

Heba Z Sailem

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5554125/publications.pdf>

Version: 2024-02-01

20
papers

586
citations

933447

10
h-index

839539

18
g-index

25
all docs

25
docs citations

25
times ranked

1172
citing authors

#	ARTICLE	IF	CITATIONS
1	A screen for morphological complexity identifies regulators of switch-like transitions between discrete cell shapes. <i>Nature Cell Biology</i> , 2013, 15, 860-871.	10.3	158
2	Microenvironmental Heterogeneity Parallels Breast Cancer Progression: A Histology-Genomic Integration Analysis. <i>PLoS Medicine</i> , 2016, 13, e1001961.	8.4	101
3	Analysis of live cell images: Methods, tools and opportunities. <i>Methods</i> , 2017, 115, 65-79.	3.8	65
4	Cross-talk between Rho and Rac GTPases drives deterministic exploration of cellular shape space and morphological heterogeneity. <i>Open Biology</i> , 2014, 4, 130132.	3.6	51
5	Visualizing cellular imaging data using PhenoPlot. <i>Nature Communications</i> , 2015, 6, 5825.	12.8	38
6	Identification of clinically predictive metagenes that encode components of a network coupling cell shape to transcription by image-omics. <i>Genome Research</i> , 2017, 27, 196-207.	5.5	33
7	Identification of molecular targets for the targeted treatment of gastric cancer using dasatinib. <i>Oncotarget</i> , 2020, 11, 535-549.	1.8	29
8	How cells explore shape space: A quantitative statistical perspective of cellular morphogenesis. <i>BioEssays</i> , 2014, 36, 1195-1203.	2.5	22
9	Visualizing quantitative microscopy data: History and challenges. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2016, 51, 96-101.	5.2	12
10	Proteomics profiling of interactome dynamics by colocalisation analysis (COLA). <i>Molecular BioSystems</i> , 2017, 13, 92-105.	2.9	11
11	HighVia: A Flexible Live-Cell High-Content Screening Pipeline to Assess Cellular Toxicity. <i>SLAS Discovery</i> , 2020, 25, 801-811.	2.7	11
12	<scp>KCML</scp> : a machine learning framework for inference of multi-scale gene functions from genetic perturbation screens. <i>Molecular Systems Biology</i> , 2020, 16, e9083.	7.2	11
13	Morphological landscape of endothelial cell networks reveals a functional role of glutamate receptors in angiogenesis. <i>Scientific Reports</i> , 2020, 10, 13829.	3.3	10
14	DeepScratch: Single-cell based topological metrics of scratch wound assays. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 2501-2509.	4.1	8
15	Differential RNAi screening provides insights into the rewiring of signalling networks during oxidative stress. <i>Molecular BioSystems</i> , 2012, 8, 2605.	2.9	7
16	Discovery of Rare Phenotypes in Cellular Images Using Weakly Supervised Deep Learning. , 2017, , .		4
17	High-Content Imaging to Phenotype Human Primary and iPSC-Derived Cells. <i>Methods in Molecular Biology</i> , 2021, 2185, 423-445.	0.9	4
18	DeepSplit: Segmentation of Microscopy Images Using Multi-task Convolutional Networks. <i>Communications in Computer and Information Science</i> , 2020, , 155-167.	0.5	3

#	ARTICLE	IF	CITATIONS
19	Efficient Bayesian inference for mechanistic modelling with high-throughput data. PLoS Computational Biology, 2022, 18, e1010191.	3.2	3
20	ShapoGraphy: A User-Friendly Web Application for Creating Bespoke and Intuitive Visualisation of Biomedical Data. Frontiers in Bioinformatics, 0, 2, .	2.1	1