Idoia Ochoa

List of Publications by Year
in descending order

40 papers	533 citations	933447 10 h-index	794594 19 g-index
51 all docs	51 docs citations	51 times ranked	351 citing authors

#	Article	IF	Citations
1	QVZ: lossy compression of quality values. Bioinformatics, 2015, 31, 3122-3129.	4.1	53
2	Effect of lossy compression of quality scores on variant calling. Briefings in Bioinformatics, 2017, 18, bbw011.	6.5	50
3	SPRING: a next-generation compressor for FASTQ data. Bioinformatics, 2019, 35, 2674-2676.	4.1	49
4	QualComp: a new lossy compressor for quality scores based on rate distortion theory. BMC Bioinformatics, 2013, 14, 187.	2.6	47
5	iDoComp: a compression scheme for assembled genomes. Bioinformatics, 2015, 31, 626-633.	4.1	40
6	Genomic Data Compression. Annual Review of Biomedical Data Science, 2019, 2, 19-37.	6.5	38
7	DeepZip: Lossless Data Compression Using Recurrent Neural Networks. , 2019, , .		33
8	FaStore: a space-saving solution for raw sequencing data. Bioinformatics, 2018, 34, 2748-2756.	4.1	30
9	CaMoDi: a new method for cancer module discovery. BMC Genomics, 2014, 15, S8.	2.8	16
10	ENANO: Encoder for NANOpore FASTQ files. Bioinformatics, 2020, 36, 4506-4507.	4.1	14
11	DZip: improved general-purpose loss less compression based on novel neural network modeling. , 2021, , .		14
12	GTRAC: fast retrieval from compressed collections of genomic variants. Bioinformatics, 2016, 32, i479-i486.	4.1	13
13	Reference based genome compression. , 2012, , .		12
14	Aligned genomic data compression via improved modeling. Journal of Bioinformatics and Computational Biology, 2014, 12, 1442002.	0.8	12
15	A Cluster-Based Approach to Compression of Quality Scores. , 2016, 2016, 261-270.		11
16	RENANO: a REference-based compressor for NANOpore FASTQ files. Bioinformatics, 2021, 37, 4862-4864.	4.1	9
17	MassComp, a lossless compressor for mass spectrometry data. BMC Bioinformatics, 2019, 20, 368.	2.6	8
18	LDPC Codes for Non-Uniform Memoryless Sources and Unequal Energy Allocation. IEEE Communications Letters, 2010, 14, 794-796.	4.1	7

#	Article	IF	Citations
19	Denoising of Aligned Genomic Data. Scientific Reports, 2019, 9, 15067.	3.3	7
20	GABAC: an arithmetic coding solution for genomic data. Bioinformatics, 2020, 36, 2275-2277.	4.1	6
21	GeneComp, a New Reference-Based Compressor for SAM Files. , 2017, 2017, 330-339.		5
22	METHCOMP: a special purpose compression platform for DNA methylation data. Bioinformatics, 2018, 34, 2654-2656.	4.1	4
23	VEF: a variant filtering tool based on ensemble methods. Bioinformatics, 2020, 36, 2328-2336.	4.1	4
24	Comment on: â€˜ERGC: an efficient referential genome compression algorithmâ€™. Bioinformatics, 2016, 32, 1115-1117.	4.1	3
25	mspack: efficient lossless and lossy mass spectrometry data compression. Bioinformatics, 2021, 37, 3923-3925.	4.1	3
26	JIND: joint integration and discrimination for automated single-cell annotation. Bioinformatics, 2022, 38, 2488-2495.	4.1	3
27	SimiC enables the inference of complex gene regulatory dynamics across cell phenotypes. Communications Biology, 2022, 5, 351.	4.4	3
28	Compression Schemes for Similarity Queries. , 2014, , .		2
29	Denoising of Quality Scores for Boosted Inference and Reduced Storage. , 2016, 2016, 251-260.		2
30	AliCo: A New Efficient Representation for SAM Files. , 2019, , .		2
31	Compression of Nanopore FASTQ Files. Lecture Notes in Computer Science, 2019, , 36-47.	1.3	2
32	DZip: Improved General-Purpose Lossless Compression Based on Novel Neural Network Modeling. , 2020, , .		2
33	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
34	Efficient similarity queries via lossy compression. , 2013, , .		1
35	CROMqs: an infinitesimal successive refinement lossy compressor for the quality scores. , 2016, 2016, 121-125.		1
36	GPress: a framework for querying general feature format (GFF) files and expression files in a compressed form. Bioinformatics, 2020, 36, 4810-4812.	4.1	1

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37	Moss enables high sensitivity single-nucleotide variant calling from multiple bulk DNA tumor samples. Nature Communications, 2021, 12, 2204.	12.8	1
38	Unsupervised ensemble learning for genome sequencing. Pattern Recognition, 2022, 129, 108721.	8.1	1
39	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
40	CROMqs: An infinitesimal successive refinement lossy compressor for the quality scores. Journal of Bioinformatics and Computational Biology, 2020, 18, 2050031.	0.8	0