

Ralph Patrick

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7638982/publications.pdf>

Version: 2024-02-01

14
papers

1,103
citations

840776

11
h-index

996975

15
g-index

19
all docs

19
docs citations

19
times ranked

1831
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-cell expression profiling reveals dynamic flux of cardiac stromal, vascular and immune cells in health and injury. <i>ELife</i> , 2019, 8, .	6.0	379
2	Single cell sequencing reveals endothelial plasticity with transient mesenchymal activation after myocardial infarction. <i>Nature Communications</i> , 2021, 12, 681.	12.8	158
3	Single cell analysis of the developing mouse kidney provides deeper insight into marker gene expression and ligand-receptor crosstalk. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	123
4	Transcriptional heterogeneity of fibroblasts is a hallmark of the aging heart. <i>JCI Insight</i> , 2019, 4, .	5.0	101
5	Hif-1a suppresses ROS-induced proliferation of cardiac fibroblasts following myocardial infarction. <i>Cell Stem Cell</i> , 2022, 29, 281-297.e12.	11.1	71
6	Sierra: discovery of differential transcript usage from polyA-captured single-cell RNA-seq data. <i>Genome Biology</i> , 2020, 21, 167.	8.8	59
7	PhosphoPICK: modelling cellular context to map kinase-substrate phosphorylation events. <i>Bioinformatics</i> , 2015, 31, 382-389.	4.1	39
8	Nkx2.5 marks angioblasts that contribute to hemogenic endothelium of the endocardium and dorsal aorta. <i>ELife</i> , 2017, 6, .	6.0	27
9	Identification of active signaling pathways by integrating gene expression and protein interaction data. <i>BMC Systems Biology</i> , 2018, 12, 120.	3.0	23
10	Predicting the Dynamics of Protein Abundance. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1330-1340.	3.8	21
11	Prediction of kinase-specific phosphorylation sites through an integrative model of protein context and sequence. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2016, 1864, 1599-1608.	2.3	16
12	PhosphoPICK-SNP: quantifying the effect of amino acid variants on protein phosphorylation. <i>Bioinformatics</i> , 2017, 33, 1773-1781.	4.1	10
13	Mapping the stabilome: a novel computational method for classifying metabolic protein stability. <i>BMC Systems Biology</i> , 2012, 6, 60.	3.0	5
14	Cardiac fibroblast heterogeneity and dynamics through the lens of single-cell dual omics. <i>Cardiovascular Research</i> , 2022, 118, 1380-1382.	3.8	3