

single cell sequencing

NCT Number		Title	Authors	Description	Identifier	Dates
1	pubmed:36116170	Chemically-induced osteogenic cells for bone tissue engineering and disease modeling	Ji-Young Yoon Nandin Mandakhbayar Jeongeun Hyun Dong Suk Yoon Kapil D Patel Keunsoo Kang Ho-Shup Shim Hae-Hyoung Lee Jung-Hwan Lee Kam W Leong Hae-Won Kim	Cell reprogramming can satisfy the demands of obtaining specific cell types for applications such as tissue regeneration and disease modeling. Here we report the reprogramming of human fibroblasts to produce chemically-induced osteogenic cells (ciOG), and explore the potential uses of ciOG in bone repair and disease treatment. A chemical cocktail of RepSox, forskolin, and phenamil was used for osteogenic induction of fibroblasts by activation of RUNX2 expression. Following a maturation, the...	pmid:36116170 doi:10.1016/j.biomaterials.2022.121792	Sun, 18 Sep 2022 06:00:00 -0400
2	pubmed:36116238	Single-nucleus RNA Sequencing reveals the mechanism of cigarette smoke exposure on diminished ovarian reserve in mice	Fang Li Ying Wang Mengting Xu Nengyin Hu Jianing Miao Yanhui Zhao Lili Wang	The systematic toxicological mechanism of cigarette smoke (CS) on ovarian reserve has not been extensively investigated. Female 8-week-old C57BL/6 mice at peak fertility were exposed to CS or indoor air only for 30 days (100 mice per group) and the effects of CS on ovarian reserve were assessed using Single-Nucleus RNA Sequencing (snRNA-seq). In addition, further biochemical experiments, including immunohistochemical staining, ELISA, immunofluorescence staining, transmission electron microscopy,...	pmid:36116238 doi:10.1016/j.ecoenv.2022.114093	Sun, 18 Sep 2022 06:00:00 -0400
3	pubmed:36116507	CD8+ T lymphocytes in hypopigmented mycosis fungoides: malignant cells or reactive clone?	Simon Cao Oleg Kruglov Oleg E Akilov	No abstract	pmid:36116507 doi:10.1016/j.jid.2022.08.047	Sun, 18 Sep 2022 06:00:00 -0400
4	pubmed:36117173	Single-cell and WGCNA uncover a prognostic model and potential oncogenes in colorectal cancer	Ziyang Di Sicheng Zhou Gaoran Xu Lian Ren Chengxin Li Zheyu Ding Kaixin Huang Leilei Liang Yihang Yuan	CONCLUSIONS: We constructed a risk model to predict the prognosis of CRC patients based on scRNA-seq and bulk RNA-seq data, which could be used for clinical application. We also identified 4 previously unreported model genes (MPZ, SCARA3, MPP2 and PBXIP1) as novel oncogenes in CRC. These results suggest that this model could potentially be used to evaluate the prognostic risk and provide potential therapeutic targets for CRC patients.	pmid:36117173 doi:10.1186/s12575-022-00175-x	Sun, 18 Sep 2022 06:00:00 -0400
5	pubmed:36117858	Single-cell analysis of gene expression in the substantia nigra pars compacta of a pesticide-induced mouse model of Parkinson's disease	Arshad H Khan Lydia K Lee Desmond J Smith	Exposure to pesticides in humans increases the risk of Parkinson's disease (PD), but the mechanisms remain poorly understood. To elucidate these pathways, we dosed C57BL/6J mice with a combination of the pesticides maneb and paraquat. Behavioral analysis revealed motor deficits consistent with PD. Single-cell RNA sequencing of substantia nigra pars compacta revealed both cell-type-specific genes and genes expressed differentially between pesticide and control, including Fam241b, Emx2os, Bivm,...	pmid:36117858 pmc:PMC9438968 doi:10.1515/tnsci-2022-0237	Mon, 19 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
6	pubmed:36118031	Acquisition of resistance to ceftazidime-avibactam during infection treatment in <i>Pseudomonas aeruginosa</i> through D179Y mutation in one of two <i>bla</i>_{KPC-2} gene copies without losing carbapenem resistance	Patricia García Bárbara Brito Manuel Alcalde-Rico José M Munita Jose R W Martínez Jorge Olivares-Pacheco Valeria Quiroz Aniela Wozniak	Ceftazidime/Avibactam (CAZ/AVI) is frequently used to treat KPC-producing <i>Pseudomonas aeruginosa</i> (KPC-PA) and Enterobacterales. CAZ/AVI resistance is driven by several mechanisms. In <i>P. aeruginosa</i> this mainly occurs through alteration of AmpC, porins, and/or efflux pump overexpression, whereas in Enterobacterales it frequently occurs through D179Y substitution in the active site of KPC enzyme. This aminoacid change abolishes AVI binding to the KPC active site, hence inhibition is impaired....	pmid:36118031 pmc:PMC9478442 doi:10.3389/fcimb.2022.981792	Mon, 19 Sep 2022 06:00:00 -0400
7	pubmed:36118132	Clinicopathologic Characteristics and Outcomes for Patients With <i>KRAS</i> G12D-Mutant NSCLC	Alissa J Cooper Alona Muzikansky Jochen Lennerz Farhaana Narinesingh Mari Mino-Kenudson Yin P Hung Zofia Piotrowska Ibiayi Dagogo-Jack Lecia V Sequist Justin F Gainor Jessica J Lin Rebecca S Heist	CONCLUSIONS: Co-occurring mutations were common in patients with <i>KRAS</i> G12D-mutant NSCLC. STK11 and KEAP1 co-mutations were associated with worse clinical outcomes, whereas co-occurring TP53 did not affect survival.	pmid:36118132 pmc:PMC9471201 doi:10.1016/j.jtocr.2022.100390	Mon, 19 Sep 2022 06:00:00 -0400
8	pubmed:36119025	High-throughput sequencing unravels the cell heterogeneity of cerebrospinal fluid in the bacterial meningitis of children	Haihan Xiao Haijuan Xiao Yun Zhang Lingyun Guo Zhenzhen Dou Linlin Liu Liang Zhu Wenya Feng Bing Liu Bing Hu Tianming Chen Gang Liu Tingyi Wen	Bacterial meningitis (BM) is a common life-threatening infection in children that occurs in the central nervous system (CNS). The cytologic examination of cerebrospinal fluid (CSF) is a key parameter in the diagnosis of BM, but the heterogeneity of cells in the CSF has not been elucidated, which limits the current understanding of BM neuroinflammation. In this study, CSF samples were collected from a number of BM patients who were in different stages of disease progression. Single-cell...	pmid:36119025 pmc:PMC9478118 doi:10.3389/fimmu.2022.872832	Mon, 19 Sep 2022 06:00:00 -0400
9	pubmed:36119084	Integrated multi-omics reveals the activated retinal microglia with intracellular metabolic reprogramming contributes to inflammation in STZ-induced early diabetic retinopathy	Kangjia Lv Hui Ying Guangyi Hu Jing Hu Qizhi Jian Fang Zhang	Diabetic retinopathy (DR) is the leading cause of visual impairment and blindness among working-age people. Inflammation is recognized as a critical driver of the DR process. However, the main retina-specific cell type producing pro-inflammatory cytokines and its mechanism underlying DR are still unclear. Here, we used single-cell sequencing to identify microglia with metabolic pathway alterations that were the main source of IL-1 in STZ-induced DR mice. To profile the full extent of local...	pmid:36119084 pmc:PMC9479211 doi:10.3389/fimmu.2022.942768	Mon, 19 Sep 2022 06:00:00 -0400
10	pubmed:36119086	MS4A6A is a new prognostic biomarker produced by macrophages in glioma patients	Chunyu Zhang Haitao Liu Yinqiu Tan Yang Xu Yuntao Li Shiao Tong Sheng Qiu Qianxue Chen Zhongzhou Su Daofeng Tian Wei Zhou Chunlong Zhong	MS4A6A has been recognized as being associated with aging and the onset of neurodegenerative disease. However, the mechanisms of MS4A6A in glioma biology and prognosis are ill-defined. Here, we show that MS4A6A is upregulated in glioma tissues, resulting in unfavorable clinical outcomes and poor responses to adjuvant chemotherapy. Multivariate Cox regression analysis suggested that MS4A6A expression can act as a strong and independent predictor for glioma outcomes (CGGA1: HR: 1.765, p	pmid:36119086 pmc:PMC9472524 doi:10.3389/fimmu.2022.865020	Mon, 19 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
11	pubmed:36119528	Tumor vessel co-option: The past & the future	Anne Cuypers Anh-Co Khanh Truong Lisa M Becker Paula Saavedra-García Peter Carmeliet	Tumor vessel co-option (VCO) is a non-angiogenic vascularization mechanism that is a possible cause of resistance to anti-angiogenic therapy (AAT). Multiple tumors are hypothesized to primarily rely on growth factor signaling-induced sprouting angiogenesis, which is often inhibited during AAT. During VCO however, tumors invade healthy tissues by hijacking pre-existing blood vessels of the host organ to secure their blood and nutrient supply. Although VCO has been described in the context of AAT...	pmid:36119528 pmc:PMC9472251 doi:10.3389/fonc.2022.965277	Mon, 19 Sep 2022 06:00:00 -0400
12	pubmed:36120466	Identification of a novel histone phosphorylation prognostic signature in hepatocellular carcinoma based on bulk and single-cell RNA sequencing	Lei Fan Ling Xu Shan Tian Xin Zheng	CONCLUSION: HPR genes risk score is closely related to the prognosis of HCC, tumor immune process and tumor cell progression.	pmid:36120466 pmc:PMC9470838 doi:10.3389/fendo.2022.965445	Mon, 19 Sep 2022 06:00:00 -0400
13	pubmed:36120564	Assessing kidney development and disease using kidney organoids and CRISPR engineering	Wajima Safi Andrés Marco Daniel Moya Patricia Prado Elena Garreta Nuria Montserrat	The differentiation of human pluripotent stem cells (hPSCs) towards organoids is one of the biggest scientific advances in regenerative medicine. Kidney organoids have not only laid the groundwork for various organ-like tissue systems but also provided insights into kidney embryonic development. Thus, several protocols for the differentiation of renal progenitors or mature cell types have been established. Insights into the interplay of developmental pathways in nephrogenesis and determination...	pmid:36120564 pmc:PMC9479189 doi:10.3389/fcell.2022.948395	Mon, 19 Sep 2022 06:00:00 -0400
14	pubmed:36121845	Analysis of low-level somatic mosaicism reveals stage and tissue-specific mutational features in human development	Ja Hye Kim Shinwon Hwang Hyeonju Son Dongsun Kim Il Bin Kim Myeong-Heui Kim Nam Suk Sim Dong-Seok Kim Yoo-Jin Ha Junehawk Lee Hoon-Chul Kang Jeong Ho Lee Sangwoo Kim	Most somatic mutations that arise during normal development are present at low levels in single or multiple tissues depending on the developmental stage and affected organs. However, the effect of human developmental stages or mutations of different organs on the features of somatic mutations is still unclear. Here, we performed a systemic and comprehensive analysis of low-level somatic mutations using deep whole-exome sequencing (average read depth ~500×) of 498 multiple organ tissues with...	pmid:36121845 doi:10.1371/journal.pgen.1010404	Mon, 19 Sep 2022 06:00:00 -0400
15	pubmed:36122177	Effects of Piperonyl Butoxide on the Accumulation of Lipid and the Transcript Levels of <i>DtMFP</i> in <i>Dunaliella tertiolecta</i>	Jv-Liang Dai De-Xing Song Hao-Hong Chen Ming-Hua Liang Jian-Guo Jiang	As one of the sources of biodiesel, microalgae are expected to solve petroleum shortage. In this study, different concentrations of piperonyl butoxide were added to the culture medium to investigate their effects on the growth, pigment content, lipid accumulation, and content of carotenoids in <i>Dunaliella tertiolecta</i> . The results showed that piperonyl butoxide addition significantly decreased the biomass, chlorophyll content, and total carotenoid content but hugely increased the lipid...	pmid:36122177 doi:10.1021/acs.jafc.2c03006	Mon, 19 Sep 2022 06:00:00 -0400

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16	pubmed:36122307	Natural coevolution of tumor and immunoenvironment in glioblastoma	Lingxiang Wu Wei Wu Junxia Zhang Zheng Zhao Liangyu Li Mengyan Zhu Min Wu Fan Wu Fengqi Zhou Yuxin Du Rui-Chao Chai Wei Zhang Xiaoguang Qiu Quanzhong Liu Ziyu Wang Jie Li Kening Li Apeng Chen Yinan Jiang Xiangwei Xiao Han Zou Rashmi Srivastava Tingting Zhang Yun Cai Yuan Liang Bin Huang Ruohan Zhang Fan Lin Lang Hu Xiuxing Wang Xu Qian Sali Lv Baoli Hu Siyuan Zheng Zhibin Hu Hongbing Shen Yongping You Roel Gw Verhaak Tao Jiang Qianghu Wang	IDH wild-type glioblastoma (GBM) has a dismal prognosis. A better understanding of tumor evolution holds the key to developing more effective treatment. Here we study glioblastoma's natural evolutionary trajectory by using rare, multifocal samples. We sequenced 61,062 single cells from eight multifocal IDH wild-type primary GBMs and defined a natural evolution signature (NES) of the tumor. We show that the NES significantly associates with the activation of transcription factors that regulate...	pmid:36122307 doi:10.1158/2159-8290.CD-22-0196	Mon, 19 Sep 2022 06:00:00 -0400
17	pubmed:36122410	Immune phenotypes and target antigens of clonally expanded bone marrow T cells in treatment-naïve multiple myeloma	Carlotta Welters María Fernanda Lammoglia Cobo Christian Alexander Stein Meng Tung Hsu Amin Ben Hamza Livius Penter Xiaojing Chen Christopher Buccitelli Oliver Popp Philipp Mertins Kerstin Dietze Lars Bullinger Andreas Moosmann Eric Blanc Dieter Beule Armin Gerbitz Julian Strobel Holger Hackstein Hans-Peter Rahn Klaus Dornmair Thomas Blankenstein Leo Hansmann	Multiple myeloma is a hematologic malignancy of monoclonal plasma cells that accumulate in the bone marrow. Despite their clinical and pathophysiological relevance, the roles of bone marrow infiltrating T cells in treatment-naïve patients are incompletely understood. We investigated whether clonally expanded T cells i) were detectable in multiple myeloma bone marrow, ii) showed characteristic immune phenotypes, and iii) whether dominant clones recognized antigens selectively presented on...	pmid:36122410 doi:10.1158/2326-6066.CIR-22-0434	Mon, 19 Sep 2022 06:00:00 -0400