyping of novel sequence insertions in many sequenced individuals. Bioinformatics, 2017, 33, i161-i169.	1.8	29
29	Abstract 2848: Identifying and targeting competing endogenous RNA (ceRNAs) networks to inhibit lung metastasis in triple negative breast cancer. , 2017, , .		0
30	Genomics technologies to study structural variations in the grapevine genome. BIO Web of Conferences, 2016, 7, 01016.	0.1	0
31	Interâ€varietal structural variation in grapevine genomes. Plant Journal, 2016, 88, 648-661.	2.8	45
32	On genomic repeats and reproducibility. Bioinformatics, 2016, 32, 2243-2247.	1.8	33
33	Optimal seed solver: optimizing seed selection in read mapping. Bioinformatics, 2016, 32, 1632-1642.	1.8	21
34	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. PLoS Genetics, 2016, 12, e1005851.	1.5	77
35	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
36	Determining the origin of synchronous multifocal bladder cancer by exome sequencing. BMC Cancer, 2015, 15, 871.	1.1	17

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37	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
38	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
39	Activating mutations of STAT5B and STAT3 in lymphomas derived from Î³Î´-T or NK cells. Nature Communications, 2015, 6, 6025.	5.8	334
40	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
41	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
42	Fast and accurate mapping of Complete Genomics reads. Methods, 2015, 79-80, 3-10.	1.9	5
43	Robustness of Massively Parallel Sequencing Platforms. PLoS ONE, 2015, 10, e0138259.	1.1	3
44	mrsFAST-Ultra: a compact, SNP-aware mapper for high performance sequencing applications. Nucleic Acids Research, 2014, 42, W494-W500.	6.5	54
45	Genome Sequencing Highlights the Dynamic Early History of Dogs. PLoS Genetics, 2014, 10, e1004016.	1.5	481
46	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
47	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
48	Reconstructing complex regions of genomes using long-read sequencing technology. Genome Research, 2014, 24, 688-696.	2.4	222
49	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
50	Annotated features of domestic cat â€“ Felis catus genome. GigaScience, 2014, 3, 13.	3.3	30
51	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. BMC Genomics, 2013, 14, 363.	1.2	48
52	Accelerating read mapping with FastHASH. BMC Genomics, 2013, 14, S13.	1.2	79
53	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
54	Great ape genetic diversity and population history. Nature, 2013, 499, 471-475.	13.7	768

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55	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
56	Frequent Activating Mutations Of JAK-STAT Pathway Genes In Natural Killer Cell Lymphomas. Blood, 2013, 122, 812-812.	0.6	1
57	Detection of structural variants and indels within exome data. Nature Methods, 2012, 9, 176-178.	9.0	109
58	SCALCE: boosting sequence compression algorithms using locally consistent encoding. Bioinformatics, 2012, 28, 3051-3057.	1.8	129
59	A High-Coverage Genome Sequence from an Archaic Denisovan Individual. Science, 2012, 338, 222-226.	6.0	1,695
60	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
61	Copy number variation of individual cattle genomes using next-generation sequencing. Genome Research, 2012, 22, 778-790.	2.4	259
62	The bonobo genome compared with the chimpanzee and human genomes. Nature, 2012, 486, 527-531.	13.7	445
63	Insights into hominid evolution from the gorilla genome sequence. Nature, 2012, 483, 169-175.	13.7	663
64	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
65	A Hexanucleotide Repeat Expansion in C9ORF72 Is the Cause of Chromosome 9p21-Linked ALS-FTD. Neuron, 2011, 72, 257-268.	3.8	3,833
66	Limitations of next-generation genome sequence assembly. Nature Methods, 2011, 8, 61-65.	9.0	685
67	Genome structural variation discovery and genotyping. Nature Reviews Genetics, 2011, 12, 363-376.	7.7	1,240
68	Comparative and demographic analysis of orang-utan genomes. Nature, 2011, 469, 529-533.	13.7	541
69	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991
70	Haplotype-resolved genome sequencing of a Gujarati Indian individual. Nature Biotechnology, 2011, 29, 59-63.	9.4	216
71	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
72	Alu repeat discovery and characterization within human genomes. Genome Research, 2011, 21, 840-849.	2.4	94

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73	Genome-wide characterization of centromeric satellites from multiple mammalian genomes. Genome Research, 2011, 21, 137-145.	2.4	78
74	Gorilla genome structural variation reveals evolutionary parallelisms with chimpanzee. Genome Research, 2011, 21, 1640-1649.	2.4	65
75	Sensitive and fast mapping of di-base encoded reads. Bioinformatics, 2011, 27, 1915-1921.	1.8	16
76	A Draft Sequence of the Neandertal Genome. Science, 2010, 328, 710-722.	6.0	3,588
77	Diversity of Human Copy Number Variation and Multicopy Genes. Science, 2010, 330, 641-646.	6.0	609
78	Complete Khoisan and Bantu genomes from southern Africa. Nature, 2010, 463, 943-947.	13.7	400
79	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
80	Genetic history of an archaic hominin group from Denisova Cave in Siberia. Nature, 2010, 468, 1053-1060.	13.7	1,537
81	A large and complex structural polymorphism at 16p12.1 underlies microdeletion disease risk. Nature Genetics, 2010, 42, 745-750.	9.4	89
82	Characterization of missing human genome sequences and copy-number polymorphic insertions. Nature Methods, 2010, 7, 365-371.	9.0	138
83	mrsFAST: a cache-oblivious algorithm for short-read mapping. Nature Methods, 2010, 7, 576-577.	9.0	248
84	Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. Bioinformatics, 2010, 26, 1277-1283.	1.8	98
85	Next-generation VariationHunter: combinatorial algorithms for transposon insertion discovery. Bioinformatics, 2010, 26, i350-i357.	1.8	190
86	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
87	Death and Resurrection of the Human IRGM Gene. PLoS Genetics, 2009, 5, e1000403.	1.5	93
88	Comparative analysis of Alu repeats in primate genomes. Genome Research, 2009, 19, 876-885.	2.4	71
89	A burst of segmental duplications in the genome of the African great ape ancestor. Nature, 2009, 457, 877-881.	13.7	222
90	Personalized copy number and segmental duplication maps using next-generation sequencing. Nature Genetics, 2009, 41, 1061-1067.	9.4	656

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91	MoDIL: detecting small indels from clone-end sequencing with mixtures of distributions. Nature Methods, 2009, 6, 473-474.	9.0	115
92	Combinatorial algorithms for structural variation detection in high-throughput sequenced genomes. Genome Research, 2009, 19, 1270-1278.	2.4	266
93	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
94	Combinatorial Algorithms for Structural Variation Detection in High Throughput Sequenced Genomes. Lecture Notes in Computer Science, 2009, , 218-219.	1.0	3
95	PERSONAL GENOMICS â€“ Session Introduction. , 2009, , 302-304.		0
96	Mapping and sequencing of structural variation from eight human genomes. Nature, 2008, 453, 56-64.	13.7	983
97	Organization and Evolution of Primate Centromeric DNA from Whole-Genome Shotgun Sequence Data. PLoS Computational Biology, 2007, 3, e181.	1.5	80
98	Optimal design of oligonucleotide microarrays for measurement of DNA copy-number. Human Molecular Genetics, 2007, 16, 2770-2779.	1.4	25
99	taveRNA: a web suite for RNA algorithms and applications. Nucleic Acids Research, 2007, 35, W325-W329.	6.5	14
100	RNAâ€“RNA Interaction Prediction and Antisense RNA Target Search. Journal of Computational Biology, 2006, 13, 267-282.	0.8	106
101	RNA Secondary Structure Prediction Via Energy Density Minimization. Lecture Notes in Computer Science, 2006, , 130-142.	1.0	9
102	Manipulating multiple sequence alignments via MaM and WebMaM. Nucleic Acids Research, 2005, 33, W295-W298.	6.5	5
103	The Role of Unequal Crossover in Alpha-Satellite DNA Evolution: A Computational Analysis. Journal of Computational Biology, 2004, 11, 933-944.	0.8	20
104	The structure and evolution of centromeric transition regions within the human genome. Nature, 2004, 430, 857-864.	13.7	179
105	Analysis of Primate Genomic Variation Reveals a Repeat-Driven Expansion of the Human Genome. Genome Research, 2003, 13, 358-368.	2.4	127
106	An algorithmic analysis of the role of unequal crossover in alpha-satellite DNA evolution. Genome Informatics, 2002, 13, 93-102.	0.4	4
107	Divergent Origins and Concerted Expansion of Two Segmental Duplications on Chromosome 16. Journal of Heredity, 2001, 92, 462-468.	1.0	25