

Jing Tang

List of Publications by Year in descending order

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Version: 2024-02-01

95
papers

6,930
citations

109137

35
h-index

69108

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. <i>BMC Bioinformatics</i> , 2008, 9, 539.	1.2	760
2	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.	8.3	607
3	Searching for Drug Synergy in Complex Dose-Response Landscapes Using an Interaction Potency Model. <i>Computational and Structural Biotechnology Journal</i> , 2015, 13, 504-513.	1.9	485
4	SynergyFinder: a web application for analyzing drug combination dose-response matrix data. <i>Bioinformatics</i> , 2017, 33, 2413-2415.	1.8	403
5	Toward more realistic drug-target interaction predictions. <i>Briefings in Bioinformatics</i> , 2015, 16, 325-337.	3.2	331
6	Network pharmacology applications to map the unexplored target space and therapeutic potential of natural products. <i>Natural Product Reports</i> , 2015, 32, 1249-1266.	5.2	331
7	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, 735-743.	2.5	284
8	Bayesian analysis of population structure based on linked molecular information. <i>Mathematical Biosciences</i> , 2007, 205, 19-31.	0.9	214
9	Association of Lipidome Remodeling in the Adipocyte Membrane with Acquired Obesity in Humans. <i>PLoS Biology</i> , 2011, 9, e1000623.	2.6	213
10	Hyper-Recombination, Diversity, and Antibiotic Resistance in <i>Pneumococcus</i> . <i>Science</i> , 2009, 324, 1454-1457.	6.0	164
11	SynergyFinder Plus: Toward Better Interpretation and Annotation of Drug Combination Screening Datasets. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 587-596.	3.0	159
12	DrugComb: an integrative cancer drug combination data portal. <i>Nucleic Acids Research</i> , 2019, 47, W43-W51.	6.5	153
13	What is synergy? The Saarisek agreement revisited. <i>Frontiers in Pharmacology</i> , 2015, 6, 181.	1.6	147
14	Methods for High-throughput Drug Combination Screening and Synergy Scoring. <i>Methods in Molecular Biology</i> , 2018, 1711, 351-398.	0.4	140
15	Chloroplot: An Online Program for the Versatile Plotting of Organelle Genomes. <i>Frontiers in Genetics</i> , 2020, 11, 576124.	1.1	135
16	Metabolome in schizophrenia and other psychotic disorders: a general population-based study. <i>Genome Medicine</i> , 2011, 3, 19.	3.6	131
17	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.	2.5	124
18	Network Pharmacology Strategies Toward Multi-Target Anticancer Therapies: From Computational Models to Experimental Design Principles. <i>Current Pharmaceutical Design</i> , 2014, 20, 23-36.	0.9	115

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19	Identifying Currents in the Gene Pool for Bacterial Populations Using an Integrative Approach. <i>PLoS Computational Biology</i> , 2009, 5, e1000455.	1.5	112
20	Phospholipids and insulin resistance in psychosis: a lipidomics study of twin pairs discordant for schizophrenia. <i>Genome Medicine</i> , 2012, 4, 1.	3.6	106
21	Drug combination sensitivity scoring facilitates the discovery of synergistic and efficacious drug combinations in cancer. <i>PLoS Computational Biology</i> , 2019, 15, e1006752.	1.5	106
22	JAK1/2 and BCL2 inhibitors synergize to counteract bone marrow stromal cell-induced protection of AML. <i>Blood</i> , 2017, 130, 789-802.	0.6	90
23	Prediction of human population responses to toxic compounds by a collaborative competition. <i>Nature Biotechnology</i> , 2015, 33, 933-940.	9.4	88
24	Target Inhibition Networks: Predicting Selective Combinations of Druggable Targets to Block Cancer Survival Pathways. <i>PLoS Computational Biology</i> , 2013, 9, e1003226.	1.5	84
25	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.	3.3	75
26	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.	2.7	74
27	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. <i>Nature Communications</i> , 2016, 7, 12460.	5.8	73
28	Exploration of databases and methods supporting drug repurposing: a comprehensive survey. <i>Briefings in Bioinformatics</i> , 2021, 22, 1656-1678.	3.2	66
29	Network-based modeling of herb combinations in traditional Chinese medicine. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	62
30	Patient-Customized Drug Combination Prediction and Testing for T-cell Prolymphocytic Leukemia Patients. <i>Cancer Research</i> , 2018, 78, 2407-2418.	0.4	60
31	Making Sense of the Epigenome Using Data Integration Approaches. <i>Frontiers in Pharmacology</i> , 2019, 10, 126.	1.6	58
32	DrugComb update: a more comprehensive drug sensitivity data repository and analysis portal. <i>Nucleic Acids Research</i> , 2021, 49, W174-W184.	6.5	54
33	Anticancer drug synergy prediction in understudied tissues using transfer learning. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021, 28, 42-51.	2.2	51
34	Comparative analysis of molecular fingerprints in prediction of drug combination effects. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	47
35	Predicting Meridian in Chinese traditional medicine using machine learning approaches. <i>PLoS Computational Biology</i> , 2019, 15, e1007249.	1.5	41
36	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.	1.4	36

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37	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, 847-857.	1.1	35
38	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, 1400.	2.0	35
39	RNA atlas of human bacterial pathogens uncovers stress dynamics linked to infection. <i>Nature Communications</i> , 2021, 12, 3282.	5.8	33
40	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. <i>Cell Reports Medicine</i> , 2022, 3, 100492.	3.3	33
41	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.	1.4	32
42	Unsupervised Learning and Multipartite Network Models: A Promising Approach for Understanding Traditional Medicine. <i>Frontiers in Pharmacology</i> , 2020, 11, 1319.	1.6	29
43	Drug repurposing for COVID-19 using graph neural network and harmonizing multiple evidence. <i>Scientific Reports</i> , 2021, 11, 23179.	1.6	28
44	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.	0.6	26
45	Integrating post-genomic approaches as a strategy to advance our understanding of health and disease. <i>Genome Medicine</i> , 2009, 1, 35.	3.6	23
46	Loss-of-function mutations with circadian rhythm regulator Per1/Per2 lead to premature ovarian insufficiency. <i>Biology of Reproduction</i> , 2019, 100, 1066-1072.	1.2	23
47	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.	0.5	23
48	Systematic Mapping of Kinase Addiction Combinations in Breast Cancer Cells by Integrating Drug Sensitivity and Selectivity Profiles. <i>Chemistry and Biology</i> , 2015, 22, 1144-1155.	6.2	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. <i>Cell Systems</i> , 2017, 5, 485-497.e3.	2.9	19
51	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.	1.7	19
52	Combined gene essentiality scoring improves the prediction of cancer dependency maps. <i>EBioMedicine</i> , 2019, 50, 67-80.	2.7	18
53	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, 1866-1868.	1.8	15
54	Bipartite network models to design combination therapies in acute myeloid leukaemia. <i>Nature Communications</i> , 2022, 13, 2128.	5.8	15

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55	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, 489-498.	9.7	14
56	Seasonal Variation in the Brain μ -Opioid Receptor Availability. <i>Journal of Neuroscience</i> , 2021, 41, 1265-1273.	1.7	14
57	From drug response profiling to target addiction scoring in cancer cell models. <i>DMM Disease Models and Mechanisms</i> , 2015, 8, 1255-1264.	1.2	13
58	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	13
59	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.	3.6	12
60	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.	1.6	12
61	Phosphorylation of human La protein at Ser ³⁶⁶ by casein kinase II contributes to hepatitis B virus replication and expression <i>in vitro</i> . <i>Journal of Viral Hepatitis</i> , 2013, 20, 24-33.	1.0	11
62	Informatics Approaches for Predicting, Understanding, and Testing Cancer Drug Combinations. <i>Methods in Molecular Biology</i> , 2017, 1636, 485-506.	0.4	11
63	The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , 2017, 14, 937-938.	9.0	9
64	Identification of Celecoxib-Targeted Proteins Using Label-Free Thermal Proteome Profiling on Rat Hippocampus. <i>Molecular Pharmacology</i> , 2021, 99, 308-318.	1.0	9
65	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.	9.7	8
66	Can We Assume the Gene Expression Profile as a Proxy for Signaling Network Activity?. <i>Biomolecules</i> , 2020, 10, 850.	1.8	8
67	A three-year survey of the antimicrobial resistance of microorganisms at a Chinese hospital. <i>Experimental and Therapeutic Medicine</i> , 2016, 11, 731-736.	0.8	7
68	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.	1.7	7
69	Minimal information for chemosensitivity assays (MICHA): a next-generation pipeline to enable the FAIRification of drug screening experiments. <i>Briefings in Bioinformatics</i> , 2022, 23, .	3.2	7
70	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.	2.5	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?. <i>Cancer Cell International</i> , 2021, 21, 646.	1.8	6
72	Using BERT to identify drug-target interactions from whole PubMed. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	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. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2007, 6, Article30.	0.2	5
74	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, 723016.	1.8	5
75	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.	0.6	5
76	Application of microfluidic chips in anticancer drug screening. <i>Bosnian Journal of Basic Medical Sciences</i> , 2021, , .	0.6	4
77	Prognosis Stratification Tools in Early-Stage Endometrial Cancer: Could We Improve Their Accuracy?. <i>Cancers</i> , 2022, 14, 912.	1.7	4
78	Quantitative changes in collagen levels following 830nm diode laser welding. <i>Lasers in Surgery and Medicine</i> , 1998, 22, 207-211.	1.1	2
79	Predictive Response Biomarkers for BET Inhibitors in AML. <i>Blood</i> , 2018, 132, 2749-2749.	0.6	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. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 7851-7872.	2.4	1
82	Bayes in Wonderland! Predictive Supervised Classification Inference Hits Unpredictability. <i>Mathematics</i> , 2022, 10, 828.	1.1	1
83	Antitumoral Effect of Plocabulin in High Grade Serous Ovarian Carcinoma Cell Line Models. <i>Frontiers in Oncology</i> , 2022, 12, 862321.	1.3	1
84	ELEVATED SERUM SPHINGOMYELIN ASSOCIATES WITH REDUCED GRAY MATTER DENSITY: EVIDENCE FROM TWINS DISCORDANT FOR SCHIZOPHRENIA. <i>Schizophrenia Research</i> , 2010, 117, 370-371.	1.1	0
85	Stromal-Derived Factors Modulate Ex Vivo Drug Responses of Primary Acute Myeloid Leukemia Cells. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2015, 15, S8-S9.	0.2	0
86	A three-term recurrence relation for accurate evaluation of transition probabilities of the simple birth-and-death process. <i>BIT Numerical Mathematics</i> , 2021, 61, 561-585.	1.0	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. <i>Blood</i> , 2015, 126, 867-867.	0.6	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. <i>Blood</i> , 2018, 132, 3836-3836.	0.6	0

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91	The ENDS of assumptions: an online tool for the epistemic non-parametric drug response scoring. <i>Bioinformatics</i> , 2022, 38, 3132-3133.	1.8	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