Can Alkan

List of Publications by Year in Descending Order

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	Fast characterization of segmental duplication structure in multiple genome assemblies.. *Algorithms for Molecular Biology*, **2022**, 17, 4	1.8	1
105	Technology dictates algorithms: recent developments in read alignment. *Genome Biology*, **2021**, 22, 249	18.3	7
104	A robust benchmark for detection of germline large deletions and insertions. *Nature Biotechnology*, **2020**, 38, 1347-1355	44.5	98
103	Apollo: a sequencing-technology-independent, scalable and accurate assembly polishing algorithm. *Bioinformatics*, **2020**, 36, 3669-3679	7.2	13
102	VALOR2: characterization of large-scale structural variants using linked-reads. *Genome Biology*, **2020**, 21, 72	18.3	4
101	GenASM: A High-Performance, Low-Power Approximate String Matching Acceleration Framework for Genome Sequence Analysis **2020**,		13
100	Accelerating Genome Analysis: A Primer on an Ongoing Journey. *IEEE Micro*, **2020**, 40, 65-75	1.8	17
99	SneakySnake: A Fast and Accurate Universal Genome Pre-Alignment Filter for CPUs, GPUs, and FPGAs. *Bioinformatics*, **2020**,	7.2	9
98	Characterizing microsatellite polymorphisms using assembly-based and mapping-based tools. *Turkish Journal of Biology*, **2019**, 43, 264-273	3.1	1
97	Shouji: a fast and efficient pre-alignment filter for sequence alignment. *Bioinformatics*, **2019**, 35, 4255-4263	7.2	20
96	Discovery of tandem and interspersed segmental duplications using high-throughput sequencing. *Bioinformatics*, **2019**, 35, 3923-3930	7.2	17
95	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	13.4	83
94	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	9.2	30
93	Computational pan-genomics: status, promises and challenges. *Briefings in Bioinformatics*, **2018**, 19, 118-135	13.4	130
92	Realizing the potential of blockchain technologies in genomics. *Genome Research*, **2018**, 28, 1255-1263	9.7	63
91	Whole-Genome Shotgun Sequence CNV Detection Using Read Depth. *Methods in Molecular Biology*, **2018**, 1833, 61-72	1.4	2
90	GRIM-Filter: Fast seed location filtering in DNA read mapping using processing-in-memory technologies. *BMC Genomics*, **2018**, 19, 89	4.5	55

89	Evaluation of genome scaffolding tools using pooled clone sequencing. *Turkish Journal of Biology*, **2018**, 42, 471-476	3.1	
88	Fast characterization of segmental duplications in genome assemblies. *Bioinformatics*, **2018**, 34, i706-i714	7.2	25
87	Hercules: a profile HMM-based hybrid error correction algorithm for long reads. *Nucleic Acids Research*, **2018**, 46, e125	20.1	13
86	Building and Improving Reference Genome Assemblies. *Proceedings of the IEEE*, **2017**, 1-14	14.3	4
85	Toolkit for automated and rapid discovery of structural variants. *Methods*, **2017**, 129, 3-7	4.6	16
84	GateKeeper: a new hardware architecture for accelerating pre-alignment in DNA short read mapping. *Bioinformatics*, **2017**, 33, 3355-3363	7.2	39
83	Discovery of large genomic inversions using long range information. *BMC Genomics*, **2017**, 18, 65	4.5	14
82	Discovery and genotyping of novel sequence insertions in many sequenced individuals. *Bioinformatics*, **2017**, 33, i161-i169	7.2	16
81	Inter-varietal structural variation in grapevine genomes. *Plant Journal*, **2016**, 88, 648-661	6.9	33
80	On genomic repeats and reproducibility. *Bioinformatics*, **2016**, 32, 2243-7	7.2	22
79	Optimal seed solver: optimizing seed selection in read mapping. *Bioinformatics*, **2016**, 32, 1632-42	7.2	14
78	Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. *PLoS Genetics*, **2016**, 12, e1005851	6	56
77	Can you Really Anonymize the Donors of Genomic Data in Today Digital World?. *Lecture Notes in Computer Science*, **2016**, 237-244	0.9	
76	Genomics technologies to study structural variations in the grapevine genome. *BIO Web of Conferences*, **2016**, 7, 01016	0.4	
75	A global reference for human genetic variation. *Nature*, **2015**, 526, 68-74	50.4	8599
74	An integrated map of structural variation in 2,504 human genomes. *Nature*, **2015**, 526, 75-81	50.4	1368
73	Fast and accurate mapping of Complete Genomics reads. *Methods*, **2015**, 79-80, 3-10	4.6	2
72	Determining the origin of synchronous multifocal bladder cancer by exome sequencing. *BMC Cancer*, **2015**, 15, 871	4.8	12

71	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, 6413-8	11.5	52
70	Shifted Hamming distance: a fast and accurate SIMD-friendly filter to accelerate alignment verification in read mapping. *Bioinformatics*, **2015**, 31, 1553-60	7.2	28
69	Activating mutations of STAT5B and STAT3 in lymphomas derived from ΒΤ or NK cells. *Nature Communications*, **2015**, 6, 6025	17.4	261
68	Robustness of Massively Parallel Sequencing Platforms. *PLoS ONE*, **2015**, 10, e0138259	3.7	3
67	Early postzygotic mutations contribute to de novo variation in a healthy monozygotic twin pair. *Journal of Medical Genetics*, **2014**, 51, 455-9	5.8	35
66	Reconstructing complex regions of genomes using long-read sequencing technology. *Genome Research*, **2014**, 24, 688-96	9.7	188
65	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, 17230-5	11.5	184
64	Annotated features of domestic cat - Felis catus genome. *GigaScience*, **2014**, 3, 13	7.6	26
63	mrsFAST-Ultra: a compact, SNP-aware mapper for high performance sequencing applications. *Nucleic Acids Research*, **2014**, 42, W494-500	20.1	41
62	Genome sequencing highlights the dynamic early history of dogs. *PLoS Genetics*, **2014**, 10, e1004016	6	372
61	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	4.5	33
60	The genome sequencing of an albino Western lowland gorilla reveals inbreeding in the wild. *BMC Genomics*, **2013**, 14, 363	4.5	30
59	Accelerating read mapping with FastHASH. *BMC Genomics*, **2013**, 14 Suppl 1, S13	4.5	53
58	Rates and patterns of great ape retrotransposition. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 13457-62	11.5	46
57	Great ape genetic diversity and population history. *Nature*, **2013**, 499, 471-5	50.4	574
56	Refinement and discovery of new hotspots of copy-number variation associated with autism spectrum disorder. *American Journal of Human Genetics*, **2013**, 92, 221-37	11	214
55	Frequent Activating Mutations Of JAK-STAT Pathway Genes In Natural Killer Cell Lymphomas. *Blood*, **2013**, 122, 812-812	2.2	1
54	A high-coverage genome sequence from an archaic Denisovan individual. *Science*, **2012**, 338, 222-6	33.3	1276

53	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
52	Copy number variation of individual cattle genomes using next-generation sequencing. *Genome Research*, **2012**, 22, 778-90	9.7	204
51	The bonobo genome compared with the chimpanzee and human genomes. *Nature*, **2012**, 486, 527-31	50.4	350
50	Insights into hominid evolution from the gorilla genome sequence. *Nature*, **2012**, 483, 169-75	50.4	517
49	SCALCE: boosting sequence compression algorithms using locally consistent encoding. *Bioinformatics*, **2012**, 28, 3051-7	7.2	89
48	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, 272-5	14.5	67
47	A hexanucleotide repeat expansion in C9ORF72 is the cause of chromosome 9p21-linked ALS-FTD. *Neuron*, **2011**, 72, 257-68	13.9	3018
46	Limitations of next-generation genome sequence assembly. *Nature Methods*, **2011**, 8, 61-5	21.6	503
45	Genome structural variation discovery and genotyping. *Nature Reviews Genetics*, **2011**, 12, 363-76	30.1	947
44	Comparative and demographic analysis of orang-utan genomes. *Nature*, **2011**, 469, 529-33	50.4	431
43	Mapping copy number variation by population-scale genome sequencing. *Nature*, **2011**, 470, 59-65	50.4	833
42	Haplotype-resolved genome sequencing of a Gujarati Indian individual. *Nature Biotechnology*, **2011**, 29, 59-63	44.5	194
41	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, 402-9	9.7	12
40	Alu repeat discovery and characterization within human genomes. *Genome Research*, **2011**, 21, 840-9	9.7	84
39	Genome-wide characterization of centromeric satellites from multiple mammalian genomes. *Genome Research*, **2011**, 21, 137-45	9.7	59
38	Gorilla genome structural variation reveals evolutionary parallelisms with chimpanzee. *Genome Research*, **2011**, 21, 1640-9	9.7	56
37	Sensitive and fast mapping of di-base encoded reads. *Bioinformatics*, **2011**, 27, 1915-21	7.2	16
36	Detection of structural variants and indels within exome data. *Nature Methods*, **2011**, 9, 176-8	21.6	93

35	Complete Khoisan and Bantu genomes from southern Africa. *Nature*, **2010**, 463, 943-7	50.4	342
34	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142
33	Genetic history of an archaic hominin group from Denisova Cave in Siberia. *Nature*, **2010**, 468, 1053-60	50.4	1169
32	A large and complex structural polymorphism at 16p12.1 underlies microdeletion disease risk. *Nature Genetics*, **2010**, 42, 745-50	36.3	81
31	Characterization of missing human genome sequences and copy-number polymorphic insertions. *Nature Methods*, **2010**, 7, 365-71	21.6	114
30	mrsFAST: a cache-oblivious algorithm for short-read mapping. *Nature Methods*, **2010**, 7, 576-7	21.6	216
29	Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. *Bioinformatics*, **2010**, 26, 1277-83	7.2	84
28	Next-generation VariationHunter: combinatorial algorithms for transposon insertion discovery. *Bioinformatics*, **2010**, 26, i350-7	7.2	161
27	A draft sequence of the Neandertal genome. *Science*, **2010**, 328, 710-722	33.3	2599
26	Diversity of human copy number variation and multicopy genes. *Science*, **2010**, 330, 641-6	33.3	491
25	New insights into centromere organization and evolution from the white-cheeked gibbon and marmoset. *Molecular Biology and Evolution*, **2009**, 26, 1889-900	8.3	37
24	Death and resurrection of the human IRGM gene. *PLoS Genetics*, **2009**, 5, e1000403	6	75
23	Comparative analysis of Alu repeats in primate genomes. *Genome Research*, **2009**, 19, 876-85	9.7	55
22	A burst of segmental duplications in the genome of the African great ape ancestor. *Nature*, **2009**, 457, 877-81	50.4	179
21	Personalized copy number and segmental duplication maps using next-generation sequencing. *Nature Genetics*, **2009**, 41, 1061-7	36.3	543
20	MoDIL: detecting small indels from clone-end sequencing with mixtures of distributions. *Nature Methods*, **2009**, 6, 473-4	21.6	103
19	Combinatorial algorithms for structural variation detection in high-throughput sequenced genomes. *Genome Research*, **2009**, 19, 1270-8	9.7	230
18	Sequence and structural variation in a human genome uncovered by short-read, massively parallel ligation sequencing using two-base encoding. *Genome Research*, **2009**, 19, 1527-41	9.7	401

17	Mapping and sequencing of structural variation from eight human genomes. *Nature*, **2008**, 453, 56-64	50.4	878
16	Organization and evolution of primate centromeric DNA from whole-genome shotgun sequence data. *PLoS Computational Biology*, **2007**, 3, 1807-18	5	66
15	Optimal design of oligonucleotide microarrays for measurement of DNA copy-number. *Human Molecular Genetics*, **2007**, 16, 2770-9	5.6	23
14	taveRNA: a web suite for RNA algorithms and applications. *Nucleic Acids Research*, **2007**, 35, W325-9	20.1	14
13	RNA-RNA interaction prediction and antisense RNA target search. *Journal of Computational Biology*, **2006**, 13, 267-82	1.7	93
12	RNA Secondary Structure Prediction Via Energy Density Minimization. *Lecture Notes in Computer Science*, **2006**, 130-142	0.9	7
11	Manipulating multiple sequence alignments via MaM and WebMaM. *Nucleic Acids Research*, **2005**, 33, W295-8	20.1	5
10	The role of unequal crossover in alpha-satellite DNA evolution: a computational analysis. *Journal of Computational Biology*, **2004**, 11, 933-44	1.7	17
9	The structure and evolution of centromeric transition regions within the human genome. *Nature*, **2004**, 430, 857-64	50.4	160
8	Analysis of primate genomic variation reveals a repeat-driven expansion of the human genome. *Genome Research*, **2003**, 13, 358-68	9.7	101
7	An algorithmic analysis of the role of unequal crossover in alpha-satellite DNA evolution. *Genome Informatics*, **2002**, 13, 93-102		4
6	Divergent origins and concerted expansion of two segmental duplications on chromosome 16. *Journal of Heredity*, **2001**, 92, 462-8	2.4	22
5	Discovery of tandem and interspersed segmental duplications using high throughput sequencing		1
4	Computational Pan-Genomics: Status, Promises and Challenges		6
3	LEAP: A Generalization of the Landau-Vishkin Algorithm with Custom Gap Penalties		1
2	Characterization of segmental duplications and large inversions using Linked-Reads		4
1	A robust benchmark for germline structural variant detection		34