

single cell sequencing

NCT Number		Title	Authors	Description	Identifier	Dates
1	pubmed:36049414	<a href="#">S100A10 might be a novel prognostic biomarker for head and neck squamous cell carcinoma based on bioinformatics analysis</a>	Shuo Gao Hao Zhang Linbin Lai Jiaqi Zhang Yu Li Zhiping Miao Siddiq Ur Rahman Honghao Zhang Airong Qian Wenjuan Zhang	Head and neck squamous cell carcinoma (HNSCC) is a frequent malignant tumor of the head and neck with a dismal survival probability due to relapse and metastasis. S100As have been identified as being involved in the tumor procession of various cancer types. However, the expressions of S100As in HNSCC and their prognostic relevance are unknown. Bioinformatics analysis was conducted to identify the prognostic value and function of S100As in HNSCC patients. In the study, we found that high mRNA...	pmid:36049414 doi:10.1016/j.compbimed.2022.106000	Thu, 01 Sep 2022 06:00:00 -0400
2	pubmed:36049533	<a href="#">Cellular and molecular profiles of larval and adult Xenopus corneal epithelia resolved at the single-cell level</a>	Surabhi Sonam Sushant Bangru Kimberly J Perry Ullas V Chembazhi Auinash Kalsotra Jonathan J Henry	Corneal Epithelial Stem Cells (CESCs) and their proliferative progeny, the Transit Amplifying Cells (TACs), are responsible for homeostasis and maintaining corneal transparency. Owing to our limited knowledge of cell fates and gene activity within the cornea, the search for unique markers to identify and isolate these cells remains crucial for ocular surface reconstruction. We performed single-cell RNA sequencing of corneal cells from larval and adult stages of Xenopus. Our results indicate that...	pmid:36049533 doi:10.1016/j.ydbio.2022.08.007	Thu, 01 Sep 2022 06:00:00 -0400
3	pubmed:36049643	<a href="#">Urinary single-cell sequencing captures kidney injury and repair processes in human acute kidney injury</a>	Jan Klocke Seung Joon Kim Christopher M Skopnik Christian Hinze Anastasiya Boltengagen Diana Metzke Emil Grothgar Luka Prskalo Leonie Wagner Paul Freund Nina Görlich Frédéric Muench Kai M Schmidt-Ott Mir-Farzin Mashreghi Christine Kocks Kai-Uwe Eckardt Nikolaus Rajewsky Philipp Enghard	Acute kidney injury (AKI) is a major health issue, the outcome of which depends primarily on damage and reparative processes of tubular epithelial cells. Mechanisms underlying AKI remain incompletely understood, specific therapies are lacking and monitoring the course of AKI in clinical routine is confined to measuring urine output and plasma levels of filtration markers. Here we demonstrate feasibility and potential of a novel approach to assess the cellular and molecular dynamics of AKI by...	pmid:36049643 doi:10.1016/j.kint.2022.07.032	Thu, 01 Sep 2022 06:00:00 -0400
4	pubmed:36050288	<a href="#">Quantification of mRNA in Single Cells Based on Dimerization-Induced Photoluminescence Nonblinking of Quantum Dots</a>	Jie Yang Chaoqing Dong Aidi Zhang Jicun Ren	Photoluminescence (PL) intermittency (or "blinking") is a unique characteristic of single quantum dot (QD) emission. Here, we report a novel single-molecule detection strategy for the intracellular mRNA of interest using the mRNA-induced nonblinking QD dimers as probes. The working principle of the method is that the DNA hybrid of the target DNA (or mRNA) with a biotin-modified ssDNA probe can induce two blinking streptavidin-modified QDs (SAV-QDs) conjugated. The formed QD dimer as a bright...	pmid:36050288 doi:10.1021/acs.analchem.2c02209	Thu, 01 Sep 2022 06:00:00 -0400

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5	pubmed:36050300	<a href="#">Heterogeneity and transcriptome changes of human CD8<sup>±</sup> T cells across nine decades of life</a>	Jian Lu Raheel Ahmad Thomas Nguyen Jeffrey Cifello Humza Hemani Jiangyuan Li Jinguo Chen Siyi Li Jing Wang Achouak Achour Joseph Chen Meagan Colie Ana Lustig Christopher Dunn Linda Zukley Chee W Chia Irina Burd Jun Zhu Luigi Ferrucci Nan-Ping Weng	The decline of CD8^(+) T cell functions contributes to deteriorating health with aging, but the mechanisms that underlie this phenomenon are not well understood. We use single-cell RNA sequencing with both cross-sectional and longitudinal samples to assess how human CD8^(+) T cell heterogeneity and transcriptomes change over nine decades of life. Eleven subpopulations of CD8^(+) T cells and their dynamic changes with age are identified. Age-related changes in gene expression result from changes...	pmid:36050300 doi:10.1038/s41467-022-32869-x	Thu, 01 Sep 2022 06:00:00 -0400
6	pubmed:36050550	<a href="#">Polygenic enrichment distinguishes disease associations of individual cells in single-cell RNA-seq data</a>	Martin Jinye Zhang Kangcheng Hou Kushal K Dey Saori Sakaue Karthik A Jagadeesh Kathryn Weinand Aris Taychameekiatchai Poorvi Rao Angela Oliveira Pisco James Zou Bruce Wang Michael Gandal Soumya Raychaudhuri Bogdan Pasaniuc Alkes L Price	Single-cell RNA sequencing (scRNA-seq) provides unique insights into the pathology and cellular origin of disease. We introduce single-cell disease relevance score (scDRS), an approach that links scRNA-seq with polygenic disease risk at single-cell resolution, independent of annotated cell types. scDRS identifies cells exhibiting excess expression across disease-associated genes implicated by genome-wide association studies (GWASs). We applied scDRS to 74 diseases/traits and 1.3 million...	pmid:36050550 doi:10.1038/s41588-022-01167-z	Thu, 01 Sep 2022 06:00:00 -0400
7	pubmed:36051239	<a href="#">Oral antibiotics perturbation on gut microbiota after prostate biopsy</a>	Joseph Kai Man Li Lynn Lin Wang Becky Su Yan Lau Ryan Tsz Hei Tse Carol Ka Lo Cheng Steven Chi Ho Leung Christine Yim Ping Wong Stephen Kwok Wing Tsui Jeremy Yuen Chun Teoh Peter Ka Fung Chiu Chi Fai Ng	CONCLUSION: A single dose of oral co-amoxiclav before TPPBx could have led to a change of gut microbiota that cannot be recovered in 5 weeks' time. Microbiome studies on prostate cancer patients should be cautioned on the use of post-prostate biopsy fecal sampling. Further studies should be conducted for the impact on gut microbiome for TPPBx alone.	pmid:36051239 pmc:PMC9425026 doi:10.3389/fcimb.2022.959903	Fri, 02 Sep 2022 06:00:00 -0400
8	pubmed:36051457	<a href="#">Somatic mutations in single human cardiomyocytes reveal age-associated DNA damage and widespread oxidative genotoxicity</a>	Sangita Choudhury August Yue Huang Junho Kim Zinan Zhou Katherine Morillo Eduardo A Maury Jessica W Tsai Michael B Miller Michael A Lodato Sarah Araten Nazia Hilal Eunjung Alice Lee Ming Hui Chen Christopher A Walsh	The accumulation of somatic DNA mutations over time is a hallmark of aging in many dividing and nondividing cells but has not been studied in postmitotic human cardiomyocytes. Using single-cell whole-genome sequencing, we identified and characterized the landscape of somatic single-nucleotide variants (sSNVs) in 56 single cardiomyocytes from 12 individuals (aged from 0.4 to 82 years). Cardiomyocyte sSNVs accumulate with age at rates that are faster than in many dividing cell types and...	pmid:36051457 pmc:PMC9432807 doi:10.1038/s43587-022-00261-5	Fri, 02 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
9	pubmed:36051694	<a href="#">Computational Analysis of Deleterious SNPs in NRAS to Assess Their Potential Correlation With Carcinogenesis</a>	Mohammed Y Behairy Mohamed A Soltan Mohamed S Adam Ahmed M Refaat Ehab M Ezz Sarah Albogami Eman Fayad Fayez Althobaiti Ahmed M Gouda Ashraf E Sileem Mahmoud A Elfaky Khaled M Darwish Muhammad Alaa Eldeen	The NRAS gene is a well-known oncogene that acts as a major player in carcinogenesis. Mutations in the NRAS gene have been linked to multiple types of human tumors. Therefore, the identification of the most deleterious single nucleotide polymorphisms (SNPs) in the NRAS gene is necessary to understand the key factors of tumor pathogenesis and therapy. We aimed to retrieve NRAS missense SNPs and analyze them comprehensively using sequence and structure approaches to determine the most deleterious...	pmid:36051694 pmc:PMC9424727 doi:10.3389/fgene.2022.872845	Fri, 02 Sep 2022 06:00:00 -0400
10	pubmed:36051873	<a href="#">Integrated analysis and validation reveal ACAP1 as a novel prognostic biomarker associated with tumor immunity in lung adenocarcinoma</a>	Ning Wang Lingye Zhu Xiaomei Xu Chang Yu Xiaoying Huang	ADP-ribosylation factor (Arf)-GTPase-activating protein (GAP) with coiled-coil, ankyrin repeat and PH domains 1 (ACAP1) has been reported to serve as an adaptor for clathrin coat complex playing a role in endocytic recycling and cellular migration. The potential role of ACAP1 in lung adenocarcinoma (LUAD) has not been yet completely defined. We performed the comprehensive analyses, including gene expression, survival analysis, genetic alteration, function enrichment, and immune characteristics....	pmid:36051873 pmc:PMC9403504 doi:10.1016/j.csbj.2022.08.026	Fri, 02 Sep 2022 06:00:00 -0400
11	pubmed:36051880	<a href="#">Exploring long non-coding RNA networks from single cell omics data</a>	Xue Zhao Yangming Lan Dijun Chen	Single-cell omics technologies provide an unprecedented opportunity to decipher molecular mechanisms underlying various biological processes in a cellular heterogeneity manner. The emergence of such techniques promotes the exploration of lncRNAs, which are known to be tissue- and cell-specific noncoding transcripts involving the regulation of multiple important cellular processes. In this review, we introduce the advancement of lncRNA studies which benefit from single-cell omics data analysis....	pmid:36051880 pmc:PMC9403499 doi:10.1016/j.csbj.2022.08.003	Fri, 02 Sep 2022 06:00:00 -0400
12	pubmed:36051881	<a href="#">Streptomyces coelicolor macrodomain hydrolase SCO6735 cleaves thymidine-linked ADP-ribosylation of DNA</a>	Andrea Hloušek-Kasun Petra Mikolevi Johannes Gregor Matthias Rack Callum Tromans-Coia Marion Schuller Gytis Jankevicius Marija Matkovi Branimir Bertoša Ivan Ahel Andreja Miko	ADP-ribosylation is an ancient, highly conserved, and reversible covalent modification critical for a variety of endogenous processes in both prokaryotes and eukaryotes. ADP-ribosylation targets proteins, nucleic acids, and small molecules (including antibiotics). ADP-ribosylation signalling involves enzymes that add ADP-ribose to the target molecule, the (ADP-ribosyl)transferases; and those that remove it, the (ADP-ribosyl)hydrolases. Recently, the toxin/antitoxin pair DarT/DarG composed of a...	pmid:36051881 pmc:PMC9411070 doi:10.1016/j.csbj.2022.08.002	Fri, 02 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
13	pubmed:36051886	<a href="#">Single-cell transcriptomics of neuroblastoma identifies chemoresistance-associated genes and pathways</a>	Marianna Avitabile Ferdinando Bonfiglio Vincenzo Aievola Sueva Cantalupo Teresa Maiorino Vito Alessandro Lasorsa Cinzia Domenicotti Barbara Marengo Heger Zbynk Adam Vojtch Achille Iolascon Mario Capasso	High-Risk neuroblastoma (NB) survival rate is still	pmid:36051886 pmc:PMC9418686 doi:10.1016/j.csbj.2022.08.031	Fri, 02 Sep 2022 06:00:00 -0400
14	pubmed:36052061	<a href="#">Bioinformatics analysis of potential pathogenesis and risk genes of immunoinflammation-promoted renal injury in severe COVID-19</a>	Zhimin Chen Caiming Chen Fengbin Chen Ruilong Lan Guo Lin Yanfang Xu	Renal injury secondary to COVID-19 is an important factor for the poor prognosis of COVID-19 patients. The pathogenesis of renal injury caused by aberrant immune inflammatory of COVID-19 remains unclear. In this study, a total of 166 samples from 4 peripheral blood transcriptomic datasets of COVID-19 patients were integrated. By using the weighted gene co-expression network (WGCNA) algorithm, we identified key genes for mild, moderate, and severe COVID-19. Subsequently, taking these genes as...	pmid:36052061 pmc:PMC9424635 doi:10.3389/fimmu.2022.950076	Fri, 02 Sep 2022 06:00:00 -0400
15	pubmed:36052088	<a href="#">Single-cell sequencing reveals heterogeneity between pancreatic adenosquamous carcinoma and pancreatic ductal adenocarcinoma with prognostic value</a>	Deyu Zhang Suna Wu Shubo Pan Meiqi Wang Zhen Wang Zixuan He Guanghao Zhang Fang Cui Yihang Song Wanshun Li Xiaohua Shi Haojie Huang Huanhai Xu	Pancreatic adenosquamous carcinoma (ASPC) is a rare subtype of pancreatic cancer with lethal malignancy, and few studies have focused on the heterogeneity of ASPC. Here, we performed a single-cell sequencing procedure on pancreatic tumor tissue from an ASPC patient and a patient with high-grade intraductal papillary mucinous neoplasm (IPMN). Through the combined analysis of single-cell sequencing data from five pancreatic ductal adenocarcinoma (PDAC) patients, one IPMN patient, and one ASPC...	pmid:36052088 pmc:PMC9424731 doi:10.3389/fimmu.2022.972298	Fri, 02 Sep 2022 06:00:00 -0400
16	pubmed:36052251	<a href="#">Minimal residual disease detection by next-generation sequencing in multiple myeloma: Promise and challenges for response-adapted therapy</a>	Valeria Ferla Elena Antonini Tommaso Perini Francesca Farina Serena Masottini Simona Malato Sarah Marktel Maria Teresa Lupo Stanghellini Cristina Tresoldi Fabio Ciceri Magda Marcatti	Assessment of minimal residual disease (MRD) is becoming a standard diagnostic tool for curable hematological malignancies such as chronic and acute myeloid leukemia. Multiple myeloma (MM) remains an incurable disease, as a major portion of patients even in complete response eventually relapse, suggesting that residual disease remains. Over the past decade, the treatment landscape of MM has radically changed with the introduction of new effective drugs and the availability of immunotherapy,....	pmid:36052251 pmc:PMC9426755 doi:10.3389/fonc.2022.932852	Fri, 02 Sep 2022 06:00:00 -0400
17	pubmed:36052535	<a href="#">A cohesin-associated gene score may predict immune checkpoint blockade in hepatocellular carcinoma</a>	Cui-Zhen Liu Jian-Di Li Gang Chen Rong-Quan He Rui Lin Zhi-Guang Huang Jian-Jun Li Xiu-Fang Du Xiao-Ping Lv	Stromal antigen 1 (STAG1), a component of cohesion, is overexpressed in various cancers, but it is unclear whether it has a role in the transcriptional regulation of hepatocellular carcinoma (HCC). To test this hypothesis, here, we screened global HCC datasets and performed multiscale embedded gene co-expression network analysis to identify the potential functional modules of differentially expressed STAG1 co-expressed genes. The putative transcriptional targets of STAG1 were identified using...	pmid:36052535 doi:10.1002/2211-5463.13474	Fri, 02 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
18	pubmed:36052737	<a href="#">Analysis of genetic profiling, pathomics signature, and prognostic features of primary lymphoepithelioma-like carcinoma of the renal pelvis</a>	Bo Fan Yuanbin Huang Hongshuo Zhang Tingyu Chen Shenghua Tao Xiaogang Wang Shuang Wen Honglong Wang Zhe Lin Tianqing Liu Hongxian Zhang Tao He Xiancheng Li	The genetic features of primary lymphoepithelioma-like carcinoma (LELC) of the upper urinary tract have not been systematically explored. In this study, tumor mutation profiling was performed using whole-genome sequencing in two patients with LELC of the renal pelvis. Novel candidate variants relevant to known disease genes were selected using rare-variant burden analysis. Subsequently, a population-based study was performed using the Surveillance, Epidemiology, and End Results (SEER), PubMed,...	pmid:36052737 doi:10.1002/1878-0261.13307	Fri, 02 Sep 2022 06:00:00 -0400
19	pubmed:36053749	<a href="#">Sex-Specific Responses to Slow Progressive Pressure Overload in a Large Animal Model of HFpEF</a>	Deborah M Eaton Remus M Berretta Jacqueline E Lynch Joshua G Travers Ryan D Pfeiffer Michelle L Hulke Huaqing Zhao Alexander R H Hobby Giana Schena Jaslyn Johnson Markus Wallner Edward Lau Maggie P Y Lam Kathleen C Woulfe Nathan R Tucker Timothy A McKinsey Marla R Wolfson Steven R Houser	Approximately 50% of all heart failure (HF) diagnoses can be classified as HF with preserved ejection fraction (HFpEF). HFpEF is more prevalent in females compared to males, but the underlying mechanisms are unknown. We previously showed that pressure overload (PO) in male felines induces a cardiopulmonary phenotype with essential features of human HFpEF. The goal of this study was to determine if slow progressive PO induces distinct cardiopulmonary phenotypes in females and males in the absence...	pmid:36053749 doi:10.1152/ajpheart.00374.2022	Fri, 02 Sep 2022 06:00:00 -0400
20	pubmed:36053827	<a href="#">Impact of measuring heteroplasmy of a pathogenic mitochondrial DNA variant at the single-cell level in individuals with mitochondrial disease</a>	Atsuko Imai-Okazaki Kazuhiro R Nitta Yukiko Yatsuka Ayumu Sugiura Masato Arai Masaru Shimura Tomohiro Ebihara Takanori Onuki Keiko Ichimoto Akira Ohtake Kei Murayama Yasushi Okazaki	Pathogenic mitochondrial DNA heteroplasmy has mainly been assessed with bulk sequencing in individuals with mitochondrial disease. However, the distribution of heteroplasmy at the single-cell level in skin fibroblasts obtained from individuals, together with detailed clinical and biochemical information, remains to be investigated. We used the mitochondrial DNA single-cell assay for the transposase-accessible chromatin sequencing method. Skin fibroblasts were obtained from six individuals with...	pmid:36053827 doi:10.1002/jimd.12547	Fri, 02 Sep 2022 06:00:00 -0400
21	pubmed:36053965	<a href="#">Single-cell RNA-seq reveals fate determination control of an individual fiber cell initiation in cotton (Gossypium hirsutum)</a>	Yuan Qin Mengling Sun Weiwen Li Mingqi Xu Lei Shao Yuqi Liu Guannan Zhao Zhenping Liu Zhongping Xu Jiaqi You Zhengxiu Ye Jiawen Xu Xiyan Yang Maojun Wang Keith Lindsey Xianlong Zhang Lili Tu	Cotton fiber is a unicellular seed trichome, and lint fiber initials per seed as a factor determines fiber yield. However, the mechanisms controlling fiber initiation from ovule epidermis are not understood well enough. Here, with single-cell RNA sequencing (scRNA-seq), a total of 14,535 cells were identified from cotton ovule outer integument of Xu142_LF line at four developmental stages (1.5, 1, 0.5 days before anthesis and the day of anthesis). Three major cell types, fiber, non-fiber...	pmid:36053965 doi:10.1111/pbi.13918	Fri, 02 Sep 2022 06:00:00 -0400



NCT Number		Title	Authors	Description	Identifier	Dates
22	pubmed:36054337	<a href="#">Autoreactive napsin A-specific T cells are enriched in lung tumors and inflammatory lung lesions during immune checkpoint blockade</a>	Fiamma Berner David Bomze Christa Lichtensteiger Vincent Walter Rebekka Niederer Omar Hasan Ali Nina Wyss Jens Bauer Lena Katharina Freudenmann Ana Marcu Eva-Maria Wolfschmitt Sebastian Haen Thorben Gross Marie-Therese Abdou Stefan Diem Stella Knöpfli Tobias Sinnberg Kathrin Hofmeister Hung-Wei Cheng Marieta Toma Niklas Klümper Mette-Triin Purde Oltin Tiberiu Pop Ann-Kristin Jochum Steve Pascolo Markus Joerger Martin Früh Wolfram Jochum Hans-Georg Rammensee Heinz Läubli Michael Hölzel Jacques Neefjes Juliane Walz Lukas Flatz	Cancer treatment with immune checkpoint blockade (ICB) often induces immune-related adverse events (irAEs). We hypothesized that proteins coexpressed in tumors and normal cells could be antigenic targets in irAEs and herein described DITAS (discovery of tumor-associated self-antigens) for their identification. DITAS computed transcriptional similarity between lung tumors and healthy lung tissue based on single-sample gene set enrichment analysis. This identified 10 lung tissue-specific genes...	pmid:36054337 doi:10.1126/sciimmunol.abn9644	Fri, 02 Sep 2022 06:00:00 -0400
23	pubmed:36054357	<a href="#">scAllele: A versatile tool for the detection and analysis of variants in scRNA-seq</a>	Giovanni Quinones-Valdez Ting Fu Tracey W Chan Xinshu Xiao	Single-cell RNA sequencing (scRNA-seq) data contain rich information at the gene, transcript, and nucleotide levels. Most analyses of scRNA-seq have focused on gene expression profiles, and it remains challenging to extract nucleotide variants and isoform-specific information. Here, we present scAllele, an integrative approach that detects single-nucleotide variants, insertions, deletions, and their allelic linkage with splicing patterns in scRNA-seq. We demonstrate that scAllele achieves better...	pmid:36054357 doi:10.1126/sciadv.abn6398	Fri, 02 Sep 2022 06:00:00 -0400
24	pubmed:36054525	<a href="#">Biochemical and genetic characterization of Botrytis cinerea laboratory mutants resistant to propamidine</a>	Xuhuan Zhang Ke Huang Mengwei Zhang Lin Jiang Yong Wang Juntao Feng Zhiqing Ma	CONCLUSION: These data suggested the resistance risk of B. cinerea to propamidine was low to moderate and the mechanism of propamidine was different from the existing fungicides. These results will increase fully understanding on the resistance mechanism of propamidine and provide critical basis for the rational design of pesticide molecules based on targets. This article is protected by copyright. All rights reserved.	pmid:36054525 doi:10.1002/ps.7150	Fri, 02 Sep 2022 06:00:00 -0400

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25	pubmed:36054819	<a href="#">Fc Fragment of IgE Receptor Ig (FCER1G) acts as a key gene involved in cancer immune infiltration and tumour microenvironment</a>	Riwei Yang Zude Chen Leqi Liang Shan Ao Jinhu Zhang Zhenglin Chang Zuomin Wang Yuhao Zhou Xiaolu Duan Tuo Deng	Although recent studies have revealed the relationship between Fc Fragment of IgE Receptor Ig (FCER1G) and human tumours, there is still a lack of a more comprehensive pan-cancer analysis of FCER1G as an immune-related gene. In this study, we investigated the expression pattern and prognostic value of FCER1G based on multiple databases. Subsequently, we further explored the role of FCER1G in tumour proliferation and metastasis, as well as its genomic alterations and DNA methylation levels, we...	pmid:36054819 doi:10.1111/imm.13557	Fri, 02 Sep 2022 06:00:00 -0400