

Rong Xu

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

89

papers

1,958

citations

22

h-index

41

g-index

96

ext. papers

3,053

ext. citations

6

avg, IF

6.61

L-index

#	Paper	IF	Citations
89	Increased risk of COVID-19 infection and mortality in people with mental disorders: analysis from electronic health records in the United States. <i>World Psychiatry</i> , 2021 , 20, 124-130	14.4	246
88	COVID-19 risk and outcomes in patients with substance use disorders: analyses from electronic health records in the United States. <i>Molecular Psychiatry</i> , 2021 , 26, 30-39	15.1	200
87	Analyses of Risk, Racial Disparity, and Outcomes Among US Patients With Cancer and COVID-19 Infection. <i>JAMA Oncology</i> , 2021 , 7, 220-227	13.4	126
86	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. <i>BMC Genomics</i> , 2015 , 16 Suppl 7, S4	4.5	103
85	Towards understanding brain-gut-microbiome connections in Alzheimer's disease. <i>BMC Systems Biology</i> , 2016 , 10 Suppl 3, 63	3.5	92
84	Large-scale extraction of accurate drug-disease treatment pairs from biomedical literature for drug repurposing. <i>BMC Bioinformatics</i> , 2013 , 14, 181	3.6	74
83	COVID-19 and dementia: Analyses of risk, disparity, and outcomes from electronic health records in the US. <i>Alzheimers and Dementia</i> , 2021 , 17, 1297-1306	1.2	68
82	Large-scale combining signals from both biomedical literature and the FDA Adverse Event Reporting System (FAERS) to improve post-marketing drug safety signal detection. <i>BMC Bioinformatics</i> , 2014 , 15, 17	3.6	50
81	Towards building a disease-phenotype knowledge base: extracting disease-manifestation relationship from literature. <i>Bioinformatics</i> , 2013 , 29, 2186-94	7.2	42
80	Tumor Necrosis Factor (TNF) blocking agents are associated with lower risk for Alzheimer's disease in patients with rheumatoid arthritis and psoriasis. <i>PLoS ONE</i> , 2020 , 15, e0229819	3.7	36
79	Phenome-driven disease genetics prediction toward drug discovery. <i>Bioinformatics</i> , 2015 , 31, i276-83	7.2	33
78	Automatic construction of a large-scale and accurate drug-side-effect association knowledge base from biomedical literature. <i>Journal of Biomedical Informatics</i> , 2014 , 51, 191-9	10.2	31
77	When hematologic malignancies meet COVID-19 in the United States: Infections, death and disparities. <i>Blood Reviews</i> , 2021 , 47, 100775	11.1	31
76	dRiskKB: a large-scale disease-disease risk relationship knowledge base constructed from biomedical text. <i>BMC Bioinformatics</i> , 2014 , 15, 105	3.6	29
75	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). <i>Journal of Biomedical Informatics</i> , 2014 , 47, 171-7	10.2	29
74	Comparative analysis of a novel disease phenotype network based on clinical manifestations. <i>Journal of Biomedical Informatics</i> , 2015 , 53, 113-20	10.2	27
73	Psoriasis and Psoriatic Arthritis Cardiovascular Disease Endotypes Identified by Red Blood Cell Distribution Width and Mean Platelet Volume. <i>Journal of Clinical Medicine</i> , 2020 , 9,	5.1	27

72	A Comprehensive Analysis of Five Million UMLS Metathesaurus Terms Using Eighteen Million MEDLINE Citations 2010 , 2010, 907-11	0.7	26
71	PhenoPredict: A disease phenome-wide drug repositioning approach towards schizophrenia drug discovery. <i>Journal of Biomedical Informatics</i> , 2015 , 56, 348-55	10.2	25
70	Disease gene prioritization by integrating tissue-specific molecular networks using a robust multi-network model. <i>BMC Bioinformatics</i> , 2016 , 17, 453	3.6	24
69	A knowledge-driven conditional approach to extract pharmacogenomics specific drug-gene relationships from free text. <i>Journal of Biomedical Informatics</i> , 2012 , 45, 827-34	10.2	23
68	Network-based gene prediction for Plasmodium falciparum malaria towards genetics-based drug discovery. <i>BMC Genomics</i> , 2015 , 16 Suppl 7, S9	4.5	22
67	A semi-supervised approach to extract pharmacogenomics-specific drug-gene pairs from biomedical literature for personalized medicine. <i>Journal of Biomedical Informatics</i> , 2013 , 46, 585-93	10.2	22
66	Mining cancer-specific disease comorbidities from a large observational health database. <i>Cancer Informatics</i> , 2014 , 13, 37-44	2.4	20
65	Unsupervised method for automatic construction of a disease dictionary from a large free text collection 2008 , 820-4	0.7	20
64	Drug repurposing for glioblastoma based on molecular subtypes. <i>Journal of Biomedical Informatics</i> , 2016 , 64, 131-138	10.2	20
63	Data-driven multiple-level analysis of gut-microbiome-immune-joint interactions in rheumatoid arthritis. <i>BMC Genomics</i> , 2019 , 20, 124	4.5	20
62	COVID-19 risk, disparities and outcomes in patients with chronic liver disease in the United States. <i>EClinicalMedicine</i> , 2021 , 31, 100688	11.3	20
61	Increased risk for COVID-19 breakthrough infection in fully vaccinated patients with substance use disorders in the United States between December 2020 and August 2021. <i>World Psychiatry</i> , 2021 ,	14.4	18
60	Oligodendroglial glycolytic stress triggers inflammasome activation and neuropathology in Alzheimer's disease. <i>Science Advances</i> , 2020 , 6,	14.3	18
59	Predict drug permeability to blood-brain-barrier from clinical phenotypes: drug side effects and drug indications. <i>Bioinformatics</i> , 2017 , 33, 901-908	7.2	17
58	Context-sensitive network-based disease genetics prediction and its implications in drug discovery. <i>Bioinformatics</i> , 2017 , 33, 1031-1039	7.2	16
57	Association of Epigenetic Clock with Consensus Molecular Subtypes and Overall Survival of Colorectal Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019 , 28, 1720-1724	4	16
56	Towards precision medicine-based therapies for glioblastoma: interrogating human disease genomics and mouse phenotypes. <i>BMC Genomics</i> , 2016 , 17 Suppl 7, 516	4.5	16
55	Immunotherapy-related adverse events (irAEs): extraction from FDA drug labels and comparative analysis. <i>JAMIA Open</i> , 2019 , 2, 173-178	2.9	15

54	Large-scale automatic extraction of side effects associated with targeted anticancer drugs from full-text oncological articles. <i>Journal of Biomedical Informatics</i> , 2015 , 55, 64-72	10.2	15
53	Streamlined alpha-synuclein RT-QuIC assay for various biospecimens in Parkinson's disease and dementia with Lewy bodies. <i>Acta Neuropathologica Communications</i> , 2021 , 9, 62	7.3	15
52	Large-scale mining disease comorbidity relationships from post-market drug adverse events surveillance data. <i>BMC Bioinformatics</i> , 2018 , 19, 500	3.6	15
51	Combining text classification and Hidden Markov Modeling techniques for categorizing sentences in randomized clinical trial abstracts 2006 , 824-8	0.7	14
50	Combining Human Disease Genetics and Mouse Model Phenotypes towards Drug Repositioning for Parkinson's disease 2015 , 2015, 1851-60	0.7	14
49	A systems biology approach to predict and characterize human gut microbial metabolites in colorectal cancer. <i>Scientific Reports</i> , 2018 , 8, 6225	4.9	13
48	Toward creation of a cancer drug toxicity knowledge base: automatically extracting cancer drug-side effect relationships from the literature. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2014 , 21, 90-6	8.6	13
47	A genomics-based systems approach towards drug repositioning for rheumatoid arthritis. <i>BMC Genomics</i> , 2016 , 17 Suppl 7, 518	4.5	12
46	Disease Comorbidity Network Guides the Detection of Molecular Evidence for the Link Between Colorectal Cancer and Obesity. <i>AMIA Summits on Translational Science Proceedings</i> , 2015 , 2015, 201-6	1.1	12
45	Phenome-based gene discovery provides information about Parkinson's disease drug targets. <i>BMC Genomics</i> , 2016 , 17 Suppl 5, 493	4.5	11
44	A Drug-Side Effect Context-Sensitive Network approach for drug target prediction. <i>Bioinformatics</i> , 2019 , 35, 2100-2107	7.2	11
43	Extracting subject demographic information from abstracts of randomized clinical trial reports. <i>Studies in Health Technology and Informatics</i> , 2007 , 129, 550-4	0.5	11
42	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.. <i>JAMA Pediatrics</i> , 2022 ,	8.3	11
41	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. <i>BMC Bioinformatics</i> , 2015 , 16 Suppl 5, S6	3.6	9
40	Combining automatic table classification and relationship extraction in extracting anticancer drug-side effect pairs from full-text articles. <i>Journal of Biomedical Informatics</i> , 2015 , 53, 128-35	10.2	9
39	Combining phenome-driven drug-target interaction prediction with patients' electronic health records-based clinical corroboration toward drug discovery. <i>Bioinformatics</i> , 2020 , 36, i436-i444	7.2	9
38	MetabolitePredict: A de novo human metabolomics prediction system and its applications in rheumatoid arthritis. <i>Journal of Biomedical Informatics</i> , 2017 , 71, 222-228	10.2	8
37	Comparison of mRNA-1273 and BNT162b2 Vaccines on Breakthrough SARS-CoV-2 Infections, Hospitalizations, and Death During the Delta-Predominant Period.. <i>JAMA - Journal of the American Medical Association</i> , 2022 ,	27.4	8

36	Unsupervised method for extracting machine understandable medical knowledge from a large free text collection 2009 , 2009, 709-13	0.7	8
35	Investigation of unsupervised pattern learning techniques for bootstrap construction of a medical treatment lexicon 2009 ,		8
34	Predict Alzheimer's disease using hippocampus MRI data: a lightweight 3D deep convolutional network model with visual and global shape representations. <i>Alzheimers Research and Therapy</i> , 2021 , 13, 104	9	8
33	COVID-19 breakthrough infections, hospitalizations and mortality in fully vaccinated patients with hematologic malignancies: A clarion call for maintaining mitigation and ramping-up research.. <i>Blood Reviews</i> , 2022 , 100931	11.1	7
32	Disease comorbidity-guided drug repositioning: a case study in schizophrenia 2018 , 2018, 1300-1309	0.7	7
31	SimQ: real-time retrieval of similar consumer health questions. <i>Journal of Medical Internet Research</i> , 2015 , 17, e43	7.6	7
30	Context-sensitive network analysis identifies food metabolites associated with Alzheimer's disease: an exploratory study. <i>BMC Medical Genomics</i> , 2019 , 12, 17	3.7	6
29	Explore Small Molecule-induced Genome-wide Transcriptional Profiles for Novel Inflammatory Bowel Disease Drug. <i>AMIA Summits on Translational Science Proceedings</i> , 2016 , 2016, 22-31	1.1	6
28	Risks of SARS-CoV-2 Breakthrough Infection and Hospitalization in Fully Vaccinated Patients With Multiple Myeloma. <i>JAMA Network Open</i> , 2021 , 4, e2137575	10.4	6
27	The Alzheimer's comorbidity phenome: mining from a large patient database and phenome-driven genetics prediction. <i>JAMIA Open</i> , 2019 , 2, 131-138	2.9	5
26	Multi-topic assignment for exploratory navigation of consumer health information in NetWellness using formal concept analysis. <i>BMC Medical Informatics and Decision Making</i> , 2014 , 14, 63	3.6	5
25	Ontology-guided organ detection to retrieve web images of disease manifestation: towards the construction of a consumer-based health image library. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2013 , 20, 1076-81	8.6	5
24	Network Analysis of Human Disease Comorbidity Patterns Based on Large-Scale Data Mining. <i>Lecture Notes in Computer Science</i> , 2014 , 243-254	0.9	5
23	Epigenetic age acceleration and clinical outcomes in gliomas. <i>PLoS ONE</i> , 2020 , 15, e0236045	3.7	5
22	Semi-supervised image classification for automatic construction of a health image library 2012 ,		4
21	Dissecting the Ambiguity of FMA Concept Names Using Taxonomy and Partonomy Structural Information. <i>AMIA Summits on Translational Science Proceedings</i> , 2013 , 2013, 157-61	1.1	4
20	Drug repurposing for opioid use disorders: integration of computational prediction, clinical corroboration, and mechanism of action analyses. <i>Molecular Psychiatry</i> , 2021 , 26, 5286-5296	15.1	4
19	Evaluating class III antiarrhythmic agents as novel MYC targeting drugs in ovarian cancer. <i>Gynecologic Oncology</i> , 2018 , 151, 525-532	4.9	4

18	COVID infection rates, clinical outcomes, and racial/ethnic and gender disparities before and after Omicron emerged in the US. 2022 ,		4
17	DenguePredict: An Integrated Drug Repositioning Approach towards Drug Discovery for Dengue 2015 , 2015, 1279-88	0.7	3
16	Combining mechanism-based prediction with patient-based profiling for psoriasis metabolomics biomarker discovery 2017 , 2017, 1734-1743	0.7	3
15	Gut-microbiota-microglia-brain interactions in Alzheimer's disease: knowledge-based, multi-dimensional characterization. <i>Alzheimers Research and Therapy</i> , 2021 , 13, 177	9	3
14	Automatic extraction, prioritization and analysis of gut microbial metabolites from biomedical literature. <i>Scientific Reports</i> , 2020 , 10, 9996	4.9	2
13	CoMNRank: An integrated approach to extract and prioritize human microbial metabolites from MEDLINE records. <i>Journal of Biomedical Informatics</i> , 2020 , 109, 103524	10.2	2
12	Potential long-term effect of tumor necrosis factor inhibitors on dementia risk: A propensity score matched retrospective cohort study in US veterans. <i>Alzheimers and Dementia</i> , 2021 ,	1.2	2
11	ATAD3A oligomerization promotes neuropathology and cognitive deficits in Alzheimer's disease models.. <i>Nature Communications</i> , 2022 , 13, 1121	17.4	2
10	Analysis of disease organ as a novel phenotype towards disease genetics understanding. <i>Journal of Biomedical Informatics</i> , 2019 , 95, 103235	10.2	1
9	An iterative searching and ranking algorithm for prioritising pharmacogenomics genes. <i>International Journal of Computational Biology and Drug Design</i> , 2013 , 6, 18-31	0.4	1
8	tcTKB: an integrated cardiovascular toxicity knowledge base for targeted cancer drugs 2015 , 2015, 1342-51	2.5	1
7	Drug repositioning for prostate cancer: using a data-driven approach to gain new insights 2017 , 2017, 1724-1733	0.7	1
6	DenseCNN: A Densely Connected CNN Model for Alzheimer's Disease Classification Based on Hippocampus MRI Data 2020 , 2020, 1277-1286	0.7	1
5	Integrating Large, Disparate Biomedical Ontologies to Boost Organ Development Network Connectivity. <i>Lecture Notes in Computer Science</i> , 2012 , 71-82	0.9	1
4	Discrimination of MSA-P and MSA-C by RT-QuIC analysis of olfactory mucosa: the first assessment of assay reproducibility between two specialized laboratories.. <i>Molecular Neurodegeneration</i> , 2021 , 16, 82	19	1
3	Computational advances in cancer informatics (a). <i>Cancer Informatics</i> , 2014 , 13, 45-8	2.4	
2	Reply to "Post-COVID 19 neurological syndrome: A new risk factor that modifies the prognosis of patients with dementia".. <i>Alzheimers and Dementia</i> , 2022 ,	1.2	
1	Interrogating Patient-level Genomics and Mouse Phenomics towards Understanding Cytokines in Colorectal Cancer Metastasis. <i>AMIA Summits on Translational Science Proceedings</i> , 2017 , 2017, 227-236	1.1	

