

single cell sequencing

| NCT Number |                 | Title   | Authors  | Description  | Identifier  | Dates                           |
|------------|-----------------|---|--|--|---|---------------------------------|
| 1          | pubmed:36054201 | <a href="#">Comparative chloroplast genomes and phylogenetic relationships of Aglaonema modestum and five variegated cultivars of Aglaonema</a>               | Dong-Mei Li<br>Gen-Fa Zhu<br>Bo Yu<br>Dan Huang  | Aglaonema, commonly called Chinese evergreens, are widely used for ornamental purposes. However, attempts to identify Aglaonema species and cultivars based on leaf morphology have been challenging. In the present study, chloroplast sequences were used to elucidate the phylogenetic relationships of cultivated Aglaonema in South China. The chloroplast genomes of one green species and five variegated cultivars of Aglaonema, Aglaonema modestum, 'Red Valentine', 'Lady Valentine', 'Hong Yan', 'Hong...   | pmid:36054201<br>pmc:PMC9439221<br>doi:10.1371/journal.pone.0274067 | Fri, 02 Sep 2022 06:00:00 -0400 |
| 2          | pubmed:36056064 | <a href="#">Genome-wide association study of the human brain functional connectome reveals strong vascular component underlying global network efficiency</a> | Steven Bell<br>Daniel J Tozer<br>Hugh S Markus   | Complex brain networks play a central role in integrating activity across the human brain, and such networks can be identified in the absence of any external stimulus. We performed 10 genome-wide association studies of resting state network measures of intrinsic brain activity in up to 36,150 participants of European ancestry in the UK Biobank. We found that the heritability of global network efficiency was largely explained by blood oxygen level-dependent (BOLD) resting state fluctuation...       | pmid:36056064<br>pmc:PMC9440133<br>doi:10.1038/s41598-022-19106-7   | Fri, 02 Sep 2022 06:00:00 -0400 |
| 3          | pubmed:36059547 | <a href="#">MX2: Identification and systematic mechanistic analysis of a novel immune-related biomarker for systemic lupus erythematosus</a>                  | Xiang-Wen Meng<br>Zhi-Luo Cheng<br>Zhi-Yuan Lu<br>Ya-Nan Tan<br>Xiao-Yi Jia<br>Min Zhang | CONCLUSION: Our study found that MX2 can serve as an immune-related biomarker for predicting the diagnosis and disease activity of SLE. It activates the NOD-like receptor signaling pathway and promotes neutrophil infiltration to aggravate SLE.  | pmid:36059547<br>pmc:PMC9433551<br>doi:10.3389/fimmu.2022.978851    | Mon, 05 Sep 2022 06:00:00 -0400 |
| 4          | pubmed:36063328 | <a href="#">Cotemporal Single-Molecule Force and Fluorescence Measurements to Determine the Mechanism of Ribosome Translocation</a>                           | Varsha P Desai<br>Filipp Frank<br>Carlos J Bustamante                                    | Ribosomes are at the core of the central dogma of life. They perform the last major step of gene expression by translating the information written in the nucleotide codon sequences into the amino acid sequence of a protein. This is a complex mechanochemical process that requires the coordination of multiple dynamic events within the ribosome such as the precise timing of decoding and the subsequent translocation along the mRNA. We have previously used a high-resolution optical tweezers...          | pmid:36063328<br>doi:10.1007/978-1-0716-2229-2_14                   | Mon, 05 Sep 2022 06:00:00 -0400 |
| 5          | pubmed:36063330 | <a href="#">Tethering Complex Proteins and Protein Complexes for Optical Tweezers Experiments</a>   | Kevin Maciuba<br>Christian M Kaiser  | Tethering proteins to force probes, typically micrometer-sized beads, is a prerequisite for dissecting their properties with optical tweezers. DNA handles serve as spacers between the tethered protein of interest and the bead surface. Attachment sites of the DNA handles to both the surface of beads and to the protein of interest must be mechanically stable for optical tweezers experiments. The most prominent method for attaching DNA handles to proteins utilizes thiol chemistry, linking modified... | pmid:36063330<br>doi:10.1007/978-1-0716-2229-2_16                   | Mon, 05 Sep 2022 06:00:00 -0400 |

| NCT Number |                 | Title  | Authors  | Description   | Identifier  | Dates                           |
|------------|-----------------|--|--|---|---|---------------------------------|
| 6          | pubmed:36064963 | <a href="#">Guest Edited Collection: Epigenetics within the tumor microenvironment</a>                                   | Aamir Ahmad  | The tumor microenvironment (TME) comprises of components that exist within the immediate vicinity of tumor cells, including fibroblasts, immune cells, the extracellular matrix, and more. Significant advances have been made in recent years in our understanding of the components of TME and their mutual interactions. Part of the focus of this research has been on epigenetic events, which are increasingly being recognized for their importance in gene regulation and cancer progression. The Collection... | pmid:36064963<br>pmc:PMC9445032<br>doi:10.1038/s41598-022-19042-6 | Tue, 06 Sep 2022 06:00:00 -0400 |
| 7          | pubmed:36066716 | <a href="#">Nontraditional Method for Telomere Staining by PNA Probes</a>  | Takamitsu A Kato   | The standard FISH uses DNA probes to hybridize to the designated complementary strands. This is DNA-DNA interaction, and it usually takes much longer time to obtain detectable signals compared to other reactions such as immunochemical reactions and simple chemical reactions. Certain proteins bind to specific DNA sequences and regulate the biological function of DNA. These DNA-binding proteins have specific domains to interact with single- or double-stranded DNA. Some of telomere proteins...         | pmid:36066716<br>doi:10.1007/978-1-0716-2433-3_13                 | Tue, 06 Sep 2022 06:00:00 -0400 |
| 8          | pubmed:36068612 | <a href="#">The associations between plasma soluble Trem1 and neurological diseases: a Mendelian randomization study</a> | Xiaolei Shi<br>Tao Wei<br>Yachun Hu<br>Meng Wang<br>Yi Tang  | CONCLUSIONS: Taken together, this study indicates suggestive association between plasma sTrem1 and AD. Moreover, higher plasma sTrem1 was associated with the increased risk of epilepsy. The findings support the hypothesis that sTrem1 may be a vital element on the causal pathway to AD and epilepsy.  | pmid:36068612<br>doi:10.1186/s12974-022-02582-z                   | Tue, 06 Sep 2022 06:00:00 -0400 |
| 9          | pubmed:36070695 | <a href="#">Landscape and age dynamics of immune cells in the Egyptian rousette bat</a>                                  | Virginia Friedrichs<br>Christophe Toussaint<br>Alexander Schäfer<br>Melanie Rissmann<br>Oliver Dietrich<br>Thomas C Mettenleiter<br>Gang Pei<br>Anne Balkema-Buschmann<br>Antoine-Emmanuel Saliba<br>Anca Dorhoi | Bats harbor high-impact zoonotic viruses often in the absence of disease manifestation. This restriction and disease tolerance possibly rely on specific immunological features. In-depth molecular characterization of cellular immunity and imprinting of age on leukocyte compartments remained unexplored in bats. We employ single-cell RNA sequencing (scRNA-seq) and establish immunostaining panels to characterize the immune cell landscape in juvenile, subadult, and adult Egyptian rousette bats...        | pmid:36070695<br>doi:10.1016/j.celrep.2022.111305                 | Wed, 07 Sep 2022 06:00:00 -0400 |

| NCT Number |                 | Title   | Authors  | Description  | Identifier  | Dates                           |
|------------|-----------------|---|--|--|---|---------------------------------|
| 10         | pubmed:36070768 | <a href="#">Induction of a colitogenic phenotype in Th1-like cells depends on interleukin-23 receptor signaling</a> | Mathias Pawlak<br>David DeTomaso<br>Alexandra Schnell<br>Gerd Meyer Zu Horste<br>Youjin Lee<br>Jackson Nyman<br>Danielle Dionne<br>Brianna M L Regan<br>Vasundhara Singh<br>Toni Delorey<br>Markus A Schramm<br>Chao Wang<br>Antonia Wallrapp<br>Patrick R Burkett<br>Samantha J Riesenfeld<br>Ana C Anderson<br>Aviv Regev<br>Ramnik J Xavier<br>Nir Yosef<br>Vijay K Kuchroo | Interleukin-23 receptor plays a critical role in inducing inflammation and autoimmunity. Here, we report that Th1-like cells differentiated in vitro with IL-12 + IL-21 showed similar IL-23R expression to that of pathogenic Th17 cells using eGFP reporter mice. Fate mapping established that these cells did not transition through a Th17 cell state prior to becoming Th1-like cells, and we observed their emergence in vivo in the T cell adoptive transfer colitis model. Using IL-23R-deficient Th1-like... | pmid:36070768<br>doi:10.1016/j.immuni.2022.08.007 | Wed, 07 Sep 2022 06:00:00 -0400 |
| 11         | pubmed:36070863 | <a href="#">Boosting single-cell gene regulatory network reconstruction via bulk-cell transcriptomic data</a>       | Hantao Shu<br>Fan Ding<br>Jingtian Zhou<br>Yexiang Xue<br>Dan Zhao<br>Jianyang Zeng<br>Jianzhu Ma  | Computational recovery of gene regulatory network (GRN) has recently undergone a great shift from bulk-cell towards designing algorithms targeting single-cell data. In this work, we investigate whether the widely available bulk-cell data could be leveraged to assist the GRN predictions for single cells. We infer cell-type-specific GRNs from both the single-cell RNA sequencing data and the generic GRN derived from the bulk cells by constructing a weakly supervised learning framework based on the... | pmid:36070863<br>doi:10.1093/bib/bbac389          | Wed, 07 Sep 2022 06:00:00 -0400 |
| 12         | pubmed:36070866 | <a href="#">SCDD: a novel single-cell RNA-seq imputation method with diffusion and denoising</a>                    | Jian Liu<br>Yichen Pan<br>Zhihan Ruan<br>Jun Guo   | Single-cell sequencing technologies are widely used to discover the evolutionary relationships and the differences in cells. Since dropout events may frustrate the analysis, many imputation approaches for single-cell RNA-seq data have appeared in previous attempts. However, previous imputation attempts usually suffer from the over-smooth problem, which may bring limited improvement or negative effect for the downstream analysis of single-cell RNA-seq data. To solve this difficulty, we propose a... | pmid:36070866<br>doi:10.1093/bib/bbac398          | Wed, 07 Sep 2022 06:00:00 -0400 |

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|------------|-----------------|---|---|---|---|---------------------------------|
| 13         | pubmed:36071032 | <a href="#">Beiging of perivascular adipose tissue regulates its inflammation and vascular remodeling</a>   | Yusuke Adachi<br>Kazutaka Ueda<br>Seitaro Nomura<br>Kaoru Ito<br>Manami Katoh<br>Mikako Katagiri<br>Shintaro Yamada<br>Masaki Hashimoto<br>Bowen Zhai<br>Genri Numata<br>Akira Otani<br>Munetoshi Hinata<br>Yuta Hiraike<br>Hironori Waki<br>Norifumi Takeda<br>Hiroyuki Morita<br>Tetsuo Ushiku<br>Toshimasa Yamauchi<br>Eiki Takimoto<br>Issei Komuro | Although inflammation plays critical roles in the development of atherosclerosis, its regulatory mechanisms remain incompletely understood. Perivascular adipose tissue (PVAT) has been reported to undergo inflammatory changes in response to vascular injury. Here, we show that vascular injury induces the beiging (brown adipose tissue-like phenotype change) of PVAT, which fine-tunes inflammatory response and thus vascular remodeling as a protective mechanism. In a mouse model of endovascular...        | pmid:36071032<br>doi:10.1038/s41467-022-32658-6 | Wed, 07 Sep 2022 06:00:00 -0400 |
| 14         | pubmed:36071103 | <a href="#">Precise identification of cancer cells from allelic imbalances in single cell transcriptomes</a>                                      | Mi K Trinh<br>Clarissa N Pacyna<br>Gerda Kildisiute<br>Christine Thevanesan<br>Alice Piapi<br>Kirsty Ambridge<br>Nathaniel D Anderson<br>Eleonora Khabirova<br>Elena Prigmore<br>Karin Straathof<br>Sam Behjati<br>Matthew D Young  | A fundamental step of tumour single cell mRNA analysis is separating cancer and non-cancer cells. We show that the common approach to separation, using shifts in average expression, can lead to erroneous biological conclusions. By contrast, allelic imbalances representing copy number changes directly detect the cancer genotype and accurately separate cancer from non-cancer cells. Our findings provide a definitive approach to identifying cancer cells from single cell mRNA sequencing data.            | pmid:36071103<br>doi:10.1038/s42003-022-03808-9 | Wed, 07 Sep 2022 06:00:00 -0400 |
| 15         | pubmed:36071107 | <a href="#">devCellPy is a machine learning-enabled pipeline for automated annotation of complex multilayered single-cell transcriptomic data</a> | Francisco X Galdos<br>Sidra Xu<br>William R Goodyer<br>Lauren Duan<br>Yuhsin V Huang<br>Soah Lee<br>Han Zhu<br>Carissa Lee<br>Nicholas Wei<br>Daniel Lee<br>Sean M Wu   | A major informatic challenge in single cell RNA-sequencing analysis is the precise annotation of datasets where cells exhibit complex multilayered identities or transitory states. Here, we present devCellPy a highly accurate and precise machine learning-enabled tool that enables automated prediction of cell types across complex annotation hierarchies. To demonstrate the power of devCellPy, we construct a murine cardiac developmental atlas from published datasets encompassing 104,199 cells from...   | pmid:36071107<br>doi:10.1038/s41467-022-33045-x | Wed, 07 Sep 2022 06:00:00 -0400 |
| 16         | pubmed:36071369 | <a href="#">The pleiotropic mode and molecular mechanism of macrophages in promoting tumor progression and metastasis</a>                         | Xingxing Zhang<br>Wenxiu Bai<br>Lisha Hu<br>Hualan Ha<br>Yuelin Du<br>Wei Xiong<br>Hongbo Wang<br>Panfeng Shang   | Macrophages are the most abundant immune cells in primary and metastatic tumor tissues. Studies have shown that macrophages mainly exhibit a tumor-promoting phenotype and play a key role in tumor progression and metastasis. Therefore, many macrophage-targeted drugs have entered clinical trials. However, compared to preclinical studies, some clinical trial results showed that macrophage-targeted therapy did not achieve the desired effect. This may be because most of what we know about macrophages... | pmid:36071369<br>doi:10.1007/s12094-022-02932-6 | Wed, 07 Sep 2022 06:00:00 -0400 |

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|------------|-----------------|--|---|--|--|---------------------------------|
| 17         | pubmed:36071475 | <a href="#">Human PMSCs-derived small extracellular vesicles alleviate neuropathic pain through miR-26a-5p/Wnt5a in SNI mice model</a>               | Yitian Lu<br>Jintao Zhang<br>Fanning Zeng<br>Peng Wang<br>Xiangna Guo<br>Haitao Wang<br>Zaisheng Qin<br>Tao Tao   | CONCLUSIONS: We reported that hPMSCs derived sEVs as a promising therapy for nerve injury induced neuropathic pain. In addition, we showed that the miR-26a-5p in the sEVs regulated Wnt5a/Ryk/CaMKII/NFAT partly take part in the analgesia through anti-neuroinflammation, which suggests an alleviating pain effect through non-canonical Wnt signaling pathway in neuropathic pain model in vivo.  | pmid:36071475<br>doi:10.1186/s12974-022-02578-9                  | Wed, 07 Sep 2022 06:00:00 -0400 |
| 18         | pubmed:36071529 | <a href="#">Abnormal molecular signatures of inflammation, energy metabolism, and vesicle biology in human Huntington disease peripheral tissues</a> | Andreas Neueder<br>Kerstin Kojer<br>Tanja Hering<br>Daniel J Lavery<br>Jian Chen<br>Nathalie Birth<br>Jaqueline Hallitsch<br>Sonja Trautmann<br>Jennifer Parker<br>Michael Flower<br>Huma Sethi<br>Salman Haider<br>Jong-Min Lee<br>Sarah J Tabrizi<br>Michael Orth | CONCLUSIONS: Our 'omics data document the involvement of inflammation, energy metabolism, and extracellular vesicle homeostasis. This demonstrates the potential to identify biological signatures from peripheral tissues in HD suitable as biomarkers in clinical trials. The generated data, complemented by the primary cell lines established from peripheral tissues, and a large panel of iPSC lines that can serve as human models of HD are a valuable and unique resource to advance the current...          | pmid:36071529<br>doi:10.1186/s13059-022-02752-5                  | Wed, 07 Sep 2022 06:00:00 -0400 |
| 19         | pubmed:36071722 | <a href="#">SIQ: easy quantitative measurement of mutation profiles in sequencing data</a>   | Robin van Schendel<br>Joost Schimmel<br>Marcel Tijsterman   | With the emergence of CRISPR-mediated genome editing, there is an increasing desire for easy-to-use tools that can process and overview the spectra of outcomes. Here, we present Sequence Interrogation and Quantification (SIQ), a simple-to-use software tool that enables researchers to retrieve, data-mine and visualize complex sets of targeted sequencing data. SIQ can analyse Sanger sequences but specifically benefit the processing of short- and long-read next-generation sequencing data (e.g....     | pmid:36071722<br>pmc:PMC9442499<br>doi:10.1093/nargab/lqac063    | Thu, 08 Sep 2022 06:00:00 -0400 |
| 20         | pubmed:36071955 | <a href="#">Microencapsulation and <i>in situ</i> incubation methodology for the cultivation of marine bacteria</a>                                  | Emily Pope<br>Christopher Cartmell<br>Bradley Haltli<br>Ali Ahmadi<br>Russell G Kerr  | Environmental microorganisms are important sources of biotechnology innovations; however, the discovery process is hampered by the inability to culture the overwhelming majority of microbes. To drive the discovery of new biotechnology products from previously unculturable microbes, several methods such as modification of media composition, incubation conditions, single-cell isolation, and in situ incubation, have been employed to improve microbial recovery from environmental samples. To improve... | pmid:36071955<br>pmc:PMC9441948<br>doi:10.3389/fmicb.2022.958660 | Thu, 08 Sep 2022 06:00:00 -0400 |
| 21         | pubmed:36072587 | <a href="#">Novel insight on marker genes and pathogenic peripheral neutrophil subtypes in acute pancreatitis</a>                                    | Deyu Zhang<br>Meiqi Wang<br>Yang Zhang<br>Chuanchao Xia<br>Lisi Peng<br>Keliang Li<br>Hua Yin<br>Shiyu Li<br>Xiaoli Yang<br>Xiaoju Su<br>Haojie Huang   | Acute pancreatitis is a common critical and acute gastrointestinal disease worldwide, with an increasing percentage of morbidity. However, the gene expression pattern in peripheral blood has not been fully analyzed. In addition, the mechanism of coronavirus disease 2019 (COVID-19)-induced acute pancreatitis has not been investigated. Here, after bioinformatic analysis with machine-learning methods of the expression data of peripheral blood cells and validation in local patients, two functional...  | pmid:36072587<br>pmc:PMC9444397<br>doi:10.3389/fimmu.2022.964622 | Thu, 08 Sep 2022 06:00:00 -0400 |

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|------------|-----------------|---|---|---|---|---------------------------------|
| 22         | pubmed:36072594 | <a href="#">The development and function of CD11c<sup>±</sup> atypical B cells - insights from single cell analysis</a>                               | Xin Gao<br>Ian A Cockburn   | CD11c <sup>+</sup> (+) T-bet <sup>+</sup> atypical B cells (ABCs) have been identified in the context of vaccination, acute and chronic infections and autoimmune disease. However, the origins and functions of ABCs remain elusive. A major obstacle in the study of ABCs, and human MBCs more generally, has been the use of different phenotypic markers in different contexts to identify what appear to be phenotypically similar cells. Advances in single-cell RNA sequencing (scRNA-seq) technology have allowed researchers to... | pmid:36072594<br>pmc:PMC9441955<br>doi:10.3389/fimmu.2022.979060  | Thu, 08 Sep 2022 06:00:00 -0400 |
| 23         | pubmed:36072672 | <a href="#">Clustering CITE-seq data with a canonical correlation-based deep learning method</a>  | Musu Yuan<br>Liang Chen<br>Minghua Deng   | Single-cell multiomics sequencing techniques have rapidly developed in the past few years. Among these techniques, single-cell cellular indexing of transcriptomes and epitopes (CITE-seq) allows simultaneous quantification of gene expression and surface proteins. Clustering CITE-seq data have the great potential of providing us with a more comprehensive and in-depth view of cell states and interactions. However, CITE-seq data inherit the properties of scRNA-seq data, being noisy,....                                     | pmid:36072672<br>pmc:PMC9441595<br>doi:10.3389/fgene.2022.977968  | Thu, 08 Sep 2022 06:00:00 -0400 |
| 24         | pubmed:36072757 | <a href="#">High-throughput scNMT protocol for multiomics profiling of single cells from mouse brain and pancreatic organoids</a>                     | Santiago Cerrizuela<br>Oguzhan Kaya<br>Lukas P M Kremer<br>Andrea Sarvari<br>Tobias Ellinger<br>Jannes Straub<br>Jan Brunken<br>Andrés Sanz-Morejón<br>Aylin Korkmaz<br>Ana Martín-Villalba | Single-cell nucleosome, methylome, and transcriptome (scNMT) sequencing is a recently developed method that allows multiomics profiling of single cells. In this scNMT protocol, we describe profiling of cells from mouse brain and pancreatic organoids, using liquid handling platforms to increase throughput from 96-well to 384-well plate format. Our approach miniaturizes reaction volumes and incorporates the latest Smart-seq3 protocol to obtain higher numbers of detected genes and genomic DNA...                           | pmid:36072757<br>pmc:PMC9441340<br>doi:10.1016/j.xpro.2022.101555 | Thu, 08 Sep 2022 06:00:00 -0400 |
| 25         | pubmed:36072840 | <a href="#">A natural mutation of the <i>NST1</i> gene arrests secondary cell wall biosynthesis in the seed coat of a hull-less pumpkin accession</a> | Xiaolong Lyu<br>Lu Shi<br>Meng Zhao<br>Zhangping Li<br>Nanqiao Liao<br>Yiqing Meng<br>Yuyuan Ma<br>Yulan Zhou<br>Qin Xue<br>Zhongyuan Hu<br>Jinghua Yang<br>Mingfang Zhang                  | Hull-less pumpkins ( <i>Cucurbita pepo</i> L.) are naturally occurring novel variants known as oilseed or naked-seeded pumpkins, and are characterized by the absence of a normal lignified seed coat. Due to a specialized seed coat structure, these variants serve as a good model for studying seed coat formation and simplify the processing of pumpkin seeds. However, causal genes for this hull-less trait still remain unknown. Here, by bulked segregant analysis and fine mapping, we found that mutation of a...               | pmid:36072840<br>pmc:PMC9437724<br>doi:10.1093/hr/uhac136         | Thu, 08 Sep 2022 06:00:00 -0400 |



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|------------|-----------------|--|---|---|---|---------------------------------|
| 26         | pubmed:36072841 | <a href="#">Construction of a high-density bin-map and identification of fruit quality-related quantitative trait loci and functional genes in pear</a>                  | Meng-Fan Qin<br>Lei-Ting Li<br>Jugpreet Singh<br>Man-Yi Sun<br>Bing Bai<br>Si-Wei Li<br>Jiang-Ping Ni<br>Jia-Ying Zhang<br>Xun Zhang<br>Wei-Lin Wei<br>Ming-Yue Zhang<br>Jia-Ming Li<br>Kai-Jie Qi<br>Shao-Ling Zhang<br>Awais Khan<br>Jun Wu | Pear (Pyrus spp.) is one of the most common fruit crops grown in temperate regions worldwide. Genetic enhancement of fruit quality is a fundamental goal of pear breeding programs. The genetic control of pear fruit quality traits is highly quantitative, and development of high-density genetic maps can facilitate fine-mapping of quantitative trait loci (QTLs) and gene identification. Bin-mapping is a powerful method of constructing high-resolution genetic maps from large-scale genotyping datasets.... | pmid:36072841<br>pmc:PMC9437719<br>doi:10.1093/hr/uhac141   | Thu, 08 Sep 2022 06:00:00 -0400 |
| 27         | pubmed:36072979 | <a href="#">A Genomic Instability-Related Long Noncoding RNA Signature for Predicting Hepatocellular Carcinoma Prognosis</a>   | Jing Lu<br>Wanyue Cao<br>Zeping He<br>Haoyu Wang<br>Jialing Hao<br>Junming Xu   | CONCLUSION: Our results showed that GIlncSig serves as a potential independent prognosis factor to predict HCC patients' prognosis for exploring potential mechanism and therapy strategy. Besides, LINC00501 plays an important role in the progression of HCC, which may be a potential therapy target.   | pmid:36072979<br>pmc:PMC9444385<br>doi:10.1155/2022/3090523 | Thu, 08 Sep 2022 06:00:00 -0400 |
| 28         | pubmed:36073931 | <a href="#">Mechanisms of IS26-Mediated Amplification of the aphA1 Gene Leading to Tobramycin Resistance in an Acinetobacter baumannii Isolate</a>                       | Christopher J Harmer<br>Francois Lebreton<br>Jason Stam<br>Patrick T McGann<br>Ruth M Hall  | Enhanced levels of resistance to antibiotics arising from amplification of an antibiotic resistance gene that impact therapeutic options are increasingly observed. Amplification can also disclose novel phenotypes leading to treatment failure. However, the mechanism is poorly understood. Here, the route to amplification of the aphA1 kanamycin and neomycin resistance gene during tobramycin treatment of an Acinetobacter baumannii clinical isolate, leading to tobramycin resistance and treatment...      | pmid:36073931<br>doi:10.1128/spectrum.02287-22              | Thu, 08 Sep 2022 06:00:00 -0400 |
| 29         | pubmed:36073947 | <a href="#">Polygenic Analysis of Tolerance to Carbon Dioxide Inhibition of Isoamyl Acetate "Banana" Flavor Production in Yeast Reveals MDS3 as Major Causative Gene</a> | Ben Souffriau<br>Sylvester Holt<br>Arne Hagman<br>Stijn De Graeve<br>Philippe Malcorps<br>Maria R Foulquié-Moreno<br>Johan M Thevelein  | The introduction in modern breweries of tall cylindroconical fermentors, replacing the traditional open fermentation vats, unexpectedly revealed strong inhibition of flavor production by the high CO(2) pressure in the fermentors. We have screened our collection of Saccharomyces cerevisiae strains for strains displaying elevated tolerance to inhibition of flavor production by +0.65 bar CO(2), using a laboratory scale CO(2) pressurized fermentation system. We focused on the production of isoamyl...   | pmid:36073947<br>doi:10.1128/aem.00814-22                   | Thu, 08 Sep 2022 06:00:00 -0400 |
| 30         | pubmed:36074152 | <a href="#">Genomic Characteristics and Single-cell Profiles after Immunotherapy in Fumarate Hydratase-deficient Renal Cell Carcinoma</a>                                | Pei Dong<br>Xinyue Zhang<br>Yulu Peng<br>Yijun Zhang<br>Ruiqi Liu<br>Yilin Li<br>Qi-Wen Pan<br>Wensu Wei<br>Shen-Jie Guo<br>Zhiling Zhang<br>Hui Han<br>FangJian Zhou<br>Yang Liu<br>Liru He  | CONCLUSIONS: Immune infiltration is frequent in FHRCC. ICI-based treatment is a promising regimen, and treatment response depends on the functional status of tumor-infiltrating lymphocytes. ICI-based treatment cannot reverse the exhaustion of CD8+ T-cells in patients with progressive disease, highlighting the need for additional therapeutic strategies.  | pmid:36074152<br>doi:10.1158/1078-0432.CCR-22-1279          | Thu, 08 Sep 2022 06:00:00 -0400 |

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|------------|-----------------|--|---|---|---|---------------------------------|
| 31         | pubmed:36074453 | <a href="#">Rational Discovery of Microtubule-Stabilizing Peptides</a>   | Brandon Úsuga-Acevedo<br>Yadiris García<br>Carola F Díaz<br>Verónica A Jiménez  | Microtubule (MT) stabilization is an attractive pharmacological strategy to hamper the progress of neurodegenerative diseases. In this regard, seeking peptides with MT-stabilizing properties has awoken great interest. This work reports the rational discovery of two structurally related MT-stabilizing octapeptides using a combination of protein-peptide docking, conventional molecular dynamics, Gaussian accelerated molecular dynamics (GaMD), and tubulin polymerization assays. FASTA sequences for... | pmid:36074453<br>doi:10.1021/acs.jcim.2c00849     | Thu, 08 Sep 2022 06:00:00 -0400 |
| 32         | pubmed:36074460 | <a href="#">Constitutional BRCA1 Methylation and Risk of Incident Triple-Negative Breast Cancer and High-grade Serous Ovarian Cancer</a> | Per E Lønning<br>Oleksii Nikolaienko<br>Kathy Pan<br>Allison W Kurian<br>Hans P Eikesdal<br>Mary Pettinger<br>Garnet L Anderson<br>Ross L Prentice<br>Rowan T Chlebowski<br>Stian Knappskog   | CONCLUSIONS AND RELEVANCE: The results of this case-control suggest that constitutional normal tissue BRCA1 promoter methylation is significantly associated with risk of incident TNBC and HGSOC, with potential implications for prediction of these cancers. These findings warrant further research to determine if constitutional methylation of tumor suppressor genes are pancancer risk factors.  | pmid:36074460<br>doi:10.1001/jamaoncol.2022.3846  | Thu, 08 Sep 2022 06:00:00 -0400 |
| 33         | pubmed:36074578 | <a href="#">The druggable transcription factor Fli-1 regulates T cell immunity and tolerance in graft-versus-host disease</a>            | Steven Schutt<br>Yongxia Wu<br>Arjun Kharel<br>David Bastian<br>Hee-Jin Choi<br>M Hanief Sofi<br>Corey Mealer<br>Brianyell McDaniel Mims<br>Hung Nguyen<br>Chen Liu<br>Kris Helke<br>Weiguo Cui<br>Xian Zhang<br>Yaacov Ben-David<br>Xue-Zhong Yu | Graft-versus-host disease (GVHD), manifesting in either acute (aGVHD) or chronic (cGVHD), presents significant life-threatening complications following allogeneic hematopoietic cell transplantation. Here, we investigated Friend Virus Leukemia Integration 1 (Fli-1) in GVHD pathogenesis and validated Fli-1 as a therapeutic target. Using genetic approaches, we found that Fli-1 dynamically regulates different T-cell subsets in allogeneic responses and pathogenicity in the development of aGVHD and...  | pmid:36074578<br>doi:10.1172/JCI143950            | Thu, 08 Sep 2022 06:00:00 -0400 |
| 34         | pubmed:36074794 | <a href="#">Measuring the latent reservoir for HIV-1: Quantification bias in near full-length genome sequencing methods</a>              | Jennifer A White<br>Joshua T Kufera<br>Niklas Bachmann<br>Weiwei Dai<br>Francesco R Simonetti<br>Ciara Armstrong<br>Jun Lai<br>Subul Beg<br>Janet D Siliciano<br>Robert F Siliciano   | Antiretroviral therapy (ART) effectively inhibits HIV-1 replication but is not curative due to the persistence of a latent viral reservoir in resting CD4+ T cells. This reservoir is a major barrier to cure. Sequencing studies have revealed that the population of proviruses persisting in ART-treated individuals is dominated by defective proviruses that cannot give rise to viral rebound due to fatal defects including large deletions and APOBEC3-mediated hypermutation. Near full genome sequencing... | pmid:36074794<br>doi:10.1371/journal.ppat.1010845 | Thu, 08 Sep 2022 06:00:00 -0400 |



| NCT Number |                 | Title  | Authors  | Description   | Identifier  | Dates                           |
|------------|-----------------|--|--|---|---|---------------------------------|
| 35         | pubmed:36074806 | <a href="#">Single-cell RNA sequencing reveals dysregulation of spinal cord cell types in a severe spinal muscular atrophy mouse model</a> | Junjie Sun<br>Jiaying Qiu<br>Qionxia Yang<br>Qianqian Ju<br>Ruobing Qu<br>Xu Wang<br>Liucheng Wu<br>Lingyan Xing | Although spinal muscular atrophy (SMA) is a motor neuron disease caused by the loss of survival of motor neuron (SMN) proteins, there is growing evidence that non-neuronal cells play important roles in SMA pathogenesis. However, transcriptome alterations occurring at the single-cell level in SMA spinal cord remain unknown, preventing us from fully comprehending the role of specific cells. Here, we performed single-cell RNA sequencing of the spinal cord of a severe SMA mouse model, and identified... | pmid:36074806<br>doi:10.1371/journal.pgen.1010392 | Thu, 08 Sep 2022 06:00:00 -0400 |