Dokyoon Kim

List of Publications by Year
in descending order

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57 papers	1,812 citations	394421 19 h-index	289244 40 g-index
66 all docs	66 docs citations	66 times ranked	3494 citing authors

#	Article	IF	Citations
1	A deep learning model for screening type 2 diabetes from retinal photographs. Nutrition, Metabolism and Cardiovascular Diseases, 2022, 32, 1218-1226.	2.6	8
2	Leveraging deep phenotyping from health check-up cohort with 10,000 Korean individuals for phenome-wide association study of 136 traits. Scientific Reports, 2022, 12, 1930.	3.3	1
3	NETMAGE: A human disease phenotype map generator for the network-based visualization of phenome-wide association study results. GigaScience, 2022, 11, .	6.4	5
4	Sex Differences in the Metabolome of Alzheimer's Disease Progression. Frontiers in Radiology, 2022, 2, .	2.0	5
5	Development and validation of a novel strong prognostic index for colon cancer through a robust combination of laboratory features for systemic inflammation: a prognostic immune nutritional index. British Journal of Cancer, 2022, , .	6.4	12
6	Dissecting the clinical relevance of polygenic risk score for obesityâ€"a cross-sectional, longitudinal analysis. International Journal of Obesity, 2022, 46, 1686-1693.	3.4	6
7	Reliability of microarray analysis for studying periodontitis: low consistency in 2 periodontitis cohort data sets from different platforms and an integrative meta-analysis. Journal of Periodontal and Implant Science, 2021, 51, 18.	2.0	1
8	Multi-layered network-based pathway activity inference using directed random walks: application to predicting clinical outcomes in urologic cancer. Bioinformatics, 2021, 37, 2405-2413.	4.1	4
9	Prognostic Effect of Inflammatory Genes on Stage Iâ€"III Colorectal Cancerâ€"Integrative Analysis of TCGA Data. Cancers, 2021, 13, 751.	3.7	8
10	HiG2Vec: hierarchical representations of Gene Ontology and genes in the PoincarÃ© ball. Bioinformatics, 2021, 37, 2971-2980.	4.1	10
11	Genetic Analysis Reveals Rare Variants in T-Cell Response Gene MR1 Associated with Poor Overall Survival after Urothelial Cancer Diagnosis. Cancers, 2021, 13, 1864.	3.7	0
12	A Novel Graph Based Semi-Supervised Learning Approach to Identify Pathways Contributing to the Development of Diabetes and Obesity. Journal of the Endocrine Society, 2021, 5, A656-A657.	0.2	0
13	Why Is the Electronic Health Record So Challenging for Research and Clinical Care?. Methods of Information in Medicine, 2021, 60, 032-048.	1.2	13
14	Epigenetic interplay between methylation and miRNA in bladder cancer: focus on isoform expression. BMC Genomics, 2021, 22, 754.	2.8	3
15	A Novel Scoring System for Response of Preoperative Chemoradiotherapy in Locally Advanced Rectal Cancer Using Early-Treatment Blood Features Derived From Machine Learning. Frontiers in Oncology, 2021, 11, 790894.	2.8	2
16	netCRS: Network-based comorbidity risk score for prediction of myocardial infarction using biobank-scaled PheWAS data. , 2021, , .		0
17	Translational Bioinformatics: Integrating Electronic Health Record and Omics Data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2021, 26, 356-359.	0.7	1
18	Identifying imaging genetics biomarkers in Alzheimerâ€™s disease via integrating graph convolutional neural network and canonical correlation analysis. Alzheimer's and Dementia, 2021, 17, .	0.8	0

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19	A Network-Based Analysis of Disease Complication Associations for Obstetric Disorders in the UK Biobank. Journal of Personalized Medicine, 2021, 11, 1382.	2.5	4
20	Interpretable temporal graph neural network for prognostic prediction of Alzheimerâ€™s disease using longitudinal neuroimaging data. , 2021, 2021, 1381-1384.		8
21	Novel polygenic risk score approach with transcriptome-based weighting for genetic risk prediction of late-onset Alzheimer's disease.. Alzheimer's and Dementia, 2021, 17 Suppl 3, e053960.	0.8	0
22	CNV Association of Diverse Clinical Phenotypes from eMERGE reveals novel disease biology underlying cardiovascular disease. International Journal of Cardiology, 2020, 298, 107-113.	1.7	7
23	Translational Bioinformatics: Integrating Electronic Health Record and Omics Data. , 2020, , .		1
24	Liver imaging features by convolutional neural network to predict the metachronous liver metastasis in stage I-III colorectal cancer patients based on preoperative abdominal CT scan. BMC Bioinformatics, 2020, 21, 382.	2.6	20
25	Genetic risk prediction of lateâ€onset Alzheimerâ€™s disease based on tissueâ€specific transcriptomic analysis and polygenic risk scores. Alzheimer's and Dementia, 2020, 16, e045184.	0.8	1
26	Ideas for how informaticians can get involved with COVID-19 research. BioData Mining, 2020, 13, 3.	4.0	20
27	MildInt: Deep Learning-Based Multimodal Longitudinal Data Integration Framework. Frontiers in Genetics, 2019, 10, 617.	2.3	35
28	Exome-Wide Rare Variant Analysis From the DiscovEHR Study Identifies Novel Candidate Predisposition Genes for Endometrial Cancer. Frontiers in Oncology, 2019, 9, 574.	2.8	18
29	Preparing next-generation scientists for biomedical big data: artificial intelligence approaches. Personalized Medicine, 2019, 16, 247-257.	1.5	28
30	An exome-wide rare variant analysis of Korean men identifies three novel genes predisposing to prostate cancer. Scientific Reports, 2019, 9, 17173.	3.3	6
31	Human-Disease Phenotype Map Derived from PheWAS across 38,682 Individuals. American Journal of Human Genetics, 2019, 104, 55-64.	6.2	54
32	Codon bias among synonymous rare variants is associated with Alzheimerâ€™s disease imaging biomarker. , 2018, , .		6
33	Population-dependent Intron Retention and DNA Methylation in Breast Cancer. Molecular Cancer Research, 2018, 16, 461-469.	3.4	23
34	Min-redundancy and max-relevance multi-view feature selection for predicting ovarian cancer survival using multi-omics data. BMC Medical Genomics, 2018, 11, 71.	1.5	41
35	The effects of alternative splicing on miRNA binding sites in bladder cancer. PLoS ONE, 2018, 13, e0190708.	2.5	17
36	The joint effect of air pollution exposure and copy number variation on risk for autism. Autism Research, 2017, 10, 1470-1480.	3.8	38

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37	Identification of epigenetic interactions between miRNA and DNA methylation associated with gene expression as potential prognostic markers in bladder cancer. BMC Medical Genomics, 2017, 10, 30.	1.5	59
38	Using knowledge-driven genomic interactions for multi-omics data analysis: metadimensional models for predicting clinical outcomes in ovarian carcinoma. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 577-587.	4.4	41
39	PLATO software provides analytic framework for investigating complexity beyond genome-wide association studies. Nature Communications, 2017, 8, 1167.	12.8	40
40	Integrative information theoretic network analysis for genome-wide association study of aspirin exacerbated respiratory disease in Korean population. BMC Medical Genomics, 2017, 10, 31.	1.5	12
41	Identifying subtype-specific associations between gene expression and DNA methylation profiles in breast cancer. BMC Medical Genomics, 2017, 10, 28.	1.5	18
42	Exome-based genome-wide association study and risk assessment using genetic risk score to prostate cancer in the Korean population. Oncotarget, 2017, 8, 43934-43943.	1.8	7
43	Integration of bioinformatics and imaging informatics for identifying rare PSEN1 variants in Alzheimerâ€™s disease. BMC Medical Genomics, 2016, 9, 30.	1.5	20
44	Identification of genetic interaction networks via an evolutionary algorithm evolved Bayesian network. BioData Mining, 2016, 9, 18.	4.0	8
45	BIOFILTER AS A FUNCTIONAL ANNOTATION PIPELINE FOR COMMON AND RARE COPY NUMBER BURDEN. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2016, 21, 357-68.	0.7	2
46	Predicting censored survival data based on the interactions between meta-dimensional omics data in breast cancer. Journal of Biomedical Informatics, 2015, 56, 220-228.	4.3	32
47	Methods of integrating data to uncover genotypeâ€“phenotype interactions. Nature Reviews Genetics, 2015, 16, 85-97.	16.3	803
48	Knowledge boosting: a graph-based integration approach with multi-omics data and genomic knowledge for cancer clinical outcome prediction. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 109-120.	4.4	79
49	Binning somatic mutations based on biological knowledge for predicting survival: an application in renal cell carcinoma. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 96-107.	0.7	11
50	Knowledge-driven genomic interactions: an application in ovarian cancer. BioData Mining, 2014, 7, 20.	4.0	21
51	Incorporating inter-relationships between different levels of genomic data into cancer clinical outcome prediction. Methods, 2014, 67, 344-353.	3.8	30
52	BINNING SOMATIC MUTATIONS BASED ON BIOLOGICAL KNOWLEDGE FOR PREDICTING SURVIVAL: AN APPLICATION IN RENAL CELL CARCINOMA. , 2014, , .		24
53	Intra-relation reconstruction from inter-relation: miRNA to gene expression. BMC Systems Biology, 2013, 7, S8.	3.0	11
54	Relative impact of multi-layered genomic data on gene expression phenotypes in serous ovarian tumors. BMC Systems Biology, 2013, 7, S9.	3.0	24

#	Article	IF	Citations
55	ATHENA: Identifying interactions between different levels of genomic data associated with cancer clinical outcomes using grammatical evolution neural network. BioData Mining, 2013, 6, 23.	4.0	64
56	Synergistic effect of different levels of genomic data for cancer clinical outcome prediction. Journal of Biomedical Informatics, 2012, 45, 1191-1198.	4.3	89
57	Reply to comment(s) on â€œDevelopment and validation of a novel strong prognostic index for colon cancer through a robust combination of laboratory features for systemic inflammation: a prognostic immune nutritional indexâ€. British Journal of Cancer, 0, , .	6.4	2