

single cell sequencing

NCT Number		Title	Authors	Description	Identifier	Dates
1	pubmed:36098604	Molecular mechanisms of male infertility: main directions of scientific research	S N Galimov Yu Yu Gromenko E F Galimova E S Bodrova K V Bulygin P F Litvitsky	This review provides up-to-date information on the molecular basis of the pathogenesis of male infertility at the cellular and subcellular levels. The emphasis is on the importance of new next-generation sequencing technologies as a high-performance tool for studying the genome and epigenomic mechanisms, transcriptome, proteome and metabolome of ejaculate, and organs of the reproductive system. This methodology made it possible to identify differentially expressed metabolic and signaling...	pmid:36098604	Tue, 13 Sep 2022 06:00:00 -0400
2	pubmed:36103820	Adipocyte mesenchymal transition contributes to mammary tumor progression	Qingzhang Zhu Yi Zhu Chelsea Hepler Qianbin Zhang Jiyoung Park Christy Gliniak Gervaise H Henry Clair Crewe Dawei Bu Zhuzhen Zhang Shangang Zhao Thomas Morley Na Li Dae-Seok Kim Douglas Strand Yingfeng Deng Jacob J Robino Oleg Varlamov Ruth Gordillo Mikhail G Kolonin Christine M Kusminski Rana K Gupta Philipp E Scherer	Obesity is associated with increased cancer incidence and progression. However, the relationship between adiposity and cancer remains poorly understood at the mechanistic level. Here, we report that adipocytes from tumor-invasive mammary fat undergo de-differentiation to fibroblast-like precursor cells during tumor progression and integrate into the tumor microenvironment. Single-cell sequencing reveals that these de-differentiated adipocytes lose their original identities and transform into...	pmid:36103820 doi:10.1016/j.celrep.2022.111362	Wed, 14 Sep 2022 06:00:00 -0400
3	pubmed:36103836	Mimicry of embryonic circulation enhances the hoxa hemogenic niche and human blood development	Jingjing Li Osmond Lao Freya F Bruveris Liyuan Wang Kajal Chaudry Ziqi Yang Nona Farbehi Elizabeth S Ng Edouard G Stanley Richard P Harvey Andrew G Elefanty Robert E Nordon	Precursors of the adult hematopoietic system arise from the aorta-gonad-mesonephros (AGM) region shortly after the embryonic circulation is established. Here, we develop a microfluidic culture system to mimic the primitive embryonic circulation and address the hypothesis that circulatory flow and shear stress enhance embryonic blood development. Embryonic (HOXA^(+)) hematopoiesis was derived from human pluripotent stem cells and induced from mesoderm by small-molecule manipulation of TGF- and...	pmid:36103836 doi:10.1016/j.celrep.2022.111339	Wed, 14 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
4	pubmed:36104333	Single-cell profiling reveals molecular basis of malignant phenotypes and tumor microenvironments in small bowel adenocarcinomas	Jingwei Yang Xin Zhou Ji Dong Wendong Wang Yongqu Lu Yuan Gao Yu Zhang Yunuo Mao Junpeng Gao Wei Wang Qingqing Li Shuai Gao Lu Wen Wei Fu Fuchou Tang	Small bowel adenocarcinomas (SBAs) are rare malignant tumors with a high mortality rate, and their molecular characteristics are still largely unexplored. Here we performed single-cell RNA sequencing for tumor samples from 12 SBA patients and predicted drug candidates for SBA. We identified four prevalent subtypes of malignant cells with distinct signatures including cell cycle program, mitochondria program, metabolism program and epithelial-mesenchymal transition (EMT) program. The progression...	pmid:36104333 doi:10.1038/s41421-022-00434-x	Wed, 14 Sep 2022 06:00:00 -0400
5	pubmed:36104364	A LILRB1 variant with a decreased ability to phosphorylate SHP-1 leads to autoimmune diseases	Thivaratana Sinthuwiat Supranee Buranapraditkun Wuttichart Kamolvisit Siraprapa Tongkobpetch Wanna Chetruengchai Chalurmpon Srichomthong Adjima Assawapitaksakul Chureerat Phokaew Patipark Kueanjinda Tanapat Palaga Tadech Boonpiyathad Kanya Suphapeetiporn Nattiya Hirankarn Vorasuk Shotelersuk	Inborn errors of immunity are known to cause not only immunodeficiencies and allergies but also autoimmunity. Leukocyte immunoglobulin-like receptor B1 (LILRB1) is a receptor on leukocytes playing a role in regulating immune responses. No phenotypes have been reported to be caused by germline mutations in LILRB1. We aimed to identify the causative variant in a three-generation family with nine members suffering from one of the three autoimmune diseases-Graves' disease, Hashimoto's thyroiditis,...	pmid:36104364 doi:10.1038/s41598-022-19334-x	Wed, 14 Sep 2022 06:00:00 -0400
6	pubmed:36104423	Oral microbial extracellular DNA initiates periodontitis through gingival degradation by fibroblast-derived cathepsin K in mice	Takeru Kondo Hiroko Okawa Akishige Hokugo Bhumika Shokeen Oskar Sundberg Yiying Zheng Charles E McKenna Renate Lux Ichiro Nishimura	Periodontitis is a highly prevalent disease leading to uncontrolled osteoclastic jawbone resorption and ultimately edentulism; however, the disease onset mechanism has not been fully elucidated. Here we propose a mechanism for initial pathology based on results obtained using a recently developed Osteoadsorptive Fluogenic Sentinel (OFS) probe that emits a fluorescent signal triggered by cathepsin K (Ctsk) activity. In a ligature-induced mouse model of periodontitis, a strong OFS signal is...	pmid:36104423 doi:10.1038/s42003-022-03896-7	Wed, 14 Sep 2022 06:00:00 -0400
7	pubmed:36104507	CRISPR FISHer enables high-sensitivity imaging of nonrepetitive DNA in living cells through phase separation-mediated signal amplification	Xin-Yuan Lyu Yuan Deng Xiao-Yan Huang Zhen-Zhen Li Guo-Qing Fang Dong Yang Feng-Liu Wang Wang Kang En-Zhi Shen Chun-Qing Song	The dynamic three-dimensional structures of chromatin and extrachromosomal DNA molecules regulate fundamental cellular processes and beyond. However, the visualization of specific DNA sequences in live cells, especially nonrepetitive sequences accounting for most of the genome, is still vastly challenging. Here, we introduce a robust CRISPR-mediated fluorescence in situ hybridization amplifier (CRISPR FISHer) system, which exploits engineered sgRNA and protein trimerization domain-mediated,...	pmid:36104507 doi:10.1038/s41422-022-00712-z	Wed, 14 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
8	pubmed:36104692	Single-cell analysis of menstrual endometrial tissues defines phenotypes associated with endometriosis	Andrew J Shih Robert P Adelson Himanshu Vashistha Houman Khalili Ashima Nayyar Radha Puran Rixsi Herrera Prodyot K Chatterjee Annette T Lee Alexander M Truskinovsky Kristine Elmaliki Margaret DeFranco Christine N Metz Peter K Gregersen	CONCLUSIONS: We propose that characterization of endometrial tissues in ME will provide an effective screening tool for identifying endometriosis in patients with chronic symptoms suggestive of this disorder. This constitutes a major advance, since delayed diagnosis for many years is a major clinical problem in the evaluation of these patients. Comprehensive analysis of ME is expected to lead to new diagnostic and therapeutic approaches to endometriosis and other associated reproductive...	pmid:36104692 doi:10.1186/s12916-022-02500-3	Wed, 14 Sep 2022 06:00:00 -0400
9	pubmed:36105026	Dexlansoprazole prevents pulmonary artery hypertension by inhibiting pulmonary artery smooth muscle cell to fibroblast transition	Qian Jiao Fangdi Zou Shiliang Li Jiawen Wang Yunping Xiao Zhihua Guan Liang Dong Jinwei Tian Shengqing Li Rui Wang Jian Zhang Honglin Li	CONCLUSIONS: Dexlansoprazole can prevent PAH through promoting cGMP generation and inhibiting pulmonary vascular remodeling through restraining PSMCs' proliferation, migration, and phenotypic transition to fibroblast-like cells. Consequently, PAH might be a new indication for dexlansoprazole.	pmid:36105026 pmc:PMC9452313	Thu, 15 Sep 2022 06:00:00 -0400
10	pubmed:36105110	Analyzing network diversity of cell-cell interactions in COVID-19 using single-cell transcriptomics	Xinyi Wang Axel A Almet Qing Nie	Cell-cell interactions (CCI) play significant roles in manipulating biological functions of cells. Analyzing the differences in CCI between healthy and diseased conditions of a biological system yields greater insight than analyzing either conditions alone. There has been a recent and rapid growth of methods to infer CCI from single-cell RNA-sequencing (scRNA-seq), revealing complex CCI networks at a previously inaccessible scale. However, the majority of current CCI analyses from scRNA-seq data...	pmid:36105110 pmc:PMC9465179 doi:10.3389/fgene.2022.948508	Thu, 15 Sep 2022 06:00:00 -0400
11	pubmed:36105400	Classification of pyroptosis patterns and construction of a novel prognostic model for prostate cancer based on bulk and single-cell RNA sequencing	Jianhan Fu Guoqiang Li Ruixiang Luo Zhijie Lu Yinhuai Wang	CONCLUSION: We have constructed a robust pyroptosis-related signature to predict the RFS of PCa patients and described the heterogeneity of prostate cancer cells in terms of pyroptosis.	pmid:36105400 pmc:PMC9465051 doi:10.3389/fendo.2022.1003594	Thu, 15 Sep 2022 06:00:00 -0400
12	pubmed:36105798	Systematic identification of cancer-associated-fibroblast-derived genes in patients with colorectal cancer based on single-cell sequencing and transcriptomics	Jia Zhao Ying Chen	Colorectal cancer (CRC) has a high incidence rate and poor prognosis, and the available treatment approaches have limited therapeutic benefits. Therefore, understanding the underlying mechanisms of occurrence and development is particularly crucial. Increasing attention has been paid to the pathophysiological role of cancer-associated fibroblasts (CAFs) in the heterogeneous tumour microenvironment. CAFs play a crucial role in tumorigenesis, tumour progression and treatment response. However,...	pmid:36105798 pmc:PMC9465173 doi:10.3389/fimmu.2022.988246	Thu, 15 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
13	pubmed:36105804	Single-cell gene expression analysis of cryopreserved equine bronchoalveolar cells	Sophie E Sage Pamela Nicholson Laureen M Peters Tosso Leeb Vidhya Jagannathan Vinzenz Gerber	The transcriptomic profile of a cell population can now be studied at the cellular level using single-cell mRNA sequencing (scRNA-seq). This novel technique provides the unprecedented opportunity to explore the cellular composition of the bronchoalveolar lavage fluid (BALF) of the horse, a species for which cell type markers are poorly described. Here, scRNA-seq technology was applied to cryopreserved equine BALF cells. Analysis of 4,631 cells isolated from three asthmatic horses in remission...	pmid:36105804 pmc:PMC9467276 doi:10.3389/fimmu.2022.929922	Thu, 15 Sep 2022 06:00:00 -0400
14	pubmed:36105817	Primitive genotypic characteristics in umbilical cord neutrophils identified by single-cell transcriptome profiling and functional prediction	Yi Chen Jiamin Huang Zaiwen Guo Zhechen Zhu Yiming Shao Linbin Li Yunxi Yang Yanzhen Yu Lu Liu Bingwei Sun	The function and heterogeneity of neutrophils in neonatal umbilical cord blood (UCB) have not been characterized. In this study, we analyzed the neutrophils in UCB and healthy adults using single-cell RNA sequencing analysis for the first time. We found that neutrophils divided into six subpopulations (G2, G3, G4, G5a, G5b, and G5c) with different marker genes and different functions under homeostasis. Compared with healthy adults, neutrophils of UCB were more naïve and have more obvious...	pmid:36105817 pmc:PMC9464600 doi:10.3389/fimmu.2022.970909	Thu, 15 Sep 2022 06:00:00 -0400
15	pubmed:36106744	DNA Methyltransferase Regulates Nitric Oxide Homeostasis and Virulence in a Chronically Adapted Pseudomonas aeruginosa Strain	Shuhong Han Jihong Liu Mianhuan Li Yizhou Zhang Xiangke Duan Yingdan Zhang Hao Chen Zhao Cai Liang Yang Yang Liu	Opportunistic pathogens such as Pseudomonas aeruginosa adapt their genomes rapidly during chronic infections. Understanding their epigenetic regulation may provide biomarkers for diagnosis and reveal novel regulatory mechanisms. We performed single-molecule real-time sequencing (SMRT-seq) to characterize the methylome of a chronically adapted P. aeruginosa clinical strain, TBCF10839. Two N-methyladenine (6mA) methylation recognition motifs (RCCANNNNNNTGAR and TRGANNNNNNTGC [modification sites...	pmid:36106744 doi:10.1128/msystems.00434-22	Thu, 15 Sep 2022 06:00:00 -0400
16	pubmed:36106829	Membrane-type 1 matrix metalloproteinase as predictor of survival and candidate therapeutic target in Ewing sarcoma	Marcus J Brookes Elizabeth A Roundhill Lee Jeys Michael Parry Susan A Burchill Kenneth S Rankin	CONCLUSIONS: MT1-MMP is expressed by ES cells, including ES-CSCs, making it a candidate therapeutic target. The level of MT1-MMP expression at diagnosis may be considered as a prognostic biomarker if validated by retrospective analysis of a larger cohort of clinical trial samples.	pmid:36106829 doi:10.1002/pbc.29959	Thu, 15 Sep 2022 06:00:00 -0400
17	pubmed:36106983	Insights into the molecular mechanisms of CRISPR/Cas9-mediated gene targeting at multiple loci in Arabidopsis	Zhengjing Zhang Wenjie Zeng Wenxin Zhang Jing Li Dali Kong Lei Zhang Rui Wang Fangnan Peng Zhe Kong Yongping Ke Heng Zhang Chanhong Kim Huiming Zhang Jose Ramón Botella Jian-Kang Zhu Daisuke Miki	Homologous recombination-mediated gene targeting (GT) enables precise sequence knock-in or sequence replacement, and thus is a powerful tool for heritable precision genome engineering. We recently established a CRISPR/Cas9-mediated approach for heritable GT in Arabidopsis (Arabidopsis thaliana), but its broad utility was not tested, and the underlying molecular mechanism was unclear. Here, we achieved precise GT at 14 out of 27 tested endogenous target loci using the sequential transformation...	pmid:36106983 doi:10.1093/plphys/kiac431	Thu, 15 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
18	pubmed:36107206	Elevating microglia TREM2 reduces amyloid seeding and suppresses disease-associated microglia	Na Zhao Wenhui Qiao Fuyao Li Yingxue Ren Jiaying Zheng Yuka A Martens Xusheng Wang Ling Li Chia-Chen Liu Kai Chen Yiyang Zhu Tadafumi C Ikezu Zonghua Li Axel D Meneses Yunjung Jin Joshua A Knight Yixing Chen Ligia Bastea Cynthia Linares Berkiye Sonustun Lucy Job Madeleine L Smith Manling Xie Yong U Liu Anthony D Umpierre Koichiro Haruwaka Zachary S Quicksall Peter Storz Yan W Asmann Long-Jun Wu Guojun Bu	TREM2 is exclusively expressed by microglia in the brain and is strongly linked to the risk for Alzheimer's disease (AD). As microglial responses modulated by TREM2 are central to AD pathogenesis, enhancing TREM2 signaling has been explored as an AD therapeutic strategy. However, the effective therapeutic window targeting TREM2 is unclear. Here, by using microglia-specific inducible mouse models overexpressing human wild-type TREM2 (TREM2-WT) or R47H risk variant (TREM2-R47H), we show that...	pmid:36107206 doi:10.1084/jem.20212479	Thu, 15 Sep 2022 06:00:00 -0400
19	pubmed:36107342	CRISPR-Cas9-Mediated Knock-In Approach to Insert the GFP₁₁ Tag into the Genome of a Human Cell Line	Ryo Tamura Daichi Kamiyama	The protocol in this chapter describes a method to label endogenous proteins using a self-complementing split green fluorescent protein (split GFP(1-10/11)) in a human cell line. By directly delivering Cas9/sgRNA ribonucleoprotein (RNP) complexes through nucleofection, this protocol allows for the efficient integration of GFP(11) into a specific genomic locus via CRISPR-Cas9-mediated homology-directed repair (HDR). We use the GFP(11) sequence in the form of a single-stranded DNA (ssDNA) as an...	pmid:36107342 doi:10.1007/978-1-0716-2667-2_8	Thu, 15 Sep 2022 06:00:00 -0400
20	pubmed:36107373	General guidelines for CRISPR/Cas-based genome editing in plants	Emre Aksoy Kubilay Yildirim Musa Kavas Ceyhun Kayihan Bayram Ali Yerlikaya Irmak Çalik Ikay Sevgen Ufuk Demirel	CRISPR (clustered regularly interspaced short palindromic repeats)/Cas (CRISPR-associated) technology is a versatile genome editing tool that has been used to improve agriculturally important plant traits. Due to its precision, CRISPR/Cas9 is more effective than either conventional plant breeding methods or standard genetic engineering approaches for the rapid development of new varieties resilient to climate change. In addition to knowledge in tissue culture-based plant transformation,...	pmid:36107373 doi:10.1007/s11033-022-07773-8	Thu, 15 Sep 2022 06:00:00 -0400

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21	pubmed:36107397	Role of lymphoid lineage cells aberrantly expressing alarmins S100A8/A9 in determining the severity of COVID-19	Joongho Lee Hanbyeol Kim Minsoo Kim Seokhyun Yoon Sanghun Lee	CONCLUSIONS: Lymphoid cells overexpressing S100A8/A9 contribute to the dysregulation of the innate immune response in patients with severe COVID-19, specifically during the early phase of infection. This study fosters a better understanding of the hyper-induction of pro-inflammatory cytokine expression and the generation of a cytokine storm in response to COVID-19 infection.	pmid:36107397 doi:10.1007/s13258-022-01285-2	Thu, 15 Sep 2022 06:00:00 -0400
22	pubmed:36107744	Scalable CRISPR-Cas9 chemical genetic screens in non-transformed human cells	Kevin Lin Ya-Chu Chang Ezequiel Marron Fernandez de Velasco Kevin Wickman Chad L Myers Anja-Katrin Bielinsky	Pooled lentiviral CRISPR-Cas9 screens are utilized for assessing the differential sensitivity or resistance of many single-gene knockouts to a compound. Here, we present a scalable approach for high-throughput compound screening by utilizing a small custom library. We describe steps to perform a proof-of-principle chemical screen in non-transformed hTERT RPE-1 TP53 ^(-/-) cells with higher coverage and greater timepoint resolution compared to genome-wide screens. This approach can be adapted for...	pmid:36107744 doi:10.1016/j.xpro.2022.101675	Thu, 15 Sep 2022 06:00:00 -0400
23	pubmed:36107768	sgcocaller and comapr: personalised haplotype assembly and comparative crossover map analysis using single-gamete sequencing data	Ruqian Lyu Vanessa Tsui Wayne Crismani Ruijie Liu Heejung Shim Davis J McCarthy	Profiling gametes of an individual enables the construction of personalised haplotypes and meiotic crossover landscapes, now achievable at larger scale than ever through the availability of high-throughput single-cell sequencing technologies. However, high-throughput single-gamete data commonly have low depth of coverage per gamete, which challenges existing gamete-based haplotype phasing methods. In addition, haplotyping a large number of single gametes from high-throughput single-cell DNA...	pmid:36107768 doi:10.1093/nar/gkac764	Thu, 15 Sep 2022 06:00:00 -0400
24	pubmed:36107780	Double-strand break toxicity is chromatin context independent	Anoek Friskes Lisa Koob Lenno Krenning Tesa M Severson Emma S Koeleman Xabier Vergara Michael Schubert Jeroen van den Berg Bastiaan Evers Anna G Manjón Stacey Joosten Yongsoo Kim Wilbert Zwart René H Medema	Cells respond to double-strand breaks (DSBs) by activating DNA damage response pathways, including cell cycle arrest. We have previously shown that a single double-strand break generated via CRISPR/Cas9 is sufficient to delay cell cycle progression and compromise cell viability. However, we also found that the cellular response to DSBs can vary, independent of the number of lesions. This implies that not all DSBs are equally toxic, and raises the question if the location of a single...	pmid:36107780 doi:10.1093/nar/gkac758	Thu, 15 Sep 2022 06:00:00 -0400
25	pubmed:36108103	The Essential Role of the Choriocapillaris in Vision: Novel Insights from Imaging and Molecular Biology	Kelly Mulfaul Jonathan F Russell Andrew P Voigt Edwin M Stone Budd A Tucker Robert F Mullins	The choriocapillaris, a dense capillary network located at the posterior pole of the eye, is essential for supporting normal vision, supplying nutrients, and removing waste products from photoreceptor cells and the retinal pigment epithelium. The anatomical location, heterogeneity, and homeostatic interactions with surrounding cell types make the choroid complex to study both in vivo and in vitro. Recent advances in single-cell RNA sequencing, in vivo imaging, and in vitro cell modeling are...	pmid:36108103 doi:10.1146/annurev-vision-100820-085958	Thu, 15 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
26	pubmed:36108145	Spatial Proteomics for Further Exploration of Missing Proteins: A Case Study of the Ovary	Loren Méar Thanadol Sutantiwanichkul Josephine Östman Pauliina Damdimopoulou Cecilia Lindskog	In the quest for "missing proteins" (MPs), the proteins encoded by the human genome still lacking evidence of existence at the protein level, novel approaches are needed to detect this challenging group of proteins. The current count stands at 1,343 MPs, and it is likely that many of these proteins are expressed at low levels, in rare cell or tissue types, or the cells in which they are expressed may only represent a small minority of the tissue. Here, we used an integrated omics approach to...	pmid:36108145 doi:10.1021/acs.jproteome.2c00392	Thu, 15 Sep 2022 06:00:00 -0400
27	pubmed:36108172	Anomalous Epithelial Variations and Ectopic Inflammatory Response in Chronic Obstructive Pulmonary Disease	Naoaki Watanabe Yu Fujita Jun Nakayama Yutaro Mori Tsukasa Kadota Yusuke Hayashi Iwao Shimomura Takashi Ohtsuka Koji Okamoto Jun Araya Kazuyoshi Kuwano Yusuke Yamamoto	Phenotypic alterations in the lung epithelium have been widely implicated in Chronic obstructive pulmonary disease (COPD) pathogenesis, but the precise mechanisms orchestrating this persistent inflammatory process remain unknown due to the complexity of lung parenchymal and mesenchymal architecture. To identify cell type-specific mechanisms and cell-cell interactions among the multiple lung resident cell types and inflammatory cells that contribute to COPD progression, we profiled 57,918 cells...	pmid:36108172 doi:10.1165/rcmb.2021-0555OC	Thu, 15 Sep 2022 06:00:00 -0400
28	pubmed:36108173	Epithelial ER Stress Enhances the Risk of Muc5b Associated Lung Fibrosis	Evgenia Dobrinskikh Corinne E Hennessy Jonathan S Kurche Eunjoo Kim Alani M Estrella Jonathan Cardwell Ivana V Yang David A Schwartz	The gain-of-function minor allele of the MUC5B promoter (rs35705950) is the strongest risk factor for idiopathic pulmonary fibrosis (IPF), a devastating fibrotic lung disease that leads to progressive respiratory failure in adults. We have previously demonstrated that Muc5b overexpression in mice worsens lung fibrosis following bleomycin exposure and have hypothesized that excess Muc5b promotes endoplasmic reticulum (ER) stress and apoptosis, stimulating fibrotic lung injury. Here, we report...	pmid:36108173 doi:10.1165/rcmb.2022-0252OC	Thu, 15 Sep 2022 06:00:00 -0400