

# Yinyin Yuan

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

8,338  
citations

185998

28  
h-index

143772

57  
g-index

76  
all docs

76  
docs citations

76  
times ranked

16261  
citing authors

#	ARTICLE	IF	CITATIONS
1	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. <i>Nature</i> , 2012, 486, 346-352.	13.7	4,708
2	Quantitative Image Analysis of Cellular Heterogeneity in Breast Tumors Complements Genomic Profiling. <i>Science Translational Medicine</i> , 2012, 4, 157ra143.	5.8	356
3	Classifying the evolutionary and ecological features of neoplasms. <i>Nature Reviews Cancer</i> , 2017, 17, 605-619.	12.8	303
4	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. <i>Cell</i> , 2018, 173, 1755-1769.e22.	13.5	261
5	Spatial Heterogeneity in the Tumor Microenvironment. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2016, 6, a026583.	2.9	194
6	Capture Hi-C identifies the chromatin interactome of colorectal cancer risk loci. <i>Nature Communications</i> , 2015, 6, 6178.	5.8	186
7	Geospatial immune variability illuminates differential evolution of lung adenocarcinoma. <i>Nature Medicine</i> , 2020, 26, 1054-1062.	15.2	181
8	Mapping spatial heterogeneity in the tumor microenvironment: a new era for digital pathology. <i>Laboratory Investigation</i> , 2015, 95, 377-384.	1.7	180
9	Relevance of Spatial Heterogeneity of Immune Infiltration for Predicting Risk of Recurrence After Endocrine Therapy of ER+ Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2018, 110, 166-175.	3.0	122
10	Beyond immune density: critical role of spatial heterogeneity in estrogen receptor-negative breast cancer. <i>Modern Pathology</i> , 2015, 28, 766-777.	2.9	117
11	Pitfalls in assessing stromal tumor infiltrating lymphocytes (sTILs) in breast cancer. <i>Npj Breast Cancer</i> , 2020, 6, 17.	2.3	106
12	Global Analysis of mRNA, Translation, and Protein Localization: Local Translation Is a Key Regulator of Cell Protrusions. <i>Developmental Cell</i> , 2015, 35, 344-357.	3.1	104
13	Microenvironmental Heterogeneity Parallels Breast Cancer Progression: A Histology-Genomic Integration Analysis. <i>PLoS Medicine</i> , 2016, 13, e1001961.	3.9	101
14	Report on computational assessment of Tumor Infiltrating Lymphocytes from the International Immuno-Oncology Biomarker Working Group. <i>Npj Breast Cancer</i> , 2020, 6, 16.	2.3	90
15	Modelling the spatial heterogeneity and molecular correlates of lymphocytic infiltration in triple-negative breast cancer. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20141153.	1.5	82
16	Patient-Specific Data Fusion Defines Prognostic Cancer Subtypes. <i>PLoS Computational Biology</i> , 2011, 7, e1002227.	1.5	81
17	An ecological measure of immune-cancer colocalization as a prognostic factor for breast cancer. <i>Breast Cancer Research</i> , 2015, 17, 131.	2.2	81
18	The T cell differentiation landscape is shaped by tumour mutations in lung cancer. <i>Nature Cancer</i> , 2020, 1, 546-561.	5.7	74

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19	Immune Surveillance in Clinical Regression of Preinvasive Squamous Cell Lung Cancer. <i>Cancer Discovery</i> , 2020, 10, 1489-1499.	7.7	60
20	Computational pathology: Exploring the spatial dimension of tumor ecology. <i>Cancer Letters</i> , 2016, 380, 296-303.	3.2	53
21	Systematic evaluation of quantotypic peptides for targeted analysis of the human kinome. <i>Nature Methods</i> , 2014, 11, 1041-1044.	9.0	52
22	Evaluation of CDK12 Protein Expression as a Potential Novel Biomarker for DNA Damage Response—Targeted Therapies in Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2018, 17, 306-315.	1.9	52
23	Topological Tumor Graphs: A Graph-Based Spatial Model to Infer Stromal Recruitment for Immunosuppression in Melanoma Histology. <i>Cancer Research</i> , 2020, 80, 1199-1209.	0.4	43
24	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. <i>Molecular Oncology</i> , 2015, 9, 115-127.	2.1	38
25	Quantitative histology analysis of the ovarian tumour microenvironment. <i>Scientific Reports</i> , 2015, 5, 16317.	1.6	35
26	Investigating the Contribution of Collagen to the Tumor Biomechanical Phenotype with Noninvasive Magnetic Resonance Elastography. <i>Cancer Research</i> , 2019, 79, 5874-5883.	0.4	35
27	Phosphoproteomic analysis of interacting tumor and endothelial cells identifies regulatory mechanisms of transendothelial migration. <i>Science Signaling</i> , 2016, 9, ra15.	1.6	34
28	Analysis of heterogeneity in T2-weighted MR images can differentiate pseudoprogression from progression in glioblastoma. <i>PLoS ONE</i> , 2017, 12, e0176528.	1.1	34
29	Microenvironmental niche divergence shapes BRCA1-dysregulated ovarian cancer morphological plasticity. <i>Nature Communications</i> , 2018, 9, 3917.	5.8	33
30	Similarity and diversity of the tumor microenvironment in multiple metastases: critical implications for overall and progression-free survival of high-grade serous ovarian cancer. <i>Oncotarget</i> , 2016, 7, 71123-71135.	0.8	32
31	The Spatiotemporal Evolution of Lymph Node Spread in Early Breast Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 4763-4770.	3.2	30
32	Directed Partial Correlation: Inferring Large-Scale Gene Regulatory Network through Induced Topology Disruptions. <i>PLoS ONE</i> , 2011, 6, e16835.	1.1	29
33	A Sparse Regulatory Network of Copy-Number Driven Gene Expression Reveals Putative Breast Cancer Oncogenes. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 947-954.	1.9	27
34	Biopsy variability of lymphocytic infiltration in breast cancer subtypes and the ImmunoSkew score. <i>Scientific Reports</i> , 2016, 6, 36231.	1.6	27
35	Systematic analysis of tumour cell-extracellular matrix adhesion identifies independent prognostic factors in breast cancer. <i>Oncotarget</i> , 2016, 7, 62939-62953.	0.8	26
36	Artificial intelligence and digital pathology: Opportunities and implications for immuno-oncology. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2021, 1875, 188520.	3.3	25

#	ARTICLE	IF	CITATIONS
37	An unsupervised conditional random fields approach for clustering gene expression time series. <i>Bioinformatics</i> , 2008, 24, 2467-2473.	1.8	23
38	Digital watermarking scheme exploiting nondeterministic dependence for image authentication. <i>Optical Engineering</i> , 2006, 45, 127001.	0.5	22
39	Superpixel-Based Conditional Random Fields (SuperCRF): Incorporating Global and Local Context for Enhanced Deep Learning in Melanoma Histopathology. <i>Frontiers in Oncology</i> , 2019, 9, 1045.	1.3	22
40	Emerging technologies and their impact on regulatory science. <i>Experimental Biology and Medicine</i> , 2022, 247, 1-75.	1.1	22
41	Unmasking the immune microecology of ductal carcinoma in situ with deep learning. <i>Npj Breast Cancer</i> , 2021, 7, 19.	2.3	20
42	Deconvolving Convolutional Neural Network for Cell Detection. , 2019, , .		18
43	SuperHistopath: A Deep Learning Pipeline for Mapping Tumor Heterogeneity on Low-Resolution Whole-Slide Digital Histopathology Images. <i>Frontiers in Oncology</i> , 2020, 10, 586292.	1.3	18
44	Partial mixture model for tight clustering of gene expression time-course. <i>BMC Bioinformatics</i> , 2008, 9, 287.	1.2	17
45	Predicting chemoin sensitivity in breast cancer with $\text{scRNA-seq}$ /digital pathology data fusion. <i>Royal Society Open Science</i> , 2016, 3, 140501.	1.1	16
46	Diffusion-weighted MRI for early detection and characterization of prostate cancer in the transgenic adenocarcinoma of the mouse prostate model. <i>Journal of Magnetic Resonance Imaging</i> , 2016, 43, 1207-1217.	1.9	15
47	Noninvasive MRI Native T1 Mapping Detects Response to <i>MYCN</i> -targeted Therapies in the Th- <i>MYCN</i> Model of Neuroblastoma. <i>Cancer Research</i> , 2020, 80, 3424-3435.	0.4	15
48	Capturing Global Spatial Context for Accurate Cell Classification in Skin Cancer Histology. <i>Lecture Notes in Computer Science</i> , 2018, , 52-60.	1.0	14
49	ConCORDe-Net: Cell Count Regularized Convolutional Neural Network for Cell Detection in Multiplex Immunohistochemistry Images. <i>Lecture Notes in Computer Science</i> , 2019, , 667-675.	1.0	14
50	MRI Imaging of the Hemodynamic Vasculature of Neuroblastoma Predicts Response to Antiangiogenic Treatment. <i>Cancer Research</i> , 2019, 79, 2978-2991.	0.4	13
51	Biomarkers for site-specific response to neoadjuvant chemotherapy in epithelial ovarian cancer: relating MRI changes to tumour cell load and necrosis. <i>British Journal of Cancer</i> , 2021, 124, 1130-1137.	2.9	11
52	Analysis of tumour ecological balance reveals resource-dependent adaptive strategies of ovarian cancer. <i>EBioMedicine</i> , 2019, 48, 224-235.	2.7	8
53	Non-Invasive Prostate Cancer Characterization with Diffusion-Weighted MRI: Insight from In silico Studies of a Transgenic Mouse Model. <i>Frontiers in Oncology</i> , 2017, 7, 290.	1.3	7
54	Stromal cell ratio based on automated image analysis as a predictor for platinum-resistant recurrent ovarian cancer. <i>BMC Cancer</i> , 2019, 19, 159.	1.1	7

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55	High interfollicular spatial co-localization of CD8+FOXP3+ with CD4+CD8+ cells predicts favorable outcome in follicular lymphoma. <i>Hematological Oncology</i> , 2022, 40, 541-553.	0.8	6
56	Unsupervised Clustering of Gene Expression Time Series with Conditional Random Fields. , 2007, , .		4
57	Fragile watermarking scheme exploiting non-deterministic block-wise dependency. , 2004, , .		3
58	Partial Mixture Model for Tight Clustering in Exploratory Gene Expression Analysis. , 2007, , .		3
59	Glioma Classification Using Multimodal Radiology and Histology Data. <i>Lecture Notes in Computer Science</i> , 2021, , 508-518.	1.0	3
60	Wisdom Of The Crowd For Early Detection In Barrett's Esophagus. , 2021, , .		3
61	Penalized regression elucidates aberration hotspots mediating subtype-specific transcriptional responses in breast cancer. <i>Bioinformatics</i> , 2011, 27, 2679-2685.	1.8	2
62	Cell Abundance Aware Deep Learning For Cell Detection On Highly Imbalanced Pathological Data. , 2021, , .		2
63	Automated Dcis Identification From Multiplex Immunohistochemistry Using Generative Adversarial Networks. , 2022, , .		1
64	Probabilistic framework for gene expression clustering validation based on gene ontology and graph theory. <i>Proceedings of the IEEE International Conference on Acoustics, Speech, and Signal Processing</i> , 2008, , .	1.8	0
65	A Bayes Random Fields Approach for Integrative Large-Scale Regulatory Network Analysis. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.0	0
66	Inferring Causal Relations from Multivariate Time Series: A Fast Method for Large-Scale Gene Expression Data. , 2009, , .		0
67	Abstract B2-55: Critical role of immune spatial heterogeneity and the molecular scaffold in estrogen receptor-negative breast cancer. , 2015, , .		0
68	Abstract B2-51: SpEeCH: Quantifying Spatial Expression of Clonal Heterogeneity in breast cancer. , 2015, , .		0
69	A Bayes random field approach for integrative large-scale regulatory network analysis. <i>Journal of Integrative Bioinformatics</i> , 2008, 5, .	1.0	0