

# Wenyu Wang

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

1,090  
citations

567281

15  
h-index

454955

30  
g-index

39  
all docs

39  
docs citations

39  
times ranked

1527  
citing authors

#	ARTICLE	IF	CITATIONS
1	nucleAlzer: A Parameter-free Deep Learning Framework for Nucleus Segmentation Using Image Style Transfer. Cell Systems, 2020, 10, 453-458.e6.	6.2	163
2	SynergyFinder Plus: Toward Better Interpretation and Annotation of Drug Combination Screening Datasets. Genomics, Proteomics and Bioinformatics, 2022, 20, 587-596.	6.9	159
3	DrugComb: an integrative cancer drug combination data portal. Nucleic Acids Research, 2019, 47, W43-W51.	14.5	153
4	Drug combination sensitivity scoring facilitates the discovery of synergistic and efficacious drug combinations in cancer. PLoS Computational Biology, 2019, 15, e1006752.	3.2	106
5	Making Sense of the Epigenome Using Data Integration Approaches. Frontiers in Pharmacology, 2019, 10, 126.	3.5	58
6	DrugComb update: a more comprehensive drug sensitivity data repository and analysis portal. Nucleic Acids Research, 2021, 49, W174-W184.	14.5	54
7	Genome-wide DNA methylation profile analysis identifies differentially methylated loci associated with ankylosis spondylitis. Arthritis Research and Therapy, 2017, 19, 177.	3.5	34
8	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. Cell Reports Medicine, 2022, 3, 100492.	6.5	33
9	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. Npj Systems Biology and Applications, 2019, 5, 20.	3.0	32
10	A Genome-wide Expression Association Analysis Identifies Genes and Pathways Associated with Amyotrophic Lateral Sclerosis. Cellular and Molecular Neurobiology, 2018, 38, 635-639.	3.3	30
11	Comparative analysis of gene expression profiles of hip articular cartilage between non-traumatic necrosis and osteoarthritis. Gene, 2016, 591, 43-47.	2.2	27
12	A Genomewide Integrative Analysis of GWAS and eQTLs Data Identifies Multiple Genes and Gene Sets Associated with Obesity. BioMed Research International, 2018, 2018, 1-5.	1.9	27
13	Tissue-specific pathway association analysis using genome-wide association study summaries. Bioinformatics, 2017, 33, 243-247.	4.1	21
14	Assessing the Associations of Blood Metabolites With Osteoporosis: A Mendelian Randomization Study. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 1850-1855.	3.6	19
15	Combined gene essentiality scoring improves the prediction of cancer dependency maps. EBioMedicine, 2019, 50, 67-80.	6.1	18
16	Genome-wide DNA methylation profiling of articular cartilage reveals significant epigenetic alterations in Kashin-Beck disease and osteoarthritis. Osteoarthritis and Cartilage, 2017, 25, 2127-2133.	1.3	16
17	Fecal microbiota transplantation for refractory diarrhea in immunocompromised diseases: a pediatric case report. Italian Journal of Pediatrics, 2019, 45, 116.	2.6	16
18	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. Briefings in Bioinformatics, 2021, 22, .	6.5	13

#	ARTICLE	IF	CITATIONS
19	Association Between Cartilage Intermediate Layer Protein and Degeneration of Intervertebral Disc. Spine, 2016, 41, E1244-E1248.	2.0	12
20	Integrating genome-wide association study and expression quantitative trait loci data identifies multiple genes and gene set associated with neuroticism. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2017, 78, 149-152.	4.8	12
21	Exome sequencing identified FGF12 as a novel candidate gene for Kashin-Beck disease. Functional and Integrative Genomics, 2016, 16, 13-17.	3.5	10
22	A bivariate genome-wide association study identifies ADAM12 as a novel susceptibility gene for Kashin-Beck disease. Scientific Reports, 2016, 6, 31792.	3.3	9
23	Survival benefit evaluation of radiotherapy in esophageal cancer patients aged 80 and older. Oncotarget, 2017, 8, 112094-112102.	1.8	9
24	PAPA: a flexible tool for identifying pleiotropic pathways using genome-wide association study summaries. Bioinformatics, 2016, 32, 946-948.	4.1	7
25	Integrating genome-wide association study summaries and element-gene interaction datasets identified multiple associations between elements and complex diseases. Genetic Epidemiology, 2018, 42, 168-173.	1.3	6
26	eQTLs Weighted Genetic Correlation Analysis Detected Brain Region Differences in Genetic Correlations for Complex Psychiatric Disorders. Schizophrenia Bulletin, 2019, 45, 709-715.	4.3	6
27	Genome-wide association study identifies COL2A1 locus involved in the hand development failure of Kashin-Beck disease. Scientific Reports, 2017, 7, 40020.	3.3	4
28	Integrating Genome-Wide Association and eQTLs Studies Identifies the Genes and Gene Sets Associated with Diabetes. BioMed Research International, 2017, 2017, 1-4.	1.9	3
29	CWAS summary-based pathway analysis correcting for the genetic confounding impact of environmental exposures. Briefings in Bioinformatics, 2018, 19, 725-730.	6.5	3
30	PPARGC1B gene is associated with Kashin-Beck disease in Han Chinese. Functional and Integrative Genomics, 2016, 16, 459-463.	3.5	1
31	Investigating the Survival Benefit of Combining Radiotherapy for Surgery Treated Locally Advanced Esophageal Squamous Cell Carcinoma Patients Aged 65 and Older. Journal of Gastrointestinal Surgery, 2019, 23, 2111-2118.	1.7	1
32	A Community Challenge for Pancancer Drug Mechanism of Action Inference from Perturbational Profile Data. SSRN Electronic Journal, 0, , .	0.4	0