Jaewoo Kang

List of Publications by Year
in descending order

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72 papers	5,045 citations	236925 25 h-index	110387 64 g-index
75 all docs	75 docs citations	75 times ranked	4982 citing authors

#	Article	IF	Citations
1	BioBERT: a pre-trained biomedical language representation model for biomedical text mining. Bioinformatics, 2020, 36, 1234-1240.	4.1	2,733
2	DSigDB: drug signatures database for gene set analysis. Bioinformatics, 2015, 31, 3069-3071.	4.1	295
3	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
4	Building a PubMed knowledge graph. Scientific Data, 2020, 7, 205.	5.3	94
5	A Neural Named Entity Recognition and Multi-Type Normalization Tool for Biomedical Text Mining. IEEE Access, 2019, 7, 73729-73740.	4.2	92
6	Detection of masses in mammograms using a one-stage object detector based on a deep convolutional neural network. PLoS ONE, 2018, 13, e0203355.	2.5	91
7	CollaboNet: collaboration of deep neural networks for biomedical named entity recognition. BMC Bioinformatics, 2019, 20, 249.	2.6	87
8	BEST: Next-Generation Biomedical Entity Search Tool for Knowledge Discovery from Biomedical Literature. PLoS ONE, 2016, 11, e0164680.	2.5	74
9	OUP accepted manuscript. Nucleic Acids Research, 2017, 45, D784-D789.	14.5	74
10	Drug drug interaction extraction from the literature using a recursive neural network. PLoS ONE, 2018, 13, e0190926.	2.5	71
11	Global Stock Market Prediction Based on Stock Chart Images Using Deep Q-Network. IEEE Access, 2019, 7, 167260-167277.	4.2	61
12	Classification of lung nodules in CT scans using three-dimensional deep convolutional neural networks with a checkpoint ensemble method. BMC Medical Imaging, 2018, 18, 48.	2.7	55
13	An automatic nuclei segmentation method based on deep convolutional neural networks for histopathology images. BMC Biomedical Engineering, 2019, 1, 24.	2.6	55
14	Chemicalâ€“gene relation extraction using recursive neural network. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	3.0	53
15	Biomedical Entity Representations with Synonym Marginalization. , 2020, , .		51
16	In silico drug combination discovery for personalized cancer therapy. BMC Systems Biology, 2018, 12, 16.	3.0	47
17	ChimerDB 4.0: an updated and expanded database of fusion genes. Nucleic Acids Research, 2020, 48, D817-D824.	14.5	44
18	Deep learning of mutation-gene-drug relations from the literature. BMC Bioinformatics, 2018, 19, 21.	2.6	43

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19	A bibliometric method for measuring the degree of technological innovation. Technological Forecasting and Social Change, 2015, 95, 152-162.	11.6	41
20	Crowdsourced mapping of unexplored target space of kinase inhibitors. Nature Communications, 2021, 12, 3307.	12.8	41
21	Improved survival analysis by learning shared genomic information from pan-cancer data. Bioinformatics, 2020, 36, i389-i398.	4.1	39
22	ReSimNet: drug response similarity prediction using Siamese neural networks. Bioinformatics, 2019, 35, 5249-5256.	4.1	37
23	BTNET : boosted tree based gene regulatory network inference algorithm using time-course measurement data. BMC Systems Biology, 2018, 12, 20.	3.0	33
24	Enhancing the interpretability of transcription factor binding site prediction using attention mechanism. Scientific Reports, 2020, 10, 13413.	3.3	33
25	Efficient quantitative assessment of facial paralysis using iris segmentation and active contour-based key points detection with hybrid classifier. BMC Medical Imaging, 2016, 16, 23.	2.7	30
26	Mut2Vec: distributed representation of cancerous mutations. BMC Medical Genomics, 2018, 11, 33.	1.5	30
27	BRONCO: Biomedical entity Relation ONcology COrpus for extracting gene-variant-disease-drug relations. Database: the Journal of Biological Databases and Curation, 2016, 2016, .	3.0	29
28	DeepNAP: Deep neural anomaly pre-detection in a semiconductor fab. Information Sciences, 2018, 457-458, 1-11.	6.9	26
29	Multipath-DenseNet: A Supervised ensemble architecture of densely connected convolutional networks. Information Sciences, 2019, 482, 63-72.	6.9	26
30	Exploring the molecular mechanisms of Traditional Chinese Medicine components using gene expression signatures and connectivity map. Computer Methods and Programs in Biomedicine, 2019, 174, 33-40.	4.7	26
31	Literature-based condition-specific miRNA-mRNA target prediction. PLoS ONE, 2017, 12, e0174999.	2.5	24
32	ARPNet: Antidepressant Response Prediction Network for Major Depressive Disorder. Genes, 2019, 10, 907.	2.4	23
33	Bioinformatics-driven discovery of rational combination for overcoming EGFR-mutant lung cancer resistance to EGFR therapy. Bioinformatics, 2014, 30, 2393-2398.	4.1	22
34	Pre-trained Language Model for Biomedical Question Answering. Communications in Computer and Information Science, 2020, , 727-740.	0.5	21
35	paraFaceTest: an ensemble of regression tree-based facial features extraction for efficient facial paralysis classification. BMC Medical Imaging, 2019, 19, 30.	2.7	20
36	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. Cell Systems, 2020, 11, 186-195.e9.	6.2	19

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37	Pandemics are catalysts of scientific novelty: Evidence from <scp>COVID</scp>â€•19. Journal of the Association for Information Science and Technology, 2022, 73, 1065-1078.	2.9	19
38	Aggregative and stochastic model of main path identification: a case study on graphene. Scientometrics, 2014, 98, 633-655.	3.0	17
39	Identifying kinase dependency in cancer cells by integrating high-throughput drug screening and kinase inhibition data. Bioinformatics, 2015, 31, 3799-3806.	4.1	17
40	Graph Transformer Networks: Learning meta-path graphs to improve GNNs. Neural Networks, 2022, 153, 104-119.	5.9	16
41	HiPub: translating PubMed and PMC texts to networks for knowledge discovery. Bioinformatics, 2016, 32, 2886-2888.	4.1	15
42	FlavorGraph: a large-scale food-chemical graph for generating food representations and recommending food pairings. Scientific Reports, 2021, 11, 931.	3.3	15
43	Look at the First Sentence: Position Bias in Question Answering. , 2020, , .		14
44	A Pilot Study of Biomedical Text Comprehension using an Attention-Based Deep Neural Reader: Design and Experimental Analysis. JMIR Medical Informatics, 2018, 6, e2.	2.6	13
45	DeepPIM: A deep neural point-of-interest imputation model. Information Sciences, 2018, 465, 61-71.	6.9	12
46	Predicting mechanism of action of novel compounds using compound structure and transcriptomic signature coembedding. Bioinformatics, 2021, 37, i376-i382.	4.1	11
47	A quantitative approach to recommend promising technologies for SME innovation: a case study on knowledge arbitrage from LCD to solar cell. Scientometrics, 2013, 96, 589-604.	3.0	10
48	Automatic Context-Specific Subnetwork Discovery from Large Interaction Networks. PLoS ONE, 2014, 9, e84227.	2.5	9
49	How Do Your Biomedical Named Entity Recognition Models Generalize to Novel Entities?. IEEE Access, 2022, 10, 31513-31523.	4.2	8
50	Adaptive pattern mining model for early detection of botnetâ€•propagation scale. Security and Communication Networks, 2012, 5, 917-927.	1.5	7
51	BEReX: Biomedical Entity-Relationship eXplorer. Bioinformatics, 2014, 30, 135-136.	4.1	7
52	Prioritizing biological pathways by recognizing context in time-series gene expression data. BMC Bioinformatics, 2016, 17, 477.	2.6	7
53	Systems Pharmacology-Based Approach of Connecting Disease Genes in Genome-Wide Association Studies with Traditional Chinese Medicine. International Journal of Genomics, 2018, 2018, 1-11.	1.6	7
54	Crowdsourced identification of multi-target kinase inhibitors for RET- and TAU- based disease: The Multi-Targeting Drug DREAM Challenge. PLoS Computational Biology, 2021, 17, e1009302.	3.2	7

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55	RecipeBowl: A Cooking Recommender for Ingredients and Recipes Using Set Transformer. IEEE Access, 2021, 9, 143623-143633.	4.2	7
56	Can Machines Learn to Comprehend Scientific Literature?. IEEE Access, 2019, 7, 16246-16256.	4.2	6
57	Effectively training neural networks for stock index prediction: Predicting the S&P 500 index without using its index data. PLoS ONE, 2020, 15, e0230635.	2.5	6
58	CONFIGURE: A pipeline for identifying context specific regulatory modules from gene expression data and its application to breast cancer. BMC Medical Genomics, 2019, 12, 97.	1.5	5
59	A Drug-Induced Liver Injury Prediction Model using Transcriptional Response Data with Graph Neural Network. , 2020, , .		5
60	BOSS: context-enhanced search for biomedical objects. BMC Medical Informatics and Decision Making, 2012, 12, S7.	3.0	4
61	Bipartite Link Prediction by Intra-Class Connection Based Triadic Closure. IEEE Access, 2020, 8, 140194-140204.	4.2	4
62	Comparative meta-analysis between human and mouse cancer microarray data reveals critical pathways. International Journal of Data Mining and Bioinformatics, 2013, 8, 349.	0.1	3
63	Using Gene Pair Combinations to Improve the Accuracy of the PAM Classifier. , 2009, , .		1
64	CLIP-GENE: a web service of the condition specific context-laid integrative analysis for gene prioritization in mouse TF knockout experiments. Biology Direct, 2016, 11, 57.	4.6	1
65	In silico experiment system for testing hypothesis on gene functions using three condition specific biological networks. Methods, 2018, 145, 10-15.	3.8	1
66	Exploring the spatial reasoning ability of neural models in human IQ tests. Neural Networks, 2021, 140, 27-38.	5.9	1
67	iCOSSY: An Online Tool for Context-Specific Subnetwork Discovery from Gene Expression Data. PLoS ONE, 2015, 10, e0131656.	2.5	1
68	Deep-Learning-Based Natural Language Processing of Serial Free-Text Radiological Reports for Predicting Rectal Cancer Patient Survival. Frontiers in Oncology, 2021, 11, 747250.	2.8	1
69	Meta-analysis of cancer microarray data reveals signaling pathway hotspots. , 2009, , .		0
70	A scalable method for detecting multiple loci associated with traits using TF-IDF weighting and association rule mining. , 2010, , .		0
71	SignatureClust: a tool for landmark gene-guided clustering. Soft Computing, 2012, 16, 411-418.	3.6	0
72	Mining Botnets and Their Evolution Patterns. Journal of Computer Science and Technology, 2013, 28, 605-615.	1.5	0