Ilan Shomorony

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/36987/publications.pdf

Version: 2024-02-01

		1163117	1125743
18	424	8	13
papers	citations	h-index	g-index
18	18	18	383
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Information-Theoretic Foundations of DNA Data Storage. Foundations and Trends in Communications and Information Theory, 2022, 19, 1-106.	3.1	11
2	Coded Shotgun Sequencing. IEEE Journal on Selected Areas in Information Theory, 2022, 3, 147-159.	2.5	4
3	JIND: joint integration and discrimination for automated single-cell annotation. Bioinformatics, 2022, 38, 2488-2495.	4.1	3
4	Achieving the Capacity of a DNA Storage Channel with Linear Coding Schemes. , 2022, , .		0
5	DNA-Based Storage: Models and Fundamental Limits. IEEE Transactions on Information Theory, 2021, 67, 3675-3689.	2.4	32
6	Sketching and Sequence Alignment: A Rate-Distortion Perspective. , 2021, , .		0
7	Torn-Paper Coding. IEEE Transactions on Information Theory, 2021, 67, 7904-7913.	2.4	5
8	Spectral Jaccard Similarity: A New Approach to Estimating Pairwise Sequence Alignments. Patterns, 2020, 1, 100081.	5.9	9
9	Communicating over the Torn-Paper Channel. , 2020, , .		5
10	Capacity Results for the Noisy Shuffling Channel., 2019,,.		38
10	Capacity Results for the Noisy Shuffling Channel., 2019,,. HINGE: long-read assembly achieves optimal repeat resolution. Genome Research, 2017, 27, 747-756.	5.5	38
		5.5	
11	HINGE: long-read assembly achieves optimal repeat resolution. Genome Research, 2017, 27, 747-756.	5.5 2.1	88
11 12	HINGE: long-read assembly achieves optimal repeat resolution. Genome Research, 2017, 27, 747-756. Fundamental limits of DNA storage systems., 2017,,. Fundamental Limits of Genome Assembly Under an Adversarial Erasure Model. IEEE Transactions on		73
11 12 13	HINGE: long-read assembly achieves optimal repeat resolution. Genome Research, 2017, 27, 747-756. Fundamental limits of DNA storage systems., 2017,,. Fundamental Limits of Genome Assembly Under an Adversarial Erasure Model. IEEE Transactions on Molecular, Biological, and Multi-Scale Communications, 2016, 2, 199-208. Information-optimal genome assembly via sparse read-overlap graphs. Bioinformatics, 2016, 32,	2.1	73 10
11 12 13 14	HINGE: long-read assembly achieves optimal repeat resolution. Genome Research, 2017, 27, 747-756. Fundamental limits of DNA storage systems., 2017,,. Fundamental Limits of Genome Assembly Under an Adversarial Erasure Model. IEEE Transactions on Molecular, Biological, and Multi-Scale Communications, 2016, 2, 199-208. Information-optimal genome assembly via sparse read-overlap graphs. Bioinformatics, 2016, 32, i494-i502. Network Compression: Worst Case Analysis. IEEE Transactions on Information Theory, 2015, 61,	2.1	88 73 10 23
11 12 13 14	HINGE: long-read assembly achieves optimal repeat resolution. Genome Research, 2017, 27, 747-756. Fundamental limits of DNA storage systems., 2017,,. Fundamental Limits of Genome Assembly Under an Adversarial Erasure Model. IEEE Transactions on Molecular, Biological, and Multi-Scale Communications, 2016, 2, 199-208. Information-optimal genome assembly via sparse read-overlap graphs. Bioinformatics, 2016, 32, i494-i502. Network Compression: Worst Case Analysis. IEEE Transactions on Information Theory, 2015, 61, 3980-3995. Degrees of Freedom of Two-Hop Wireless Networks: Everyone Gets the Entire Cake. IEEE Transactions	2.1 4.1 2.4	88 73 10 23