

Su-In Lee

List of Publications by Year in descending order

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Version: 2024-02-01

41
papers

7,932
citations

304368

22
h-index

329751

37
g-index

48
all docs

48
docs citations

48
times ranked

10439
citing authors

#	ARTICLE	IF	CITATIONS
1	From local explanations to global understanding with explainable AI for trees. <i>Nature Machine Intelligence</i> , 2020, 2, 56-67.	8.3	2,869
2	Sequencing of <i>Aspergillus nidulans</i> and comparative analysis with <i>A. fumigatus</i> and <i>A. oryzae</i> . <i>Nature</i> , 2005, 438, 1105-1115.	13.7	1,250
3	Explainable machine-learning predictions for the prevention of hypoxaemia during surgery. <i>Nature Biomedical Engineering</i> , 2018, 2, 749-760.	11.6	1,033
4	Massively parallel functional dissection of mammalian enhancers in vivo. <i>Nature Biotechnology</i> , 2012, 30, 265-270.	9.4	468
5	Learning generative models for protein fold families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1061-1078.	1.5	293
6	AI for radiographic COVID-19 detection selects shortcuts over signal. <i>Nature Machine Intelligence</i> , 2021, 3, 610-619.	8.3	230
7	Application of independent component analysis to microarrays. <i>Genome Biology</i> , 2003, 4, R76.	13.9	207
8	A machine learning approach to integrate big data for precision medicine in acute myeloid leukemia. <i>Nature Communications</i> , 2018, 9, 42.	5.8	194
9	The Proteomic Landscape of Triple-Negative Breast Cancer. <i>Cell Reports</i> , 2015, 11, 630-644.	2.9	179
10	Learning a Prior on Regulatory Potential from eQTL Data. <i>PLoS Genetics</i> , 2009, 5, e1000358.	1.5	177
11	Identifying regulatory mechanisms using individual variation reveals key role for chromatin modification. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14062-14067.	3.3	126
12	Reproducibility standards for machine learning in the life sciences. <i>Nature Methods</i> , 2021, 18, 1132-1135.	9.0	96
13	Brn3a and Islet1 Act Epistatically to Regulate the Gene Expression Program of Sensory Differentiation. <i>Journal of Neuroscience</i> , 2011, 31, 9789-9799.	1.7	90
14	Visualizing the Impact of Feature Attribution Baselines. <i>Distill</i> , 2020, 5, .	5.3	73
15	Improving performance of deep learning models with axiomatic attribution priors and expected gradients. <i>Nature Machine Intelligence</i> , 2021, 3, 620-631.	8.3	69
16	Node-Based Learning of Multiple Gaussian Graphical Models. <i>Journal of Machine Learning Research</i> , 2014, 15, 445-488.	62.4	59
17	A pluripotency signature predicts histologic transformation and influences survival in follicular lymphoma patients. <i>Blood</i> , 2009, 114, 3158-3166.	0.6	52
18	Automated Detection of Glaucoma With Interpretable Machine Learning Using Clinical Data and Multimodal Retinal Images. <i>American Journal of Ophthalmology</i> , 2021, 231, 154-169.	1.7	43

#	ARTICLE	IF	CITATIONS
19	Identifying Network Perturbation in Cancer. PLoS Computational Biology, 2016, 12, e1004888.	1.5	35
20	ChromNet: Learning the human chromatin network from all ENCODE ChIP-seq data. Genome Biology, 2016, 17, 82.	3.8	31
21	Adversarial deconfounding autoencoder for learning robust gene expression embeddings. Bioinformatics, 2020, 36, i573-i582.	1.8	30
22	Learning Graphical Models With Hubs. Journal of Machine Learning Research, 2014, 15, 3297-3331.	62.4	30
23	Sparse expression bases in cancer reveal tumor drivers. Nucleic Acids Research, 2015, 43, 1332-1344.	6.5	27
24	A Systematic Approach to Multifactorial Cardiovascular Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2012, 32, 2821-2835.	1.1	26
25	Forecasting adverse surgical events using self-supervised transfer learning for physiological signals. Npj Digital Medicine, 2021, 4, 167.	5.7	25
26	A Distributed Network for Intensive Longitudinal Monitoring in Metastatic Triple-Negative Breast Cancer. Journal of the National Comprehensive Cancer Network: JNCCN, 2016, 14, 8-17.	2.3	21
27	Extracting a low-dimensional description of multiple gene expression datasets reveals a potential driver for tumor-associated stroma in ovarian cancer. Genome Medicine, 2016, 8, 66.	3.6	18
28	Associations Between Genetic Data and Quantitative Assessment of Normal Facial Asymmetry. Frontiers in Genetics, 2018, 9, 659.	1.1	14
29	Efficient and Explainable Risk Assessments for Imminent Dementia in an Aging Cohort Study. IEEE Journal of Biomedical and Health Informatics, 2021, 25, 2409-2420.	3.9	14
30	An adversarial approach for the robust classification of pneumonia from chest radiographs. , 2020, , .		14
31	A cost-aware framework for the development of AI models for healthcare applications. Nature Biomedical Engineering, 2022, 6, 1384-1398.	11.6	12
32	Epigenome-wide analysis of long-term air pollution exposure and DNA methylation in monocytes: results from the Multi-Ethnic Study of Atherosclerosis. Epigenetics, 2022, 17, 1-17.	1.3	11
33	Structured Learning of Gaussian Graphical Models. Advances in Neural Information Processing Systems, 2012, 2012, 629-637.	2.8	10
34	AIControl: replacing matched control experiments with machine learning improves ChIP-seq peak identification. Nucleic Acids Research, 2019, 47, e58-e58.	6.5	9
35	Unified AI framework to uncover deep interrelationships between gene expression and Alzheimer's disease neuropathologies. Nature Communications, 2021, 12, 5369.	5.8	8
36	High Throughput Drug Screening of Leukemia Stem Cells Reveals Resistance to Standard Therapies and Sensitivity to Other Agents in Acute Myeloid Leukemia. Blood, 2018, 132, 180-180.	0.6	5

#	ARTICLE	IF	CITATIONS
37	Personalized Approach To Treatment of Acute Myeloid Leukemia Using a High-Throughput Chemosensitivity Assay. <i>Blood</i> , 2013, 122, 483-483.	0.6	2
38	University of Washington Nathan Shock Center: innovation to advance aging research. <i>GeroScience</i> , 2021, 43, 2161-2165.	2.1	1
39	An automatic integrative method for learning interpretable communities of biological pathways. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	1.5	1
40	Course corrections for clinical AI. <i>Kidney360</i> , 2021, 2, 10.34067/KID.0004152021.	0.9	0
41	Mini-Chromosome Maintenance (MCM) DNA Helicase Genes Influence Acute Myeloid Leukemia (AML) Replication and Response to Chemotherapy-Induced DNA Damage. <i>Blood</i> , 2015, 126, 3629-3629.	0.6	0