

# David N Tse

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7880034/publications.pdf>

Version: 2024-02-01

38  
papers

2,314  
citations

567281

15  
h-index

610901

24  
g-index

42  
all docs

42  
docs citations

42  
times ranked

3544  
citing authors

#	ARTICLE	IF	CITATIONS
1	Spectrum sharing for unlicensed bands. IEEE Journal on Selected Areas in Communications, 2007, 25, 517-528.	14.0	642
2	Longitudinal multi-omics of host-microbe dynamics in prediabetes. Nature, 2019, 569, 663-671.	27.8	391
3	The two-user Gaussian interference channel: a deterministic view. European Transactions on Telecommunications, 2008, 19, 333-354.	1.2	187
4	FinisherSC: a repeat-aware tool for upgrading <i>de novo</i> assembly using long reads. Bioinformatics, 2015, 31, 3207-3209.	4.1	123
5	Fast and accurate single-cell RNA-seq analysis by clustering of transcript-compatibility counts. Genome Biology, 2016, 17, 112.	8.8	109
6	HINGE: long-read assembly achieves optimal repeat resolution. Genome Research, 2017, 27, 747-756.	5.5	88
7	Large dataset enables prediction of repair after CRISPR-Cas9 editing in primary T cells. Nature Biotechnology, 2019, 37, 1034-1037.	17.5	87
8	Distributed algorithms for optimal power flow problem. , 2012, , .		82
9	Determining sequencing depth in a single-cell RNA-seq experiment. Nature Communications, 2020, 11, 774.	12.8	74
10	Optimal assembly for high throughput shotgun sequencing. BMC Bioinformatics, 2013, 14, S18.	2.6	63
11	An interpretable framework for clustering single-cell RNA-Seq datasets. BMC Bioinformatics, 2018, 19, 93.	2.6	49
12	Valid Post-clustering Differential Analysis for Single-Cell RNA-Seq. Cell Systems, 2019, 9, 383-392.e6.	6.2	45
13	Capacity-achieving rateless polar codes. , 2016, , .		44
14	Network Risk Limiting Dispatch: Optimal Control and Price of Uncertainty. IEEE Transactions on Automatic Control, 2014, 59, 2442-2456.	5.7	34
15	Efficient file synchronization: A distributed source coding approach. , 2011, , .		30
16	Reduce the Complexity of List Decoding of Polar Codes by Tree-Pruning. IEEE Communications Letters, 2016, 20, 204-207.	4.1	29
17	Asynchronous Capacity per Unit Cost. IEEE Transactions on Information Theory, 2013, 59, 1213-1226.	2.4	27
18	Channel Identification: Secret Sharing using Reciprocity in Ultrawideband Channels. , 2007, , .		23

#	ARTICLE	IF	CITATIONS
19	Prediction and Modeling for the Time-Evolving Ultra-Wideband Channel. IEEE Journal on Selected Topics in Signal Processing, 2007, 1, 340-356.	10.8	22
20	Optimal DNA shotgun sequencing: Noisy reads are as good as noiseless reads. , 2013, , .		22
21	Interference neutralization in distributed lossy source coding. , 2010, , .		15
22	Optimal compressed representation of high throughput sequence data via light assembly. Nature Communications, 2018, 9, 566.	12.8	14
23	RefShannon: A genome-guided transcriptome assembler using sparse flow decomposition. PLoS ONE, 2020, 15, e0232946.	2.5	13
24	A compression algorithm using mis-aligned side-information. , 2012, , .		12
25	Hidden Hamiltonian Cycle Recovery via Linear Programming. Operations Research, 2020, 68, 53-70.	1.9	11
26	Fundamental Limits of Genome Assembly Under an Adversarial Erasure Model. IEEE Transactions on Molecular, Biological, and Multi-Scale Communications, 2016, 2, 199-208.	2.1	10
27	Spectral Jaccard Similarity: A New Approach to Estimating Pairwise Sequence Alignments. Patterns, 2020, 1, 100081.	5.9	9
28	A framework for robust measurement-based admission control. Computer Communication Review, 1997, 27, 237-248.	1.8	8
29	Polarization degrees of freedom. , 2008, , .		8
30	Information theory for DNA sequencing: Part I: A basic model. , 2012, , .		8
31	Reference-based DNA shotgun sequencing: Information theoretic limits. , 2013, , .		7
32	Prism Removes Consensus Bottleneck for Smart Contracts. , 2020, , .		7
33	Optimal haplotype assembly from high-throughput mate-pair reads. , 2015, , .		6
34	Novel probabilistic models of spatial genetic ancestry with applications to stratification correction in genome-wide association studies. Bioinformatics, 2017, 33, 879-885.	4.1	6
35	Fundamental Limits of Search. Cell Systems, 2015, 1, 102-103.	6.2	4
36	Polar Coding for Parallel Gaussian Channels. , 2019, , .		1

#	ARTICLE	IF	CITATIONS
37	Somatic mutations render human exome and pathogen DNA more similar. PLoS ONE, 2019, 14, e0197949.	2.5	0
38	Spectral Jaccard Similarity: A New Approach to Estimating Pairwise Sequence Alignments. Lecture Notes in Computer Science, 2020, , 223-225.	1.3	0