Yinyin Yuan

List of Publications by Year
in descending order

69	8,338	185998	143772
papers	citations	28	57
		h-index	g-index

76	76	76	16261
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Emerging technologies and their impact on regulatory science. Experimental Biology and Medicine, 2022, 247, 1-75.	1.1	22
2	High interâ€follicular spatial coâ€localization of CD8+FOXP3+ with CD4+CD8+ cells predicts favorable outcome in follicular lymphoma. Hematological Oncology, 2022, 40, 541-553.	0.8	6
3	Automated Dcis Identification From Multiplex Immunohistochemistry Using Generative Adversarial Networks. , 2022, , .		1
4	Glioma Classification Using Multimodal Radiology and Histology Data. Lecture Notes in Computer Science, 2021, , 508-518.	1.0	3
5	Biomarkers for site-specific response to neoadjuvant chemotherapy in epithelial ovarian cancer: relating MRI changes to tumour cell load and necrosis. British Journal of Cancer, 2021, 124, 1130-1137.	2.9	11
6	Unmasking the immune microecology of ductal carcinoma in situ with deep learning. Npj Breast Cancer, 2021, 7, 19.	2.3	20
7	Artificial intelligence and digital pathology: Opportunities and implications for immuno-oncology. Biochimica Et Biophysica Acta: Reviews on Cancer, 2021, 1875, 188520.	3.3	25
8	Wisdom Of The Crowd For Early Detection In Barrettâ€™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. Cancer Discovery, 2020, 10, 1489-1499.	7.7	60
11	Report on computational assessment of Tumor Infiltrating Lymphocytes from the International Immuno-Oncology Biomarker Working Group. Npj Breast Cancer, 2020, 6, 16.	2.3	90
12	Pitfalls in assessing stromal tumor infiltrating lymphocytes (sTILs) in breast cancer. Npj Breast Cancer, 2020, 6, 17.	2.3	106
13	Geospatial immune variability illuminates differential evolution of lung adenocarcinoma. Nature Medicine, 2020, 26, 1054-1062.	15.2	181
14	Noninvasive MRI Native T1 Mapping Detects Response to $MYCN$-targeted Therapies in the Th-$MYCN$ Model of Neuroblastoma. Cancer Research, 2020, 80, 3424-3435.	0.4	15
15	Topological Tumor Graphs: A Graph-Based Spatial Model to Infer Stromal Recruitment for Immunosuppression in Melanoma Histology. Cancer Research, 2020, 80, 1199-1209.	0.4	43
16	SuperHistopath: A Deep Learning Pipeline for Mapping Tumor Heterogeneity on Low-Resolution Whole-Slide Digital Histopathology Images. Frontiers in Oncology, 2020, 10, 586292.	1.3	18
17	The T cell differentiation landscape is shaped by tumour mutations in lung cancer. Nature Cancer, 2020, 1, 546-561.	5.7	74
18	Investigating the Contribution of Collagen to the Tumor Biomechanical Phenotype with Noninvasive Magnetic Resonance Elastography. Cancer Research, 2019, 79, 5874-5883.	0.4	35

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19	Superpixel-Based Conditional Random Fields (SuperCRF): Incorporating Global and Local Context for Enhanced Deep Learning in Melanoma Histopathology. Frontiers in Oncology, 2019, 9, 1045.	1.3	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. Cancer Research, 2019, 79, 2978-2991.	0.4	13
22	Stromal cell ratio based on automated image analysis as a predictor for platinum-resistant recurrent ovarian cancer. BMC Cancer, 2019, 19, 159.	1.1	7
23	Analysis of tumour ecological balance reveals resource-dependent adaptive strategies of ovarian cancer. EBioMedicine, 2019, 48, 224-235.	2.7	8
24	ConCORDe-Net: Cell Count Regularized Convolutional Neural Network for Cell Detection in Multiplex Immunohistochemistry Images. Lecture Notes in Computer Science, 2019, , 667-675.	1.0	14
25	Evaluation of CDK12 Protein Expression as a Potential Novel Biomarker for DNA Damage Responseâ€"Targeted Therapies in Breast Cancer. Molecular Cancer Therapeutics, 2018, 17, 306-315.	1.9	52
26	Relevance of Spatial Heterogeneity of Immune Infiltration for Predicting Risk of Recurrence After Endocrine Therapy of ER+ Breast Cancer. Journal of the National Cancer Institute, 2018, 110, 166-175.	3.0	122
27	Microenvironmental niche divergence shapes BRCA1-dysregulated ovarian cancer morphological plasticity. Nature Communications, 2018, 9, 3917.	5.8	33
28	Capturing Global Spatial Context for Accurate Cell Classification in Skin Cancer Histology. Lecture Notes in Computer Science, 2018, , 52-60.	1.0	14
29	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. Cell, 2018, 173, 1755-1769.e22.	13.5	261
30	The Spatiotemporal Evolution of Lymph Node Spread in Early Breast Cancer. Clinical Cancer Research, 2018, 24, 4763-4770.	3.2	30
31	Classifying the evolutionary and ecological features of neoplasms. Nature Reviews Cancer, 2017, 17, 605-619.	12.8	303
32	Non-Invasive Prostate Cancer Characterization with Diffusion-Weighted MRI: Insight from In silico Studies of a Transgenic Mouse Model. Frontiers in Oncology, 2017, 7, 290.	1.3	7
33	Analysis of heterogeneity in T2-weighted MR images can differentiate pseudoprogression from progression in glioblastoma. PLoS ONE, 2017, 12, e0176528.	1.1	34
34	Systematic analysis of tumour cell-extracellular matrix adhesion identifies independent prognostic factors in breast cancer. Oncotarget, 2016, 7, 62939-62953.	0.8	26
35	Microenvironmental Heterogeneity Parallels Breast Cancer Progression: A Histologyâ€"Genomic Integration Analysis. PLoS Medicine, 2016, 13, e1001961.	3.9	101
36	Spatial Heterogeneity in the Tumor Microenvironment. Cold Spring Harbor Perspectives in Medicine, 2016, 6, a026583.	2.9	194

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37	Biopsy variability of lymphocytic infiltration in breast cancer subtypes and the ImmunoSkew score. Scientific Reports, 2016, 6, 36231.	1.6	27
38	Predicting chemoinsensitivity in breast cancer with â€™omics/digital pathology data fusion. Royal Society Open Science, 2016, 3, 140501.	1.1	16
39	Diffusionâ€weighted MRI for early detection and characterization of prostate cancer in the transgenic adenocarcinoma of the mouse prostate model. Journal of Magnetic Resonance Imaging, 2016, 43, 1207-1217.	1.9	15
40	Phosphoproteomic analysis of interacting tumor and endothelial cells identifies regulatory mechanisms of transendothelial migration. Science Signaling, 2016, 9, ra15.	1.6	34
41	Computational pathology: Exploring the spatial dimension of tumor ecology. Cancer Letters, 2016, 380, 296-303.	3.2	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. Oncotarget, 2016, 7, 71123-71135.	0.8	32
43	Global Analysis of mRNA, Translation, and Protein Localization: Local Translation Is a Key Regulator of Cell Protrusions. Developmental Cell, 2015, 35, 344-357.	3.1	104
44	Quantitative histology analysis of the ovarian tumour microenvironment. Scientific Reports, 2015, 5, 16317.	1.6	35
45	An ecological measure of immune-cancer colocalization as a prognostic factor for breast cancer. Breast Cancer Research, 2015, 17, 131.	2.2	81
46	A tumor DNA complex aberration index is an independent predictor of survival in breast and ovarian cancer. Molecular Oncology, 2015, 9, 115-127.	2.1	38
47	Beyond immune density: critical role of spatial heterogeneity in estrogen receptor-negative breast cancer. Modern Pathology, 2015, 28, 766-777.	2.9	117
48	Capture Hi-C identifies the chromatin interactome of colorectal cancer risk loci. Nature Communications, 2015, 6, 6178.	5.8	186
49	Modelling the spatial heterogeneity and molecular correlates of lymphocytic infiltration in triple-negative breast cancer. Journal of the Royal Society Interface, 2015, 12, 20141153.	1.5	82
50	Mapping spatial heterogeneity in the tumor microenvironment: a new era for digital pathology. Laboratory Investigation, 2015, 95, 377-384.	1.7	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. Nature Methods, 2014, 11, 1041-1044.	9.0	52
54	Quantitative Image Analysis of Cellular Heterogeneity in Breast Tumors Complements Genomic Profiling. Science Translational Medicine, 2012, 4, 157ra143.	5.8	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.	1.9	27
56	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.	13.7	4,708
57	Directed Partial Correlation: Inferring Large-Scale Gene Regulatory Network through Induced Topology Disruptions. PLoS ONE, 2011, 6, e16835.	1.1	29
58	Penalized regression elucidates aberration hotspots mediating subtype-specific transcriptional responses in breast cancer. Bioinformatics, 2011, 27, 2679-2685.	1.8	2
59	Patient-Specific Data Fusion Defines Prognostic Cancer Subtypes. PLoS Computational Biology, 2011, 7, e1002227.	1.5	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.	1.2	17
62	An unsupervised conditional random fields approach for clustering gene expression time series. Bioinformatics, 2008, 24, 2467-2473.	1.8	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, .	1.0	0
65	A Bayes random field approach for integrative large-scale regulatory network analysis. Journal of Integrative Bioinformatics, 2008, 5, .	1.0	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.	0.5	22
69	Fragile watermarking scheme exploiting non-deterministic block-wise dependency. , 2004, , .		3