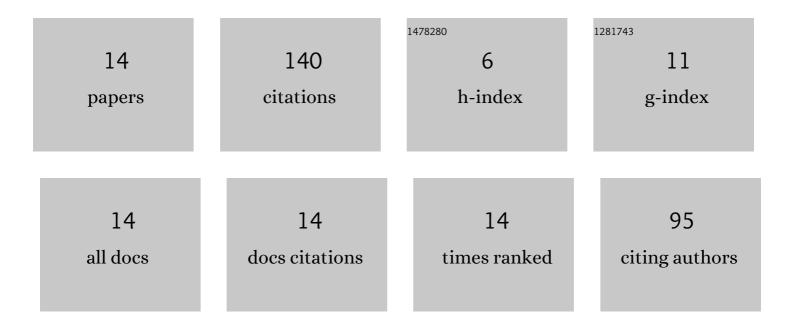
Minhyeok Lee

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8407829/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Controllable Generative Adversarial Network. IEEE Access, 2019, 7, 28158-28169.	2.6	45
2	Portfolio management via two-stage deep learning with a joint cost. Expert Systems With Applications, 2020, 143, 113041.	4.4	27
3	Stock Price Prediction Through the Sentimental Analysis of News Articles. , 2019, , .		15
4	Serum biomarkers from cell-based assays for AhRL and MIS strongly predicted the future development of diabetes in a large community-based prospective study in Korea. Scientific Reports, 2020, 10, 6339.	1.6	9
5	Estimation with Uncertainty via Conditional Generative Adversarial Networks. Sensors, 2021, 21, 6194.	2.1	9
6	Improved recurrent generative adversarial networks with regularization techniques and a controllable framework. Information Sciences, 2020, 538, 428-443.	4.0	7
7	HRGAN: A Generative Adversarial Network Producing Higher-Resolution Images than Training Sets. Sensors, 2022, 22, 1435.	2.1	7
8	An Ensemble Deep Learning Model with a Gene Attention Mechanism for Estimating the Prognosis of Low-Grade Glioma. Biology, 2022, 11, 586.	1.3	7
9	Clinical Implication of Concordant or Discordant Genomic Profiling between Primary and Matched Metastatic Tissues in Patients with Colorectal Cancer. Cancer Research and Treatment, 2020, 52, 764-778.	1.3	6
10	A Comparison of Two-Stage Approaches Based on Penalized Regression for Estimating Gene Networks. Journal of Computational Biology, 2017, 24, 709-720.	0.8	2
11	The estimation of probability distribution for factor variables with many categorical values. PLoS ONE, 2018, 13, e0202547.	1.1	2
12	Long Term Traffic Prediction in Highway Using Parallel CNN. , 2020, , .		2
13	Prediction of survival risks with adjusted gene expression through risk-gene networks. Bioinformatics, 2019, 35, 4898-4906.	1.8	1
14	Regression-Based Network Estimation for High-Dimensional Genetic Data. Journal of Computational Biology, 2019, 26, 336-349.	0.8	1