

Jing Tang

List of Publications by Citations

Source: <https://exaly.com/author-pdf/1187665/jing-tang-publications-by-citations.pdf>

Version: 2024-04-24

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.

99
papers

3,916
citations

28
h-index

62
g-index

126
ext. papers

5,466
ext. citations

8.3
avg, IF

5.75
L-index

#	Paper	IF	Citations
99	Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations. <i>BMC Bioinformatics</i> , 2008 , 9, 539	3.6	612
98	SynergyFinder: a web application for analyzing drug combination dose-response matrix data. <i>Bioinformatics</i> , 2017 , 33, 2413-2415	7.2	249
97	Searching for Drug Synergy in Complex Dose-Response Landscapes Using an Interaction Potency Model. <i>Computational and Structural Biotechnology Journal</i> , 2015 , 13, 504-13	6.8	232
96	Common pitfalls and recommendations for using machine learning to detect and prognosticate for COVID-19 using chest radiographs and CT scans. <i>Nature Machine Intelligence</i> , 2021 , 3, 199-217	22.5	200
95	Network pharmacology applications to map the unexplored target space and therapeutic potential of natural products. <i>Natural Product Reports</i> , 2015 , 32, 1249-66	15.1	198
94	Bayesian analysis of population structure based on linked molecular information. <i>Mathematical Biosciences</i> , 2007 , 205, 19-31	3.9	185
93	Toward more realistic drug-target interaction predictions. <i>Briefings in Bioinformatics</i> , 2015 , 16, 325-37	13.4	182
92	Association of lipidome remodeling in the adipocyte membrane with acquired obesity in humans. <i>PLoS Biology</i> , 2011 , 9, e1000623	9.7	169
91	Hyper-recombination, diversity, and antibiotic resistance in pneumococcus. <i>Science</i> , 2009 , 324, 1454-7	33.3	138
90	Making sense of large-scale kinase inhibitor bioactivity data sets: a comparative and integrative analysis. <i>Journal of Chemical Information and Modeling</i> , 2014 , 54, 735-43	6.1	113
89	Metabolome in schizophrenia and other psychotic disorders: a general population-based study. <i>Genome Medicine</i> , 2011 , 3, 19	14.4	110
88	What is synergy? The Saariselkä Agreement revisited. <i>Frontiers in Pharmacology</i> , 2015 , 6, 181	5.6	88
87	Network pharmacology strategies toward multi-target anticancer therapies: from computational models to experimental design principles. <i>Current Pharmaceutical Design</i> , 2014 , 20, 23-36	3.3	86
86	Methods for High-throughput Drug Combination Screening and Synergy Scoring. <i>Methods in Molecular Biology</i> , 2018 , 1711, 351-398	1.4	80
85	Phospholipids and insulin resistance in psychosis: a lipidomics study of twin pairs discordant for schizophrenia. <i>Genome Medicine</i> , 2012 , 4, 1	14.4	80
84	Identifying currents in the gene pool for bacterial populations using an integrative approach. <i>PLoS Computational Biology</i> , 2009 , 5, e1000455	5	78
83	DrugComb: an integrative cancer drug combination data portal. <i>Nucleic Acids Research</i> , 2019 , 47, W43-W50	10.1	71

82	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015 , 33, 933-40	44.5	70
81	Target inhibition networks: predicting selective combinations of druggable targets to block cancer survival pathways. <i>PLoS Computational Biology</i> , 2013 , 9, e1003226	5	66
80	JAK1/2 and BCL2 inhibitors synergize to counteract bone marrow stromal cell-induced protection of AML. <i>Blood</i> , 2017 , 130, 789-802	2.2	63
79	Discovery of novel drug sensitivities in T-PLL by high-throughput ex vivo drug testing and mutation profiling. <i>Leukemia</i> , 2018 , 32, 774-787	10.7	56
78	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. <i>Nature Communications</i> , 2016 , 7, 12460	17.4	54
77	Drug combination sensitivity scoring facilitates the discovery of synergistic and efficacious drug combinations in cancer. <i>PLoS Computational Biology</i> , 2019 , 15, e1006752	5	53
76	Drug Target Commons: A Community Effort to Build a Consensus Knowledge Base for Drug-Target Interactions. <i>Cell Chemical Biology</i> , 2018 , 25, 224-229.e2	8.2	51
75	Patient-Customized Drug Combination Prediction and Testing for T-cell Prolymphocytic Leukemia Patients. <i>Cancer Research</i> , 2018 , 78, 2407-2418	10.1	40
74	Making Sense of the Epigenome Using Data Integration Approaches. <i>Frontiers in Pharmacology</i> , 2019 , 10, 126	5.6	35
73	Genomic, transcriptomic, and lipidomic profiling highlights the role of inflammation in individuals with low high-density lipoprotein cholesterol. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013 , 33, 847-57	9.4	33
72	Drug synergy of combinatory treatment with remdesivir and the repurposed drugs fluoxetine and itraconazole effectively impairs SARS-CoV-2 infection in vitro. <i>British Journal of Pharmacology</i> , 2021 , 178, 2339-2350	8.6	32
71	Chloroplot: An Online Program for the Versatile Plotting of Organelle Genomes. <i>Frontiers in Genetics</i> , 2020 , 11, 576124	4.5	25
70	Exploration of databases and methods supporting drug repurposing: a comprehensive survey. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1656-1678	13.4	25
69	Systematic drug sensitivity testing reveals synergistic growth inhibition by dasatinib or mTOR inhibitors with paclitaxel in ovarian granulosa cell tumor cells. <i>Gynecologic Oncology</i> , 2017 , 144, 621-630 ⁴⁻⁹	4.9	22
68	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	5	21
67	Predicting Meridian in Chinese traditional medicine using machine learning approaches. <i>PLoS Computational Biology</i> , 2019 , 15, e1007249	5	21
66	Systematic Mapping of Kinase Addiction Combinations in Breast Cancer Cells by Integrating Drug Sensitivity and Selectivity Profiles. <i>Chemistry and Biology</i> , 2015 , 22, 1144-55		20
65	Integrating post-genomic approaches as a strategy to advance our understanding of health and disease. <i>Genome Medicine</i> , 2009 , 1, 35	14.4	19

64	Drug Target Commons 2.0: a community platform for systematic analysis of drug-target interaction profiles. <i>Database: the Journal of Biological Databases and Curation</i> , 2018 , 2018, 1-13	5	18
63	Unsupervised Learning and Multipartite Network Models: A Promising Approach for Understanding Traditional Medicine. <i>Frontiers in Pharmacology</i> , 2020 , 11, 1319	5.6	16
62	Anticancer drug synergy prediction in understudied tissues using transfer learning. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021 , 28, 42-51	8.6	16
61	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. <i>Cell Systems</i> , 2017 , 5, 485-497.e3	10.6	14
60	TIMMA-R: an R package for predicting synergistic multi-targeted drug combinations in cancer cell lines or patient-derived samples. <i>Bioinformatics</i> , 2015 , 31, 1866-8	7.2	14
59	Quantitative changes in collagen levels following 830-nm diode laser welding. <i>Lasers in Surgery and Medicine</i> , 1998 , 22, 207-11	3.6	14
58	SynergyFinder Plus: Toward Better Interpretation and Annotation of Drug Combination Screening Datasets.. <i>Genomics, Proteomics and Bioinformatics</i> , 2022 ,	6.5	14
57	Drug Repurposing for COVID-19 using Graph Neural Network with Genetic, Mechanistic, and Epidemiological Validation 2020 ,		13
56	Metastasis associated in colon cancer 1 (MACC1) promotes growth and metastasis processes of colon cancer cells. <i>European Review for Medical and Pharmacological Sciences</i> , 2016 , 20, 2825-34	2.9	13
55	Network-based modeling of herb combinations in traditional Chinese medicine. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	11
54	DrugComb update: a more comprehensive drug sensitivity data repository and analysis portal. <i>Nucleic Acids Research</i> , 2021 , 49, W174-W184	20.1	11
53	Phosphorylation of human La protein at Ser 366 by casein kinase II contributes to hepatitis B virus replication and expression in vitro. <i>Journal of Viral Hepatitis</i> , 2013 , 20, 24-33	3.4	10
52	Seed-effect modeling improves the consistency of genome-wide loss-of-function screens and identifies synthetic lethal vulnerabilities in cancer cells. <i>Genome Medicine</i> , 2017 , 9, 51	14.4	10
51	Combined gene essentiality scoring improves the prediction of cancer dependency maps. <i>EBioMedicine</i> , 2019 , 50, 67-80	8.8	10
50	Loss-of-function mutations with circadian rhythm regulator Per1/Per2 lead to premature ovarian insufficiency <i>Biology of Reproduction</i> , 2019 , 100, 1066-1072	3.9	10
49	From drug response profiling to target addiction scoring in cancer cell models. <i>DMM Disease Models and Mechanisms</i> , 2015 , 8, 1255-64	4.1	9
48	A Bayesian Predictive Model for Clustering Data of Mixed Discrete and Continuous Type. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2015 , 37, 489-98	13.3	9
47	The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , 2017 , 14, 937-938	21.6	8

46	Can we assume the gene expression profile as a proxy for signaling network activity?		8
45	Multi-parametric single cell evaluation defines distinct drug responses in healthy hematologic cells that are retained in corresponding malignant cell types. <i>Haematologica</i> , 2020 , 105, 1527-1538	6.6	8
44	Bayesian clustering of fuzzy feature vectors using a quasi-likelihood approach. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , 2009 , 31, 74-85	13.3	7
43	A three-year survey of the antimicrobial resistance of microorganisms at a Chinese hospital. <i>Experimental and Therapeutic Medicine</i> , 2016 , 11, 731-736	2.1	7
42	Combination Therapy with Fluoxetine and the Nucleoside Analog GS-441524 Exerts Synergistic Antiviral Effects against Different SARS-CoV-2 Variants In Vitro. <i>Pharmaceutics</i> , 2021 , 13,	6.4	7
41	Informatics Approaches for Predicting, Understanding, and Testing Cancer Drug Combinations. <i>Methods in Molecular Biology</i> , 2017 , 1636, 485-506	1.4	6
40	Treatment of novel IL17A inhibitor in glioblastoma implementing 3rd generation co-culture cell line and patient-derived tumor model. <i>European Journal of Pharmacology</i> , 2017 , 803, 24-38	5.3	5
39	Can We Assume the Gene Expression Profile as a Proxy for Signaling Network Activity?. <i>Biomolecules</i> , 2020 , 10,	5.9	5
38	T-BAPS: a Bayesian statistical tool for comparison of microbial communities using terminal-restriction fragment length polymorphism (T-RFLP) data. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2007 , 6, Article30	1.2	5
37	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data.. <i>Cell Reports Medicine</i> , 2022 , 3, 100492	18	5
36	Drug repurposing for COVID-19 using graph neural network and harmonizing multiple evidence. <i>Scientific Reports</i> , 2021 , 11, 23179	4.9	5
35	Drug synergy of combinatory treatment with remdesivir and the repurposed drugs fluoxetine and itraconazole effectively impairs SARS-CoV-2 infection in vitro		5
34	RNA atlas of human bacterial pathogens uncovers stress dynamics linked to infection. <i>Nature Communications</i> , 2021 , 12, 3282	17.4	5
33	Methods for High-Throughput Drug Combination Screening and Synergy Scoring		4
32	CD73 contributes to anti-inflammatory properties of afferent lymphatic endothelial cells in humans and mice. <i>European Journal of Immunology</i> , 2021 , 51, 231-246	6.1	4
31	Seasonal Variation in the Brain μ Opioid Receptor Availability. <i>Journal of Neuroscience</i> , 2021 , 41, 1265-1273	3.6	3
30	A Community Challenge for Pancancer Drug Mechanism of Action Inference from Perturbational Profile Data		3
29	Comparative analysis of molecular fingerprints in prediction of drug combination effects. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	3

28	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	3
27	Identification of Celecoxib-Targeted Proteins Using Label-Free Thermal Proteome Profiling on Rat Hippocampus. <i>Molecular Pharmacology</i> , 2021 , 99, 308-318	4.3	2
26	S100 Calcium Binding Protein Family Members Associate With Poor Patient Outcome and Response to Proteasome Inhibition in Multiple Myeloma. <i>Frontiers in Cell and Developmental Biology</i> , 2021 , 9, 7230-7246	5.7	2
25	Quantitative changes in collagen levels following 830-nm diode laser welding 1998 , 22, 207		2
24	NIMAA: an R/CRAN package to accomplish NomInal data Mining AnAlysis		1
23	Multi-Parametric Single Cell Profiling Defines Distinct Drug Responses in Healthy Hematological Cell Lineages That Are Retained in Corresponding Malignant Cell Types. <i>Blood</i> , 2018 , 132, 264-264	2.2	1
22	Eribulin activity in soft tissue sarcoma monolayer and three-dimensional cell line models: could the combination with other drugs improve its antitumoral effect?. <i>Cancer Cell International</i> , 2021 , 21, 646	6.4	1
21	Anti-cancer Drug Synergy Prediction in Understudied Tissues using Transfer Learning		1
20	RNA Atlas of Human Bacterial Pathogens Uncovers Stress Dynamics Linked to Infection		1
19	DrugComb - an integrative cancer drug combination data portal		1
18	Facilitating the design of combination therapy in cancer using multipartite network models: Emphasis on acute myeloid leukemia		1
17	DrugComb update: a more comprehensive drug sensitivity data repository and analysis portal		1
16	Comparative analysis of molecular representations in prediction of drug combination effects		1
15	Minimal information for chemosensitivity assays (MICHA): a next-generation pipeline to enable the FAIRification of drug screening experiments. <i>Briefings in Bioinformatics</i> , 2021 ,	13.4	1
14	Bipartite network models to design combination therapies in acute myeloid leukaemia.. <i>Nature Communications</i> , 2022 , 13, 2128	17.4	1
13	Predictive Response Biomarkers for BET Inhibitors in AML. <i>Blood</i> , 2018 , 132, 2749-2749	2.2	0
12	Vascular adhesion protein-1 defines a unique subpopulation of human hematopoietic stem cells and regulates their proliferation. <i>Cellular and Molecular Life Sciences</i> , 2021 , 78, 7851-7872	10.3	0
11	Heterogeneous modulation of Bcl-2 family members and drug efflux mediate MCL-1 inhibitor resistance in multiple myeloma. <i>Blood Advances</i> , 2021 , 5, 4125-4139	7.8	0

- 10 Antitumoral Effect of Plocabulin in High Grade Serous Ovarian Carcinoma Cell Line Models.. *Frontiers in Oncology*, **2022**, 12, 862321 5.3 0
- 9 ELEVATED SERUM SPHINGOMYELIN ASSOCIATES WITH REDUCED GRAY MATTER DENSITY: EVIDENCE FROM TWINS DISCORDANT FOR SCHIZOPHRENIA. *Schizophrenia Research*, **2010**, 117, 370-374^{3,6}
- 8 Eltrombopag Promotes Megakaryocyte Survival and Signaling in the Presence of Specific Cytotoxic Agents. *Blood*, **2018**, 132, 3836-3836 2.2
- 7 JAK1/2 and BCL2 Inhibitors Synergize to Counter-Act Bone Marrow Stromal Cell-Induced Protection of AML. *Blood*, **2015**, 126, 867-867 2.2
- 6 A three-term recurrence relation for accurate evaluation of transition probabilities of the simple birth-and-death process. *BIT Numerical Mathematics*, **2021**, 61, 561-585 1.7
- 5 Bayes in Wonderland! Predictive Supervised Classification Inference Hits Unpredictability. *Mathematics*, **2022**, 10, 828 2.3
- 4 Predicting Meridian in Chinese traditional medicine using machine learning approaches **2019**, 15, e1007249
- 3 Predicting Meridian in Chinese traditional medicine using machine learning approaches **2019**, 15, e1007249
- 2 Predicting Meridian in Chinese traditional medicine using machine learning approaches **2019**, 15, e1007249
- 1 Predicting Meridian in Chinese traditional medicine using machine learning approaches **2019**, 15, e1007249