

Gary Benson

List of Publications by Year in descending order

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35
papers

8,629
citations

393982

19
h-index

414034

32
g-index

37
all docs

37
docs citations

37
times ranked

14419
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide characterization of human minisatellite VNTRs: population-specific alleles and gene expression differences. <i>Nucleic Acids Research</i> , 2021, 49, 4308-4324.	6.5	15
2	Sleep-wake disorders in Alzheimer's disease: further genetic analyses in relation to objective sleep measures. <i>International Psychogeriatrics</i> , 2020, 32, 807-813.	0.6	6
3	An SIMD Algorithm for Wraparound Tandem Alignment. <i>Lecture Notes in Computer Science</i> , 2017, , 140-149.	1.0	2
4	BitPAL: a bit-parallel, general integer-scoring sequence alignment algorithm. <i>Bioinformatics</i> , 2014, 30, 3166-3173.	1.8	24
5	VNTRseek—a computational tool to detect tandem repeat variants in high-throughput sequencing data. <i>Nucleic Acids Research</i> , 2014, 42, 8884-8894.	6.5	39
6	A Bit-Parallel, General Integer-Scoring Sequence Alignment Algorithm. <i>Lecture Notes in Computer Science</i> , 2013, , 50-61.	1.0	7
7	Mining poly-regions in DNA. <i>International Journal of Data Mining and Bioinformatics</i> , 2012, 6, 406.	0.1	5
8	Targeted analysis of glycomics liquid chromatography/mass spectrometry data. <i>Analytical and Bioanalytical Chemistry</i> , 2011, 399, 727-735.	1.9	19
9	The distribution of inverted repeat sequences in the <i>Saccharomyces cerevisiae</i> genome. <i>Current Genetics</i> , 2010, 56, 321-340.	0.8	27
10	Mutations in the Hepatitis C Virus <i>core</i> Gene Are Associated with Advanced Liver Disease and Hepatocellular Carcinoma. <i>Clinical Cancer Research</i> , 2009, 15, 3205-3213.	3.2	67
11	All hits all the time: parameter-free calculation of spaced seed sensitivity. <i>Bioinformatics</i> , 2009, 25, 302-308.	1.8	11
12	Pattern matching with address errors: Rearrangement distances. <i>Journal of Computer and System Sciences</i> , 2009, 75, 359-370.	0.9	22
13	Evolutionary History of Mammalian Transposons Determined by Genome-Wide Defragmentation. <i>PLoS Computational Biology</i> , 2007, 3, e137.	1.5	124
14	TRDB--The Tandem Repeats Database. <i>Nucleic Acids Research</i> , 2007, 35, D80-D87.	6.5	174
15	Elevated Basal Slippage Mutation Rates among the Canidae. <i>Journal of Heredity</i> , 2007, 98, 452-460.	1.0	31
16	ALL HITS ALL THE TIME: PARAMETER FREE CALCULATION OF SEED SENSITIVITY. , 2007, , .		4
17	Discovering Frequent Poly-Regions in DNA Sequences. , 2006, , .		8
18	Tandem cyclic alignment. <i>Discrete Applied Mathematics</i> , 2005, 146, 124-133.	0.5	9

#	ARTICLE	IF	CITATIONS
19	Evaluating distance functions for clustering tandem repeats. <i>Genome Informatics</i> , 2005, 16, 3-12.	0.4	5
20	Inverted Repeat Structure of the Human Genome: The X-Chromosome Contains a Preponderance of Large, Highly Homologous Inverted Repeats That Contain Testes Genes. <i>Genome Research</i> , 2004, 14, 1861-1869.	2.4	237
21	Minimal entropy probability paths between genome families. <i>Journal of Mathematical Biology</i> , 2004, 48, 563-590.	0.8	1
22	Predicting Human Minisatellite Polymorphism. <i>Genome Research</i> , 2003, 13, 856-867.	2.4	43
23	A new distance measure for comparing sequence profiles based on path lengths along an entropy surface. <i>Bioinformatics</i> , 2002, 18, S44-S53.	1.8	14
24	Mutation Master: Profiles of substitutions in hepatitis C virus RNA of the core, alternate reading frame, and NS2 coding regions. <i>Rna</i> , 2002, 8, 557-571.	1.6	41
25	Replication and compartmentalization of HIV-1 in kidney epithelium of patients with HIV-associated nephropathy. <i>Nature Medicine</i> , 2002, 8, 522-526.	15.2	286
26	A tandem repeats database for bacterial genomes: application to the genotyping of <i>Yersinia pestis</i> and <i>Bacillus anthracis</i> . <i>BMC Microbiology</i> , 2001, 1, 2.	1.3	222
27	Tandem repeats finder: a program to analyze DNA sequences. <i>Nucleic Acids Research</i> , 1999, 27, 573-580.	6.5	6,803
28	Optimal Parallel Two Dimensional Text Searching on a CREW PRAM. <i>Information and Computation</i> , 1998, 144, 1-17.	0.5	14
29	On the Distribution of K-tuple Matches for Sequence Homology: A Constant Time Exact Calculation of the Variance. <i>Journal of Computational Biology</i> , 1998, 5, 87-100.	0.8	12
30	Pooling Strategies for Establishing Physical Genome Maps Using FISH. <i>Journal of Computational Biology</i> , 1997, 4, 467-486.	0.8	0
31	Sequence Alignment with Tandem Duplication. <i>Journal of Computational Biology</i> , 1997, 4, 351-367.	0.8	51
32	Optimal Two-Dimensional Compressed Matching. <i>Journal of Algorithms</i> , 1997, 24, 354-379.	0.9	22
33	Let Sleeping Files Lie: Pattern Matching in Z-Compressed Files. <i>Journal of Computer and System Sciences</i> , 1996, 52, 299-307.	0.9	136
34	A method for fast database search for allk-nucleotide repeats. <i>Nucleic Acids Research</i> , 1994, 22, 4828-4836.	6.5	70
35	An Alphabet Independent Approach to Two-Dimensional Pattern Matching. <i>SIAM Journal on Computing</i> , 1994, 23, 313-323.	0.8	77