

Rong Xu

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/8678226/rong-xu-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	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
88	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
87	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	
86	COVID infection rates, clinical outcomes, and racial/ethnic and gender disparities before and after Omicron emerged in the US. 2022 ,		4
85	ATAD3A oligomerization promotes neuropathology and cognitive deficits in Alzheimer's disease models.. <i>Nature Communications</i> , 2022 , 13, 1121	17.4	2
84	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
83	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
82	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
81	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
80	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
79	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
78	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
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	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
75	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
74	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
73	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

72	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
71	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
70	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
69	Automatic extraction, prioritization and analysis of gut microbial metabolites from biomedical literature. <i>Scientific Reports</i> , 2020 , 10, 9996	4.9	2
68	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
67	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
66	DenseCNN: A Densely Connected CNN Model for Alzheimer's Disease Classification Based on Hippocampus MRI Data 2020 , 2020, 1277-1286	0.7	1
65	Epigenetic age acceleration and clinical outcomes in gliomas. <i>PLoS ONE</i> , 2020 , 15, e0236045	3.7	5
64	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
63	Oligodendroglial glycolytic stress triggers inflammasome activation and neuropathology in Alzheimer's disease. <i>Science Advances</i> , 2020 , 6,	14.3	18
62	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
61	Analysis of disease organ as a novel phenotype towards disease genetics understanding. <i>Journal of Biomedical Informatics</i> , 2019 , 95, 103235	10.2	1
60	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
59	Immunotherapy-related adverse events (irAEs): extraction from FDA drug labels and comparative analysis. <i>JAMIA Open</i> , 2019 , 2, 173-178	2.9	15
58	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
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	Data-driven multiple-level analysis of gut-microbiome-immune-joint interactions in rheumatoid arthritis. <i>BMC Genomics</i> , 2019 , 20, 124	4.5	20
55	A Drug-Side Effect Context-Sensitive Network approach for drug target prediction. <i>Bioinformatics</i> , 2019 , 35, 2100-2107	7.2	11

54	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
53	Disease comorbidity-guided drug repositioning: a case study in schizophrenia 2018 , 2018, 1300-1309	0.7	7
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	Evaluating class III antiarrhythmic agents as novel MYC targeting drugs in ovarian cancer. <i>Gynecologic Oncology</i> , 2018 , 151, 525-532	4.9	4
50	Context-sensitive network-based disease genetics prediction and its implications in drug discovery. <i>Bioinformatics</i> , 2017 , 33, 1031-1039	7.2	16
49	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
48	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	
47	Drug repositioning for prostate cancer: using a data-driven approach to gain new insights 2017 , 2017, 1724-1733	0.7	1
46	Combining mechanism-based prediction with patient-based profiling for psoriasis metabolomics biomarker discovery 2017 , 2017, 1734-1743	0.7	3
45	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
44	Towards understanding brain-gut-microbiome connections in Alzheimer's disease. <i>BMC Systems Biology</i> , 2016 , 10 Suppl 3, 63	3.5	92
43	A genomics-based systems approach towards drug repositioning for rheumatoid arthritis. <i>BMC Genomics</i> , 2016 , 17 Suppl 7, 518	4.5	12
42	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
41	Phenome-based gene discovery provides information about Parkinson's disease drug targets. <i>BMC Genomics</i> , 2016 , 17 Suppl 5, 493	4.5	11
40	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
39	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
38	Drug repurposing for glioblastoma based on molecular subtypes. <i>Journal of Biomedical Informatics</i> , 2016 , 64, 131-138	10.2	20
37	Phenome-driven disease genetics prediction toward drug discovery. <i>Bioinformatics</i> , 2015 , 31, i276-83	7.2	33

36	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
35	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
34	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
33	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
32	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
31	Network-based gene prediction for <i>Plasmodium falciparum</i> malaria towards genetics-based drug discovery. <i>BMC Genomics</i> , 2015 , 16 Suppl 7, S9	4.5	22
30	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
29	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
28	DenguePredict: An Integrated Drug Repositioning Approach towards Drug Discovery for Dengue 2015 , 2015, 1279-88	0.7	3
27	tcTKB: an integrated cardiovascular toxicity knowledge base for targeted cancer drugs 2015 , 2015, 1342-51	0.7	1
26	Combining Human Disease Genetics and Mouse Model Phenotypes towards Drug Repositioning for Parkinson's disease 2015 , 2015, 1851-60	0.7	14
25	SimQ: real-time retrieval of similar consumer health questions. <i>Journal of Medical Internet Research</i> , 2015 , 17, e43	7.6	7
24	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
23	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
22	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
21	dRiskKB: a large-scale disease-disease risk relationship knowledge base constructed from biomedical text. <i>BMC Bioinformatics</i> , 2014 , 15, 105	3.6	29
20	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
19	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

18	Mining cancer-specific disease comorbidities from a large observational health database. <i>Cancer Informatics</i> , 2014 , 13, 37-44	2.4	20
17	Computational advances in cancer informatics (a). <i>Cancer Informatics</i> , 2014 , 13, 45-8	2.4	
16	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
15	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
14	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
13	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
12	Towards building a disease-phenotype knowledge base: extracting disease-manifestation relationship from literature. <i>Bioinformatics</i> , 2013 , 29, 2186-94	7.2	42
11	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
10	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
9	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
8	Semi-supervised image classification for automatic construction of a health image library 2012 ,		4
7	Integrating Large, Disparate Biomedical Ontologies to Boost Organ Development Network Connectivity. <i>Lecture Notes in Computer Science</i> , 2012 , 71-82	0.9	1
6	A Comprehensive Analysis of Five Million UMLS Metathesaurus Terms Using Eighteen Million MEDLINE Citations 2010 , 2010, 907-11	0.7	26
5	Unsupervised method for extracting machine understandable medical knowledge from a large free text collection 2009 , 2009, 709-13	0.7	8
4	Investigation of unsupervised pattern learning techniques for bootstrap construction of a medical treatment lexicon 2009 ,		8
3	Unsupervised method for automatic construction of a disease dictionary from a large free text collection 2008 , 820-4	0.7	20
2	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
1	Combining text classification and Hidden Markov Modeling techniques for categorizing sentences in randomized clinical trial abstracts 2006 , 824-8	0.7	14

