

Wenyu Wang

List of Publications by Year in descending order

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Version: 2024-02-01

32
papers

1,090
citations

643344

15
h-index

511568

30
g-index

39
all docs

39
docs citations

39
times ranked

1672
citing authors

#	ARTICLE	IF	CITATIONS
1	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. <i>Cell Reports Medicine</i> , 2022, 3, 100492.	3.3	33
2	SynergyFinder Plus: Toward Better Interpretation and Annotation of Drug Combination Screening Datasets. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 587-596.	3.0	159
3	DrugComb update: a more comprehensive drug sensitivity data repository and analysis portal. <i>Nucleic Acids Research</i> , 2021, 49, W174-W184.	6.5	54
4	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	13
5	nucleAlzer: A Parameter-free Deep Learning Framework for Nucleus Segmentation Using Image Style Transfer. <i>Cell Systems</i> , 2020, 10, 453-458.e6.	2.9	163
6	eQTLs Weighted Genetic Correlation Analysis Detected Brain Region Differences in Genetic Correlations for Complex Psychiatric Disorders. <i>Schizophrenia Bulletin</i> , 2019, 45, 709-715.	2.3	6
7	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. <i>Npj Systems Biology and Applications</i> , 2019, 5, 20.	1.4	32
8	Fecal microbiota transplantation for refractory diarrhea in immunocompromised diseases: a pediatric case report. <i>Italian Journal of Pediatrics</i> , 2019, 45, 116.	1.0	16
9	Drug combination sensitivity scoring facilitates the discovery of synergistic and efficacious drug combinations in cancer. <i>PLoS Computational Biology</i> , 2019, 15, e1006752.	1.5	106
10	DrugComb: an integrative cancer drug combination data portal. <i>Nucleic Acids Research</i> , 2019, 47, W43-W51.	6.5	153
11	Investigating the Survival Benefit of Combining Radiotherapy for Surgery Treated Locally Advanced Esophageal Squamous Cell Carcinoma Patients Aged 65 and Older. <i>Journal of Gastrointestinal Surgery</i> , 2019, 23, 2111-2118.	0.9	1
12	Making Sense of the Epigenome Using Data Integration Approaches. <i>Frontiers in Pharmacology</i> , 2019, 10, 126.	1.6	58
13	Combined gene essentiality scoring improves the prediction of cancer dependency maps. <i>EBioMedicine</i> , 2019, 50, 67-80.	2.7	18
14	Integrating genome-wide association study summaries and element-gene interaction datasets identified multiple associations between elements and complex diseases. <i>Genetic Epidemiology</i> , 2018, 42, 168-173.	0.6	6
15	Assessing the Associations of Blood Metabolites With Osteoporosis: A Mendelian Randomization Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 1850-1855.	1.8	19
16	GWAS summary-based pathway analysis correcting for the genetic confounding impact of environmental exposures. <i>Briefings in Bioinformatics</i> , 2018, 19, 725-730.	3.2	3
17	A Genome-wide Expression Association Analysis Identifies Genes and Pathways Associated with Amyotrophic Lateral Sclerosis. <i>Cellular and Molecular Neurobiology</i> , 2018, 38, 635-639.	1.7	30
18	A Genomewide Integrative Analysis of GWAS and eQTLs Data Identifies Multiple Genes and Gene Sets Associated with Obesity. <i>BioMed Research International</i> , 2018, 2018, 1-5.	0.9	27

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19	Genome-wide association study identifies COL2A1 locus involved in the hand development failure of Kashin-Beck disease. <i>Scientific Reports</i> , 2017, 7, 40020.	1.6	4
20	Integrating genome-wide association study and expression quantitative trait loci data identifies multiple genes and gene set associated with neuroticism. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2017, 78, 149-152.	2.5	12
21	Genome-wide DNA methylation profiling of articular cartilage reveals significant epigenetic alterations in Kashin-Beck disease and osteoarthritis. <i>Osteoarthritis and Cartilage</i> , 2017, 25, 2127-2133.	0.6	16
22	Tissue-specific pathway association analysis using genome-wide association study summaries. <i>Bioinformatics</i> , 2017, 33, 243-247.	1.8	21
23	Integrating Genome-Wide Association and eQTLs Studies Identifies the Genes and Gene Sets Associated with Diabetes. <i>BioMed Research International</i> , 2017, 2017, 1-4.	0.9	3
24	Genome-wide DNA methylation profile analysis identifies differentially methylated loci associated with ankylosis spondylitis. <i>Arthritis Research and Therapy</i> , 2017, 19, 177.	1.6	34
25	Survival benefit evaluation of radiotherapy in esophageal cancer patients aged 80 and older. <i>Oncotarget</i> , 2017, 8, 112094-112102.	0.8	9
26	Comparative analysis of gene expression profiles of hip articular cartilage between non-traumatic necrosis and osteoarthritis. <i>Gene</i> , 2016, 591, 43-47.	1.0	27
27	Association Between Cartilage Intermediate Layer Protein and Degeneration of Intervertebral Disc. <i>Spine</i> , 2016, 41, E1244-E1248.	1.0	12
28	A bivariate genome-wide association study identifies ADAM12 as a novel susceptibility gene for Kashin-Beck disease. <i>Scientific Reports</i> , 2016, 6, 31792.	1.6	9
29	PAPA: a flexible tool for identifying pleiotropic pathways using genome-wide association study summaries. <i>Bioinformatics</i> , 2016, 32, 946-948.	1.8	7
30	PPARGC1B gene is associated with Kashin-Beck disease in Han Chinese. <i>Functional and Integrative Genomics</i> , 2016, 16, 459-463.	1.4	1
31	Exome sequencing identified FGF12 as a novel candidate gene for Kashin-Beck disease. <i>Functional and Integrative Genomics</i> , 2016, 16, 13-17.	1.4	10
32	A Community Challenge for Pancancer Drug Mechanism of Action Inference from Perturbational Profile Data. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0