

Henrik Failmezger

List of Publications by Year in descending order

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Version: 2024-02-01

10
papers

760
citations

1163117

8
h-index

1372567

10
g-index

11
all docs

11
docs citations

11
times ranked

1823
citing authors

#	ARTICLE	IF	CITATIONS
1	Computational Tumor Infiltration Phenotypes Enable the Spatial and Genomic Analysis of Immune Infiltration in Colorectal Cancer. <i>Frontiers in Oncology</i> , 2021, 11, 552331.	2.8	4
2	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
3	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
4	Clustering of samples with a tree-shaped dependence structure, with an application to microscopic time lapse imaging. <i>Bioinformatics</i> , 2019, 35, 2291-2299.	4.1	12
5	MowJoe: a method for automated-high throughput dissected leaf phenotyping. <i>Plant Methods</i> , 2018, 14, 27.	4.3	5
6	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
7	Interfaces of Malignant and Immunologic Clonal Dynamics in Ovarian Cancer. <i>Cell</i> , 2018, 173, 1755-1769.e22.	28.9	261
8	Unsupervised automated high throughput phenotyping of RNAi time-lapse movies. <i>BMC Bioinformatics</i> , 2013, 14, 292.	2.6	21
9	Semi-automated 3D Leaf Reconstruction and Analysis of Trichome Patterning from Light Microscopic Images. <i>PLoS Computational Biology</i> , 2013, 9, e1003029.	3.2	20
10	Quantitative Image Analysis of Cellular Heterogeneity in Breast Tumors Complements Genomic Profiling. <i>Science Translational Medicine</i> , 2012, 4, 157ra143.	12.4	356