

Joshua J Levy

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

21
papers

94
citations

5
h-index

9
g-index

47
ext. papers

251
ext. citations

4.6
avg, IF

3.02
L-index

#	Paper	IF	Citations
21	MethylNet: an automated and modular deep learning approach for DNA methylation analysis. <i>BMC Bioinformatics</i> , 2020 , 21, 108	3.6	23
20	Gradual polyploid genome evolution revealed by pan-genomic analysis of <i>Brachypodium hybridum</i> and its diploid progenitors. <i>Nature Communications</i> , 2020 , 11, 3670	17.4	22
19	Don't dismiss logistic regression: the case for sensible extraction of interactions in the era of machine learning. <i>BMC Medical Research Methodology</i> , 2020 , 20, 171	4.7	10
18	A large-scale internal validation study of unsupervised virtual trichrome staining technologies on nonalcoholic steatohepatitis liver biopsies. <i>Modern Pathology</i> , 2021 , 34, 808-822	9.8	7
17	PyMethylProcess-convenient high-throughput preprocessing workflow for DNA methylation data. <i>Bioinformatics</i> , 2019 , 35, 5379-5381	7.2	6
16	PathFlowAI: A High-Throughput Workflow for Preprocessing, Deep Learning and Interpretation in Digital Pathology. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2020 , 25, 403-414	1.3	5
15	Topological Feature Extraction and Visualization of Whole Slide Images using Graph Neural Networks. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2021 , 26, 285-296	1.3	3
14	Preliminary Evaluation of the Utility of Deep Generative Histopathology Image Translation at a Mid-Sized NCI Cancer Center		3
13	PolyCRACKER, a robust method for the unsupervised partitioning of polyploid subgenomes by signatures of repetitive DNA evolution. <i>BMC Genomics</i> , 2019 , 20, 580	4.5	2
12	PathFlow-MixMatch for Whole Slide Image Registration: An Investigation of a Segment-Based Scalable Image Registration Method		2
11	Journey across epidemiology's third variables: an anesthesiologist's guide for successfully navigating confounding, mediation, and effect modification. <i>Regional Anesthesia and Pain Medicine</i> , 2021 , 46, 936-940	3.4	2
10	Using molecular testing to improve the management of thyroid nodules with indeterminate cytology: an institutional experience with review of molecular alterations. <i>Journal of the American Society of Cytopathology</i> , 2021 ,	2.4	2
9	Does the timing of postoperative showering impact infection rates? A systematic review and meta-analysis. <i>Journal of Plastic, Reconstructive and Aesthetic Surgery</i> , 2020 , 73, 1306-1311	1.7	1
8	Comparison of Machine-Learning Algorithms for the Prediction of Current Procedural Terminology (CPT) Codes from Pathology Reports.. <i>Journal of Pathology Informatics</i> , 2022 , 13, 3	4.4	1
7	Comparison of Machine Learning Algorithms for the Prediction of Current Procedural Terminology (CPT) Codes from Pathology Reports		1
6	Artificial Intelligence in Anatomic Pathology. <i>Advances in Molecular Pathology</i> , 2021 , 4, 145-171	0.3	0
5	Evaluating the mediating effects of perceived vulnerability to disease in the relation between disgust and contamination-based OCD. <i>Journal of Anxiety Disorders</i> , 2021 , 79, 102384	10.9	0

4	Atypia of undetermined significance in thyroid cytology: Nuclear atypia and architectural atypia are associated with different molecular alterations and risks of malignancy. <i>Cancer Cytopathology</i> , 2021 , 129, 966-972	3.9	o
3	MethylSPWNet and MethylCapsNet: Biologically Motivated Organization of DNAm Neural Networks, Inspired by Capsule Networks. <i>Npj Systems Biology and Applications</i> , 2021 , 7, 33	5	o
2	DNA 5-hydroxymethylcytosine in pediatric central nervous system tumors may impact tumor classification and is a positive prognostic marker. <i>Clinical Epigenetics</i> , 2021 , 13, 176	7.7	o
1	Mixed Effects Machine Learning Models for Colon Cancer Metastasis Prediction using Spatially Localized Immuno-Oncology Markers. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2022 , 27, 175-186	1.3	