Rong Xu

List of Publications by Year in descending order

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172386 143943 4,002 93 29 57 citations h-index g-index papers 96 96 96 5135 citing authors docs citations times ranked all docs

#	Article	IF	CITATIONS
1	Increased risk of $\langle scp \rangle COVID \langle scp \rangle \hat{a} \in 19$ infection and mortality in people with mental disorders: analysis from electronic health records in the United States. World Psychiatry, 2021, 20, 124-130.	4.8	491
2	COVID-19 risk and outcomes in patients with substance use disorders: analyses from electronic health records in the United States. Molecular Psychiatry, 2021, 26, 30-39.	4.1	455
3	Analyses of Risk, Racial Disparity, and Outcomes Among US Patients With Cancer and COVID-19 Infection. JAMA Oncology, 2021, 7, 220.	3.4	304
4	COVIDâ€19 and dementia: Analyses of risk, disparity, and outcomes from electronic health records in the US. Alzheimer's and Dementia, 2021, 17, 1297-1306.	0.4	177
5	A genome-wide systems analysis reveals strong link between colorectal cancer and trimethylamine N-oxide (TMAO), a gut microbial metabolite of dietary meat and fat. BMC Genomics, 2015, 16, S4.	1.2	143
6	Towards understanding brain-gut-microbiome connections in Alzheimer's disease. BMC Systems Biology, 2016, 10, 63.	3.0	128
7	Incidence Rates and Clinical Outcomes of SARS-CoV-2 Infection With the Omicron and Delta Variants in Children Younger Than 5 Years in the US. JAMA Pediatrics, 2022, 176, 811.	3.3	108
8	Increased risk for <scp>COVID</scp> â€19 breakthrough infection in fully vaccinated patients with substance use disorders in the United States between December 2020 and August 2021. World Psychiatry, 2022, 21, 124-132.	4.8	105
9	Large-scale extraction of accurate drug-disease treatment pairs from biomedical literature for drug repurposing. BMC Bioinformatics, 2013, 14, 181.	1.2	92
10	Tumor Necrosis Factor (TNF) blocking agents are associated with lower risk for Alzheimer's disease in patients with rheumatoid arthritis and psoriasis. PLoS ONE, 2020, 15, e0229819.	1.1	92
11	Oligodendroglial glycolytic stress triggers inflammasome activation and neuropathology in Alzheimer's disease. Science Advances, 2020, 6, .	4.7	79
12	Streamlined alpha-synuclein RT-QuIC assay for various biospecimens in Parkinson's disease and dementia with Lewy bodies. Acta Neuropathologica Communications, 2021, 9, 62.	2.4	79
13	Large-scale combining signals from both biomedical literature and the FDA Adverse Event Reporting System (FAERS) to improve post-marketing drug safety signal detection. BMC Bioinformatics, 2014, 15, 17.	1.2	71
14	Predict drug permeability to blood–brain-barrier from clinical phenotypes: drug side effects and drug indications. Bioinformatics, 2017, 33, 901-908.	1.8	61
15	Breakthrough SARS-CoV-2 Infections, Hospitalizations, and Mortality in Vaccinated Patients With Cancer in the US Between December 2020 and November 2021. JAMA Oncology, 2022, 8, 1027.	3.4	61
16	When hematologic malignancies meet COVID-19 in the United States: Infections, death and disparities. Blood Reviews, 2021, 47, 100775.	2.8	59
17	Towards building a disease-phenotype knowledge base: extracting disease-manifestation relationship from literature. Bioinformatics, 2013, 29, 2186-2194.	1.8	56
18	Comparison of mRNA-1273 and BNT162b2 Vaccines on Breakthrough SARS-CoV-2 Infections, Hospitalizations, and Death During the Delta-Predominant Period. JAMA - Journal of the American Medical Association, 2022, 327, 678.	3.8	53

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19	Psoriasis and Psoriatic Arthritis Cardiovascular Disease Endotypes Identified by Red Blood Cell Distribution Width and Mean Platelet Volume. Journal of Clinical Medicine, 2020, 9, 186.	1.0	50
20	COVID-19 breakthrough infections, hospitalizations and mortality in fully vaccinated patients with hematologic malignancies: A clarion call for maintaining mitigation and ramping-up research. Blood Reviews, 2022, 54, 100931.	2.8	49
21	COVID-19 risk, disparities and outcomes in patients with chronic liver disease in the United States. EClinicalMedicine, 2021, 31, 100688.	3.2	44
22	dRiskKB: a large-scale disease-disease risk relationship knowledge base constructed from biomedical text. BMC Bioinformatics, 2014, 15, 105.	1.2	41
23	Automatic construction of a large-scale and accurate drug-side-effect association knowledge base from biomedical literature. Journal of Biomedical Informatics, 2014, 51, 191-199.	2.5	40
24	Phenome-driven disease genetics prediction toward drug discovery. Bioinformatics, 2015, 31, i276-i283.	1.8	37
25	Association of Epigenetic Clock with Consensus Molecular Subtypes and Overall Survival of Colorectal Cancer. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1720-1724.	1.1	37
26	Risks of SARS-CoV-2 Breakthrough Infection and Hospitalization in Fully Vaccinated Patients With Multiple Myeloma. JAMA Network Open, 2021, 4, e2137575.	2.8	35
27	Automatic signal extraction, prioritizing and filtering approaches in detecting post-marketing cardiovascular events associated with targeted cancer drugs from the FDA Adverse Event Reporting System (FAERS). Journal of Biomedical Informatics, 2014, 47, 171-177.	2.5	33
28	Comparative analysis of a novel disease phenotype network based on clinical manifestations. Journal of Biomedical Informatics, 2015, 53, 113-120.	2.5	33
29	Predict Alzheimer's disease using hippocampus MRI data: a lightweight 3D deep convolutional network model with visual and global shape representations. Alzheimer's Research and Therapy, 2021, 13, 104.	3.0	32
30	Disease gene prioritization by integrating tissue-specific molecular networks using a robust multi-network model. BMC Bioinformatics, 2016, 17, 453.	1.2	31
31	A knowledge-driven conditional approach to extract pharmacogenomics specific drug–gene relationships from free text. Journal of Biomedical Informatics, 2012, 45, 827-834.	2.5	30
32	A semi-supervised approach to extract pharmacogenomics-specific drug–gene pairs from biomedical literature for personalized medicine. Journal of Biomedical Informatics, 2013, 46, 585-593.	2.5	30
33	PhenoPredict: A disease phenome-wide drug repositioning approach towards schizophrenia drug discovery. Journal of Biomedical Informatics, 2015, 56, 348-355.	2.5	30
34	Data-driven multiple-level analysis of gut-microbiome-immune-joint interactions in rheumatoid arthritis. BMC Genomics, 2019, 20, 124.	1,2	30
35	Drug repurposing for glioblastoma based on molecular subtypes. Journal of Biomedical Informatics, 2016, 64, 131-138.	2.5	29
36	Immunotherapy-related adverse events (irAEs): extraction from FDA drug labels and comparative analysis. JAMIA Open, 2019, 2, 173-178.	1.0	29

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37	Discrimination of MSA-P and MSA-C by RT-QuIC analysis of olfactory mucosa: the first assessment of assay reproducibility between two specialized laboratories. Molecular Neurodegeneration, 2021, 16, 82.	4.4	28
38	KG-Predict: A knowledge graph computational framework for drug repurposing. Journal of Biomedical Informatics, 2022, 132, 104133.	2.5	28
39	Network-based gene prediction for Plasmodium falciparum malaria towards genetics-based drug discovery. BMC Genomics, 2015, 16, S9.	1.2	26
40	A Comprehensive Analysis of Five Million UMLS Metathesaurus Terms Using Eighteen Million MEDLINE Citations. AMIA Annual Symposium proceedings, 2010, 2010, 907-11.	0.2	26
41	COVIDâ€19 breakthrough infections and hospitalizations among vaccinated patients with dementia in the United States between December 2020 and August 2021. Alzheimer's and Dementia, 2023, 19, 421-432.	0.4	26
42	ATAD3A oligomerization promotes neuropathology and cognitive deficits in Alzheimer's disease models. Nature Communications, 2022, 13, 1121.	5.8	24
43	Mining Cancer-Specific Disease Comorbidities from a Large Observational Health Database. Cancer Informatics, 2014, 13s1, CIN.S13893.	0.9	22
44	Unsupervised method for automatic construction of a disease dictionary from a large free text collection. AMIA Annual Symposium proceedings, 2008, , 820-4.	0.2	22
45	Large-scale mining disease comorbidity relationships from post-market drug adverse events surveillance data. BMC Bioinformatics, 2018, 19, 500.	1.2	21
46	Large-scale automatic extraction of side effects associated with targeted anticancer drugs from full-text oncological articles. Journal of Biomedical Informatics, 2015, 55, 64-72.	2.5	20
47	Context-sensitive network-based disease genetics prediction and its implications in drug discovery. Bioinformatics, 2017, 33, 1031-1039.	1.8	20
48	Combining phenome-driven drug-target interaction prediction with patients' electronic health records-based clinical corroboration toward drug discovery. Bioinformatics, 2020, 36, i436-i444.	1.8	20
49	Drug repurposing for opioid use disorders: integration of computational prediction, clinical corroboration, and mechanism of action analyses. Molecular Psychiatry, 2021, 26, 5286-5296.	4.1	19
50	A genomics-based systems approach towards drug repositioning for rheumatoid arthritis. BMC Genomics, 2016, 17, 518.	1.2	18
51	A Drug-Side Effect Context-Sensitive Network approach for drug target prediction. Bioinformatics, 2019, 35, 2100-2107.	1.8	18
52	Towards precision medicine-based therapies for glioblastoma: interrogating human disease genomics and mouse phenotypes. BMC Genomics, 2016, 17, 516.	1.2	17
53	SimQ: Real-Time Retrieval of Similar Consumer Health Questions. Journal of Medical Internet Research, 2015, 17, e43.	2.1	15
54	Gut–microbiota–microglia–brain interactions in Alzheimer's disease: knowledge-based, multi-dimensional characterization. Alzheimer's Research and Therapy, 2021, 13, 177.	3.0	15

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55	A systems biology approach to predict and characterize human gut microbial metabolites in colorectal cancer. Scientific Reports, 2018, 8, 6225.	1.6	14
56	Epigenetic age acceleration and clinical outcomes in gliomas. PLoS ONE, 2020, 15, e0236045.	1.1	14
57	Combining text classification and Hidden Markov Modeling techniques for categorizing sentences in randomized clinical trial abstracts. AMIA Annual Symposium proceedings, 2006, , 824-8.	0.2	14
58	Combining Human Disease Genetics and Mouse Model Phenotypes towards Drug Repositioning for Parkinson's disease. AMIA Annual Symposium proceedings, 2015, 2015, 1851-60.	0.2	14
59	Toward creation of a cancer drug toxicity knowledge base: automatically extracting cancer drugâ€"side effect relationships from the literature. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 90-96.	2.2	13
60	Combining automatic table classification and relationship extraction in extracting anticancer drug–side effect pairs from full-text articles. Journal of Biomedical Informatics, 2015, 53, 128-135.	2.5	12
61	Phenome-based gene discovery provides information about Parkinson's disease drug targets. BMC Genomics, 2016, 17, 493.	1.2	12
62	Investigation of unsupervised pattern learning techniques for bootstrap construction of a medical treatment lexicon., 2009,,.		12
63	Disease Comorbidity Network Guides the Detection of Molecular Evidence for the Link Between Colorectal Cancer and Obesity. AMIA Summits on Translational Science Proceedings, 2015, 2015, 2016.	0.4	12
64	Comparing a knowledge-driven approach to a supervised machine learning approach in large-scale extraction of drug-side effect relationships from free-text biomedical literature. BMC Bioinformatics, 2015, 16, S6.	1.2	11
65	Extracting subject demographic information from abstracts of randomized clinical trial reports. Studies in Health Technology and Informatics, 2007, 129, 550-4.	0.2	11
66	Context-sensitive network analysis identifies food metabolites associated with Alzheimer's disease: an exploratory study. BMC Medical Genomics, 2019, 12, 17.	0.7	10
67	MetabolitePredict: A de novo human metabolomics prediction system and its applications in rheumatoid arthritis. Journal of Biomedical Informatics, 2017, 71, 222-228.	2.5	9
68	The Alzheimer's comorbidity phenome: mining from a large patient database and phenome-driven genetics prediction. JAMIA Open, 2019, 2, 131-138.	1.0	9
69	Unsupervised method for extracting machine understandable medical knowledge from a large free text collection. AMIA Annual Symposium proceedings, 2009, 2009, 709-13.	0.2	8
70	Ontology-guided organ detection to retrieve web images of disease manifestation: towards the construction of a consumer-based health image library. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 1076-1081.	2.2	7
71	Evaluating class III antiarrhythmic agents as novel MYC targeting drugs in ovarian cancer. Gynecologic Oncology, 2018, 151, 525-532.	0.6	7
72	Potential longâ€term effect of tumor necrosis factor inhibitors on dementia risk: A propensity score matched retrospective cohort study in US veterans. Alzheimer's and Dementia, 2022, 18, 1248-1259.	0.4	7

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73	Network Analysis of Human Disease Comorbidity Patterns Based on Large-Scale Data Mining. Lecture Notes in Computer Science, 2014, , 243-254.	1.0	7
74	Disease comorbidity-guided drug repositioning: a case study in schizophrenia. AMIA Annual Symposium proceedings, 2018, 2018, 1300-1309.	0.2	7
75	Semi-supervised image classification for automatic construction of a health image library. , 2012, , .		6
76	Explore Small Molecule-induced Genome-wide Transcriptional Profiles for Novel Inflammatory Bowel Disease Drug. AMIA Summits on Translational Science Proceedings, 2016, 2016, 22-31.	0.4	6
77	Multi-topic assignment for exploratory navigation of consumer health information in NetWellness using formal concept analysis. BMC Medical Informatics and Decision Making, 2014, 14, 63.	1.5	5
78	CoMNRank: An integrated approach to extract and prioritize human microbial metabolites from MEDLINE records. Journal of Biomedical Informatics, 2020, 109, 103524.	2.5	4
79	Dissecting the Ambiguity of FMA Concept Names Using Taxonomy and Partonomy Structural Information. AMIA Summits on Translational Science Proceedings, 2013, 2013, 157-61.	0.4	4
80	Mining comorbidities of opioid use disorder from FDA adverse event reporting system and patient electronic health records. BMC Medical Informatics and Decision Making, 2022, 22, .	1.5	4
81	DenguePredict: An Integrated Drug Repositioning Approach towards Drug Discovery for Dengue. AMIA Annual Symposium proceedings, 2015, 2015, 1279-88.	0.2	3
82	Combining mechanism-based prediction with patient-based profiling for psoriasis metabolomics biomarker discovery. AMIA Annual Symposium proceedings, 2017, 2017, 1734-1743.	0.2	3
83	An iterative searching and ranking algorithm for prioritising pharmacogenomics genes. International Journal of Computational Biology and Drug Design, 2013, 6, 18.	0.3	2
84	Automatic extraction, prioritization and analysis of gut microbial metabolites from biomedical literature. Scientific Reports, 2020, 10, 9996.	1.6	2
85	Integrating Large, Disparate Biomedical Ontologies to Boost Organ Development Network Connectivity. Lecture Notes in Computer Science, 2012, , 71-82.	1.0	2
86	Ontology-Guided Approach to Retrieving Disease Manifestation Images for Health Image Base Construction., 2012,,.		1
87	Analysis of disease organ as a novel phenotype towards disease genetics understanding. Journal of Biomedical Informatics, 2019, 95, 103235.	2.5	1
88	tcTKB: an integrated cardiovascular toxicity knowledge base for targeted cancer drugs. AMIA Annual Symposium proceedings, 2015, 2015, 1342-51.	0.2	1
89	Drug repositioning for prostate cancer: using a data-driven approach to gain new insights. AMIA Annual Symposium proceedings, 2017, 2017, 1724-1733.	0.2	1
90	DenseCNN: A Densely Connected CNN Model for Alzheimer's Disease Classification Based on Hippocampus MRI Data. AMIA Annual Symposium proceedings, 2020, 2020, 1277-1286.	0.2	1

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91	Reply to "Post OVID 19 neurological syndrome: A new risk factor that modifies the prognosis of patients with dementia― Alzheimer's and Dementia, 2022, 18, 544-544.	0.4	1
92	Computational Advances in Cancer Informatics (A). Cancer Informatics, 2014, 13s1, CIN.S19243.	0.9	0
93	Interrogating Patient-level Genomics and Mouse Phenomics towards Understanding Cytokines in Colorectal Cancer Metastasis. AMIA Summits on Translational Science Proceedings, 2017, 2017, 227-236.	0.4	0