

Mikel Hernaez

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

684
citations

759233

12
h-index

677142

22
g-index

56
all docs

56
docs citations

56
times ranked

848
citing authors

#	ARTICLE	IF	CITATIONS
1	JIND: joint integration and discrimination for automated single-cell annotation. <i>Bioinformatics</i> , 2022, 38, 2488-2495.	4.1	3
2	SimiC enables the inference of complex gene regulatory dynamics across cell phenotypes. <i>Communications Biology</i> , 2022, 5, 351.	4.4	3
3	Cellular plasticity balances the metabolic and proliferation dynamics of a regenerating liver. <i>Genome Research</i> , 2021, 31, 576-591.	5.5	53
4	An Introduction to MPEG-G: The First Open ISO/IEC Standard for the Compression and Exchange of Genomic Sequencing Data. <i>Proceedings of the IEEE</i> , 2021, 109, 1607-1622.	21.3	10
5	Single-Cell Transcriptomics Study of Human Hematopoietic Progenitors Reveals Alterations Associated with Aging and Myeloid Malignancies. <i>Blood</i> , 2021, 138, 1082-1082.	1.4	0
6	Comparison of single and module-based methods for modeling gene regulatory networks. <i>Bioinformatics</i> , 2020, 36, 558-567.	4.1	12
7	GABAC: an arithmetic coding solution for genomic data. <i>Bioinformatics</i> , 2020, 36, 2275-2277.	4.1	6
8	Imaging-AMARETTO: An Imaging Genomics Software Tool to Interrogate Multiomics Networks for Relevance to Radiography and Histopathology Imaging Biomarkers of Clinical Outcomes. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 421-435.	2.1	10
9	GPress: a framework for querying general feature format (GFF) files and expression files in a compressed form. <i>Bioinformatics</i> , 2020, 36, 4810-4812.	4.1	1
10	CROMqs: An infinitesimal successive refinement lossy compressor for the quality scores. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2050031.	0.8	0
11	Sentieon DNaseq Variant Calling Workflow Demonstrates Strong Computational Performance and Accuracy. <i>Frontiers in Genetics</i> , 2019, 10, 736.	2.3	131
12	AliCo: A New Efficient Representation for SAM Files. , 2019, , .		2
13	Genomic Data Compression. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 19-37.	6.5	38
14	Benchmark of long non-coding RNA quantification for RNA sequencing of cancer samples. <i>GigaScience</i> , 2019, 8, .	6.4	32
15	Denoising of Aligned Genomic Data. <i>Scientific Reports</i> , 2019, 9, 15067.	3.3	7
16	SPRING: a next-generation compressor for FASTQ data. <i>Bioinformatics</i> , 2019, 35, 2674-2676.	4.1	49
17	Cell-type specific polysome profiling from mammalian tissues. <i>Methods</i> , 2019, 155, 131-139.	3.8	15
18	CALQ: compression of quality values of aligned sequencing data. <i>Bioinformatics</i> , 2018, 34, 1650-1658.	4.1	16

#	ARTICLE	IF	CITATIONS
19	FaStore: a space-saving solution for raw sequencing data. <i>Bioinformatics</i> , 2018, 34, 2748-2756.	4.1	30
20	Abstract 2472: Benchmark of lncRNA quantification in RNA-Seq of cancer samples. , 2018, , .		0
21	Effect of lossy compression of quality scores on variant calling. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw011.	6.5	50
22	GeneComp, a New Reference-Based Compressor for SAM Files. , 2017, 2017, 330-339.		5
23	An Evaluation Framework for Lossy Compression of Genome Sequencing Quality Values. , 2016, 2016, 221-230.		13
24	A Cluster-Based Approach to Compression of Quality Scores. , 2016, 2016, 261-270.		11
25	Denoising of Quality Scores for Boosted Inference and Reduced Storage. , 2016, 2016, 251-260.		2
26	CROMqs: an infinitesimal successive refinement lossy compressor for the quality scores. , 2016, 2016, 121-125.		1
27	GTRAC: fast retrieval from compressed collections of genomic variants. <i>Bioinformatics</i> , 2016, 32, i479-i486.	4.1	13
28	Comment on: "ERGC: an efficient referential genome compression algorithm". <i>Bioinformatics</i> , 2016, 32, 1115-1117.	4.1	3
29	Design of a new scheme for multi-hop wireless networks using decode-and-forward strategy. <i>Eurasip Journal on Wireless Communications and Networking</i> , 2015, 2015, .	2.4	0
30	QVZ: lossy compression of quality values. <i>Bioinformatics</i> , 2015, 31, 3122-3129.	4.1	53
31	iDoComp: a compression scheme for assembled genomes. <i>Bioinformatics</i> , 2015, 31, 626-633.	4.1	40
32	Aligned genomic data compression via improved modeling. <i>Journal of Bioinformatics and Computational Biology</i> , 2014, 12, 1442002.	0.8	12
33	A Decode-and-Forward Scheme for Multihop Wireless Networks. , 2013, , .		0
34	Teaching information theory via a simulation tool for communications systems. , 2013, , .		0
35	On the design of a novel joint network-channel coding scheme for the multiple access relay channel. <i>IEEE Journal on Selected Areas in Communications</i> , 2013, 31, 1368-1378.	14.0	12
36	Flexible Channel Coding Approach for Short-Length Codewords. <i>IEEE Communications Letters</i> , 2012, 16, 1508-1511.	4.1	6

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37	A Novel Scheme for Message-Forwarding in Multi-Hop Ad-Hoc Wireless Networks. , 2011, , .		1
38	Joint Non-Binary LDPC-BICM and Network Coding with Iterative Decoding for the Multiple Access Relay Channel. , 2011, , .		5
39	Erratum to "serially-concatenated LDGM codes for correlated sources over Gaussian broadcast channels". IEEE Communications Letters, 2010, 14, 235-235.	4.1	1
40	Turbo joint source-channel coding of non-uniform memoryless sources in the bandwidth-limited regime. IEEE Communications Letters, 2010, 14, 336-338.	4.1	1
41	LDPC Codes for Non-Uniform Memoryless Sources and Unequal Energy Allocation. IEEE Communications Letters, 2010, 14, 794-796.	4.1	7
42	Joint Turbo Coding and Source-Controlled Modulation of Cycle-Stationary Sources in the Bandwidth-Limited Regime. Lecture Notes of the Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering, 2010, , 618-625.	0.3	0
43	Serially-concatenated LDGM codes for correlated sources over gaussian broadcast channels. IEEE Communications Letters, 2009, 13, 788-790.	4.1	5
44	Towards scalable genomic data access. Nature Computational Science, 0, , .	8.0	0