

Jean Fan

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2496451/publications.pdf>

Version: 2024-02-01

31
papers

9,844
citations

430754

18
h-index

526166

27
g-index

38
all docs

38
docs citations

38
times ranked

17074
citing authors

#	ARTICLE	IF	CITATIONS
1	Fast, sensitive and accurate integration of single-cell data with Harmony. <i>Nature Methods</i> , 2019, 16, 1289-1296.	9.0	3,494
2	RNA velocity of single cells. <i>Nature</i> , 2018, 560, 494-498.	13.7	2,602
3	Integrative single-cell analysis of transcriptional and epigenetic states in the human adult brain. <i>Nature Biotechnology</i> , 2018, 36, 70-80.	9.4	762
4	Spatial transcriptome profiling by MERFISH reveals subcellular RNA compartmentalization and cell cycle-dependent gene expression. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 19490-19499.	3.3	460
5	Characterizing transcriptional heterogeneity through pathway and gene set overdispersion analysis. <i>Nature Methods</i> , 2016, 13, 241-244.	9.0	356
6	Locally Disordered Methylation Forms the Basis of Intratumor Methylome Variation in Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2014, 26, 813-825.	7.7	323
7	Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. <i>Nature Communications</i> , 2016, 7, 11589.	5.8	285
8	Cell-Type-Specific Alternative Splicing Governs Cell Fate in the Developing Cerebral Cortex. <i>Cell</i> , 2016, 166, 1147-1162.e15.	13.5	276
9	Interactions between cancer cells and immune cells drive transitions to mesenchymal-like states in glioblastoma. <i>Cancer Cell</i> , 2021, 39, 779-792.e11.	7.7	245
10	Transcriptomic Characterization of SF3B1 Mutation Reveals Its Pleiotropic Effects in Chronic Lymphocytic Leukemia. <i>Cancer Cell</i> , 2016, 30, 750-763.	7.7	173
11	Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. <i>Genome Research</i> , 2018, 28, 1217-1227.	2.4	172
12	Single-cell transcriptomics in cancer: computational challenges and opportunities. <i>Experimental and Molecular Medicine</i> , 2020, 52, 1452-1465.	3.2	108
13	Rewiring of human neurodevelopmental gene regulatory programs by human accelerated regions. <i>Neuron</i> , 2021, 109, 3239-3251.e7.	3.8	91
14	Characterizing spatial gene expression heterogeneity in spatially resolved single-cell transcriptomic data with nonuniform cellular densities. <i>Genome Research</i> , 2021, 31, 1843-1855.	2.4	79
15	A Murine Model of Chronic Lymphocytic Leukemia Based on B Cell-Restricted Expression of Sf3b1 Mutation and Atm Deletion. <i>Cancer Cell</i> , 2019, 35, 283-296.e5.	7.7	71
16	Reference-free cell type deconvolution of multi-cellular pixel-resolution spatially resolved transcriptomics data. <i>Nature Communications</i> , 2022, 13, 2339.	5.8	68
17	Integrated single-cell genetic and transcriptional analysis suggests novel drivers of chronic lymphocytic leukemia. <i>Genome Research</i> , 2017, 27, 1300-1311.	2.4	67
18	Computational challenges and opportunities in spatially resolved transcriptomic data analysis. <i>Nature Communications</i> , 2021, 12, 5283.	5.8	34

#	ARTICLE	IF	CITATIONS
19	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. <i>Human Mutation</i> , 2017, 38, 1266-1276.	1.1	14
20	VeloViz: RNA velocity-informed embeddings for visualizing cellular trajectories. <i>Bioinformatics</i> , 2022, 38, 391-396.	1.8	11
21	Single-cell analysis reveals immune dysfunction from the earliest stages of CLL that can be reversed by ibrutinib. <i>Blood</i> , 2022, 139, 2252-2256.	0.6	7
22	Differential Pathway Analysis. <i>Methods in Molecular Biology</i> , 2019, 1935, 97-114.	0.4	5
23	Multi scale diffeomorphic metric mapping of spatial transcriptomics datasets. , 2021, , .		4
24	Single cell biologyâ€™a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2021, 1506, 74-97.	1.8	3
25	Comprehensive Bulk and Single Cell Transcriptomic Characterization of SF3B1 Mutation Reveals Its Pleiotropic Effects in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2015, 126, 2906-2906.	0.6	2
26	Integrated Single-Cell Detection of Genotype and Phenotype in SF3B1-Mutated Chronic Lymphocytic Leukemia Cells. <i>Blood</i> , 2014, 124, 1943-1943.	0.6	1
27	Expression of Sf3b1-K700E in Murine B Cells Causes Pre-mRNA Splicing and Altered B Cell Differentiation and Function. <i>Blood</i> , 2015, 126, 366-366.	0.6	1
28	Single Cell Transcriptomic Characterization of the Immune Microenvironment in Naturally Progressing Chronic Lymphocytic Leukemia (CLL). <i>Blood</i> , 2018, 132, 3112-3112.	0.6	1
29	From Human Genetic to Mouse Model: SF3B1 Mutation and its Impact on Chronic Lymphocytic Leukemia. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2016, 16, S52.	0.2	0
30	OTME-7. Cancer - immune cell interactions drive transitions to mesenchymal-like state in glioblastoma. <i>Neuro-Oncology Advances</i> , 2021, 3, ii14-ii15.	0.4	0
31	Abstract 669: Compound heterozygous Sf3b1-K700E mutation and Atm deletion in B cells leads to CLL in mice. , 2016, , .		0