

# Jing Tang

## List of Publications by Year in Descending Order

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**Version:** 2024-04-24

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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.

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	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data.. <i>Cell Reports Medicine</i> , <b>2022</b> , 3, 100492	18	5
98	SynergyFinder Plus: Toward Better Interpretation and Annotation of Drug Combination Screening Datasets.. <i>Genomics, Proteomics and Bioinformatics</i> , <b>2022</b> ,	6.5	14
97	Bayes in Wonderland! Predictive Supervised Classification Inference Hits Unpredictability. <i>Mathematics</i> , <b>2022</b> , 10, 828	2.3	
96	Antitumoral Effect of Plocabulin in High Grade Serous Ovarian Carcinoma Cell Line Models.. <i>Frontiers in Oncology</i> , <b>2022</b> , 12, 862321	5.3	0
95	Bipartite network models to design combination therapies in acute myeloid leukaemia.. <i>Nature Communications</i> , <b>2022</b> , 13, 2128	17.4	1
94	Seasonal Variation in the Brain $\mu$ Opioid Receptor Availability. <i>Journal of Neuroscience</i> , <b>2021</b> , 41, 1265-1273	13.6	3
93	Drug repurposing for COVID-19 using graph neural network and harmonizing multiple evidence. <i>Scientific Reports</i> , <b>2021</b> , 11, 23179	4.9	5
92	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> , <b>2021</b> , 21, 646	6.4	1
91	Vascular adhesion protein-1 defines a unique subpopulation of human hematopoietic stem cells and regulates their proliferation. <i>Cellular and Molecular Life Sciences</i> , <b>2021</b> , 78, 7851-7872	10.3	0
90	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> , <b>2021</b> , 3, 199-217	22.5	200
89	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> , <b>2021</b> , 178, 2339-2350	8.6	32
88	Network-based modeling of herb combinations in traditional Chinese medicine. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	11
87	RNA atlas of human bacterial pathogens uncovers stress dynamics linked to infection. <i>Nature Communications</i> , <b>2021</b> , 12, 3282	17.4	5
86	DrugComb update: a more comprehensive drug sensitivity data repository and analysis portal. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, W174-W184	20.1	11
85	Exploration of databases and methods supporting drug repurposing: a comprehensive survey. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22, 1656-1678	13.4	25
84	Anticancer drug synergy prediction in understudied tissues using transfer learning. <i>Journal of the American Medical Informatics Association: JAMIA</i> , <b>2021</b> , 28, 42-51	8.6	16
83	CD73 contributes to anti-inflammatory properties of afferent lymphatic endothelial cells in humans and mice. <i>European Journal of Immunology</i> , <b>2021</b> , 51, 231-246	6.1	4

82	A three-term recurrence relation for accurate evaluation of transition probabilities of the simple birth-and-death process. <i>BIT Numerical Mathematics</i> , <b>2021</b> , 61, 561-585	1.7	
81	Identification of Celecoxib-Targeted Proteins Using Label-Free Thermal Proteome Profiling on Rat Hippocampus. <i>Molecular Pharmacology</i> , <b>2021</b> , 99, 308-318	4.3	2
80	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> , <b>2021</b> , 9, 723016	5.7	2
79	Comparative analysis of molecular fingerprints in prediction of drug combination effects. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	3
78	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	3
77	Minimal information for chemosensitivity assays (MICHA): a next-generation pipeline to enable the FAIRification of drug screening experiments. <i>Briefings in Bioinformatics</i> , <b>2021</b> ,	13.4	1
76	Heterogeneous modulation of Bcl-2 family members and drug efflux mediate MCL-1 inhibitor resistance in multiple myeloma. <i>Blood Advances</i> , <b>2021</b> , 5, 4125-4139	7.8	0
75	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> , <b>2021</b> , 13,	6.4	7
74	Can We Assume the Gene Expression Profile as a Proxy for Signaling Network Activity?. <i>Biomolecules</i> , <b>2020</b> , 10,	5.9	5
73	Drug Repurposing for COVID-19 using Graph Neural Network with Genetic, Mechanistic, and Epidemiological Validation <b>2020</b> ,		13
72	Chloroplot: An Online Program for the Versatile Plotting of Organelle Genomes. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 576124	4.5	25
71	Unsupervised Learning and Multipartite Network Models: A Promising Approach for Understanding Traditional Medicine. <i>Frontiers in Pharmacology</i> , <b>2020</b> , 11, 1319	5.6	16
70	Multi-parametric single cell evaluation defines distinct drug responses in healthy hematologic cells that are retained in corresponding malignant cell types. <i>Haematologica</i> , <b>2020</b> , 105, 1527-1538	6.6	8
69	Drug combination sensitivity scoring facilitates the discovery of synergistic and efficacious drug combinations in cancer. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1006752	5	53
68	DrugComb: an integrative cancer drug combination data portal. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, W43-W50.	10.1	71
67	Making Sense of the Epigenome Using Data Integration Approaches. <i>Frontiers in Pharmacology</i> , <b>2019</b> , 10, 126	5.6	35
66	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. <i>Npj Systems Biology and Applications</i> , <b>2019</b> , 5, 20	5	21
65	Predicting Meridian in Chinese traditional medicine using machine learning approaches. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1007249	5	21

64	Combined gene essentiality scoring improves the prediction of cancer dependency maps. <i>EBioMedicine</i> , <b>2019</b> , 50, 67-80	8.8	10
63	Loss-of-function mutations with circadian rhythm regulator Per1/Per2 lead to premature ovarian insufficiency <i>Biology of Reproduction</i> , <b>2019</b> , 100, 1066-1072	3.9	10
62	Predicting Meridian in Chinese traditional medicine using machine learning approaches <b>2019</b> , 15, e1007249		
61	Predicting Meridian in Chinese traditional medicine using machine learning approaches <b>2019</b> , 15, e1007249		
60	Predicting Meridian in Chinese traditional medicine using machine learning approaches <b>2019</b> , 15, e1007249		
59	Predicting Meridian in Chinese traditional medicine using machine learning approaches <b>2019</b> , 15, e1007249		
58	Patient-Customized Drug Combination Prediction and Testing for T-cell Prolymphocytic Leukemia Patients. <i>Cancer Research</i> , <b>2018</b> , 78, 2407-2418	10.1	40
57	Methods for High-throughput Drug Combination Screening and Synergy Scoring. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1711, 351-398	1.4	80
56	Drug Target Commons: A Community Effort to Build a Consensus Knowledge Base for Drug-Target Interactions. <i>Cell Chemical Biology</i> , <b>2018</b> , 25, 224-229.e2	8.2	51
55	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> , <b>2018</b> , 132, 264-264	2.2	1
54	Predictive Response Biomarkers for BET Inhibitors in AML. <i>Blood</i> , <b>2018</b> , 132, 2749-2749	2.2	0
53	Eltrombopag Promotes Megakaryocyte Survival and Signaling in the Presence of Specific Cytotoxic Agents. <i>Blood</i> , <b>2018</b> , 132, 3836-3836	2.2	
52	Discovery of novel drug sensitivities in T-PLL by high-throughput ex vivo drug testing and mutation profiling. <i>Leukemia</i> , <b>2018</b> , 32, 774-787	10.7	56
51	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> , <b>2018</b> , 2018, 1-13	5	18
50	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> , <b>2017</b> , 144, 621-630	4.9	22
49	JAK1/2 and BCL2 inhibitors synergize to counteract bone marrow stromal cell-induced protection of AML. <i>Blood</i> , <b>2017</b> , 130, 789-802	2.2	63
48	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> , <b>2017</b> , 803, 24-38	5.3	5
47	SynergyFinder: a web application for analyzing drug combination dose-response matrix data. <i>Bioinformatics</i> , <b>2017</b> , 33, 2413-2415	7.2	249

46	The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , <b>2017</b> , 14, 937-938	21.6	8
45	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. <i>Cell Systems</i> , <b>2017</b> , 5, 485-497.e3	10.6	14
44	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> , <b>2017</b> , 9, 51	14.4	10
43	Informatics Approaches for Predicting, Understanding, and Testing Cancer Drug Combinations. <i>Methods in Molecular Biology</i> , <b>2017</b> , 1636, 485-506	1.4	6
42	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. <i>Nature Communications</i> , <b>2016</b> , 7, 12460	17.4	54
41	A three-year survey of the antimicrobial resistance of microorganisms at a Chinese hospital. <i>Experimental and Therapeutic Medicine</i> , <b>2016</b> , 11, 731-736	2.1	7
40	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> , <b>2016</b> , 20, 2825-34	2.9	13
39	Searching for Drug Synergy in Complex Dose-Response Landscapes Using an Interaction Potency Model. <i>Computational and Structural Biotechnology Journal</i> , <b>2015</b> , 13, 504-13	6.8	232
38	From drug response profiling to target addiction scoring in cancer cell models. <i>DMM Disease Models and Mechanisms</i> , <b>2015</b> , 8, 1255-64	4.1	9
37	What is synergy? The Saariselkä agreement revisited. <i>Frontiers in Pharmacology</i> , <b>2015</b> , 6, 181	5.6	88
36	Toward more realistic drug-target interaction predictions. <i>Briefings in Bioinformatics</i> , <b>2015</b> , 16, 325-37	13.4	182
35	Network pharmacology applications to map the unexplored target space and therapeutic potential of natural products. <i>Natural Product Reports</i> , <b>2015</b> , 32, 1249-66	15.1	198
34	TIMMA-R: an R package for predicting synergistic multi-targeted drug combinations in cancer cell lines or patient-derived samples. <i>Bioinformatics</i> , <b>2015</b> , 31, 1866-8	7.2	14
33	Systematic Mapping of Kinase Addiction Combinations in Breast Cancer Cells by Integrating Drug Sensitivity and Selectivity Profiles. <i>Chemistry and Biology</i> , <b>2015</b> , 22, 1144-55		20
32	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 933-40	44.5	70
31	A Bayesian Predictive Model for Clustering Data of Mixed Discrete and Continuous Type. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , <b>2015</b> , 37, 489-98	13.3	9
30	JAK1/2 and BCL2 Inhibitors Synergize to Counter-Act Bone Marrow Stromal Cell-Induced Protection of AML. <i>Blood</i> , <b>2015</b> , 126, 867-867	2.2	
29	Making sense of large-scale kinase inhibitor bioactivity data sets: a comparative and integrative analysis. <i>Journal of Chemical Information and Modeling</i> , <b>2014</b> , 54, 735-43	6.1	113

28	Network pharmacology strategies toward multi-target anticancer therapies: from computational models to experimental design principles. <i>Current Pharmaceutical Design</i> , <b>2014</b> , 20, 23-36	3.3	86
27	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> , <b>2013</b> , 20, 24-33	3.4	10
26	Target inhibition networks: predicting selective combinations of druggable targets to block cancer survival pathways. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003226	5	66
25	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> , <b>2013</b> , 33, 847-57	9.4	33
24	Phospholipids and insulin resistance in psychosis: a lipidomics study of twin pairs discordant for schizophrenia. <i>Genome Medicine</i> , <b>2012</b> , 4, 1	14.4	80
23	Metabolome in schizophrenia and other psychotic disorders: a general population-based study. <i>Genome Medicine</i> , <b>2011</b> , 3, 19	14.4	110
22	Association of lipidome remodeling in the adipocyte membrane with acquired obesity in humans. <i>PLoS Biology</i> , <b>2011</b> , 9, e1000623	9.7	169
21	ELEVATED SERUM SPHINGOMYELIN ASSOCIATES WITH REDUCED GRAY MATTER DENSITY: EVIDENCE FROM TWINS DISCORDANT FOR SCHIZOPHRENIA. <i>Schizophrenia Research</i> , <b>2010</b> , 117, 370-374 <sup>3,6</sup>		
20	Identifying currents in the gene pool for bacterial populations using an integrative approach. <i>PLoS Computational Biology</i> , <b>2009</b> , 5, e1000455	5	78
19	Integrating post-genomic approaches as a strategy to advance our understanding of health and disease. <i>Genome Medicine</i> , <b>2009</b> , 1, 35	14.4	19
18	Bayesian clustering of fuzzy feature vectors using a quasi-likelihood approach. <i>IEEE Transactions on Pattern Analysis and Machine Intelligence</i> , <b>2009</b> , 31, 74-85	13.3	7
17	Hyper-recombination, diversity, and antibiotic resistance in pneumococcus. <i>Science</i> , <b>2009</b> , 324, 1454-7	33.3	138
16	Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 539	3.6	612
15	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> , <b>2007</b> , 6, Article30	1.2	5
14	Bayesian analysis of population structure based on linked molecular information. <i>Mathematical Biosciences</i> , <b>2007</b> , 205, 19-31	3.9	185
13	Quantitative changes in collagen levels following 830-nm diode laser welding. <i>Lasers in Surgery and Medicine</i> , <b>1998</b> , 22, 207-11	3.6	14
12	Quantitative changes in collagen levels following 830-nm diode laser welding <b>1998</b> , 22, 207		2
11	NIMAA: an R/CRAN package to accomplish Nomlnal data Mining AnAllysis		1

10	Can we assume the gene expression profile as a proxy for signaling network activity?	8
9	Methods for High-Throughput Drug Combination Screening and Synergy Scoring	4
8	Anti-cancer Drug Synergy Prediction in Understudied Tissues using Transfer Learning	1
7	RNA Atlas of Human Bacterial Pathogens Uncovers Stress Dynamics Linked to Infection	1
6	Drug synergy of combinatory treatment with remdesivir and the repurposed drugs fluoxetine and itraconazole effectively impairs SARS-CoV-2 infection in vitro	5
5	A Community Challenge for Pancancer Drug Mechanism of Action Inference from Perturbational Profile Data	3
4	DrugComb - an integrative cancer drug combination data portal	1
3	Facilitating the design of combination therapy in cancer using multipartite network models: Emphasis on acute myeloid leukemia	1
2	DrugComb update: a more comprehensive drug sensitivity data repository and analysis portal	1
1	Comparative analysis of molecular representations in prediction of drug combination effects	1