

# Su-In Lee

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/398917/publications.pdf>

Version: 2024-02-01

41  
papers

7,932  
citations

304743

22  
h-index

330143

37  
g-index

48  
all docs

48  
docs citations

48  
times ranked

10439  
citing authors

#	ARTICLE	IF	CITATIONS
1	Epigenome-wide analysis of long-term air pollution exposure and DNA methylation in monocytes: results from the Multi-Ethnic Study of Atherosclerosis. <i>Epigenetics</i> , 2022, 17, 1-17.	2.7	11
2	A cost-aware framework for the development of AI models for healthcare applications. <i>Nature Biomedical Engineering</i> , 2022, 6, 1384-1398.	22.5	12
3	An automatic integrative method for learning interpretable communities of biological pathways. <i>NAR Genomics and Bioinformatics</i> , 2022, 4, .	3.2	1
4	Improving performance of deep learning models with axiomatic attribution priors and expected gradients. <i>Nature Machine Intelligence</i> , 2021, 3, 620-631.	16.0	69
5	AI for radiographic COVID-19 detection selects shortcuts over signal. <i>Nature Machine Intelligence</i> , 2021, 3, 610-619.	16.0	230
6	University of Washington Nathan Shock Center: innovation to advance aging research. <i>GeroScience</i> , 2021, 43, 2161-2165.	4.6	1
7	Efficient and Explainable Risk Assessments for Imminent Dementia in an Aging Cohort Study. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2021, 25, 2409-2420.	6.3	14
8	Reproducibility standards for machine learning in the life sciences. <i>Nature Methods</i> , 2021, 18, 1132-1135.	19.0	96
9	Unified AI framework to uncover deep interrelationships between gene expression and Alzheimer's disease neuropathologies. <i>Nature Communications</i> , 2021, 12, 5369.	12.8	8
10	Course corrections for clinical AI. <i>Kidney360</i> , 2021, 2, 10.34067/KID.0004152021.	2.1	0
11	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.	3.3	43
12	Forecasting adverse surgical events using self-supervised transfer learning for physiological signals. <i>Npj Digital Medicine</i> , 2021, 4, 167.	10.9	25
13	From local explanations to global understanding with explainable AI for trees. <i>Nature Machine Intelligence</i> , 2020, 2, 56-67.	16.0	2,869
14	Adversarial deconfounding autoencoder for learning robust gene expression embeddings. <i>Bioinformatics</i> , 2020, 36, i573-i582.	4.1	30
15	An adversarial approach for the robust classification of pneumonia from chest radiographs. , 2020, , .		14
16	Visualizing the Impact of Feature Attribution Baselines. <i>Distill</i> , 2020, 5, .	5.3	73
17	AIControl: replacing matched control experiments with machine learning improves ChIP-seq peak identification. <i>Nucleic Acids Research</i> , 2019, 47, e58-e58.	14.5	9
18	A machine learning approach to integrate big data for precision medicine in acute myeloid leukemia. <i>Nature Communications</i> , 2018, 9, 42.	12.8	194

#	ARTICLE	IF	CITATIONS
19	Associations Between Genetic Data and Quantitative Assessment of Normal Facial Asymmetry. <i>Frontiers in Genetics</i> , 2018, 9, 659.	2.3	14
20	Explainable machine-learning predictions for the prevention of hypoxaemia during surgery. <i>Nature Biomedical Engineering</i> , 2018, 2, 749-760.	22.5	1,033
21	High Throughput Drug Screening of Leukemia Stem Cells Reveals Resistance to Standard Therapies and Sensitivity to Other Agents in Acute Myeloid Leukemia. <i>Blood</i> , 2018, 132, 180-180.	1.4	5
22	Extracting a low-dimensional description of multiple gene expression datasets reveals a potential driver for tumor-associated stroma in ovarian cancer. <i>Genome Medicine</i> , 2016, 8, 66.	8.2	18
23	Identifying Network Perturbation in Cancer. <i>PLoS Computational Biology</i> , 2016, 12, e1004888.	3.2	35
24	A Distributed Network for Intensive Longitudinal Monitoring in Metastatic Triple-Negative Breast Cancer. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2016, 14, 8-17.	4.9	21
25	ChromNet: Learning the human chromatin network from all ENCODE ChIP-seq data. <i>Genome Biology</i> , 2016, 17, 82.	8.8	31
26	Sparse expression bases in cancer reveal tumor drivers. <i>Nucleic Acids Research</i> , 2015, 43, 1332-1344.	14.5	27
27	The Proteomic Landscape of Triple-Negative Breast Cancer. <i>Cell Reports</i> , 2015, 11, 630-644.	6.4	179
28	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.	1.4	0
29	Node-Based Learning of Multiple Gaussian Graphical Models. <i>Journal of Machine Learning Research</i> , 2014, 15, 445-488.	62.4	59
30	Learning Graphical Models With Hubs. <i>Journal of Machine Learning Research</i> , 2014, 15, 3297-3331.	62.4	30
31	Personalized Approach To Treatment of Acute Myeloid Leukemia Using a High-Throughput Chemosensitivity Assay. <i>Blood</i> , 2013, 122, 483-483.	1.4	2
32	A Systematic Approach to Multifactorial Cardiovascular Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2012, 32, 2821-2835.	2.4	26
33	Massively parallel functional dissection of mammalian enhancers in vivo. <i>Nature Biotechnology</i> , 2012, 30, 265-270.	17.5	468
34	Structured Learning of Gaussian Graphical Models. <i>Advances in Neural Information Processing Systems</i> , 2012, 2012, 629-637.	2.8	10
35	Learning generative models for protein fold families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1061-1078.	2.6	293
36	Brn3a and Islet1 Act Epistatically to Regulate the Gene Expression Program of Sensory Differentiation. <i>Journal of Neuroscience</i> , 2011, 31, 9789-9799.	3.6	90

#	ARTICLE	IF	CITATIONS
37	Learning a Prior on Regulatory Potential from eQTL Data. PLoS Genetics, 2009, 5, e1000358.	3.5	177
38	A pluripotency signature predicts histologic transformation and influences survival in follicular lymphoma patients. Blood, 2009, 114, 3158-3166.	1.4	52
39	Identifying regulatory mechanisms using individual variation reveals key role for chromatin modification. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14062-14067.	7.1	126
40	Sequencing of Aspergillus nidulans and comparative analysis with A. fumigatus and A. oryzae. Nature, 2005, 438, 1105-1115.	27.8	1,250
41	Application of independent component analysis to microarrays. Genome Biology, 2003, 4, R76.	9.6	207