single cell sequencing

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36058061	[Intestinal epithelial organoids: regeneration and maintenance of the intestinal epithelium](#)	Mayumi Oda Yoshiko Hatano Toshiro Sato	Vital functions of the intestines: digestion, absorption, and surface barrier are performed by the intestinal epithelium, which consists of various differentiated cells and intestinal stem cells. Recent technological advances in sequencing technology, including single-cell transcriptomics and epigenetic analysis, have facilitated the genetic characterization of diverse intestinal epithelial cell types and surrounding mesenchymal niche environments. Organoids have allowed biological analysis of...	pmid:36058061 doi:10.1016/j.gde.2022.101977	Sun, 04 Sep 2022 06:00:00 -0400
2	pubmed:36059147	[Interleukin-18 signaling promotes activation of hepatic stellate cells in murine liver fibrosis](#)	Jana Knorr Benedikt Kaufmann Maria Eugenia Inzaugarat Theresa Maria Holtmann Lukas Geisler Jana Hundertmark Marlene Sophia Kohlhepp Laela M Boosheri Daisy R Chilin-Fuentes Amanda Birmingham Kathleen M Fisch Joel D Schilling Sven H Loosen Christian Trautwein Christoph Roderburg Münevver Demir Frank Tacke Hal M Hoffman Ariel E Feldstein Alexander Wree	CONCLUSIONS: Our study highlights the role of IL-18 in the development of liver fibrosis by its direct effect on HSC activation identifying IL-18 as a novel target to treat liver fibrosis.	pmid:36059147 doi:10.1002/hep.32776	Mon, 05 Sep 2022 06:00:00 -0400
3	pubmed:36059185	[Cutting edge technologies in chronic inflammation research](#)	Jon D Laman	This concise review provides the broad background and selection from the literature for a Keynote lecture at EHSF 2022 on state of the art technologies in inflammation research, with an emphasis on disease of the skin and the nervous system. The value of ex vivo skin explant models is discussed, as well as the innovative use of animal models, wherein the crucial roles of antigen experience and "wild" microbiota are emphasized. Spectral flow cytometry allowing large surface marker panels to be...	pmid:36059185 doi:10.1111/exd.14648	Mon, 05 Sep 2022 06:00:00 -0400
4	pubmed:36059490	[Single-cell RNA-Seq reveals the potential risk of anti-mesothelin CAR T Cell therapy toxicity to different organs in humans](#)	Lu Wen Yu Huang Ling Peng Kaiping Zhao Yan Sun Zhicai Lin Yuanyuan Chen Zhong Li Qijun Qian Fan Tong Ruiguang Zhang Xiaorong Dong	"On-target off-tumor" toxicity is a major challenge to the use of chimeric antigen receptor (CAR)-engineered T cells in the treatment of solid malignancies, because of the expression of target antigens in normal tissues. Mesothelin overexpression is associated with poor prognosis of multiple solid tumors, and would therefore appear to be a suitable antigen target. To understand the risk of toxicity to different organs on anti-mesothelin CAR T cell therapy, single-cell RNA sequencing (scRNA-seq)...	pmid:36059490 pmc:PMC9428152 doi:10.3389/fimmu.2022.807915	Mon, 05 Sep 2022 06:00:00 -0400

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5	pubmed:36059506	Research progress on application of single-cell TCR/BCR sequencing technology to the tumor immune microenvironment, autoimmune diseases, and infectious diseases	Jinhua He Jian Shen Wenfeng Luo Zeping Han Fangmei Xie Ting Pang Liyin Liao Zhonghui Guo Jianhao Li Yuguang Li Hanwei Chen	Single-cell omics is the profiling of individual cells through sequencing and other technologies including high-throughput analysis for single-cell resolution, cell classification, and identification as well as time series analyses. Unlike multicellular studies, single-cell omics overcomes the problem of cellular heterogeneity. It provides new methods and perspectives for in-depth analyses of the behavior and mechanism of individual cells in the cell population and their relationship with the...	pmid:36059506 pmc:PMC9434330 doi:10.3389/fimmu.2022.969808	Mon, 05 Sep 2022 06:00:00 -0400
6	pubmed:36059514	Key molecules associated with thyroid carcinoma prognosis: A study based on transcriptome sequencing and GEO datasets	Miaoyu Bai Shanjia Ke Hongjun Yu Yanan Xu Yue Yu Shounan Lu Chaoqun Wang Jingjing Huang Yong Ma Wenjie Dai Yaohua Wu	CONCLUSIONS: RGS8, DGKI and OCA2 might be promising prognostic molecular markers in patients with THCA and reveal the clinical significance of RGS8, DGKI and OCA2 in THCA.	pmid:36059514 pmc:PMC9428590 doi:10.3389/fimmu.2022.964891	Mon, 05 Sep 2022 06:00:00 -0400
7	pubmed:36059518	Fucose as a potential therapeutic molecule against the immune-mediated inflammation in IgA nepharopathy: An unrevealed link	Jianbo Qing Xueli Hu Changqun Li Wenzhu Song Hasna Tirichen Hasnaa Yaigoub Yafeng Li	CONCLUSION: The increase of macrophages and the decrease of iTregs in glomeruli represent the immune-mediated inflammation of IgAN, and fucose may be a potential therapeutic molecule against IgAN because it affects genes involved in the severe inflammation of IgAN.	pmid:36059518 pmc:PMC9428610 doi:10.3389/fimmu.2022.929138	Mon, 05 Sep 2022 06:00:00 -0400
8	pubmed:36059685	Selinexor inhibits growth of patient derived chordomas *in vivo* as a single agent and in combination with abemaciclib through diverse mechanisms	Christopher J Walker Hua Chang Leah Henegar Trinayan Kashyap Sharon Shacham Josh Sommer Michael J Wick Joan Levy Yosef Landesman	Chordoma is a rare cancer that grows in the base of the skull and along the mobile spine from remnants of embryonic notochord tissue. The cornerstone of current treatments is surgical excision with adjuvant radiation therapy, although complete surgical removal is not always possible. Chordomas have high rates of metastasis and recurrence, with no approved targeted agents. Selinexor and eltanexor are selective inhibitors of nuclear export (SINE) that prevent the karyopherin protein exportin-1...	pmid:36059685 pmc:PMC9434827 doi:10.3389/fonc.2022.808021	Mon, 05 Sep 2022 06:00:00 -0400
9	pubmed:36060279	Profiling mouse cochlear cell maturation using 10× Genomics single-cell transcriptomics	Zhenhang Xu Shu Tu Caroline Pass Yan Zhang Huizhan Liu Jack Diers Yusi Fu David Z Z He Jian Zuo	Juvenile and mature mouse cochleae contain various low-abundant, vulnerable sensory epithelial cells embedded in the calcified temporal bone, making it challenging to profile the dynamic transcriptome changes of these cells during maturation at the single-cell level. Here we performed the 10x Genomics single-cell RNA sequencing (scRNA-seq) of mouse cochleae at postnatal days 14 (P14) and 28. We attained the transcriptomes of multiple cell types, including hair cells, supporting cells, spiral...	pmid:36060279 pmc:PMC9434313 doi:10.3389/fncel.2022.962106	Mon, 05 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
10	pubmed:36061826	Identifying potential signatures for atherosclerosis in the context of predictive, preventive, and personalized medicine using integrative bioinformatics approaches and machine-learning strategies	Jinling Xu Hui Zhou Yangyang Cheng Guangda Xiang	CONCLUSIONS: Our findings are the first to report the involvement of DHRS9 in the atherogenesis, and the proatherogenic effect of DHRS9 is mediated by immune mechanism. In addition, we confirm that DHRS9 is localized in macrophages within atherosclerotic plaques. Therefore, upregulated DHRS9 could be a novel potential target for the future predictive diagnostics, targeted prevention, patient stratification, and personalization of medical services in atherosclerosis.	pmid:36061826 pmc:PMC9437201 doi:10.1007/s13167-022-00289-y	Mon, 05 Sep 2022 06:00:00 -0400
11	pubmed:36062157	Accelerated aging-related transcriptome alterations in neurovascular unit cells in the brain of Alzheimer's disease	Yan Zhao Yong-Zhi Xie You-Shuo Liu	Alzheimer's disease (AD) is the most common cause of dementia with no effective therapies. Aging is a dominant risk factor for AD. The neurovascular unit (NVU) plays an important role in maintaining homeostasis of the brain microenvironment. The accelerated aging of NVU cells may directly impair NVU function and contribute to AD pathogenesis. However, the expression patterns of aging-related genes (AGs) in NVU cells of AD remain unclear. In this study, we performed single-nucleus transcriptome...	pmid:36062157 pmc:PMC9435434 doi:10.3389/fnagi.2022.949074	Mon, 05 Sep 2022 06:00:00 -0400
12	pubmed:36063335	Single-Molecule Studies on the Motion and Force Generation of the Kinesin-3 Motor KIF1A	Lu Rao Arne Gennerich	KIF1A is a neuron-specific member of the kinesin-3 family of microtubule (MT) plus-end-directed motor proteins. It powers the migration of nuclei in differentiating brain stem cells and the transport of synaptic precursors and dense core vesicles in axons. Its dysfunction causes severe neurodevelopmental and neurodegenerative diseases termed KIF1A-associated neurological disorders (KAND). KAND mutations span the entirety of the KIF1A protein sequence, of which the majority are located within the...	pmid:36063335 doi:10.1007/978-1-0716-2229-2_21	Mon, 05 Sep 2022 06:00:00 -0400
13	pubmed:36063454	CCPLS reveals cell-type-specific spatial dependence of transcriptomes in single cells	Takaho Tsuchiya Hiroki Hori Haruka Ozaki	MOTIVATION: Cell-cell communications regulate internal cellular states, e.g., gene expression and cell functions, and play pivotal roles in normal development and disease states. Furthermore, single-cell RNA sequencing methods have revealed cell-to-cell expression variability of highly variable genes (HVGs), which is also crucial. Nevertheless, the regulation on cell-to-cell expression variability of HVGs via cell-cell communications is still largely unexplored. The recent advent of spatial...	pmid:36063454 doi:10.1093/bioinformatics/btac599	Mon, 05 Sep 2022 06:00:00 -0400
14	pubmed:36063455	SD2: Spatially resolved transcriptomics deconvolution through integration of dropout and spatial information	Haoyang Li Hanmin Li Juexiao Zhou Xin Gao	MOTIVATION: Unveiling the heterogeneity in the tissues is crucial to explore cell-cell interactions and cellular targets of human diseases. Spatial transcriptomics (ST) supplies spatial gene expression profile which has revolutionized our biological understanding, but variations in cell type proportions of each spot with dozens of cells would confound downstream analysis. Therefore, deconvolution of ST has been an indispensable step and a technical challenge towards the higher-resolution...	pmid:36063455 doi:10.1093/bioinformatics/btac605	Mon, 05 Sep 2022 06:00:00 -0400

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15	pubmed:36063544	A scalable and unbiased discordance metric with H	Nathan Dyjack Daniel N Baker Vladimir Braverman Ben Langmead Stephanie C Hicks	A standard unsupervised analysis is to cluster observations into discrete groups using a dissimilarity measure, such as Euclidean distance. If there does not exist a ground-truth label for each observation necessary for external validity metrics, then internal validity metrics, such as the tightness or separation of the clusters, are often used. However, the interpretation of these internal metrics can be problematic when using different dissimilarity measures as they have different magnitudes...	pmid:36063544 doi:10.1093/biostatistics/kxac035	Mon, 05 Sep 2022 06:00:00 -0400