Hojung Nam

List of Publications by Year
in descending order

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44 papers	2,693 citations	304743 22 h-index	302126 39 g-index
45 all docs	45 docs citations	45 times ranked	3902 citing authors

#	Article	IF	Citations
1	A comprehensive genomeâ€scale reconstruction of Escherichia coli metabolismâ€”2011. Molecular Systems Biology, 2011, 7, 535.	7.2	917
2	DeepConv-DTI: Prediction of drug-target interactions via deep learning with convolution on protein sequences. PLoS Computational Biology, 2019, 15, e1007129.	3.2	320
3	Network Context and Selection in the Evolution to Enzyme Specificity. Science, 2012, 337, 1101-1104.	12.6	249
4	The CH25Hâ€“CYP7B1â€“RORÎ± axis of cholesterol metabolism regulates osteoarthritis. Nature, 2019, 566, 254-258.	27.8	172
5	Combining tissue transcriptomics and urine metabolomics for breast cancer biomarker identification. Bioinformatics, 2009, 25, 3151-3157.	4.1	107
6	A Systems Approach to Predict Oncometabolites via Context-Specific Genome-Scale Metabolic Networks. PLoS Computational Biology, 2014, 10, e1003837.	3.2	63
7	Systems assessment of transcriptional regulation on central carbon metabolism by Cra and CRP. Nucleic Acids Research, 2018, 46, 2901-2917.	14.5	62
8	Discovering Health Benefits of Phytochemicals with Integrated Analysis of the Molecular Network, Chemical Properties and Ethnopharmacological Evidence. Nutrients, 2018, 10, 1042.	4.1	62
9	Virmid: accurate detection of somatic mutations with sample impurity inference. Genome Biology, 2013, 14, R90.	9.6	58
10	Cross-species oncogenic signatures of breast cancer in canine mammary tumors. Nature Communications, 2020, 11, 3616.	12.8	58
11	SELF-BLM: Prediction of drug-target interactions via self-training SVM. PLoS ONE, 2017, 12, e0171839.	2.5	57
12	Prediction models for drug-induced hepatotoxicity by using weighted molecular fingerprints. BMC Bioinformatics, 2017, 18, 227.	2.6	44
13	The use of technical replication for detection of low-level somatic mutations in next-generation sequencing. Nature Communications, 2019, 10, 1047.	12.8	43
14	Artificial Intelligence in Drug Discovery: A Comprehensive Review of Data-driven and Machine Learning Approaches. Biotechnology and Bioprocess Engineering, 2020, 25, 895-930.	2.6	43
15	Identification of drug-target interaction by a random walk with restart method on an interactome network. BMC Bioinformatics, 2018, 19, 208.	2.6	42
16	Predicting the Absorption Potential of Chemical Compounds Through a Deep Learning Approach. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2018, 15, 432-440.	3.0	38
17	Drug repositioning of herbal compounds via a machine-learning approach. BMC Bioinformatics, 2019, 20, 247.	2.6	37
18	The role of cellular objectives and selective pressures in metabolic pathway evolution. Current Opinion in Biotechnology, 2011, 22, 595-600.	6.6	31

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19	hERG-Att: Self-attention-based deep neural network for predicting hERG blockers. Computational Biology and Chemistry, 2020, 87, 107286.	2.3	28
20	Prognostic factor analysis for breast cancer using gene expression profiles. BMC Medical Informatics and Decision Making, 2016, 16, 56.	3.0	25
21	Prediction of compound-target interactions of natural products using large-scale drug and protein information. BMC Bioinformatics, 2016, 17, 219.	2.6	24
22	Whole-exome and whole-transcriptome sequencing of canine mammary gland tumors. Scientific Data, 2019, 6, 147.	5.3	24
23	Identification of temporal association rules from time-series microarray data sets. BMC Bioinformatics, 2009, 10, S6.	2.6	22
24	Development of Tissue-Specific Age Predictors Using DNA Methylation Data. Genes, 2019, 10, 888.	2.4	21
25	Sequence-based prediction of protein binding regions and drugâ€“target interactions. Journal of Cheminformatics, 2022, 14, 5.	6.1	16
26	HiDRA: Hierarchical Network for Drug Response Prediction with Attention. Journal of Chemical Information and Modeling, 2021, 61, 3858-3867.	5.4	15
27	bZIPDB : A database of regulatory information for human bZIP transcription factors. BMC Genomics, 2007, 8, 136.	2.8	13
28	In silico profiling of systemic effects of drugs to predict unexpected interactions. Scientific Reports, 2018, 8, 1612.	3.3	13
29	DeSIDE-DDI: interpretable prediction of drug-drug interactions using drug-induced gene expressions. Journal of Cheminformatics, 2022, 14, 9.	6.1	13
30	Computational identification of altered metabolism using gene expression and metabolic pathways. Biotechnology and Bioengineering, 2009, 103, 835-843.	3.3	11
31	A Data-Driven Approach for Identifying Medicinal Combinations of Natural Products. IEEE Access, 2018, 6, 58106-58118.	4.2	11
32	Phenotype-oriented network analysis for discovering pharmacological effects of natural compounds. Scientific Reports, 2018, 8, 11667.	3.3	11
33	Identification of genomic features in the classification of loss- and gain-of-function mutation. BMC Medical Informatics and Decision Making, 2015, 15, S6.	3.0	10
34	Exploring molecular links between lymph node invasion and cancer prognosis in human breast cancer. BMC Systems Biology, 2011, 5, S4.	3.0	8
35	BayeshERG: a robust, reliable and interpretable deep learning model for predicting hERG channel blockers. Briefings in Bioinformatics, 2022, 23, .	6.5	6
36	AI-based prediction of new binding site and virtual screening for the discovery of novel P2X3 receptor antagonists. European Journal of Medicinal Chemistry, 2022, 240, 114556.	5.5	6

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37	SoloDel: a probabilistic model for detecting low-frequent somatic deletions from unmatched sequencing data. Bioinformatics, 2015, 31, 3105-3113.	4.1	3
38	Prediction model construction of mouse stem cell pluripotency using CpG and non-CpG DNA methylation markers. BMC Bioinformatics, 2020, 21, 175.	2.6	3
39	1H NMR based urinary metabolites profiling dataset of canine mammary tumors. Scientific Data, 2022, 9, 132.	5.3	3
40	Identification of a Specific Base Sequence of Pathogenic E. Coli through a Genomic Analysis. , 2014, , .		1
41	Identification of temporal association rules from time-series microarray data set. , 2008, , .		0
42	mvp- an open-source preprocessor for cleaning duplicate records and missing values in mass spectrometry data. FEBS Open Bio, 2017, 7, 1051-1059.	2.3	0
43	Computational identification of significantly regulated metabolic reactions by integration of data on enzyme activity and gene expression. BMB Reports, 2008, 41, 609-614.	2.4	0
44	In Silico Simulation of Signal Cascades in Biomedical Networks Based on the Production Rule System. Lecture Notes in Computer Science, 2017, , 356-361.	1.3	0