

BBKNN: fast batch alignment of single cell transcriptom

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Citation Report

#	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	Cellular resolution in clinical MALDI mass spectrometry imaging: the latest advancements and current challenges. <i>Clinical Chemistry and Laboratory Medicine</i> , 2020, 58, 914-929.	1.4	84
3	The emergence and promise of single-cell temporal-omics approaches. <i>Current Opinion in Biotechnology</i> , 2020, 63, 70-78.	3.3	34
4	In vitro characterization of the human segmentation clock. <i>Nature</i> , 2020, 580, 113-118.	13.7	152
5	scRNA-seq assessment of the human lung, spleen, and esophagus tissue stability after cold preservation. <i>Genome Biology</i> , 2020, 21, 1.	3.8	572
6	Using single-cell technologies to map the human immune system – implications for nephrology. <i>Nature Reviews Nephrology</i> , 2020, 16, 112-128.	4.1	39
7	Reverse engineering human brain evolution using organoid models. <i>Brain Research</i> , 2020, 1729, 146582.	1.1	25
8	Sequencing dropout-and-batch effect normalization for single-cell mRNA profiles: a survey and comparative analysis. <i>Briefings in Bioinformatics</i> , 2020, 22, .	3.2	4
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10	Alveolar regeneration through a Krt8+ transitional stem cell state that persists in human lung fibrosis. <i>Nature Communications</i> , 2020, 11, 3559.	5.8	378
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16	Multi-Omics Resolves a Sharp Disease-State Shift between Mild and Moderate COVID-19. <i>Cell</i> , 2020, 183, 1479-1495.e20.	13.5	449
17	Interactions between lineage-associated transcription factors govern haematopoietic progenitor states. <i>EMBO Journal</i> , 2020, 39, e104983.	3.5	20
18	Unsupervised Inference of Developmental Directions for Single Cells Using VECTOR. <i>Cell Reports</i> , 2020, 32, 108069.	2.9	11

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20	A multicenter study benchmarking single-cell RNA sequencing technologies using reference samples. <i>Nature Biotechnology</i> , 2021, 39, 1103-1114.	9.4	69
21	FR-Match: robust matching of cell type clusters from single cell RNA sequencing data using the Friedman-Rafsky non-parametric test. <i>Briefings in Bioinformatics</i> , 2020, 22, .	3.2	12
22	Single-Cell Sequencing of Developing Human Gut Reveals Transcriptional Links to Childhood Crohn's Disease. <i>Developmental Cell</i> , 2020, 55, 771-783.e5.	3.1	164
23	Molecular design of hypothalamus development. <i>Nature</i> , 2020, 582, 246-252.	13.7	105
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54	iMAP: integration of multiple single-cell datasets by adversarial paired transfer networks. <i>Genome Biology</i> , 2021, 22, 63.	3.8	26

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