single cell sequencing

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36095842	The end of the beginning: Application of single cell sequencing to chronic lymphocytic leukemia (CLL)	Adi Nagler Catherine J Wu	Single cell analysis has emerged over the past decade as a transformative technology informative for the systematic analysis of complex cell populations such as in cancers and the tumor immune microenvironment. The methodologic and analytical advancements in this realm have rapidly evolved, scaling from but a few cells at its outset to the current capabilities of processing and analyzing hundreds of thousands of individual cells at a time. The types of profiling attainable at individual cell	pmid:36095842 doi:10.1182/blood.2021014669	Mon, 12 Sep 2022 06:00:00 -0400
2	pubmed:36095948	MSR1 characterized by chromatin accessibility mediates M2 macrophage polarization to promote gastric cancer progression	Xin Chen Jiebang Jiang Hailong Liu Ajian Li Wenchao Wang Zhizhan Ni Moubin Lin	CONCLUSION: We identified a gene-MSR1-characterized by chromatin accessibility, associated with poor prognosis in gastric cancer. This gene dictates the progression of gastric cancer by facilitating M2 macrophage polarization.	pmid:36095948 doi:10.1016/j.intimp.2022.109217	Mon, 12 Sep 2022 06:00:00 -0400
3	pubmed:36096099	Gray Blight Disease on Euonymus japonicas Caused by Pestalotiopsis disseminata in China	Tan Wang Guangling Xu Suo Zhou Qiuhong Niu Jiaxiang Zang Tiantian Yang FaHu Pang FengXia Tian	Euonymus japonicas is widely planted as an important landscape species throughout China. In June 2021, a serious gray blight disease was detected on E. japonicas in Henan Province (32°30'58" N, 112°19'44" E), causing severe defoliation of infected trees with a foliar disease incidence of 52 to 70% (n = 100). Gray spots initially appeared on leaves, gradually expanded into irregular white blotches with dark brown borders, eventually leading to wilting and death of the leaves. The junctions	pmid:36096099 doi:10.1094/PDIS-06-22-1373-PDN	Mon, 12 Sep 2022 06:00:00 -0400
4	pubmed:36096106	First report of leaf blight caused by Pantoea agglomerans on wheat in China	Long Gao Wenqiang Li Bin Ren Yaolong Hu Xiaoyun Ma Yanxia Jia Zhangjun Wang	Wheat (Triticum aestivum L.) is the main grain crop in Ningxia Hui Autonomous Region, China. A new leaf blight disease of wheat was observed in many wheat fields in Yinchuan City and Wuzhong City of Ningxia during 2020-2021. The average disease incidence of the cultivar Ningchun 50 was 5 to 15%, and there appeared the evident disease symptoms from the heading stage, then the symptoms got more serious until the mature stage. The tips of the leaves were chlorotic and turned bright yellow at the	pmid:36096106 doi:10.1094/PDIS-07-22-1606-PDN	Mon, 12 Sep 2022 06:00:00 -0400
5	pubmed:36096729	Identification and characterization of the T cell receptor (TCR) repertoire of the cynomolgus macaque (Macaca Fascicularis)	Swati Jaiswal Sarah K Nyquist Shayla Boyce Tasneem Jivanjee Samira Ibrahim Joshua D Bromley G James Gatter Hannah Gideon Kush Patel Sharie Keanne Ganchua Bonnie Berger Sarah M Fortune JoAnne L Flynn Alex K Shalek Samuel M Behar	CONCLUSION: The genomic organization of the cynomolgus macaque has great similarity with the rhesus macaque and they shared > 90% sequence similarity with the human TCR repertoire. The identification of the TCR repertoire facilitates analysis of T cell immunity in cynomolgus macaques.	pmid:36096729 doi:10.1186/s12864-022-08867-0	Mon, 12 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
6	pubmed:36096847	Liquid biopsy: current technology and clinical applications	Mina Nikanjam Shumei Kato Razelle Kurzrock	Liquid biopsies are increasingly used for cancer molecular profiling that enables a precision oncology approach. Circulating extracellular nucleic acids (cell-free DNA; cfDNA), circulating tumor DNA (ctDNA), and circulating tumor cells (CTCs) can be isolated from the blood and other body fluids. This review will focus on current technologies and clinical applications for liquid biopsies. ctDNA/cfDNA has been isolated and analyzed using many techniques, e.g., droplet digital polymerase chain	pmid:36096847 doi:10.1186/s13045-022-01351-y	Mon, 12 Sep 2022 06:00:00 -0400
7	pubmed:36097044	Semibulk RNA-seq analysis as a convenient method for measuring gene expression statuses in a local cellular environment	Kyoko Muto Issei Tsuchiya Soo Hyeon Kim Satoi Nagasawa Mariko Takishita Koichiro Tsugawa Hiroaki Saito Yusuke Komazaki Toru Torii Teruo Fujii Yutaka Suzuki Ayako Suzuki Masahide Seki	When biologically interpretation of the data obtained from the single-cell RNA sequencing (scRNA-seq) analysis is attempted, additional information on the location of the single cells, behavior of the surrounding cells, and the microenvironment they generate, would be very important. We developed an inexpensive, high throughput application while preserving spatial organization, named "semibulk RNA-seq" (sbRNA-seq). We utilized a microfluidic device specifically designed for the experiments to	pmid:36097044 doi:10.1038/s41598-022-19391-2	Mon, 12 Sep 2022 06:00:00 -0400
8	pubmed:36097056	The choanoflagellate pore-forming lectin SaroL-1 punches holes in cancer cells by targeting the tumor-related glycosphingolipid Gb3	Simona Notova François Bonnardel Francesca Rosato Lina Siukstaite Jessica Schwaiger Jia Hui Lim Nicolai Bovin Annabelle Varrot Yu Ogawa Winfried Römer Frédérique Lisacek Anne Imberty	Choanoflagellates are primitive protozoa used as models for animal evolution. They express a large variety of multi-domain proteins contributing to adhesion and cell communication, thereby providing a rich repertoire of molecules for biotechnology. Adhesion often involves proteins adopting a trefoil fold with carbohydrate-binding properties therefore classified as lectins. Sequence database screening with a dedicated method resulted in TrefLec, a database of 44714 -trefoil candidate lectins	pmid:36097056 doi:10.1038/s42003-022-03869-w	Mon, 12 Sep 2022 06:00:00 -0400
9	pubmed:36097076	The role of goblet cells and mucus in intestinal homeostasis	Jenny K Gustafsson Malin E V Johansson	The intestinal tract faces numerous challenges that require several layers of defence. The tight epithelium forms a physical barrier that is further protected by a mucus layer, which provides various sitespecific protective functions. Mucus is produced by goblet cells, and as a result of single-cell RNA sequencing identifying novel goblet cell subpopulations, our understanding of their various contributions to intestinal homeostasis has improved. Goblet cells not only produce mucus but also are	pmid:36097076 doi:10.1038/s41575-022-00675-x	Mon, 12 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
10	pubmed:36097221	Distinct cellular dynamics associated with response to CAR-T therapy for refractory B cell lymphoma	Nicholas J Haradhvala Mark B Leick Katie Maurer Satyen H Gohil Rebecca C Larson Ning Yao Kathleen M E Gallagher Katelin Katsis Matthew J Frigault Jackson Southard Shuqiang Li Michael C Kann Harrison Silva Max Jan Kahn Rhrissorrakrai Filippo Utro Chaya Levovitz Raquel A Jacobs Kara Slowik Brian P Danysh Kenneth J Livak Laxmi Parida Judith Ferry Caron Jacobson Catherine J Wu Gad Getz Marcela V Maus	Chimeric antigen receptor (CAR)-T cell therapy has revolutionized the treatment of hematologic malignancies. Approximately half of patients with refractory large B cell lymphomas achieve durable responses from CD19-targeting CAR-T treatment; however, failure mechanisms are identified in only a fraction of cases. To gain new insights into the basis of clinical response, we performed single-cell transcriptome sequencing of 105 pretreatment and post-treatment peripheral blood mononuclear cell	pmid:36097221 doi:10.1038/s41591-022-01959-0	Tue, 13 Sep 2022 06:00:00 -0400
11	pubmed:36097543	Single-cell transcriptome landscape and antigen receptor dynamic during SARS-CoV-2 vaccination	Xiaojian Cao Xiaohua Chen Yaqi Zhu Xiaojuan Gou Keyi Yan Bing Yang Dong Men Lei Liu Yong-An Zhang Gang Cao	Vaccination by inactivated vaccine is an effective strategy to prevent the COVID-19 pandemic. However, the detailed molecular immune response at single-cell level is poorly understood. In this study, we systematically delineated the landscape of the pre- and post-vaccination single-cell transcriptome, TCR (T cell antigen receptor) and BCR (B cell antigen receptor) expression profile of vaccinated candidates. The bulk TCR sequencing analysis of COVID-19 patients was also performed. Enrichment of	pmid:36097543 pmc:PMC9454148 doi:10.1016/j.gendis.2022.08.020	Tue, 13 Sep 2022 06:00:00 -0400