

single cell sequencing

| NCT Number | | Title | Authors | Description | Identifier | Dates |
|------------|-----------------|---|---|---|---|---------------------------------|
| 1 | pubmed:36076168 | Newly reported chloroplast genome of Sinosenecio albonervius Y. Liu & Q. E. Yang and comparative analyses with other Sinosenecio species | Jing-Yi Peng Xiao-Shuang Zhang Dai-Gui Zhang Yi Wang Tao Deng Xian-Han Huang Tian-Hui Kuang Qiang Zhou | CONCLUSIONS: The complete chloroplast genome of Sinosenecio albonervius was revealed in this study, which included a comparison of Sinosenecio chloroplast genome structure, variation, and phylogenetic analysis for related species. These will help future research on Sinosenecio taxonomy, identification, origin, and evolution to some extent. | pmid:36076168 pmc:PMC9454173 doi:10.1186/s12864-022-08872-3 | Thu, 08 Sep 2022 06:00:00 -0400 |
| 2 | pubmed:36077110 | Chromosome-Level Genome Assembly of a Fragrant Japonica Rice Cultivar 'Changxianggeng 1813' Provides Insights into Genomic Variations between Fragrant and Non-Fragrant Japonica Rice | Ruisen Lu Jia Liu Xuegang Wang Zhao Song Xiangdong Ji Naiwei Li Gang Ma Xiaoqin Sun | East Asia has an abundant resource of fragrant japonica rice that is gaining increasing interest among both consumers and producers. However, genomic resources and in particular complete genome sequences currently available for the breeding of fragrant japonica rice are still scarce. Here, integrating Nanopore long-read sequencing, Illumina short-read sequencing, and Hi-C methods, we presented a high-quality chromosome-level genome assembly (~378.78 Mb) for a new fragrant japonica cultivar... | pmid:36077110 pmc:PMC9456513 doi:10.3390/ijms23179705 | Fri, 09 Sep 2022 06:00:00 -0400 |
| 3 | pubmed:36077333 | Delving into the Heterogeneity of Different Breast Cancer Subtypes and the Prognostic Models Utilizing scRNA-Seq and Bulk RNA-Seq | Jieyun Xu Shijie Qin Yunmeng Yi Hanyu Gao Xiaoqi Liu Fei Ma Miao Guan | CONCLUSIONS: Comparative analysis of the three BC subtypes based on cancer cell heterogeneity in this study will be of great clinical significance for the diagnosis, prognosis and targeted therapy for BC patients. | pmid:36077333 pmc:PMC9456551 doi:10.3390/ijms23179936 | Fri, 09 Sep 2022 06:00:00 -0400 |
| 4 | pubmed:36088998 | Single-cell RNA analysis of chemokine expression in heterogeneous CD14⁺ monocytes with lipopolysaccharide-induced bone resorption | Junpan Luo Jiarui Lu Jie Zeng Yuanyuan Ma Qimei Gong Zhuyu Wang Xiaolei Zhang Jingjing Quan | Lipopolysaccharide (LPS)-induced bone resorption has normally been found in inflammatory bone diseases, but the underlying mechanism is currently unclear. Since LPS binds to CD14 and activates Toll-like receptor 4 (TLR4) in monocytes, the present study focused on CD14 ⁽⁺⁾ monocytes and observed their responses after LPS treatment during the progression of local bone destruction. CD14 ⁽⁺⁾ monocytes were obtained from human peripheral blood mononuclear cells (PBMCs) by magnetic cell separation... | pmid:36088998 doi:10.1016/j.yexcr.2022.113343 | Sun, 11 Sep 2022 06:00:00 -0400 |
| 5 | pubmed:36089561 | Self-supervised contrastive learning for integrative single cell RNA-seq data analysis | Wenkai Han Yuqi Cheng Jiayang Chen Huawen Zhong Zhihang Hu Siyuan Chen Licheng Zong Liang Hong Ting-Fung Chan Irwin King Xin Gao Yu Li | We present a novel self-supervised Contrastive LEArning framework for single-cell ribonucleic acid (RNA)-sequencing (CLEAR) data representation and the downstream analysis. Compared with current methods, CLEAR overcomes the heterogeneity of the experimental data with a specifically designed representation learning task and thus can handle batch effects and dropout events simultaneously. It achieves superior performance on a broad range of fundamental tasks, including clustering, visualization,... | pmid:36089561 doi:10.1093/bib/bbac377 | Sun, 11 Sep 2022 06:00:00 -0400 |

| NCT Number | | Title | Authors | Description | Identifier | Dates |
|------------|-----------------|--|--|--|---|---------------------------------|
| 6 | pubmed:36089578 | Characterization of the T cell receptor repertoire and melanoma tumor microenvironment upon combined treatment with ipilimumab and hTERT vaccination | Espen Basmo Ellingsen Gergana Bounova Iliana Kerzeli Irantzu Anzar Donjete Simnica Elin Aamdal Tormod Guren Trevor Clancy Artur Mezheyeuski Else Marit Inderberg Sara M Mangsbo Mascha Binder Eivind Hovig Gustav Gaudernack | CONCLUSION: Clinical responses were observed irrespective of established predictive biomarkers for checkpoint inhibitor efficacy, indicating an added benefit of the vaccine-induced T cells. The clinical and immunological read-out warrants further investigation of UV1 in combination with checkpoint inhibitors. Trial registration Clinicaltrials.gov identifier: NCT02275416. Registered October 27, 2014. https://clinicaltrials.gov/ct2/show/NCT02275416?term=uv1&draw=2&rank=6 . | pmid:36089578 doi:10.1186/s12967-022-03624-z | Sun, 11 Sep 2022 06:00:00 -0400 |
| 7 | pubmed:36090759 | CRISPR-Cas9-directed gene tagging using a single integrase-defective lentiviral vector carrying a transposase-based Cas9 off switch | Emil Aagaard Thomsen Kristian Alsbjerg Skipper Sofie Andersen Didde Haslund Thomas Wisbech Skov Jacob Giehm Mikkelsen | Locus-directed DNA cleavage induced by the CRISPR-Cas9 system triggers DNA repair mechanisms allowing gene repair or targeted insertion of foreign DNA. For gene insertion to be successful, availability of a homologous donor template needs to be timed with cleavage of the DNA by the Cas9 endonuclease guided by a target-specific single guide RNA (sgRNA). We present a novel approach for targeted gene insertion based on a single integrase-defective lentiviral vector (IDLV) carrying a Cas9 off... | pmid:36090759 pmc:PMC9403905 doi:10.1016/j.omtn.2022.08.005 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 8 | pubmed:36090803 | Targeted therapy for pediatric diffuse intrinsic pontine glioma: a single-center experience | Giada Del Baldo Andrea Carai Rachid Abbas Antonella Cacchione Mara Vinci Valentina Di Ruscio Giovanna Stefania Colafati Sabrina Rossi Francesca Diomedi Camassei Nicola Maestro Sara Temelso Giulia Pericoli Emmanuel De Billy Isabella Giovannoni Alessia Carboni Martina Rinelli Emanuele Agolini Alan Mackay Chris Jones Silvia Chiesa Mario Balducci Franco Locatelli Angela Mastronuzzi | CONCLUSION: Despite the small simple size of our study, our data suggest a prognostic advantage and a safe profile of targeted therapies in DIPG patients, and we strongly advocate to reconsider the role of biopsy for these patients. | pmid:36090803 pmc:PMC9459464 doi:10.1177/17588359221113693 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 9 | pubmed:36090907 | ATAXIC: An Algorithm to Quantify Transcriptomic Perturbation Heterogeneity in Single Cancer Cells | Qian Liu Qiqi Lu Xiaosheng Wang | The single-cell RNA sequencing (scRNA-seq) has recently been widely utilized to quantify transcriptomic profiles in single cells of bulk tumors. The transcriptomic profiles in single cells facilitate the investigation of intratumor heterogeneity that is unlikely confounded by the nontumor components. We proposed an algorithm (ATAXIC) to quantify the heterogeneity of transcriptomic perturbations (TPs) in single cancer cells. ATAXIC calculated the TP heterogeneity level of a single cell based on... | pmid:36090907 pmc:PMC9452944 doi:10.1155/2022/4106736 | Mon, 12 Sep 2022 06:00:00 -0400 |

| NCT Number | | Title | Authors | Description | Identifier | Dates |
|------------|-----------------|--|--|---|--|---------------------------------|
| 10 | pubmed:36091018 | Bioinformatics analysis identified apolipoprotein E as a hub gene regulating neuroinflammation in macrophages and microglia following spinal cord injury | Xin-Qiang Yao Jia-Ying Chen Zi-Han Yu Zu-Cheng Huang Regan Hamel Yong-Qiang Zeng Zhi-Ping Huang Ke-Wu Tu Jun-Hao Liu Yan-Meng Lu Zhi-Tao Zhou Stefano Pluchino Qing-An Zhu Jian-Ting Chen | Macrophages and microglia play important roles in chronic neuroinflammation following spinal cord injury (SCI). Although macrophages and microglia have similar functions, their phagocytic and homeostatic abilities differ. It is difficult to distinguish between these two populations in vivo, but single-cell analysis can improve our understanding of their identity and heterogeneity. We conducted bioinformatics analysis of the single-cell RNA sequencing dataset GSE159638, identifying apolipoprotein... | pmid:36091018 pmc:PMC9448857 doi:10.3389/fimmu.2022.964138 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 11 | pubmed:36091022 | An immunotherapy response prediction model derived from proliferative CD4⁺ T cells and antigen-presenting monocytes in ccRCC | Kun Zheng Lianchong Gao Jie Hao Xin Zou Xiaoyong Hu | Most patients with clear cell renal cell carcinoma (ccRCC) have an impaired response to immune checkpoint blockade (ICB) therapy. Few biomarkers can predict responsiveness, and there is insufficient evidence to extend them to ccRCC clinical use. To explore subtypes and signatures of immunocytes with good predictive performance for ICB outcomes in the ccRCC context, we reanalyzed two ccRCC single-cell RNA sequencing (scRNA-seq) datasets from patients receiving ICB treatment. A subtype of... | pmid:36091022 pmc:PMC9452905 doi:10.3389/fimmu.2022.972227 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 12 | pubmed:36091370 | Long term high glucose exposure induces premature senescence in retinal endothelial cells | Pietro Maria Bertelli Edoardo Pedrini David Hughes Shannon McDonnell Varun Pathak Elisa Peixoto Jasenska Guduric-Fuchs Alan W Stitt Reinhold J Medina | Purpose: Features of cellular senescence have been described in diabetic retinal vasculature. The aim of this study was to investigate how the high glucose microenvironment impacts on the senescence program of retinal endothelial cells. Methods: Human retinal microvascular endothelial cells were cultured under control and high glucose conditions of 5 mM and 25 mM D-glucose, respectively. Isomeric l-glucose was used as the osmotic control. Cells were counted using CASY technology until they... | pmid:36091370 pmc:PMC9459081 doi:10.3389/fphys.2022.929118 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 13 | pubmed:36091434 | Effects of <i>HSD11B1</i> knockout and overexpression on local cortisol production and differentiation of mesenchymal stem cells | Angelique Kragl Janosch Schoon Ana Tzvetkova Christoph Wenzel Martina Blaschke Wolfgang Böcker Heide Siggelkow Mladen V Tzvetkov | Exogenous glucocorticoids increase the risk for osteoporosis, but the role of endogenous glucocorticoids remains elusive. Here, we describe the generation and validation of a loss- and a gain-of-function model of the cortisol producing enzyme 11-HSD1 (HSD11B1) to modulate the endogenous glucocorticoid conversion in SCP-1 cells - a model for human mesenchymal stem cells capable of adipogenic and osteogenic differentiation. CRISPR-Cas9 was successfully used to generate a cell line carrying a... | pmid:36091434 pmc:PMC9453430 doi:10.3389/fbioe.2022.953034 | Mon, 12 Sep 2022 06:00:00 -0400 |

| NCT Number | | Title | Authors | Description | Identifier | Dates |
|------------|-----------------|--|---|---|--|---------------------------------|
| 14 | pubmed:36091579 | Programmable endonuclease combined with isothermal polymerase amplification to selectively enrich for rare mutant allele fractions | Junman Chen Tian Qiud Michael G Mauk Zheng Su Yaguang Fan Dennis J Yuan Qinghua Zhou Youlin Qiao Haim H Bau Jianming Ying Jinzhao Song | Liquid biopsy is a highly promising method for non-invasive detection of tumor-associated nucleic acid fragments in body fluids but is challenged by the low abundance of nucleic acids of clinical interest and their sequence homology with the vast background of nucleic acids from healthy cells. Recently, programmable endonucleases such as clustered regularly interspaced short palindromic repeat (CRISPR) associated protein (Cas) and prokaryotic Argonautes have been successfully used to remove... | pmid:36091579 pmc:PMC9454931 doi:10.1016/j.cclet.2021.11.065 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 15 | pubmed:36091706 | COL17A1 editing via homology-directed repair in junctional epidermolysis bullosa | Igor Petkovi Johannes Bischof Thomas Kocher Oliver Patrick March Bernadette Liemberger Stefan Hainzl Dirk Strunk Anna Maria Raninger Heide-Marie Binder Julia Reichelt Christina Guttmann-Gruber Verena Wally Josefina Piñón Hofbauer Johann Wolfgang Bauer Ulrich Koller | CONCLUSION: Here we present a gene editing approach capable of reducing end joining-generated repair products while increasing the level of seamless HDR-mediated gene repair outcomes, thereby providing a promising CRISPR/Cas9-based gene editing approach for JEB. | pmid:36091706 pmc:PMC9454317 doi:10.3389/fmed.2022.976604 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 16 | pubmed:36091935 | Identification and Characterization of Genes Related to the Prognosis of Hepatocellular Carcinoma Based on Single-Cell Sequencing | Wenbiao Chen Feng Zhang Huixuan Xu Xianliang Hou Donge Tang Yong Dai | The heterogeneity of hepatocellular carcinoma (HCC) highlights the importance of precision therapy. In recent years, single-cell RNA sequencing has been used to reveal the expression of genes at the single-cell level and comprehensively study cell heterogeneity. This study combined big data analytics and single-cell data mining to study the influence of genes on HCC prognosis. The cells and genes closely related to the HCC were screened through single-cell RNA sequencing (71,915 cells, including... | pmid:36091935 pmc:PMC9454301 doi:10.3389/pore.2022.1610199 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 17 | pubmed:36092319 | The role of tumor-infiltrating B cells in the tumor microenvironment of hepatocellular carcinoma and its prognostic value: a bioinformatics analysis | Jixue Zou Chubin Luo Haoyang Xin Tongchun Xue Xiaoying Xie Rongxin Chen Lan Zhang | CONCLUSIONS: Tumor-infiltrating B cells potentially exert a tumor-suppressive function in the microenvironment of HCC and the higher levels of B cell infiltration are associated with a favorable outcome of HCC. Targeted activation of B cells may improve the tumor immune-targeted therapy. | pmid:36092319 pmc:PMC9459216 doi:10.21037/jgo-22-717 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 18 | pubmed:36092325 | A novel senescence-associated LncRNA signature predicts the prognosis and tumor microenvironment of patients with colorectal cancer: a bioinformatics analysis | Enmin Huang Tao Ma Junyi Zhou Ning Ma Weisheng Yang Chuangxiong Liu Zehui Hou Shuang Chen Zhen Zong Bing Zeng Yingru Li Taicheng Zhou | CONCLUSIONS: SenALSig can better predict survival and risk in CRC patients, as well as help develop new anti-cancer treatment strategies for CRC. | pmid:36092325 pmc:PMC9459181 doi:10.21037/jgo-22-721 | Mon, 12 Sep 2022 06:00:00 -0400 |

| NCT Number | | Title | Authors | Description | Identifier | Dates |
|------------|-----------------|--|--|--|--|---------------------------------|
| 19 | pubmed:36092714 | Transcriptional comparison of adult human primary Retinal Pigment Epithelium, human pluripotent stem cell-derived Retinal Pigment Epithelium, and ARPE19 cells | Elke K Markert Holger Klein Coralie Viollet Werner Rust Benjamin Strobel Stefan G Kauschke Bar Makovoz Heike Neubauer Remko A Bakker Timothy A Blenkinsop | The therapeutic potential of pluripotent stem cells is great as they promise to usher in a new era of medicine where cells or organs may be prescribed to replace dysfunctional tissue. At the forefront are efforts in the eye to develop this technology as it lends itself to in vivo monitoring and sophisticated non-invasive imaging modalities. In the retina, retinal pigment epithelium (RPE) is the most promising replacement cell as it has a single layer, is relatively simple to transplant, and is... | pmid:36092714 pmc:PMC9461284 doi:10.3389/fcell.2022.910040 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 20 | pubmed:36092896 | Network analysis of hepatocellular carcinoma liquid biopsies augmented by single-cell sequencing data | Aram Safrastyan Damian Wollny | Liquid biopsy, the analysis of body fluids, represents a promising approach for disease diagnosis and prognosis with minimal intervention. Sequencing cell-free RNA derived from liquid biopsies has been very promising for the diagnosis of several diseases. Cancer research, in particular, has emerged as a prominent candidate since early diagnosis has been shown to be a critical determinant of disease prognosis. Although high-throughput analysis of liquid biopsies has uncovered many differentially... | pmid:36092896 pmc:PMC9452847 doi:10.3389/fgene.2022.921195 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 21 | pubmed:36092910 | XBP1 impacts lung adenocarcinoma progression by promoting plasma cell adaptation to the tumor microenvironment | Zhaoqian Zhong Junhao Wang Qizheng Han Hong Lin Haihua Luo Danyan Guo Yong Jiang Aihua Liu | Background: The activation of X-box binding protein 1 (XBP1) plays an essential role in the unfolded protein response (UPR) of the endoplasmic reticulum (ER). XBP1 is commonly expressed in various tumors and is closely related to tumorigenesis and progression. However, the role of XBP1 in lung adenocarcinoma (LUAD), especially the prognostic value of its alternative splicing isoforms, remains largely unknown. Methods: The LUAD datasets were retrieved from the The Cancer Genome Atlas,... | pmid:36092910 pmc:PMC9448868 doi:10.3389/fgene.2022.969536 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 22 | pubmed:36092920 | Repression of enhancer RNA PHLDA1 promotes tumorigenesis and progression of Ewing sarcoma via decreasing infiltrating T-lymphocytes: A bioinformatic analysis | Runzhi Huang Dan Huang Siqiao Wang Shuyuan Xian Yifan Liu Minghao Jin Xinkun Zhang Shaofeng Chen Xi Yue Wei Zhang Jianyu Lu Huizhen Liu Zongqiang Huang Hao Zhang Huabin Yin | Background: The molecular mechanisms of EWS-FLI-mediating target genes and downstream pathways may provide a new way in the targeted therapy of Ewing sarcoma. Meanwhile, enhancers transcript non-coding RNAs, known as enhancer RNAs (eRNAs), which may serve as potential diagnosis markers and therapeutic targets in Ewing sarcoma. Materials and methods: Differentially expressed genes (DEGs) were identified between 85 Ewing sarcoma samples downloaded from the Treehouse database and 3 normal bone... | pmid:36092920 pmc:PMC9453160 doi:10.3389/fgene.2022.952162 | Mon, 12 Sep 2022 06:00:00 -0400 |

| NCT Number | | Title | Authors | Description | Identifier | Dates |
|------------|-----------------|--|--|--|--|---------------------------------|
| 23 | pubmed:36093045 | Probabilistic boolean networks predict transcription factor targets to induce transdifferentiation | Bahar Tercan Boris Aguilar Sui Huang Edward R Dougherty Ilya Shmulevich | We developed a computational approach to find the best intervention to achieve transcription factor (TF) mediated transdifferentiation. We construct probabilistic Boolean networks (PBNs) from single-cell RNA sequencing data of two different cell states to model hematopoietic transcription factors cross-talk. This was achieved by a "sampled network" approach, which enabled us to construct large networks. The interventions to induce transdifferentiation consisted of permanently activating or... | pmid:36093045 pmc:PMC9460527 doi:10.1016/j.jisci.2022.104951 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 24 | pubmed:36093191 | Single-cell RNA profiling of <i>Plasmodium vivax</i>-infected hepatocytes reveals parasite- and host- specific transcriptomic signatures and therapeutic targets | Anthony A Ruberto Steven P Maher Amélie Vantaux Chester J Joyner Caitlin Bourke Balu Balan Aaron Jex Ivo Mueller Benoit Witkowski Dennis E Kyle | The resilience of Plasmodium vivax, the most widely-distributed malaria-causing parasite in humans, is attributed to its ability to produce dormant liver forms known as hypnozoites, which can activate weeks, months, or even years after an initial mosquito bite. The factors underlying hypnozoite formation and activation are poorly understood, as is the parasite's influence on the host hepatocyte. Here, we shed light on transcriptome-wide signatures of both the parasite and the infected host cell... | pmid:36093191 pmc:PMC9453201 doi:10.3389/fcimb.2022.986314 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 25 | pubmed:36093192 | The relationship between the number of stenotic coronary arteries and the gut microbiome in coronary heart disease patients | Hao Yu Le Li Yu Deng Guolan Zhang Mimi Jiang He Huang Cheng Li Zhiyu Lv Yingshun Zhou Xing Liu | An increasing number of studies have shown that the gut microbiome plays an important role in the development of coronary heart disease (CHD). However, there are no clear studies on the relationship between the gut microbiome and the number of stenotic coronary arteries. To clarify whether the gut microbiome is associated with the number of stenotic coronary arteries in CHD, we performed the 16S rRNA gene sequencing for the V3-V4 region in the gut microbiota from 9 healthy controls (C) and 36... | pmid:36093192 pmc:PMC9458979 doi:10.3389/fcimb.2022.903828 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 26 | pubmed:36093324 | Growth and differentiation of human induced pluripotent stem cell (hiPSC)-derived kidney organoids using fully synthetic peptide hydrogels | Niall J Treacy Shane Clerkin Jessica L Davis Ciarán Kennedy Aline F Miller Alberto Saiani Jacek K Wychowaniec Dermot F Brougham John Crean | Human induced pluripotent stem cell (hiPSC)-derived kidney organoids have prospective applications ranging from basic disease modelling to personalised medicine. However, there remains a necessity to refine the biophysical and biochemical parameters that govern kidney organoid formation. Differentiation within fully-controllable and physiologically relevant 3D growth environments will be critical to improving organoid reproducibility and maturation. Here, we matured hiPSC-derived kidney... | pmid:36093324 pmc:PMC9420433 doi:10.1016/j.bioactmat.2022.08.003 | Mon, 12 Sep 2022 06:00:00 -0400 |

| | NCT Number | Title | Authors | Description | Identifier | Dates |
|----|-----------------|---|--|--|--|---------------------------------|
| 27 | pubmed:36093346 | Microfluidic immuno-serology assay revealed a limited diversity of protection against COVID-19 in patients with altered immunity | Dongjoo Kim Giulia Biancon Zhiliang Bai Jennifer VanOudenhove Yuxin Liu Shalin Kothari Lohith Gowda Jennifer M Kwan Nicholas Carlos Buitrago-Pocasangre Nikhil Lele Hiromitsu Asashima Michael K Racke JoDell E Wilson Tara S Givens Mary M Tomayko Wade L Schulz Erin E Longbrake David A Hafler Stephanie Halene Rong Fan | The immune response to SARS-CoV-2 for patients with altered immunity such as hematologic malignancies and autoimmune disease may differ substantially from that in general population. These patients remain at high risk despite wide-spread adoption of vaccination. It is critical to examine the differences at the systems level between the general population and the patients with altered immunity in terms of immunologic and serological responses to COVID-19 infection and vaccination. Here, we... | pmid:36093346 pmc:PMC9460970 doi:10.1101/2022.08.31.506117 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 28 | pubmed:36093522 | E2F1 as a potential prognostic and therapeutic biomarker by affecting tumor development and immune microenvironment in hepatocellular carcinoma | Zhibo Tan Min Chen Feng Peng Pengfei Yang Zhaoming Peng Zhe Zhang Xin Li Xiaopeng Zhu Lei Zhang Yujie Zhao Yajie Liu | CONCLUSIONS: This study elucidated that E2F1 could affect tumor development and immune microenvironment in LIHC. Thus, E2F1 might be a potential prognostic biomarker and therapeutic target for LIHC. | pmid:36093522 pmc:PMC9459514 doi:10.21037/tcr-22-218 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 29 | pubmed:36093576 | The astroglial and stem cell functions of adult rat folliculostellate cells | Patrick A Fletcher Kosara Smiljanic Rafael M Prévide Stephanie Constantin Arthur S Sherman Steven L Coon Stanko S Stojilkovic | The mammalian pituitary gland is a complex organ consisting of hormone-producing cells, anterior lobe folliculostellate cells (FSCs), posterior lobe pituicytes, vascular pericytes and endothelial cells, and Sox2-expressing stem cells. We present single-cell RNA sequencing and immunohistofluorescence analyses of pituitary cells of adult female rats with a focus on the transcriptomic profiles of nonhormonal cell types. Samples obtained from whole pituitaries and separated anterior and posterior... | pmid:36093576 doi:10.1002/glia.24267 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 30 | pubmed:36094248 | Analysis of primary uveal melanomas using single cell RNA sequencing | Eva Grandjean-Closson Camille Heckmann Corentin Le Coz Isaline Louvet Matthieu Neri Corine Bertolotto | No abstract | pmid:36094248 doi:10.1051/medsci/2022113 | Mon, 12 Sep 2022 06:00:00 -0400 |
| 31 | pubmed:36095330 | Transcriptomic Response to Calcium in Normal Colon Organoids is Impacted by Colon Location and Sex | Matthew A M Devall Christopher H Dampier Stephen Eaton Mourad Wagdy Ali Sarah J Plummer Jennifer Bryant W James Gauderman Ulrike Peters Steven M Powell Graham Casey | Observational studies indicate that calcium supplementation may protect against colorectal cancer. Stratified analyses suggest that this protective effect may differ based on anatomic subsite and sex, but these hypotheses have been difficult to test experimentally. Here, we exposed 36 patient-derived organoid lines derived from normal colon biopsies (21 right colons, 15 left colons) of unrelated subjects (18 female, 18 male) to moderate (1.66 mmol/L) or high (5.0 mmol/L) concentrations of... | pmid:36095330 doi:10.1158/1940-6207.CAPR-22-0068 | Mon, 12 Sep 2022 06:00:00 -0400 |