Yang Xie

List of Publications by Year
in descending order

125 papers	9,397 citations	50276 46 h-index	43889 91 g-index
136 all docs	136 docs citations	136 times ranked	17639 citing authors

#	Article	IF	Citations
1	The U6 snRNA m 6 A Methyltransferase METTL16 Regulates SAM Synthetase Intron Retention. Cell, 2017, 169, 824-835.e14.	28.9	756
2	Noncoding RNA NORAD Regulates Genomic Stability by Sequestering PUMILIO Proteins. Cell, 2016, 164, 69-80.	28.9	723
3	Poly-dipeptides encoded by the <i>C9orf72</i> repeats bind nucleoli, impede RNA biogenesis, and kill cells. Science, 2014, 345, 1139-1145.	12.6	551
4	Targeting renal cell carcinoma with a HIF-2 antagonist. Nature, 2016, 539, 112-117.	27.8	521
5	Metagenomic Shotgun Sequencing and Unbiased Metabolomic Profiling Identify Specific Human Gut Microbiota and Metabolites Associated with Immune Checkpoint Therapy Efficacy in Melanoma Patients. Neoplasia, 2017, 19, 848-855.	5.3	475
6	Anticancer sulfonamides target splicing by inducing RBM39 degradation via recruitment to DCAF15. Science, 2017, 356, .	12.6	441
7	Activation of HIF-1Î± and LL-37 by commensal bacteria inhibits Candida albicans colonization. Nature Medicine, 2015, 21, 808-814.	30.7	333
8	A community computational challenge to predict the activity of pairs of compounds. Nature Biotechnology, 2014, 32, 1213-1222.	17.5	264
9	Beclin-1-Dependent Autophagy Protects the Heart During Sepsis. Circulation, 2018, 138, 2247-2262.	1.6	255
10	An Argonaute phosphorylation cycle promotes microRNA-mediated silencing. Nature, 2017, 542, 197-202.	27.8	232
11	Transforming activity of an oncoprotein-encoding circular RNA from human papillomavirus. Nature Communications, 2019, 10, 2300.	12.8	218
12	Trends in leukemia incidence and survival in the United States (1973â€"1998). Cancer, 2003, 97, 2229-2235.	4.1	192
13	Artificial Intelligence in Lung Cancer Pathology Image Analysis. Cancers, 2019, 11, 1673.	3.7	152
14	Robust Gene Expression Signature from Formalin-Fixed Paraffin-Embedded Samples Predicts Prognosis of Nonâ€"Small-Cell Lung Cancer Patients. Clinical Cancer Research, 2011, 17, 5705-5714.	7.0	150
15	An Expression Signature as an Aid to the Histologic Classification of Nonâ€"Small Cell Lung Cancer. Clinical Cancer Research, 2016, 22, 4880-4889.	7.0	140
16	Comprehensive Computational Pathological Image Analysis Predicts Lung Cancer Prognosis. Journal of Thoracic Oncology, 2017, 12, 501-509.	1.1	138
17	Development and Validation of a Nomogram Prognostic Model for SCLC Patients. Journal of Thoracic Oncology, 2018, 13, 1338-1348.	1.1	138
18	Antibiotic-Induced Depletion of Anti-inflammatory Clostridia Is Associated with the Development of Graft-versus-Host Disease in Pediatric Stem Cell Transplantation Patients. Biology of Blood and Marrow Transplantation, 2017, 23, 820-829.	2.0	130

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19	Immune dysregulation in cancer patients developing immune-related adverse events. British Journal of Cancer, 2019, 120, 63-68.	6.4	126
20	Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. Lancet Oncology, The, 2017, 18, 132-142.	10.7	124
21	Increased autophagy blocks HER2-mediated breast tumorigenesis. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4176-4181.	7.1	106
22	A note on using permutation-based false discovery rate estimates to compare different analysis methods for microarray data. Bioinformatics, 2005, 21, 4280-4288.	4.1	104
23	Targeting glutamine metabolism sensitizes pancreatic cancer to PARP-driven metabolic catastrophe induced by ÃŸ-lapachone. Cancer & Metabolism, 2015, 3, 12.	5.0	104
24	FMAP: Functional Mapping and Analysis Pipeline for metagenomics and metatranscriptomics studies. BMC Bioinformatics, 2016, 17, 420.	2.6	98
25	Decreased BECN1 mRNA Expression in Human Breast Cancer is Associated With Estrogen Receptor-Negative Subtypes and Poor Prognosis. EBioMedicine, 2015, 2, 255-263.	6.1	95
26	Comprehensive functional characterization of cancerâ€"testis antigens defines obligate participation in multiple hallmarks of cancer. Nature Communications, 2015, 6, 8840.	12.8	94
27	Predictors and Intensity of Online Access to Electronic Medical Records Among Patients With Cancer. Journal of Oncology Practice, 2014, 10, e307-e312.	2.5	90
28	Computational Staining of Pathology Images to Study the Tumor Microenvironment in Lung Cancer. Cancer Research, 2020, 80, 2056-2066.	0.9	88
29	Aryl Sulfonamides Degrade RBM39 and RBM23 by Recruitment to CRL4-DCAF15. Cell Reports, 2019, 29, 1499-1510.e6.	6.4	84
30	The antitumor toxin CD437 is a direct inhibitor of DNA polymerase Î±. Nature Chemical Biology, 2016, 12, 511-515.	8.0	83
31	LCE: an open web portal to explore gene expression and clinical associations in lung cancer. Oncogene, 2019, 38, 2551-2564.	5.9	78
32	Comprehensive analysis of lung cancer pathology images to discover tumor shape and boundary features that predict survival outcome. Scientific Reports, 2018, 8, 10393.	3.3	77
33	Real-time resolution of point mutations that cause phenovariance in mice. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E440-9.	7.1	75
34	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. Nature Communications, 2016, 7, 12460.	12.8	73
35	eIF5B drives integrated stress response-dependent translation of PD-L1 in lung cancer. Nature Cancer, 2020, 1, 533-545.	13.2	73
36	Statistical methods of background correction for Illumina BeadArray data. Bioinformatics, 2009, 25, 751-757.	4.1	72

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37	The Hormone FGF21 Stimulates Water Drinking in Response to Ketogenic Diet and Alcohol. Cell Metabolism, 2018, 27, 1338-1347.e4.	16.2	72
38	Phase 1 study of ARQ 761, a Î²-lapachone analogue that promotes NQO1-mediated programmed cancer cell necrosis. British Journal of Cancer, 2018, 119, 928-936.	6.4	66
39	ConvPath: A software tool for lung adenocarcinoma digital pathological image analysis aided by a convolutional neural network. EBioMedicine, 2019, 50, 103-110.	6.1	66
40	Design and bioinformatics analysis of genome-wide CLIP experiments. Nucleic Acids Research, 2015, 43, 5263-5274.	14.5	65
41	PUMILIO hyperactivity drives premature aging of Norad-deficient mice. ELife, 2019, 8, .	6.0	65
42	Evaluation of the 7th and 8th editions of the AJCC/UICC TNM staging systems for lung cancer in a large North American cohort. Oncotarget, 2017, 8, 66784-66795.	1.8	63
43	A Phase I Dose-Escalation Trial of Single-Fraction Stereotactic Radiation Therapy for Liver Metastases. Annals of Surgical Oncology, 2016, 23, 218-224.	1.5	61
44	Sorting nexin 5 mediates virus-induced autophagy and immunity. Nature, 2021, 589, 456-461.	27.8	61
45	Severe Gut Microbiota Dysbiosis Is Associated With Poor Growth in Patients With Short Bowel Syndrome. Journal of Parenteral and Enteral Nutrition, 2017, 41, 1202-1212.	2.6	58
46	Variation in the Assessment of Immune-Related Adverse Event Occurrence, Grade, and Timing in Patients Receiving Immune Checkpoint Inhibitors. JAMA Network Open, 2019, 2, e1911519.	5.9	57
47	PROTOCADHERIN 7 Acts through SET and PP2A to Potentiate MAPK Signaling by EGFR and KRAS during Lung Tumorigenesis. Cancer Research, 2017, 77, 187-197.	0.9	55
48	High-dimensional genomic data bias correction and data integration using MANCIE. Nature Communications, 2016, 7, 11305.	12.8	52
49	VAMPr: VAriant Mapping and Prediction of antibiotic resistance via explainable features and machine learning. PLoS Computational Biology, 2020, 16, e1007511.	3.2	50
50	Tumor-suppressor function of Beclin 1 in breast cancer cells requires E-cadherin. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	50
51	Cell-autonomous immune gene expression is repressed in pulmonary neuroendocrine cells and small cell lung cancer. Communications Biology, 2021, 4, 314.	4.4	44
52	Phase 1 study of romidepsin plus erlotinib in advanced non-small cell lung cancer. Lung Cancer, 2015, 90, 534-541.	2.0	43
53	A Systematic Analysis Reveals Heterogeneous Changes in the Endocytic Activities of Cancer Cells. Cancer Research, 2015, 75, 4640-4650.	0.9	43
54	The Nuclear Receptor DAF-12 Regulates Nutrient Metabolism and Reproductive Growth in Nematodes. PLoS Genetics, 2015, 11, e1005027.	3.5	41

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55	Loss of *Dis3l2* partially phenocopies Perlman syndrome in mice and results in up-regulation of *Igf2* in nephron progenitor cells. Genes and Development, 2018, 32, 903-908.	5.9	34
56	Association between immune-related adverse event timing and treatment outcomes. OncoImmunology, 2022, 11, 2017162.	4.6	33
57	Automatic extraction of cell nuclei from H&E-stained histopathological images. Journal of Medical Imaging, 2017, 4, 027502.	1.5	32
58	Nuclear receptor NR4A1 is a tumor suppressor down-regulated in triple-negative breast cancer. Oncotarget, 2017, 8, 54364-54377.	1.8	32
59	Microvessel prediction in H&E Stained Pathology Images using fully convolutional neural networks. BMC Bioinformatics, 2018, 19, 64.	2.6	32
60	GeNeCK: a web server for gene network construction and visualization. BMC Bioinformatics, 2019, 20, 12.	2.6	29
61	Ensemble-Based Network Aggregation Improves the Accuracy of Gene Network Reconstruction. PLoS ONE, 2014, 9, e106319.	2.5	26
62	Increase in Cancer Center Staff Effort Related to Electronic Patient Portal Use. Journal of Oncology Practice, 2016, 12, e981-e990.	2.5	24
63	A deep learning-based model for screening and staging pneumoconiosis. Scientific Reports, 2021, 11, 2201.	3.3	24
64	A Model-Based Approach to Identify Binding Sites in CLIP-Seq Data. PLoS ONE, 2014, 9, e93248.	2.5	22
65	The Kub5-Hera/RPRD1B interactome: a novel role in preserving genetic stability by regulating DNA mismatch repair. Nucleic Acids Research, 2016, 44, 1718-1731.	14.5	21
66	Usage and survival implications of surgical staging of inguinal lymph nodes in intermediate- to high-risk, clinical localized penile cancer: A propensity-score matched analysis. Urologic Oncology: Seminars and Original Investigations, 2018, 36, 159.e7-159.e17.	1.6	21
67	Unique mutation patterns in anaplastic thyroid cancer identified by comprehensive genomic profiling. Head and Neck, 2019, 41, 1928-1934.	2.0	21
68	Identification of scavenger receptor B1 as the airway microfold cell receptor for Mycobacterium tuberculosis. ELife, 2020, 9, .	6.0	21
69	Association of Healthcare Access With Intensive Care Unit Utilization and Mortality in Patients of Hispanic Ethnicity Hospitalized With COVID-19. Journal of Hospital Medicine, 2021, 16, 659-666.	1.4	20
70	Identifying CDKN3 Gene Expression as a Prognostic Biomarker in Lung Adenocarcinoma via Meta-analysis. Cancer Informatics, 2015, 14s2, CIN.S17287.	1.9	19
71	HITS-CLIP Analysis Uncovers a Link between the Kaposi's Sarcoma-Associated Herpesvirus ORF57 Protein and Host Pre-mRNA Metabolism. PLoS Pathogens, 2015, 11, e1004652.	4.7	19
72	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

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73	Type and case volume of health care facility influences survival and surgery selection in cases with early-stage non–small cell lung cancer. Cancer, 2019, 125, 4252-4259.	4.1	19
74	Biomarkers for RBM39 degradation in acute myeloid leukemia. Leukemia, 2020, 34, 1924-1928.	7.2	19
75	TK216 targets microtubules in Ewing sarcoma cells. Cell Chemical Biology, 2022, 29, 1325-1332.e4.	5.2	19
76	A Bayesian hidden Potts mixture model for analyzing lung cancer pathology images. Biostatistics, 2019, 20, 565-581.	1.5	17
77	Late-Onset Immunotherapy Toxicity and Delayed Autoantibody Changes: Checkpoint Inhibitor–Induced Raynaud's-Like Phenomenon. Oncologist, 2020, 25, e753-e757.	3.7	17
78	Large-Scale Profiling of RBP-circRNA Interactions from Public CLIP-Seq Datasets. Genes, 2020, 11, 54.	2.4	17
79	Experience, Perceptions, and Recommendations Concerning COVID-19–Related Clinical Research Adjustments. Journal of the National Comprehensive Cancer Network: JNCCN, 2021, 19, 505-512.	4.9	17
80	Characteristics of Patients Using Patient Portals in Oncology. JAMA Oncology, 2018, 4, 416.	7.1	16
81	Main bronchus location is a predictor for metastasis and prognosis in lung adenocarcinoma: A large cohort analysis. Lung Cancer, 2018, 120, 22-26.	2.0	16
82	Engineering Forward Genetics into Cultured Cancer Cells for Chemical Target Identification. Cell Chemical Biology, 2019, 26, 1315-1321.e3.	5.2	16
83	Divergent prognostic effects of pre-existing and treatment-emergent thyroid dysfunction in patients treated with immune checkpoint inhibitors. Cancer Immunology, Immunotherapy, 2022, 71, 2169-2181.	4.2	16
84	Mobile Device Applications for Electronic Patient Portals in Oncology. JCO Clinical Cancer Informatics, 2019, 3, 1-8.	2.1	15
85	A Case Study on Choosing Normalization Methods and Test Statistics for Two-Channel Microarray Data. Comparative and Functional Genomics, 2004, 5, 432-444.	2.0	14
86	Practice Patterns and Impact of Postchemotherapy Retroperitoneal Lymph Node Dissection on Testicular Cancer Outcomes. European Urology Oncology, 2018, 1, 242-251.	5.4	14
87	MB-GAN: Microbiome Simulation via Generative Adversarial Network. GigaScience, 2021, 10, .	6.4	14
88	Systematic Analysis of Gene Expression in Lung Adenocarcinoma and Squamous Cell Carcinoma with a Case Study of FAM83A and FAM83B. Cancers, 2019, 11, 886.	3.7	13
89	Validation of the 12-gene Predictive Signature for Adjuvant Chemotherapy Response in Lung Cancer. Clinical Cancer Research, 2019, 25, 150-157.	7.0	13
90	Closing the gap: Contribution of surgical best practices to outcome differences between high-and low-volume centers for lung cancer resection. Cancer Medicine, 2020, 9, 4137-4147.	2.8	13

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91	Intramolecular circularization increases efficiency of RNA sequencing and enables CLIP-Seq of nuclear RNA from human cells. Nucleic Acids Research, 2015, 43, e75-e75.	14.5	12
92	Kub5-Hera<i>RPRD1B</i> Deficiency Promotes â€œBRCAnessâ€•and Vulnerability to PARP Inhibition in BRCA-proficient Breast Cancers. Clinical Cancer Research, 2018, 24, 6459-6470.	7.0	11
93	Development and Validation of a Nomogram Prognostic Model for Patients With Advanced Non-Small-Cell Lung Cancer. Cancer Informatics, 2019, 18, 117693511983754.	1.9	10
94	Statin Intolerance, Anti-HMGCR Antibodies, and Immune Checkpoint Inhibitor-Associated Myositis: A â€œTwo-Hitâ€•Autoimmune Toxicity or Clinical Predisposition?. Oncologist, 2020, 25, e1242-e1245.	3.7	10
95	Deep Learning of Rhabdomyosarcoma Pathology Images for Classification and Survival Outcome Prediction. American Journal of Pathology, 2022, 192, 917-925.	3.8	10
96	A Bayesian approach to joint modeling of proteinâ€"DNA binding, gene expression and sequence data. Statistics in Medicine, 2010, 29, 489-503.	1.6	9
97	A Multipronged Approach Establishes Covalent Modification of Î²-Tubulin as the Mode of Action of Benzamide Anti-cancer Toxins. Journal of Medicinal Chemistry, 2020, 63, 14054-14066.	6.4	9
98	BepiTBR: T-B reciprocity enhances B cell epitope prediction. IScience, 2022, 25, 103764.	4.1	9
99	Association between Antibiotic Exposure and Systemic Immune Parameters in Cancer Patients Receiving Checkpoint Inhibitor Therapy. Cancers, 2022, 14, 1327.	3.7	9
100	DIGREM: an integrated web-based platform for detecting effective multi-drug combinations. Bioinformatics, 2019, 35, 1792-1794.	4.1	8
101	Development and Validation of a Pathology Image Analysis-based Predictive Model for Lung Adenocarcinoma Prognosis - A Multi-cohort Study. Scientific Reports, 2019, 9, 6886.	3.3	8
102	Evaluating short-term forecasting of COVID-19 cases among different epidemiological models under a Bayesian framework. GigaScience, 2021, 10, .	6.4	8
103	Longitudinal Experience With and Impressions of COVID-19â€"Related Clinical Research Changes. JCO Oncology Practice, 2022, 18, e98-e107.	2.9	8
104	Lack of Association Between Radiographic Tumor Burden and Efficacy of Immune Checkpoint Inhibitors in Advanced Lung Cancer. Oncologist, 2020, 25, 515-522.	3.7	7
105	iScreen: Image-Based High-Content RNAi Screening Analysis Tools. Journal of Biomolecular Screening, 2015, 20, 998-1002.	2.6	6
106	Development of a Data Model and Data Commons for Germ Cell Tumors. JCO Clinical Cancer Informatics, 2020, 4, 555-566.	2.1	6
107	Statistical Methods for Integrating Multiple Types of High-Throughput Data. Methods in Molecular Biology, 2010, 620, 511-529.	0.9	5
108	Usefulness of a Simple Algorithm to Identify Hypertensive Patients Who Benefit from Intensive Blood Pressure Lowering. American Journal of Cardiology, 2018, 122, 248-254.	1.6	5

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109	A Bayesian hierarchical model for analyzing methylated RNA immunoprecipitation sequencing data. Quantitative Biology, 2018, 6, 275-286.	0.5	5
110	Experience, Perceptions, and Recommendations Concerning COVID-19-Related Clinical Research Adjustments. Journal of the National Comprehensive Cancer Network: JNCCN, 2021, 19, 505-512.	4.9	5
111	Incorporating prior information via shrinkage: a combined analysis of genome-wide location data and gene expression data. Statistics in Medicine, 2007, 26, 2258-2275.	1.6	4
112	DEFOR: depth- and frequency-based somatic copy number alteration detector. Bioinformatics, 2019, 35, 3824-3825.	4.1	4
113	Assessing consistency across functional screening datasets in cancer cells. Bioinformatics, 2021, 37, 4540-4547.	4.1	4
114	Finding RNAâ€"Protein Interaction Sites Using HMMs. Methods in Molecular Biology, 2017, 1552, 177-184.	0.9	3
115	Identifying genes with tri-modal association with survival and tumor grade in cancer patients. BMC Bioinformatics, 2019, 20, 13.	2.6	3
116	Molecular differences across invasive lung adenocarcinoma morphological subgroups. Translational Lung Cancer Research, 2020, 9, 1029-1040.	2.8	3
117	SCT Promoter Methylation Is a Highly Discriminative Biomarker for Lung and Many Other Cancers. IEEE Life Sciences Letters, 2015, 1, 30-33.	1.2	2
118	Upfront Brain Treatments Followed by Lung Surgery Improves Survival for Stage IV Non-small Cell Lung Cancer Patients With Brain Metastases: A Large Cohort Analysis. Frontiers in Surgery, 2021, 8, 649531.	1.4	2
119	Phase I and pharmacodynamic study of the histone deacetylase (HDAC) inhibitor romidepsin plus erlotinib in previously treated advanced non-small cell lung cancer (NSCLC).. Journal of Clinical Oncology, 2013, 31, 8088-8088.	1.6	2
120	MetaPrism: A versatile toolkit for joint taxa/gene analysis of metagenomic sequencing data. G3: Genes, Genomes, Genetics, 2021, 11, .	1.8	1
121	Developing and Using a Data Commons for Understanding the Molecular Characteristics of Germ Cell Tumors. Methods in Molecular Biology, 2021, 2195, 263-275.	0.9	1
122	Lung Cancer Computational Biology and Resources. Cold Spring Harbor Perspectives in Medicine, 2022, 12, a038273.	6.2	1
123	RCRdiff: A fully integrated Bayesian method for differential expression analysis using raw NanoString nCounter data. Statistics in Medicine, 2022, 41, 665-680.	1.6	1
124	Prevalence and predictors of online patient access to electronic medical records among patients with cancer.. Journal of Clinical Oncology, 2013, 31, 35-35.	1.6	0
125	Abstract P5-17-09: A genome-wide CRISPR screen identifies PRMT5 as a novel therapeutic target in ER+/*RB1*-deficient breast cancer. Cancer Research, 2022, 82, P5-17-09-P5-17-09.	0.9	0