

# Yinyin Yuan

## List of Publications by Year in descending order

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Version: 2024-02-01

69  
papers

8,338  
citations

186265  
28  
h-index

144013  
57  
g-index

76  
all docs

76  
docs citations

76  
times ranked

16261  
citing authors

#	ARTICLE	IF	CITATIONS
1	Emerging technologies and their impact on regulatory science. <i>Experimental Biology and Medicine</i> , 2022, 247, 1-75.	2.4	22
2	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.	1.7	6
3	Automated Dcis Identification From Multiplex Immunohistochemistry Using Generative Adversarial Networks. , 2022, , .		1
4	Glioma Classification Using Multimodal Radiology and Histology Data. <i>Lecture Notes in Computer Science</i> , 2021, , 508-518.	1.3	3
5	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.	6.4	11
6	Unmasking the immune microecology of ductal carcinoma in situ with deep learning. <i>Npj Breast Cancer</i> , 2021, 7, 19.	5.2	20
7	Artificial intelligence and digital pathology: Opportunities and implications for immuno-oncology. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2021, 1875, 188520.	7.4	25
8	Wisdom Of The Crowd For Early Detection In Barrett's Esophagus. , 2021, , .		3
9	Cell Abundance Aware Deep Learning For Cell Detection On Highly Imbalanced Pathological Data. , 2021, , .		2
10	Immune Surveillance in Clinical Regression of Preinvasive Squamous Cell Lung Cancer. <i>Cancer Discovery</i> , 2020, 10, 1489-1499.	9.4	60
11	Report on computational assessment of Tumor Infiltrating Lymphocytes from the International Immuno-Oncology Biomarker Working Group. <i>Npj Breast Cancer</i> , 2020, 6, 16.	5.2	90
12	Pitfalls in assessing stromal tumor infiltrating lymphocytes (sTILs) in breast cancer. <i>Npj Breast Cancer</i> , 2020, 6, 17.	5.2	106
13	Geospatial immune variability illuminates differential evolution of lung adenocarcinoma. <i>Nature Medicine</i> , 2020, 26, 1054-1062.	30.7	181
14	Noninvasive MRI Native T1 Mapping Detects Response to MYCN-targeted Therapies in the Th-MYCN Model of Neuroblastoma. <i>Cancer Research</i> , 2020, 80, 3424-3435.	0.9	15
15	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.	0.9	43
16	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.	2.8	18
17	The T cell differentiation landscape is shaped by tumour mutations in lung cancer. <i>Nature Cancer</i> , 2020, 1, 546-561.	13.2	74
18	Investigating the Contribution of Collagen to the Tumor Biomechanical Phenotype with Noninvasive Magnetic Resonance Elastography. <i>Cancer Research</i> , 2019, 79, 5874-5883.	0.9	35

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19	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.	2.8	22
20	Deconvolving Convolutional Neural Network for Cell Detection. , 2019, , .		18
21	MRI Imaging of the Hemodynamic Vasculature of Neuroblastoma Predicts Response to Antiangiogenic Treatment. <i>Cancer Research</i> , 2019, 79, 2978-2991.	0.9	13
22	Stromal cell ratio based on automated image analysis as a predictor for platinum-resistant recurrent ovarian cancer. <i>BMC Cancer</i> , 2019, 19, 159.	2.6	7
23	Analysis of tumour ecological balance reveals resource-dependent adaptive strategies of ovarian cancer. <i>EBioMedicine</i> , 2019, 48, 224-235.	6.1	8
24	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.	1.3	14
25	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.	4.1	52
26	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.	6.3	122
27	Microenvironmental niche divergence shapes BRCA1-dysregulated ovarian cancer morphological plasticity. <i>Nature Communications</i> , 2018, 9, 3917.	12.8	33
28	Capturing Global Spatial Context for Accurate Cell Classification in Skin Cancer Histology. <i>Lecture Notes in Computer Science</i> , 2018, , 52-60.	1.3	14
29	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. <i>Cell</i> , 2018, 173, 1755-1769.e22.	28.9	261
30	The Spatiotemporal Evolution of Lymph Node Spread in Early Breast Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 4763-4770.	7.0	30
31	Classifying the evolutionary and ecological features of neoplasms. <i>Nature Reviews Cancer</i> , 2017, 17, 605-619.	28.4	303
32	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.	2.8	7
33	Analysis of heterogeneity in T2-weighted MR images can differentiate pseudoprogression from progression in glioblastoma. <i>PLoS ONE</i> , 2017, 12, e0176528.	2.5	34
34	Systematic analysis of tumour cell-extracellular matrix adhesion identifies independent prognostic factors in breast cancer. <i>Oncotarget</i> , 2016, 7, 62939-62953.	1.8	26
35	Microenvironmental Heterogeneity Parallels Breast Cancer Progression: A Histology—Genomic Integration Analysis. <i>PLoS Medicine</i> , 2016, 13, e1001961.	8.4	101
36	Spatial Heterogeneity in the Tumor Microenvironment. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2016, 6, a026583.	6.2	194

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37	Biopsy variability of lymphocytic infiltration in breast cancer subtypes and the ImmunoSkew score. <i>Scientific Reports</i> , 2016, 6, 36231.	3.3	27
38	Predicting chemoin sensitivity in breast cancer with $\delta$ ™omics/digital pathology data fusion. <i>Royal Society Open Science</i> , 2016, 3, 140501.	2.4	16
39	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.	3.4	15
40	Phosphoproteomic analysis of interacting tumor and endothelial cells identifies regulatory mechanisms of transendothelial migration. <i>Science Signaling</i> , 2016, 9, ra15.	3.6	34
41	Computational pathology: Exploring the spatial dimension of tumor ecology. <i>Cancer Letters</i> , 2016, 380, 296-303.	7.2	53
42	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.	1.8	32
43	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.	7.0	104
44	Quantitative histology analysis of the ovarian tumour microenvironment. <i>Scientific Reports</i> , 2015, 5, 16317.	3.3	35
45	An ecological measure of immune-cancer colocalization as a prognostic factor for breast cancer. <i>Breast Cancer Research</i> , 2015, 17, 131.	5.0	81
46	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.	4.6	38
47	Beyond immune density: critical role of spatial heterogeneity in estrogen receptor-negative breast cancer. <i>Modern Pathology</i> , 2015, 28, 766-777.	5.5	117
48	Capture Hi-C identifies the chromatin interactome of colorectal cancer risk loci. <i>Nature Communications</i> , 2015, 6, 6178.	12.8	186
49	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.	3.4	82
50	Mapping spatial heterogeneity in the tumor microenvironment: a new era for digital pathology. <i>Laboratory Investigation</i> , 2015, 95, 377-384.	3.7	180
51	Abstract B2-55: Critical role of immune spatial heterogeneity and the molecular scaffold in estrogen receptor-negative breast cancer. , 2015, , .		0
52	Abstract B2-51: SpEeCH: Quantifying Spatial Expression of Clonal Heterogeneity in breast cancer. , 2015, , .		0
53	Systematic evaluation of quantotypic peptides for targeted analysis of the human kinome. <i>Nature Methods</i> , 2014, 11, 1041-1044.	19.0	52
54	Quantitative Image Analysis of Cellular Heterogeneity in Breast Tumors Complements Genomic Profiling. <i>Science Translational Medicine</i> , 2012, 4, 157ra143.	12.4	356

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55	A Sparse Regulatory Network of Copy-Number Driven Gene Expression Reveals Putative Breast Cancer Oncogenes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 947-954.	3.0	27
56	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.	27.8	4,708
57	Directed Partial Correlation: Inferring Large-Scale Gene Regulatory Network through Induced Topology Disruptions. PLoS ONE, 2011, 6, e16835.	2.5	29
58	Penalized regression elucidates aberration hotspots mediating subtype-specific transcriptional responses in breast cancer. Bioinformatics, 2011, 27, 2679-2685.	4.1	2
59	Patient-Specific Data Fusion Defines Prognostic Cancer Subtypes. PLoS Computational Biology, 2011, 7, e1002227.	3.2	81
60	Inferring Causal Relations from Multivariate Time Series: A Fast Method for Large-Scale Gene Expression Data. , 2009, , .		0
61	Partial mixture model for tight clustering of gene expression time-course. BMC Bioinformatics, 2008, 9, 287.	2.6	17
62	An unsupervised conditional random fields approach for clustering gene expression time series. Bioinformatics, 2008, 24, 2467-2473.	4.1	23
63	Probabilistic framework for gene expression clustering validation based on gene ontology and graph theory. Proceedings of the IEEE International Conference on Acoustics, Speech, and Signal Processing, 2008, , .	1.8	0
64	A Bayes Random Fields Approach for Integrative Large-Scale Regulatory Network Analysis. Journal of Integrative Bioinformatics, 2008, 5, .	1.5	0
65	A Bayes random field approach for integrative large-scale regulatory network analysis. Journal of Integrative Bioinformatics, 2008, 5, .	1.5	0
66	Unsupervised Clustering of Gene Expression Time Series with Conditional Random Fields. , 2007, , .		4
67	Partial Mixture Model for Tight Clustering in Exploratory Gene Expression Analysis. , 2007, , .		3
68	Digital watermarking scheme exploiting nondeterministic dependence for image authentication. Optical Engineering, 2006, 45, 127001.	1.0	22
69	Fragile watermarking scheme exploiting non-deterministic block-wise dependency. , 2004, , .		3