

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Compositional Structure of the Genome: A Review. <i>Biology</i> , 2023, 12, 849.	2.9	3
2	Functional characterization of the tomato <i>HAIRPLUS</i> gene reveals the implication of the epigenome in the control of glandular trichome formation. <i>Horticulture Research</i> , 2022, 9, .	6.5	5
3	Decoding Gene Expression Signatures Underlying Vegetative to Inflorescence Meristem Transition in the Common Bean. <i>International Journal of Molecular Sciences</i> , 2022, 23, 14783.	4.2	1
4	Driven progressive evolution of genome sequence complexity in Cyanobacteria. <i>Scientific Reports</i> , 2020, 10, 19073.	3.4	7
5	Transcriptional Dynamics and Candidate Genes Involved in Pod Maturation of Common Bean (<i>Phaseolus vulgaris</i> L.). <i>Plants</i> , 2020, 9, 545.	3.6	5
6	Prediction of CpG Islands as an Intrinsic Clustering Property Found in Many Eukaryotic DNA Sequences and Its Relation to DNA Methylation. <i>Methods in Molecular Biology</i> , 2018, 1766, 31-47.	0.0	6
7	sRNAtoolboxVM: Small RNA Analysis in a Virtual Machine. <i>Methods in Molecular Biology</i> , 2017, 1580, 149-174.	0.0	2
8	NGSmethDB 2017: enhanced methylomes and differential methylation. <i>Nucleic Acids Research</i> , 2017, 45, D97-D103.	14.0	16
9	sRNAtoolbox: an integrated collection of small RNA research tools. <i>Nucleic Acids Research</i> , 2015, 43, W467-W473.	14.0	243
10	NGSmethDB: an updated genome resource for high quality, single-cytosine resolution methylomes. <i>Nucleic Acids Research</i> , 2014, 42, D53-D59.	14.0	22
11	DNA clustering and genome complexity. <i>Computational Biology and Chemistry</i> , 2014, 53, 71-78.	2.4	12
12	<i>CpGislandEVO</i> : A Database and Genome Browser for Comparative Evolutionary Genomics of CpG Islands. <i>BioMed Research International</i> , 2013, 2013, 1-6.	2.0	4
13	MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. <i>F1000Research</i> , 2013, 2, 217.	1.6	44
14	MethylExtract: High-Quality methylation maps and SNV calling from whole genome bisulfite sequencing data. <i>F1000Research</i> , 2013, 2, 217.	1.6	30
15	Clustering of DNA words and biological function: A proof of principle. <i>Journal of Theoretical Biology</i> , 2012, 297, 127-136.	1.7	22
16	WordCluster: detecting clusters of DNA words and genomic elements. <i>Algorithms for Molecular Biology</i> , 2011, 6, 2.	1.4	21
17	NGSmethDB: a database for next-generation sequencing single-cytosine-resolution DNA methylation data. <i>Nucleic Acids Research</i> , 2011, 39, D75-D79.	14.0	51
18	Prediction of CpG-island function: CpG clustering vs. sliding-window methods. <i>BMC Genomics</i> , 2010, 11, 327.	2.9	40

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19	Phylogenetic distribution of large-scale genome patchiness. <i>BMC Evolutionary Biology</i> , 2008, 8, 107.	3.1	8
20	CpGcluster: a distance-based algorithm for CpG-island detection. <i>BMC Bioinformatics</i> , 2006, 7, 446.	2.7	158
21	The Biased Distribution of Alus in Human Isochores Might Be Driven by Recombination. <i>Journal of Molecular Evolution</i> , 2005, 60, 365-377.	1.9	42
22	Compositional searching of CpG islands in the human genome. <i>Physical Review E</i> , 2005, 71, 061925.	2.1	14
23	IsoFinder: computational prediction of isochores in genome sequences. <i>Nucleic Acids Research</i> , 2004, 32, W287-W292.	14.0	78
24	Quantifying intrachromosomal GC heterogeneity in prokaryotic genomes. <i>Gene</i> , 2004, 333, 121-133.	2.3	29
25	GC-Biased Mutation Pressure and ORF Lengthening. <i>Journal of Molecular Evolution</i> , 2003, 56, 371-372.	1.9	1
26	Isochores merit the prefix "iso"™. <i>Computational Biology and Chemistry</i> , 2003, 27, 5-10.	2.4	46
27	Isochores Merit the Prefix 'Iso'. <i>Genome Biology</i> , 2002, 3, preprint0009.1.	7.3	0
28	Isochore chromosome maps of the human genome. <i>Gene</i> , 2002, 300, 117-127.	2.3	56
29	Isochore chromosome maps of eukaryotic genomes. <i>Gene</i> , 2001, 276, 47-56.	2.3	92
30	Finding Borders between Coding and Noncoding DNA Regions by an Entropic Segmentation Method. <i>Physical Review Letters</i> , 2000, 85, 1342-1345.	8.0	116
31	Decomposition of DNA Sequence Complexity. <i>Physical Review Letters</i> , 1999, 83, 3336-3339.	8.0	33
32	Compositional Correlation Between Open Reading Frames with Opposite Transcriptional Orientations in <i>Escherichia coli</i> . <i>Journal of Molecular Evolution</i> , 1999, 48, 712-716.	1.9	0
33	Sequence Compositional Complexity of DNA through an Entropic Segmentation Method. <i>Physical Review Letters</i> , 1998, 80, 1344-1347.	8.0	82
34	Compositional Heterogeneity within, and Uniformity between, DNA Sequences of Yeast Chromosomes. <i>Genome Research</i> , 1998, 8, 916-928.	5.6	66
35	A possible relationship between vsp mismatch repair and gene expression level. <i>Journal of Molecular Evolution</i> , 1996, 43, 161-163.	1.9	2
36	A relationship between GC content and coding-sequence length. <i>Journal of Molecular Evolution</i> , 1996, 43, 216-223.	1.9	100

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37	Compositional segmentation and long-range fractal correlations in DNA sequences. <i>Physical Review E</i> , 1996, 53, 5181-5189.	2.1	182
38	Compositional heterogeneity of the <i>Escherichia coli</i> genome: A role for VSP repair?. <i>Journal of Molecular Evolution</i> , 1994, 39, 340-346.	1.9	23
39	Molecular characterization and transcription of the histone H2B gene from the protozoan parasite <i>Trypanosoma cruzi</i> . <i>Molecular Microbiology</i> , 1994, 13, 1033-1043.	2.5	39
40	SDSE: A software package to simulate the evolution of a pair of DNA sequences. <i>Bioinformatics</i> , 1989, 5, 47-50.	4.2	3
41	Inferring the phylogeny of archaeobacteria: The use of ribosomal sensitivity to protein-synthesis inhibitors. <i>Journal of Molecular Evolution</i> , 1987, 24, 281-288.	1.9	10
42	GENETIC ANALYSIS OF ISOZYME LOCI IN TETRAPLOID POTATOES (<i>SOLANUM TUBEROSUM</i> L.). <i>Genetics</i> , 1984, 108, 669-679.	2.9	42
43	B-Chromosomes and E-1 isozyme activity in mosaic bulbs of <i>Scilla autumnalis</i> (Liliaceae). <i>Chromosoma</i> , 1982, 85, 399-403.	2.1	20
44	Genetic variability in <i>Muscari comosum</i> (Liliaceae). I. A comparative analysis of chromosome polymorphisms in Spanish and Aegean populations. <i>Heredity</i> , 1981, 47, 403-407.	2.7	15