Jean Fan

**List of Publications by Year
in descending order**

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	VeloViz: RNA velocity-informed embeddings for visualizing cellular trajectories. Bioinformatics, 2022, 38, 391-396.	1.8	11
2	Single-cell analysis reveals immune dysfunction from the earliest stages of CLL that can be reversed by ibrutinib. Blood, 2022, 139, 2252-2256.	0.6	7
3	Reference-free cellÂtype deconvolution of multi-cellular pixel-resolution spatially resolved transcriptomics data. Nature Communications, 2022, 13, 2339.	5.8	68
4	Characterizing spatial gene expression heterogeneity in spatially resolved single-cell transcriptomic data with nonuniform cellular densities. Genome Research, 2021, 31, 1843-1855.	2.4	79
5	Interactions between cancer cells and immune cells drive transitions to mesenchymal-like states in glioblastoma. Cancer Cell, 2021, 39, 779-792.e11.	7.7	245
6	Multi scale diffeomorphic metric mapping of spatial transcriptomics datasets. , 2021, , .		4
7	OTME-7. Cancer - immune cell interactions drive transitions to mesenchymal-like state in glioblastoma. Neuro-Oncology Advances, 2021, 3, ii14-ii15.	0.4	0
8	Rewiring of human neurodevelopmental gene regulatory programs by human accelerated regions. Neuron, 2021, 109, 3239-3251.e7.	3.8	91
9	Computational challenges and opportunities in spatially resolved transcriptomic data analysis. Nature Communications, 2021, 12, 5283.	5.8	34
10	Single cell biologyâ€"a Keystone Symposia report. Annals of the New York Academy of Sciences, 2021, 1506, 74-97.	1.8	3
11	Single-cell transcriptomics in cancer: computational challenges and opportunities. Experimental and Molecular Medicine, 2020, 52, 1452-1465.	3.2	108
12	Spatial transcriptome profiling by MERFISH reveals subcellular RNA compartmentalization and cell cycle-dependent gene expression. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19490-19499.	3.3	460
13	A Murine Model of Chronic Lymphocytic Leukemia Based on B Cell-Restricted Expression of Sf3b1 Mutation and Atm Deletion. Cancer Cell, 2019, 35, 283-296.e5.	7.7	71
14	Differential Pathway Analysis. Methods in Molecular Biology, 2019, 1935, 97-114.	0.4	5
15	Fast, sensitive and accurate integration of single-cell data with Harmony. Nature Methods, 2019, 16, 1289-1296.	9.0	3,494
16	Integrative single-cell analysis of transcriptional and epigenetic states in the human adult brain. Nature Biotechnology, 2018, 36, 70-80.	9.4	762
17	RNA velocity of single cells. Nature, 2018, 560, 494-498.	13.7	2,602
18	Linking transcriptional and genetic tumor heterogeneity through allele analysis of single-cell RNA-seq data. Genome Research, 2018, 28, 1217-1227.	2.4	172

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19	Single Cell Transcriptomic Characterization of the Immune Microenvironment in Naturally Progressing Chronic Lymphocytic Leukemia (CLL). Blood, 2018, 132, 3112-3112.	0.6	1
20	Matching phenotypes to whole genomes: Lessons learned from four iterations of the personal genome project community challenges. Human Mutation, 2017, 38, 1266-1276.	1.1	14
21	Integrated single-cell genetic and transcriptional analysis suggests novel drivers of chronic lymphocytic leukemia. Genome Research, 2017, 27, 1300-1311.	2.4	67
22	From Human Genetic to Mouse Model: SF3B1 Mutation and its Impact on Chronic Lymphocytic Leukemia. Clinical Lymphoma, Myeloma and Leukemia, 2016, 16, S52.	0.2	0
23	Cell-Type-Specific Alternative Splicing Governs Cell Fate in the Developing Cerebral Cortex. Cell, 2016, 166, 1147-1162.e15.	13.5	276
24	Clonal evolution in patients with chronic lymphocytic leukaemia developing resistance to BTK inhibition. Nature Communications, 2016, 7, 11589.	5.8	285
25	Transcriptomic Characterization of SF3B1 Mutation Reveals Its Pleiotropic Effects in Chronic Lymphocytic Leukemia. Cancer Cell, 2016, 30, 750-763.	7.7	173
26	Characterizing transcriptional heterogeneity through pathway and gene set overdispersion analysis. Nature Methods, 2016, 13, 241-244.	9.0	356
27	Abstract 669: Compound heterozygous Sf3b1-K700E mutation and Atm deletion in B cells leads to CLL in mice. , 2016, , .		0
28	Expressionof Sf3b1- K700Ein Murine B Cells Causes Pre-mRNA Splicing and Altered B Cell Differentiation and Function. Blood, 2015, 126, 366-366.	0.6	1
29	Comprehensive Bulk and Single Cell Transcriptomic Characterization of SF3B1 Mutation Reveals Its Pleiotropic Effects in Chronic Lymphocytic Leukemia. Blood, 2015, 126, 2906-2906.	0.6	2
30	Locally Disordered Methylation Forms the Basis of Intratumor Methylome Variation in Chronic Lymphocytic Leukemia. Cancer Cell, 2014, 26, 813-825.	7.7	323
31	Integrated Single-Cell Detection of Genotype and Phenotype in SF3B1-Mutated Chronic Lymphocytic Leukemia Cells. Blood, 2014, 124, 1943-1943.	0.6	1