

Hyunghoon Cho

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

1,008
citations

759233

12
h-index

888059

17
g-index

25
all docs

25
docs citations

25
times ranked

1385
citing authors

#	ARTICLE	IF	CITATIONS
1	Mechanisms for Hiding Sensitive Genotypes With Information-Theoretic Privacy. IEEE Transactions on Information Theory, 2022, 68, 4090-4105.	2.4	3
2	Bayesian information sharing enhances detection of regulatory associations in rare cell types. Bioinformatics, 2021, 37, i349-i357.	4.1	1
3	Privacy-preserving genotype imputation in a trusted execution environment. Cell Systems, 2021, 12, 983-993.e7.	6.2	13
4	Assessing single-cell transcriptomic variability through density-preserving data visualization. Nature Biotechnology, 2021, 39, 765-774.	17.5	74
5	Truly privacy-preserving federated analytics for precision medicine with multiparty homomorphic encryption. Nature Communications, 2021, 12, 5910.	12.8	64
6	Privacy-Preserving Biomedical Database Queries with Optimal Privacy-Utility Trade-Offs. Cell Systems, 2020, 10, 408-416.e9.	6.2	14
7	Emerging technologies towards enhancing privacy in genomic data sharing. Genome Biology, 2019, 20, 128.	8.8	45
8	Geometric Sketching Compactly Summarizes the Single-Cell Transcriptomic Landscape. Cell Systems, 2019, 8, 483-493.e7.	6.2	95
9	Large-Margin Classification in Hyperbolic Space. Proceedings of Machine Learning Research, 2019, 89, 1832-1840.	0.3	1
10	Realizing private and practical pharmacological collaboration. Science, 2018, 362, 347-350.	12.6	52
11	Principles of Systems Biology, No. 31. Cell Systems, 2018, 7, 133-135.	6.2	0
12	Secure genome-wide association analysis using multiparty computation. Nature Biotechnology, 2018, 36, 547-551.	17.5	139
13	Generalizable and Scalable Visualization of Single-Cell Data Using Neural Networks. Cell Systems, 2018, 7, 185-191.e4.	6.2	49
14	Compact Integration of Multi-Network Topology for Functional Analysis of Genes. Cell Systems, 2016, 3, 540-548.e5.	6.2	207
15	Reconstructing Causal Biological Networks through Active Learning. PLoS ONE, 2016, 11, e0150611.	2.5	13
16	Exploiting ontology graph for predicting sparsely annotated gene function. Bioinformatics, 2015, 31, i357-i364.	4.1	97
17	Diffusion Component Analysis: Unraveling Functional Topology in Biological Networks. Lecture Notes in Computer Science, 2015, 9029, 62-64.	1.3	63
18	High-Resolution Transcriptome Analysis with Long-Read RNA Sequencing. PLoS ONE, 2014, 9, e108095.	2.5	47