

Sungdong Kim

List of Publications by Year in descending order

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Version: 2024-02-01

17
papers

3,348
citations

687220

13
h-index

940416

16
g-index

19
all docs

19
docs citations

19
times ranked

3065
citing authors

#	ARTICLE	IF	CITATIONS
1	BioBERT: a pre-trained biomedical language representation model for biomedical text mining. <i>Bioinformatics</i> , 2020, 36, 1234-1240.	1.8	2,733
2	Building a PubMed knowledge graph. <i>Scientific Data</i> , 2020, 7, 205.	2.4	94
3	BEST: Next-Generation Biomedical Entity Search Tool for Knowledge Discovery from Biomedical Literature. <i>PLoS ONE</i> , 2016, 11, e0164680.	1.1	74
4	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2017, 45, D784-D789.	6.5	74
5	In silico drug combination discovery for personalized cancer therapy. <i>BMC Systems Biology</i> , 2018, 12, 16.	3.0	47
6	ChimerDB 4.0: an updated and expanded database of fusion genes. <i>Nucleic Acids Research</i> , 2020, 48, D817-D824.	6.5	44
7	Deep learning of mutation-gene-drug relations from the literature. <i>BMC Bioinformatics</i> , 2018, 19, 21.	1.2	43
8	Crowdsourced mapping of unexplored target space of kinase inhibitors. <i>Nature Communications</i> , 2021, 12, 3307.	5.8	41
9	Improved survival analysis by learning shared genomic information from pan-cancer data. <i>Bioinformatics</i> , 2020, 36, i389-i398.	1.8	39
10	ReSimNet: drug response similarity prediction using Siamese neural networks. <i>Bioinformatics</i> , 2019, 35, 5249-5256.	1.8	37
11	Mut2Vec: distributed representation of cancerous mutations. <i>BMC Medical Genomics</i> , 2018, 11, 33.	0.7	30
12	BRONCO: Biomedical entity Relation ONcology COrpus for extracting gene-variant-disease-drug relations. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, .	1.4	29
13	Community Assessment of the Predictability of Cancer Protein and Phosphoprotein Levels from Genomics and Transcriptomics. <i>Cell Systems</i> , 2020, 11, 186-195.e9.	2.9	19
14	Predicting mechanism of action of novel compounds using compound structure and transcriptomic signature coembedding. <i>Bioinformatics</i> , 2021, 37, i376-i382.	1.8	11
15	Bipartite Link Prediction by Intra-Class Connection Based Triadic Closure. <i>IEEE Access</i> , 2020, 8, 140194-140204.	2.6	4
16	Deep-Learning-Based Natural Language Processing of Serial Free-Text Radiological Reports for Predicting Rectal Cancer Patient Survival. <i>Frontiers in Oncology</i> , 2021, 11, 747250.	1.3	1
17	Characterization of hyperprogressive disease in patients with advanced biliary tract cancer treated with anti-PD-1 inhibitor: A multicenter retrospective study. <i>Journal of Clinical Oncology</i> , 2021, 39, 339-339.	0.8	0