

single cell sequencing

NCT Number		Title	Authors	Description	Identifier	Dates
1	pubmed:36127250	<a href="#">Bioinformatics in bioscience and bioengineering: Recent advances, applications, and perspectives</a>	Kazuma Uesaka Hiroya Oka Ryuji Kato Kei Kanie Takaaki Kojima Hiroshi Tsugawa Yosuke Toda Takaaki Horinouchi	Recent advances have led to the emergence of highly comprehensive and analytical approaches, such as omics analysis and high-resolution, time-resolved bioimaging analysis. These technologies have made it possible to obtain vast data from a single measurement. Subsequently, large datasets have pioneered the data-driven approach, an alternative to the traditional hypothesis-testing system, for researchers. However, processing, interpreting, and elucidating enormous datasets is no longer possible...	pmid:36127250 doi:10.1016/j.jbiosc.2022.08.004	Tue, 20 Sep 2022 06:00:00 -0400
2	pubmed:36127326	<a href="#">An anti-inflammatory activation sequence governs macrophage transcriptional dynamics during tissue injury in zebrafish</a>	Nicolas Denans Nhung T T Tran Madeleine E Swall Daniel C Diaz Jillian Blanck Tatjana Piotrowski	Macrophages are essential for tissue repair and regeneration. Yet, the molecular programs, as well as the timing of their activation during and after tissue injury are poorly defined. Using a high spatio-temporal resolution single cell analysis of macrophages coupled with live imaging after sensory hair cell death in zebrafish, we find that the same population of macrophages transitions through a sequence of three major anti-inflammatory activation states. Macrophages first show a signature of...	pmid:36127326 doi:10.1038/s41467-022-33015-3	Tue, 20 Sep 2022 06:00:00 -0400
3	pubmed:36127333	<a href="#">Single-cell transcriptome reveals cellular hierarchies and guides p-EMT-targeted trial in skull base chordoma</a>	Qilin Zhang Lijiang Fei Rui Han Ruofan Huang Yongfei Wang Hong Chen Boyuan Yao Nidan Qiao Zhe Wang Zengyi Ma Zhao Ye Yichao Zhang Weiwei Wang Ye Wang Lin Kong Xuefei Shou Xiaoyun Cao Xiang Zhou Ming Shen Haixia Cheng Zhenwei Yao Chao Zhang Guoji Guo Yao Zhao	Skull base chordoma (SBC) is a bone cancer with a high recurrence rate, high radioresistance rate, and poorly understood mechanism. Here, we profiled the transcriptomes of 90,691 single cells, revealed the SBC cellular hierarchies, and explored novel treatment targets. We identified a cluster of stem-like SBC cells that tended to be distributed in the inferior part of the tumor. Combining radiated UM-Chor1 RNA-seq data and in vitro validation, we further found that this stem-like cell cluster is...	pmid:36127333 doi:10.1038/s41421-022-00459-2	Tue, 20 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
4	pubmed:36127427	<a href="#">Single cell atlas identifies lipid-processing and immunomodulatory endothelial cells in healthy and malignant breast</a>	Vincent Geldhof Laura P M H de Rooij Liliana Sokol Jacob Amersfoort Maxim De Schepper Katerina Rohlenova Griet Hoste Adriaan Vanderstichele Anne-Marie Delsupehe Edoardo Isnaldi Naima Dai Federico Taverna Shawez Khan Anh-Co K Truong Laure-Anne Teuwen François Richard Lucas Treps Ann Smeets Ines Nevelsteen Birgit Weynand Stefan Vinckier Luc Schoonjans Joanna Kalucka Christine Desmedt Patrick Neven Massimiliano Mazzone Giuseppe Floris Kevin Punie Mieke Dewerchin Guy Eelen Hans Wildiers Xuri Li Yonglun Luo Peter Carmeliet	Since a detailed inventory of endothelial cell (EC) heterogeneity in breast cancer (BC) is lacking, here we perform single cell RNA-sequencing of 26,515 cells (including 8433 ECs) from 9 BC patients and compare them to published EC taxonomies from lung tumors. Angiogenic ECs are phenotypically similar, while other EC subtypes are different. Predictive interactome analysis reveals known but also previously unreported receptor-ligand interactions between ECs and immune cells, suggesting an...	pmid:36127427 doi:10.1038/s41467-022-33052-y	Tue, 20 Sep 2022 06:00:00 -0400
5	pubmed:36127466	<a href="#">Macrophage-specific inhibition of the histone demethylase JMJD3 decreases STING and pathologic inflammation in diabetic wound repair</a>	Christopher O Audu William J Melvin Amrita D Joshi Sonya J Wolf Jadie Y Moon Frank M Davis Emily C Barrett Kevin D Mangum Hongping Deng Xianying Xing Rachel Wasikowski Lam C Tsoi Sriganesh B Sharma Tyler M Bauer James Shadiow Matthew A Corriere Andrea T Obi Steven L Kunkel Benjamin Levi Bethany B Moore Johann E Gudjonsson Andrew M Smith Katherine A Gallagher	Macrophage plasticity is critical for normal tissue repair following injury. In pathologic states such as diabetes, macrophage plasticity is impaired, and macrophages remain in a persistent proinflammatory state; however, the reasons for this are unknown. Here, using single-cell RNA sequencing of human diabetic wounds, we identified increased JMJD3 in diabetic wound macrophages, resulting in increased inflammatory gene expression. Mechanistically, we report that in wound healing, JMJD3 directs...	pmid:36127466 doi:10.1038/s41423-022-00919-5	Tue, 20 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
6	pubmed:36127475	<a href="#">Construction and characterisation of glycoprotein E and glycoprotein I deficient mutants of Australian strains of infectious laryngotracheitis virus using traditional and CRISPR/Cas9-assisted homologous recombination techniques</a>	Marzieh Armat Paola K Vaz Glenn F Browning Amir H Noormohammadi Carol A Hartley Joanne M Devlin	In alphaherpesviruses, glycoproteins E and I (gE and gI, respectively) form a heterodimer that facilitates cell-to-cell spread of virus. Using traditional homologous recombination techniques, as well as CRISPR/Cas9-assisted homologous recombination, we separately deleted gE and gI coding sequences from an Australian field strain (CSW-1) and a vaccine strain (A20) of infectious laryngotracheitis virus (ILTV) and replaced each coding sequence with sequence encoding green fluorescent protein (GFP)....	pmid:36127475 doi:10.1007/s11262-022-01933-5	Tue, 20 Sep 2022 06:00:00 -0400
7	pubmed:36127695	<a href="#">Combining single-cell RNA sequencing of peripheral blood mononuclear cells and exosomal transcriptome to reveal the cellular and genetic profiles in COPD</a>	Yanli Pei Yuxi Wei Boshizhang Peng Mengqi Wang Wei Xu Zhe Chen Xindi Ke Lei Rong	CONCLUSIONS: We generated exosomal RNA profiling and single-cell transcriptomic profiling of PBMCs in COPD, described possible connection between impaired immune function and COPD development, and finally determined the possible role of exosomes in mediating local and systemic immune reactions.	pmid:36127695 doi:10.1186/s12931-022-02182-8	Tue, 20 Sep 2022 06:00:00 -0400
8	pubmed:36128218	<a href="#">SARS-CoV-2 infection of human pluripotent stem cell-derived liver organoids reveals potential mechanisms of liver pathology</a>	Alexsia Richards Max Friesen Andrew Khalil M Inmaculada Barrasa Lee Gehrke Rudolf Jaenisch	Although respiratory symptoms are the most prevalent disease manifestation of infection by Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2), infection can also damage other organs, including the brain, gut, and liver. Symptoms of liver damage are observed in nearly half of patients that succumb to severe SARS-CoV-2 infection. Here we use human induced pluripotent stem cell-derived liver organoids (HLOs) to recapitulate and characterize liver pathology following virus exposure....	pmid:36128218 pmc:PMC9477603 doi:10.1016/j.jisci.2022.105146	Wed, 21 Sep 2022 06:00:00 -0400
9	pubmed:36128423	<a href="#">SPROUT: spectral sparsification helps restore the spatial structure at single-cell resolution</a>	Jingwan Wang Shiying Li Lingxi Chen Shuai Cheng Li	Single-cell RNA sequencing thoroughly quantifies the individual cell transcriptomes but renounces the spatial structure. Conversely, recently emerged spatial transcriptomics technologies capture the cellular spatial structure but skimp cell or gene resolutions. Ligand-receptor interactions reveal the potential of cell proximity since they are spatially constrained. Cell-cell affinity values estimated by ligand-receptor interaction can partially represent the structure of cells but falsely...	pmid:36128423 pmc:PMC9477078 doi:10.1093/nargab/lqac069	Wed, 21 Sep 2022 06:00:00 -0400
10	pubmed:36129301	<a href="#">Microevolution of CG23-I Hypervirulent Klebsiella pneumoniae during Recurrent Infections in a Single Patient</a>	Yao-Chen Wang Min-Chi Lu Yia-Ting Li Hui-Ling Tang Pei-Yi Hsiao Bo-Han Chen Ru-Hsiou Teng Chien-Shun Chiou Yi-Chyi Lai	CG23-I lineage constitutes the majority of hypervirulent Klebsiella pneumoniae. A diabetic patient suffered six episodes of infections caused by CG23-I K. pneumoniae. A total of nine isolates were collected in 2020. We performed whole-genome sequencing to elucidate the within-patient evolution of CG23-I K. pneumoniae. The maximum pairwise difference among the nine longitudinally collected isolates was five single nucleotide polymorphisms. One of the mutations was at the Asp87 position of GyrA....	pmid:36129301 doi:10.1128/spectrum.02077-22	Wed, 21 Sep 2022 06:00:00 -0400

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11	pubmed:36129636	<a href="#">Single-cell profile of tumor and immune cells in primary breast cancer, sentinel lymph node, and metastatic lymph node</a>	Ning Liao Cheukfai Li Li Cao Yanhua Chen Chongyang Ren Xiaoqing Chen Hsiaopei Mok Lingzhu Wen Kai Li Yulei Wang Yuchen Zhang Yingzi Li Jiaoyi Lv Fangrong Cao Yuting Luo Hongrui Li Wendy Wu Charles M Balch Armando E Giuliano	PURPOSE: Little is known about the host-tumor interaction in the lymph-node basin at a single cell level. This study examines single cell sequences in breast cancer nodal metastases of a patient with triple-negative breast cancer.	pmid:36129636 doi:10.1007/s12282-022-01400-x	Wed, 21 Sep 2022 06:00:00 -0400
12	pubmed:36129760	<a href="#">Unraveling unique features of plasma cell clones in POEMS syndrome by single-cell analysis</a>	Yusuke Isshiki Motohiko Oshima Naoya Mimura Kensuke Kayamori Yurie Miyamoto-Nagai Masahide Seki Yaeko Nakajima-Takagi Takashi Kanamori Eisuke Iwamoto Tomoya Muto Shokichi Tsukamoto Yusuke Takeda Chikako Ohwada Sonoko Misawa Jun-Ichiro Ikeda Masashi Sanada Satoshi Kuwabara Yutaka Suzuki Emiko Sakaida Chiaki Nakaseko Atsushi Iwama	POEMS syndrome is a rare monoclonal plasma cell disorder with unique symptoms distinct from other plasma cell neoplasms, including high serum VEGF levels. Since the prospective isolation of POEMS clones has not yet been successful, their real nature remains unclear. We herein performed the single-cell RNA sequencing of bone marrow plasma cells from patients with POEMS syndrome and identified POEMS clones that had immunoglobulin light chain (IGL) sequences (IGLV1-36, 40, 44, and 47) with amino...	pmid:36129760 doi:10.1172/jci.insight.151482	Wed, 21 Sep 2022 06:00:00 -0400
13	pubmed:36129833	<a href="#">Cancer-associated fibroblasts subtypes and role in invasion and metastasis of gastric cancer</a>	Meng Zhang Wen-Bin Guan Jun-Lei Li Ling-Xuan Li Ke-Zhou Wang Rui-Fen Wang Li-Feng Wang	Gastric cancer (GC) is the fifth most common malignancy and the fourth leading cause of cancer-related death worldwide. Cancer-associated fibroblasts (CAFs), an important cell type in the tumor microenvironment, play an important role in GC development. In this review, we describe the current knowledge of CAFs' heterogeneity and their role in GC invasion and metastasis. Currently, CAF-targeted cancer therapies are being rapidly explored and developed. However, the heterogeneity of CAFs limits...	pmid:36129833 doi:10.4149/neo_2022_220513N511	Wed, 21 Sep 2022 06:00:00 -0400

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14	pubmed:36130266	<a href="#">HTCA: a database with an in-depth characterization of the single-cell human transcriptome</a>	Lu Pan Shaobo Shan Roman Tremmel Weiyuan Li Zehuan Liao Hangyu Shi Qishuang Chen Xiaolu Zhang Xuexin Li	Single-cell RNA-sequencing (scRNA-seq) is one of the most used single-cell omics in recent decades. The exponential growth of single-cell data has immense potential for large-scale integration and in-depth explorations that are more representative of the study population. Efforts have been made to consolidate published data, yet extensive characterization is still lacking. Many focused on raw-data database constructions while others concentrate mainly on gene expression queries. Hereby, we...	pmid:36130266 doi:10.1093/nar/gkac791	Wed, 21 Sep 2022 06:00:00 -0400
15	pubmed:36130281	<a href="#">Integrated analysis of multimodal single-cell data with structural similarity</a>	Yingxin Cao Laiyi Fu Jie Wu Qinke Peng Qing Nie Jing Zhang Xiaohui Xie	Multimodal single-cell sequencing technologies provide unprecedented information on cellular heterogeneity from multiple layers of genomic readouts. However, joint analysis of two modalities without properly handling the noise often leads to overfitting of one modality by the other and worse clustering results than vanilla single-modality analysis. How to efficiently utilize the extra information from single cell multi-omics to delineate cell states and identify meaningful signal remains as a...	pmid:36130281 doi:10.1093/nar/gkac781	Wed, 21 Sep 2022 06:00:00 -0400