Jing Tang

List of Publications by Year
in descending order

95 papers	6,930 citations	125106 35 h-index	78623 77 g-index
126 all docs	126 docs citations	126 times ranked	11885 citing authors

#	Article	IF	Citations
1	Minimal information for chemosensitivity assays (MICHA): a next-generation pipeline to enable the FAIRification of drug screening experiments. Briefings in Bioinformatics, 2022, 23, .	3.2	7
2	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. Cell Reports Medicine, 2022, 3, 100492.	3.3	33
3	SynergyFinder Plus: Toward Better Interpretation and Annotation of Drug Combination Screening Datasets. Genomics, Proteomics and Bioinformatics, 2022, 20, 587-596.	3.0	159
4	Prognosis Stratification Tools in Early-Stage Endometrial Cancer: Could We Improve Their Accuracy?. Cancers, 2022, 14, 912.	1.7	4
5	Bayes in Wonderland! Predictive Supervised Classification Inference Hits Unpredictability. Mathematics, 2022, 10, 828.	1.1	1
6	Antitumoral Effect of Plocabulin in High Grade Serous Ovarian Carcinoma Cell Line Models. Frontiers in Oncology, 2022, 12, 862321.	1.3	1
7	The ENDS of assumptions: an online tool for the epistemic non-parametric drug–response scoring. Bioinformatics, 2022, 38, 3132-3133.	1.8	0
8	Bipartite network models to design combination therapies in acute myeloid leukaemia. Nature Communications, 2022, 13, 2128.	5.8	15
9	Using BERT to identify drug-target interactions from whole PubMed. BMC Bioinformatics, 2022, 23, .	1.2	6
10	Exploration of databases and methods supporting drug repurposing: a comprehensive survey. Briefings in Bioinformatics, 2021, 22, 1656-1678.	3.2	66
11	Anticancer drug synergy prediction in understudied tissues using transfer learning. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 42-51.	2.2	51
12	CD73 contributes to anti‐inflammatory properties of afferent lymphatic endothelial cells in humans and mice. European Journal of Immunology, 2021, 51, 231-246.	1.6	12
13	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.	1.0	0
14	Identification of Celecoxib-Targeted Proteins Using Label-Free Thermal Proteome Profiling on Rat Hippocampus. Molecular Pharmacology, 2021, 99, 308-318.	1.0	9
15	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.	8.3	607
16	Drug synergy of combinatory treatment with remdesivir and the repurposed drugs fluoxetine and itraconazole effectively impairs SARS‐CoV‐2 infection in vitro. British Journal of Pharmacology, 2021, 178, 2339-2350.	2.7	74
17	Network-based modeling of herb combinations in traditional Chinese medicine. Briefings in Bioinformatics, 2021, 22, .	3.2	62
18	RNA atlas of human bacterial pathogens uncovers stress dynamics linked to infection. Nature Communications, 2021, 12, 3282.	5.8	33

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19	DrugComb update: a more comprehensive drug sensitivity data repository and analysis portal. Nucleic Acids Research, 2021, 49, W174-W184.	6.5	54
20	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.	1.8	5
21	Comparative analysis of molecular fingerprints in prediction of drug combination effects. Briefings in Bioinformatics, 2021, 22, .	3.2	47
22	Network-guided identification of cancer-selective combinatorial therapies in ovarian cancer. Briefings in Bioinformatics, 2021, 22, .	3.2	13
23	Application of microfluidic chips in anticancer drug screening. Bosnian Journal of Basic Medical Sciences, 2021, , .	0.6	4
24	Heterogeneous modulation of Bcl-2 family members and drug efflux mediate MCL-1 inhibitor resistance in multiple myeloma. Blood Advances, 2021, 5, 4125-4139.	2.5	6
25	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.	2.0	35
26	Seasonal Variation in the Brain μ-Opioid Receptor Availability. Journal of Neuroscience, 2021, 41, 1265-1273.	1.7	14
27	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.	2.4	1
28	Drug repurposing for COVID-19 using graph neural network and harmonizing multiple evidence. Scientific Reports, 2021, 11, 23179.	1.6	28
29	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.	1.8	6
30	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.	1.7	19
31	Chloroplot: An Online Program for the Versatile Plotting of Organelle Genomes. Frontiers in Genetics, 2020, 11, 576124.	1.1	135
32	Unsupervised Learning and Multipartite Network Models: A Promising Approach for Understanding Traditional Medicine. Frontiers in Pharmacology, 2020, 11, 1319.	1.6	29
33	Can We Assume the Gene Expression Profile as a Proxy for Signaling Network Activity?. Biomolecules, 2020, 10, 850.	1.8	8
34	Network pharmacology modeling identifies synergistic Aurora B and ZAK interaction in triple-negative breast cancer. Npj Systems Biology and Applications, 2019, 5, 20.	1.4	32
35	Drug combination sensitivity scoring facilitates the discovery of synergistic and efficacious drug combinations in cancer. PLoS Computational Biology, 2019, 15, e1006752.	1.5	106
36	DrugComb: an integrative cancer drug combination data portal. Nucleic Acids Research, 2019, 47, W43-W51.	6.5	153

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37	Making Sense of the Epigenome Using Data Integration Approaches. Frontiers in Pharmacology, 2019, 10, 126.	1.6	58
38	Predicting Meridian in Chinese traditional medicine using machine learning approaches. PLoS Computational Biology, 2019, 15, e1007249.	1.5	41
39	Combined gene essentiality scoring improves the prediction of cancer dependency maps. EBioMedicine, 2019, 50, 67-80.	2.7	18
40	Loss-of-function mutations with circadian rhythm regulator Per1/Per2 lead to premature ovarian insufficiencyâ€. Biology of Reproduction, 2019, 100, 1066-1072.	1.2	23
41	Predicting Meridian in Chinese traditional medicine using machine learning approaches. , 2019, 15, e1007249.		0
42	Predicting Meridian in Chinese traditional medicine using machine learning approaches. , 2019, 15, e1007249.		0
43	Predicting Meridian in Chinese traditional medicine using machine learning approaches. , 2019, 15, e1007249.		0
44	Predicting Meridian in Chinese traditional medicine using machine learning approaches. , 2019, 15, e1007249.		0
45	Patient-Customized Drug Combination Prediction and Testing for T-cell Prolymphocytic Leukemia Patients. Cancer Research, 2018, 78, 2407-2418.	0.4	60
46	Methods for High-throughput Drug Combination Screening and Synergy Scoring. Methods in Molecular Biology, 2018, 1711, 351-398.	0.4	140
47	Drug Target Commons: A Community Effort to Build a Consensus Knowledge Base for Drug-Target Interactions. Cell Chemical Biology, 2018, 25, 224-229.e2.	2.5	124
48	Discovery of novel drug sensitivities in T-PLL by high-throughput ex vivo drug testing and mutation profiling. Leukemia, 2018, 32, 774-787.	3.3	75
49	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.	1.4	36
50	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.	0.6	5
51	Predictive Response Biomarkers for BET Inhibitors in AML. Blood, 2018, 132, 2749-2749.	0.6	2
52	Eltrombopag Promotes Megakaryocyte Survival and Signaling in the Presence of Specific Cytotoxic Agents. Blood, 2018, 132, 3836-3836.	0.6	0
53	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.	0.6	26
54	JAK1/2 and BCL2 inhibitors synergize to counteract bone marrow stromal cellâ€"induced protection of AML. Blood, 2017, 130, 789-802.	0.6	90

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55	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.	1.7	7
56	SynergyFinder: a web application for analyzing drug combination dose–response matrix data. Bioinformatics, 2017, 33, 2413-2415.	1.8	403
57	The inconvenience of data of convenience: computational research beyond post-mortem analyses. Nature Methods, 2017, 14, 937-938.	9.0	9
58	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.	2.9	19
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.	3.6	12
60	Informatics Approaches for Predicting, Understanding, and Testing Cancer Drug Combinations. Methods in Molecular Biology, 2017, 1636, 485-506.	0.4	11
61	Abstract A26: Prediction of synergistic anticancer drug combinations by integrating chemical and genetic screens. , 2017, , .		0
62	A three-year survey of the antimicrobial resistance of microorganisms at a Chinese hospital. Experimental and Therapeutic Medicine, 2016, 11, 731-736.	0.8	7
63	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460.	5.8	73
64	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.	0.5	23
65	From drug response profiling to target addiction scoring in cancer cell models. DMM Disease Models and Mechanisms, 2015, 8, 1255-1264.	1.2	13
66	What is synergy? The Saariselkä agreement revisited. Frontiers in Pharmacology, 2015, 6, 181.	1.6	147
67	Toward more realistic drug-target interaction predictions. Briefings in Bioinformatics, 2015, 16, 325-337.	3.2	331
68	Network pharmacology applications to map the unexplored target space and therapeutic potential of natural products. Natural Product Reports, 2015, 32, 1249-1266.	5.2	331
69	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.	1.8	15
70	Systematic Mapping of Kinase Addiction Combinations in Breast Cancer Cells by Integrating Drug Sensitivity and Selectivity Profiles. Chemistry and Biology, 2015, 22, 1144-1155.	6.2	22
71	Prediction of human population responses to toxic compounds by a collaborative competition. Nature Biotechnology, 2015, 33, 933-940.	9.4	88
72	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.	9.7	14

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73	Stromal-Derived Factors Modulate Ex Vivo Drug Responses of Primary Acute Myeloid Leukemia Cells. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, S8-S9.	0.2	0
74	Searching for Drug Synergy in Complex Dose–Response Landscapes Using an Interaction Potency Model. Computational and Structural Biotechnology Journal, 2015, 13, 504-513.	1.9	485
75	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
76	JAK1/2 and BCL2 Inhibitors Synergize to Counter-Act Bone Marrow Stromal Cell-Induced Protection of AML. Blood, 2015, 126, 867-867.	0.6	0
77	Network Pharmacology Strategies Toward Multi-Target Anticancer Therapies: From Computational Models to Experimental Design Principles. Current Pharmaceutical Design, 2014, 20, 23-36.	0.9	115
78	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.	2.5	284
79	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.	1.0	11
80	Target Inhibition Networks: Predicting Selective Combinations of Druggable Targets to Block Cancer Survival Pathways. PLoS Computational Biology, 2013, 9, e1003226.	1.5	84
81	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.	1.1	35
82	Abstract 5220: Identifying AML-specific key targeted drugs using high-throughput drug sensitivity and resistance testing profiles of AML cells.. , 2013, , .		0
83	Phospholipids and insulin resistance in psychosis: a lipidomics study of twin pairs discordant for schizophrenia. Genome Medicine, 2012, 4, 1.	3.6	106
84	Metabolome in schizophrenia and other psychotic disorders: a general population-based study. Genome Medicine, 2011, 3, 19.	3.6	131
85	Association of Lipidome Remodeling in the Adipocyte Membrane with Acquired Obesity in Humans. PLoS Biology, 2011, 9, e1000623.	2.6	213
86	ELEVATED SERUM SPHINGOMYELIN ASSOCIATES WITH REDUCED GRAY MATTER DENSITY: EVIDENCE FROM TWINS DISCORDANT FOR SCHIZOPHRENIA. Schizophrenia Research, 2010, 117, 370-371.	1.1	0
87	Identifying Currents in the Gene Pool for Bacterial Populations Using an Integrative Approach. PLoS Computational Biology, 2009, 5, e1000455.	1.5	112
88	Integrating post-genomic approaches as a strategy to advance our understanding of health and disease. Genome Medicine, 2009, 1, 35.	3.6	23
89	Bayesian Clustering of Fuzzy Feature Vectors Using a Quasi-Likelihood Approach. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2009, 31, 74-85.	9.7	8
90	Hyper-Recombination, Diversity, and Antibiotic Resistance in Pneumococcus. Science, 2009, 324, 1454-1457.	6.0	164

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91	Enhanced Bayesian modelling in BAPS software for learning genetic structures of populations. BMC Bioinformatics, 2008, 9, 539.	1.2	760
92	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.	0.2	5
93	Bayesian analysis of population structure based on linked molecular information. Mathematical Biosciences, 2007, 205, 19-31.	0.9	214
94	Quantitative changes in collagen levels following 830-nm diode laser welding. , 1998, 22, 207-211.		21
95	Quantitative changes in collagen levels following 830â€‘nm diode laser welding. Lasers in Surgery and Medicine, 1998, 22, 207-211.	1.1	2