Jing Tang

List of Publications by Year
in descending order

95 papers	6,930 citations	109321 35 h-index	69250 77 g-index
126 all docs	126 docs citations	126 times ranked	10916 citing authors

#	Article	IF	Citations
1	Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations. BMC Bioinformatics, 2008, 9, 539.	2.6	760
2	Common pitfalls and recommendations for using machine learning to detect and prognosticate for COVID-19 using chest radiographs and CT scans. Nature Machine Intelligence, 2021, 3, 199-217.	16.0	607
3	Searching for Drug Synergy in Complex Dose–Response Landscapes Using an Interaction Potency Model. Computational and Structural Biotechnology Journal, 2015, 13, 504-513.	4.1	485
4	SynergyFinder: a web application for analyzing drug combination dose–response matrix data. Bioinformatics, 2017, 33, 2413-2415.	4.1	403
5	Toward more realistic drug-target interaction predictions. Briefings in Bioinformatics, 2015, 16, 325-337.	6.5	331
6	Network pharmacology applications to map the unexplored target space and therapeutic potential of natural products. Natural Product Reports, 2015, 32, 1249-1266.	10.3	331
7	Making Sense of Large-Scale Kinase Inhibitor Bioactivity Data Sets: A Comparative and Integrative Analysis. Journal of Chemical Information and Modeling, 2014, 54, 735-743.	5.4	284
8	Bayesian analysis of population structure based on linked molecular information. Mathematical Biosciences, 2007, 205, 19-31.	1.9	214
9	Association of Lipidome Remodeling in the Adipocyte Membrane with Acquired Obesity in Humans. PLoS Biology, 2011, 9, e1000623.	5.6	213
10	Hyper-Recombination, Diversity, and Antibiotic Resistance in Pneumococcus. Science, 2009, 324, 1454-1457.	12.6	164
11	SynergyFinder Plus: Toward Better Interpretation and Annotation of Drug Combination Screening Datasets. Genomics, Proteomics and Bioinformatics, 2022, 20, 587-596.	6.9	159
12	DrugComb: an integrative cancer drug combination data portal. Nucleic Acids Research, 2019, 47, W43-W51.	14.5	153
13	What is synergy? The Saariselkä agreement revisited. Frontiers in Pharmacology, 2015, 6, 181.	3.5	147
14	Methods for High-throughput Drug Combination Screening and Synergy Scoring. Methods in Molecular Biology, 2018, 1711, 351-398.	0.9	140
15	Chloroplot: An Online Program for the Versatile Plotting of Organelle Genomes. Frontiers in Genetics, 2020, 11, 576124.	2.3	135
16	Metabolome in schizophrenia and other psychotic disorders: a general population-based study. Genome Medicine, 2011, 3, 19.	8.2	131
17	Drug Target Commons: A Community Effort to Build a Consensus Knowledge Base for Drug-Target Interactions. Cell Chemical Biology, 2018, 25, 224-229.e2.	5.2	124
18	Network Pharmacology Strategies Toward Multi-Target Anticancer Therapies: From Computational Models to Experimental Design Principles. Current Pharmaceutical Design, 2014, 20, 23-36.	1.9	115

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19	Identifying Currents in the Gene Pool for Bacterial Populations Using an Integrative Approach. PLoS Computational Biology, 2009, 5, e1000455.	3.2	112
20	Phospholipids and insulin resistance in psychosis: a lipidomics study of twin pairs discordant for schizophrenia. Genome Medicine, 2012, 4, 1.	8.2	106
21	Drug combination sensitivity scoring facilitates the discovery of synergistic and efficacious drug combinations in cancer. PLoS Computational Biology, 2019, 15, e1006752.	3.2	106
22	JAK1/2 and BCL2 inhibitors synergize to counteract bone marrow stromal cellâ€"induced protection of AML. Blood, 2017, 130, 789-802.	1.4	90
23	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	17.5	88
24	Target Inhibition Networks: Predicting Selective Combinations of Druggable Targets to Block Cancer Survival Pathways. PLoS Computational Biology, 2013, 9, e1003226.	3.2	84
25	Discovery of novel drug sensitivities in T-PLL by high-throughput ex vivo drug testing and mutation profiling. Leukemia, 2018, 32, 774-787.	7.2	75
26	Drug synergy of combinatory treatment with remdesivir and the repurposed drugs fluoxetine and itraconazole effectively impairs SARSâ€CoVâ€2 infection in vitro. British Journal of Pharmacology, 2021, 178, 2339-2350.	5.4	74
27	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460.	12.8	73
28	Exploration of databases and methods supporting drug repurposing: a comprehensive survey. Briefings in Bioinformatics, 2021, 22, 1656-1678.	6.5	66
29	Network-based modeling of herb combinations in traditional Chinese medicine. Briefings in Bioinformatics, 2021, 22, .	6.5	62
30	Patient-Customized Drug Combination Prediction and Testing for T-cell Prolymphocytic Leukemia Patients. Cancer Research, 2018, 78, 2407-2418.	0.9	60
31	Making Sense of the Epigenome Using Data Integration Approaches. Frontiers in Pharmacology, 2019, 10, 126.	3.5	58
32	DrugComb update: a more comprehensive drug sensitivity data repository and analysis portal. Nucleic Acids Research, 2021, 49, W174-W184.	14.5	54
33	Anticancer drug synergy prediction in understudied tissues using transfer learning. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 42-51.	4.4	51
34	Comparative analysis of molecular fingerprints in prediction of drug combination effects. Briefings in Bioinformatics, 2021, 22, .	6.5	47
35	Predicting Meridian in Chinese traditional medicine using machine learning approaches. PLoS Computational Biology, 2019, 15, e1007249.	3.2	41
36	Drug Target Commons 2.0: a community platform for systematic analysis of drugâ€"target interaction profiles. Database: the Journal of Biological Databases and Curation, 2018, 2018, 1-13.	3.0	36

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37	Genomic, Transcriptomic, and Lipidomic Profiling Highlights the Role of Inflammation in Individuals With Low High-density Lipoprotein Cholesterol. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 847-857.	2.4	35
38	Combination Therapy with Fluoxetine and the Nucleoside Analog GS-441524 Exerts Synergistic Antiviral Effects against Different SARS-CoV-2 Variants In Vitro. Pharmaceutics, 2021, 13, 1400.	4.5	35
39	RNA atlas of human bacterial pathogens uncovers stress dynamics linked to infection. Nature Communications, 2021, 12, 3282.	12.8	33
40	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. Cell Reports Medicine, 2022, 3, 100492.	6.5	33
41	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. Npj Systems Biology and Applications, 2019, 5, 20.	3.0	32
42	Unsupervised Learning and Multipartite Network Models: A Promising Approach for Understanding Traditional Medicine. Frontiers in Pharmacology, 2020, 11, 1319.	3.5	29
43	Drug repurposing for COVID-19 using graph neural network and harmonizing multiple evidence. Scientific Reports, 2021, 11, 23179.	3.3	28
44	Systematic drug sensitivity testing reveals synergistic growth inhibition by dasatinib or mTOR inhibitors with paclitaxel in ovarian granulosa cell tumor cells. Gynecologic Oncology, 2017, 144, 621-630.	1.4	26
45	Integrating post-genomic approaches as a strategy to advance our understanding of health and disease. Genome Medicine, 2009, 1, 35.	8.2	23
46	Loss-of-function mutations with circadian rhythm regulator Per1/Per2 lead to premature ovarian insufficiencyâ€. Biology of Reproduction, 2019, 100, 1066-1072.	2.7	23
47	Metastasis associated in colon cancer 1 (MACC1) promotes growth and metastasis processes of colon cancer cells. European Review for Medical and Pharmacological Sciences, 2016, 20, 2825-34.	0.7	23
48	Systematic Mapping of Kinase Addiction Combinations in Breast Cancer Cells by Integrating Drug Sensitivity and Selectivity Profiles. Chemistry and Biology, 2015, 22, 1144-1155.	6.0	22
49	Quantitative changes in collagen levels following 830-nm diode laser welding. , 1998, 22, 207-211.		21
50	A Community Challenge for Inferring Genetic Predictors of Gene Essentialities through Analysis of a Functional Screen of Cancer Cell Lines. Cell Systems, 2017, 5, 485-497.e3.	6.2	19
51	Multi-parametric single cell evaluation defines distinct drug responses in healthy hematologic cells that are retained in corresponding malignant cell types. Haematologica, 2020, 105, 1527-1538.	3.5	19
52	Combined gene essentiality scoring improves the prediction of cancer dependency maps. EBioMedicine, 2019, 50, 67-80.	6.1	18
53	TIMMA-R: an R package for predicting synergistic multi-targeted drug combinations in cancer cell lines or patient-derived samples. Bioinformatics, 2015, 31, 1866-1868.	4.1	15
54	Bipartite network models to design combination therapies in acute myeloid leukaemia. Nature Communications, 2022, 13, 2128.	12.8	15

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55	A Bayesian Predictive Model for Clustering Data of Mixed Discrete and Continuous Type. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2015, 37, 489-498.	13.9	14
56	Seasonal Variation in the Brain Î¼-Opioid Receptor Availability. Journal of Neuroscience, 2021, 41, 1265-1273.	3.6	14
57	From drug response profiling to target addiction scoring in cancer cell models. DMM Disease Models and Mechanisms, 2015, 8, 1255-1264.	2.4	13
58	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. Briefings in Bioinformatics, 2021, 22, .	6.5	13
59	Seed-effect modeling improves the consistency of genome-wide loss-of-function screens and identifies synthetic lethal vulnerabilities in cancer cells. Genome Medicine, 2017, 9, 51.	8.2	12
60	CD73 contributes to antiâ€inflammatory properties of afferent lymphatic endothelial cells in humans and mice. European Journal of Immunology, 2021, 51, 231-246.	2.9	12
61	Phosphorylation of human La protein at Ser^{366} by casein kinase II contributes to hepatitis B virus replication and expression *in vitro*. Journal of Viral Hepatitis, 2013, 20, 24-33.	2.0	11
62	Informatics Approaches for Predicting, Understanding, and Testing Cancer Drug Combinations. Methods in Molecular Biology, 2017, 1636, 485-506.	0.9	11
63	The inconvenience of data of convenience: computational research beyond post-mortem analyses. Nature Methods, 2017, 14, 937-938.	19.0	9
64	Identification of Celecoxib-Targeted Proteins Using Label-Free Thermal Proteome Profiling on Rat Hippocampus. Molecular Pharmacology, 2021, 99, 308-318.	2.3	9
65	Bayesian Clustering of Fuzzy Feature Vectors Using a Quasi-Likelihood Approach. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2009, 31, 74-85.	13.9	8
66	Can We Assume the Gene Expression Profile as a Proxy for Signaling Network Activity?. Biomolecules, 2020, 10, 850.	4.0	8
67	A three-year survey of the antimicrobial resistance of microorganisms at a Chinese hospital. Experimental and Therapeutic Medicine, 2016, 11, 731-736.	1.8	7
68	Treatment of novel IL17A inhibitor in glioblastoma implementing 3rd generation co-culture cell line and patient-derived tumor model. European Journal of Pharmacology, 2017, 803, 24-38.	3.5	7
69	Minimal information for chemosensitivity assays (MICHA): a next-generation pipeline to enable the FAIRification of drug screening experiments. Briefings in Bioinformatics, 2022, 23, .	6.5	7
70	Heterogeneous modulation of Bcl-2 family members and drug efflux mediate MCL-1 inhibitor resistance in multiple myeloma. Blood Advances, 2021, 5, 4125-4139.	5.2	6
71	Eribulin activity in soft tissue sarcoma monolayer and three-dimensional cell line models: could the combination with other drugs improve its antitumoral effect?. Cancer Cell International, 2021, 21, 646.	4.1	6
72	Using BERT to identify drug-target interactions from whole PubMed. BMC Bioinformatics, 2022, 23, .	2.6	6

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73	T-BAPS: A Bayesian Statistical Tool for Comparison of Microbial Communities Using Terminal-restriction Fragment Length Polymorphism (T-RFLP) Data. Statistical Applications in Genetics and Molecular Biology, 2007, 6, Article30.	0.6	5
74	S100 Calcium Binding Protein Family Members Associate With Poor Patient Outcome and Response to Proteasome Inhibition in Multiple Myeloma. Frontiers in Cell and Developmental Biology, 2021, 9, 723016.	3.7	5
75	Multi-Parametric Single Cell Profiling Defines Distinct Drug Responses in Healthy Hematological Cell Lineages That Are Retained in Corresponding Malignant Cell Types. Blood, 2018, 132, 264-264.	1.4	5
76	Application of microfluidic chips in anticancer drug screening. Bosnian Journal of Basic Medical Sciences, 2021, , .	1.0	4
77	Prognosis Stratification Tools in Early-Stage Endometrial Cancer: Could We Improve Their Accuracy?. Cancers, 2022, 14, 912.	3.7	4
78	Quantitative changes in collagen levels following 830â€nm diode laser welding. Lasers in Surgery and Medicine, 1998, 22, 207-211.	2.1	2
79	Predictive Response Biomarkers for BET Inhibitors in AML. Blood, 2018, 132, 2749-2749.	1.4	2
80	Abstract 3746: Novel therapeutic possibilities for chemorefractory ovarian cancer patients identified by functional ex vivo drug sensitivity testing of primary cells from ascites. , 2015, , .		1
81	Vascular adhesion protein-1 defines a unique subpopulation of human hematopoietic stem cells and regulates their proliferation. Cellular and Molecular Life Sciences, 2021, 78, 7851-7872.	5.4	1
82	Bayes in Wonderland! Predictive Supervised Classification Inference Hits Unpredictability. Mathematics, 2022, 10, 828.	2.2	1
83	Antitumoral Effect of Plocabulin in High Grade Serous Ovarian Carcinoma Cell Line Models. Frontiers in Oncology, 2022, 12, 862321.	2.8	1
84	ELEVATED SERUM SPHINGOMYELIN ASSOCIATES WITH REDUCED GRAY MATTER DENSITY: EVIDENCE FROM TWINS DISCORDANT FOR SCHIZOPHRENIA. Schizophrenia Research, 2010, 117, 370-371.	2.0	0
85	Stromal-Derived Factors Modulate Ex Vivo Drug Responses of Primary Acute Myeloid Leukemia Cells. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, S8-S9.	0.4	0
86	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.	2.0	0
87	Abstract 5220: Identifying AML-specific key targeted drugs using high-throughput drug sensitivity and resistance testing profiles of AML cells.. , 2013, , .		0
88	JAK1/2 and BCL2 Inhibitors Synergize to Counter-Act Bone Marrow Stromal Cell-Induced Protection of AML. Blood, 2015, 126, 867-867.	1.4	0
89	Abstract A26: Prediction of synergistic anticancer drug combinations by integrating chemical and genetic screens. , 2017, , .		0
90	Eltrombopag Promotes Megakaryocyte Survival and Signaling in the Presence of Specific Cytotoxic Agents. Blood, 2018, 132, 3836-3836.	1.4	0

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91	The ENDS of assumptions: an online tool for the epistemic non-parametric drug–response scoring. Bioinformatics, 2022, 38, 3132-3133.	4.1	0
92	Predicting Meridian in Chinese traditional medicine using machine learning approaches. , 2019, 15, e1007249.		0
93	Predicting Meridian in Chinese traditional medicine using machine learning approaches. , 2019, 15, e1007249.		0
94	Predicting Meridian in Chinese traditional medicine using machine learning approaches. , 2019, 15, e1007249.		0
95	Predicting Meridian in Chinese traditional medicine using machine learning approaches. , 2019, 15, e1007249.		0