

single cell sequencing

NCT Number		Title	Authors	Description	Identifier	Dates
1	pubmed:36122200	Nanomolar inhibition of SARS-CoV-2 infection by an unmodified peptide targeting the prehairpin intermediate of the spike protein	Kailu Yang Chuchu Wang Alex J B Kreutzberger Ravi Ojha Suvi Kuivanen Sergio Couoh-Cardel Serena Muratcioglu Timothy J Eisen K Ian White Richard G Held Subu Subramanian Kendra Marcus Richard A Pfuetzner Luis Esquivies Catherine A Doyle John Kuriyan Olli Vapalahti Giuseppe Balistreri Tom Kirchhausen Axel T Brunger	Variants of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) challenge currently available coronavirus disease 2019 vaccines and monoclonal antibody therapies through epitope change on the receptor binding domain of the viral spike glycoprotein. Hence, there is a specific urgent need for alternative antivirals that target processes less likely to be affected by mutation, such as the membrane fusion step of viral entry into the host cell. One such antiviral class includes peptide...	pmid:36122200 doi:10.1073/pnas.2210990119	Mon, 19 Sep 2022 06:00:00 -0400
2	pubmed:36130423	Construction of tomato plants with suppressed endo--N-acetylglucosaminidase activity using CRISPR-Cas9 mediated genome editing	Naoko Okamoto Megumi Maeda Chiharu Yamamoto Reo Kodama Koichi Sugimoto Yoshihito Shinozaki Hiroshi Ezura Yoshinobu Kimura	High mannose-type free N-glycans with a single N-acetyl-D-glucosamine (GlcNAc) residue at the reducing end (GN1-HMT-FNGs) are produced by cytosolic endo--N-acetylglucosaminidase (EC:3.2.1.96) (ENGase) and are ubiquitous in differentiating and growing plant cells. To elucidate the physiological functions of HMT-FNGs in plants, we identified the ENGase gene in tomato (Soly06g050930) and detected ENGase activity and increased production of GN1-HMT-FNGs during tomato fruit maturation. However, the...	pmid:36130423 doi:10.1016/j.plaphy.2022.08.009	Wed, 21 Sep 2022 06:00:00 -0400
3	pubmed:36130486	Single-cell sequencing reveals activation of core transcription factors in PRC2-deficient malignant peripheral nerve sheath tumor	Xiyuan Zhang Hannah E Lou Vishaka Gopalan Zhihui Liu Hilda M Jafarah Haiyan Lei Paige Jones Carly M Sayers Marielle E Yohe Prashant Chittiboina Brigitte C Widemann Carol J Thiele Michael C Kelly Sridhar Hannenhalli Jack F Shern	Loss-of-function mutations in the polycomb repressive complex 2 (PRC2) occur frequently in malignant peripheral nerve sheath tumor, an aggressive sarcoma that arises from NF1-deficient Schwann cells. To define the oncogenic mechanisms underlying PRC2 loss, we use engineered cells that dynamically reassemble a competent PRC2 coupled with single-cell sequencing from clinical samples. We discover a two-pronged oncogenic process: first, PRC2 loss leads to remodeling of the bivalent chromatin and...	pmid:36130486 doi:10.1016/j.celrep.2022.111363	Wed, 21 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
4	pubmed:36130508	Circulating monocytes associated with anti-PD-1 resistance in human biliary cancer induce T cell paralysis	Bridget P Keenan Elizabeth E McCarthy Arielle Ilano Hai Yang Li Zhang Kathryn Allaire Zenghua Fan Tony Li David S Lee Yang Sun Alexander Cheung Diamond Luong Hewitt Chang Brandon Chen Jaqueline Marquez Brenna Sheldon Robin K Kelley Chun Jimmie Ye Lawrence Fong	Suppressive myeloid cells can contribute to immunotherapy resistance, but their role in response to checkpoint inhibition (CPI) in anti-PD-1 refractory cancers, such as biliary tract cancer (BTC), remains elusive. We use multiplexed single-cell transcriptomic and epitope sequencing to profile greater than 200,000 peripheral blood mononuclear cells from advanced BTC patients (n = 9) and matched healthy donors (n = 8). Following anti-PD-1 treatment, CD14^(+) monocytes expressing high levels of...	pmid:36130508 doi:10.1016/j.celrep.2022.111384	Wed, 21 Sep 2022 06:00:00 -0400
5	pubmed:36130520	Single-cell transcriptomics identifies conserved regulators of neuroglandular lineages	Julia Steger Alison G Cole Andreas Denner Tatiana Lebedeva Grigory Genikhovich Alexander Ries Robert Reischl Elisabeth Taudes Mark Lassnig Ulrich Technau	Communication in bilaterian nervous systems is mediated by electrical and secreted signals; however, the evolutionary origin and relation of neurons to other secretory cell types has not been elucidated. Here, we use developmental single-cell RNA sequencing in the cnidarian Nematostella vectensis, representing an early evolutionary lineage with a simple nervous system. Validated by transgenics, we demonstrate that neurons, stinging cells, and gland cells arise from a common multipotent...	pmid:36130520 doi:10.1016/j.celrep.2022.111370	Wed, 21 Sep 2022 06:00:00 -0400
6	pubmed:36130957	Intrinsic bias estimation for improved analysis of bulk and single-cell chromatin accessibility profiles using SELMA	Shengen Shawn Hu Lin Liu Qi Li Wenjing Ma Michael J Guertin Clifford A Meyer Ke Deng Tingting Zhang Chongzhi Zang	Genome-wide profiling of chromatin accessibility by DNase-seq or ATAC-seq has been widely used to identify regulatory DNA elements and transcription factor binding sites. However, enzymatic DNA cleavage exhibits intrinsic sequence biases that confound chromatin accessibility profiling data analysis. Existing computational tools are limited in their ability to account for such intrinsic biases and not designed for analyzing single-cell data. Here, we present Simplex Encoded Linear Model for...	pmid:36130957 doi:10.1038/s41467-022-33194-z	Wed, 21 Sep 2022 06:00:00 -0400
7	pubmed:36131068	Executable models of immune signaling pathways in HIV-associated atherosclerosis	Mukta G Palshikar Rohith Palli Alicia Tyrell Sanjay Maggirwar Giovanni Schifitto Meera V Singh Juilee Thakar	Atherosclerosis (AS)-associated cardiovascular disease is an important cause of mortality in an aging population of people living with HIV (PLWH). This elevated risk has been attributed to viral infection, anti-retroviral therapy, chronic inflammation, and lifestyle factors. However, the rates at which PLWH develop AS vary even after controlling for length of infection, treatment duration, and for lifestyle factors. To investigate the molecular signaling underlying this variation, we sequenced...	pmid:36131068 doi:10.1038/s41540-022-00246-5	Wed, 21 Sep 2022 06:00:00 -0400
8	pubmed:36131234	Evaluation of classification in single cell atac-seq data with machine learning methods	Hongzhe Guo Zhongbo Yang Tao Jiang Shiqi Liu Yadong Wang Zhe Cui	CONCLUSIONS: Both in intra-dataset and in inter-dataset experiment, SVM and NMC are overall outperformed others across all 4 datasets. Thus, we recommend researchers to use SVM and NMC as the underlying classifier when developing an automatic cell-type classification method for scATAC-seq.	pmid:36131234 doi:10.1186/s12859-022-04774-z	Wed, 21 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
9	pubmed:36131282	Malignant clonal evolution drives multiple myeloma cellular ecological diversity and microenvironment reprogramming	Yuanzheng Liang Haiyan He Weida Wang Henan Wang Shaowen Mo Ruiying Fu Xindi Liu Qiong Song Zhongjun Xia Liang Wang	CONCLUSIONS: This characterization of the malignant clonal evolution pattern of MM at the single-cell level provides a theoretical basis and scientific evidence for a personalized precision therapy strategy and further development of a potential new adjuvant strategy combining epigenetic agent and immune checkpoint blockade.	pmid:36131282 doi:10.1186/s12943-022-01648-z	Wed, 21 Sep 2022 06:00:00 -0400
10	pubmed:36131292	The architecture of clonal expansions in morphologically normal tissue from cancerous and non-cancerous prostates	Claudia Buhigas Anne Y Warren Wing-Kit Leung Hayley C Whitaker Hayley J Luxton Steve Hawkins Jonathan Kay Adam Butler Yaobo Xu Dan J Woodcock Sue Merson Fiona M Frame Atef Sahli Federico Abascal CRUK-ICGC Prostate Cancer Group Iñigo Martincorena G Steven Bova Christopher S Foster Peter Campbell Norman J Maitland David E Neal Charlie E Massie Andy G Lynch Rosalind A Eeles Colin S Cooper David C Wedge Daniel S Brewer	CONCLUSIONS: Cells within regions of morphologically normal tissue (both BPH and non-BPH) can expand under selective pressure by mechanisms that are distinct from those occurring in adjacent cancer, but that are allied to the presence of cancer. Expansions, which are probably stromal in origin, are characterised by lack of recurrent driver mutations, by almost complete absence of structural variants/copy number alterations, and mutational processes similar to malignant tissue. Our findings have...	pmid:36131292 doi:10.1186/s12943-022-01644-3	Wed, 21 Sep 2022 06:00:00 -0400
11	pubmed:36131498	First report of Corn Ear Rot Caused by <i>Fusarium asiaticum</i> in China	Baiwen Jiang Dian Yao Wang Jiangruihang Zhou Juan Cai Jujuan Jiang Lianxia Wang Yonggang Li	Corn (<i>Zea mays</i> L.) ear rot, caused by various pathogens, is one of the most significant diseases of corn worldwide. In September 2020, a survey was undertaken to identify pathogenic fungi associated with corn ear rot in Suihua city (46.63°N 126.98°E), Heilongjiang Province, China. The average disease incidence was 14.2% and 15.6% in each of two fields sampled (~5 ha) using a five-point method (100 plants/each point). Twenty tissue samples from 20 diseased ears, showing white or pink mold on the...	pmid:36131498 doi:10.1094/PDIS-08-22-1934-PDN	Thu, 22 Sep 2022 06:00:00 -0400
12	pubmed:36131930	RAB20 deficiency promotes the development of silicosis via NLRP3 inflammasome	Zhouyangfan Peng Mingwu Duan Kai Zhao Yiting Tang Fang Liang	Silicosis is a worldwide serious occupational disease that is caused by inhalation of silica crystals. However, little is known about the pathogenesis mechanism of silicosis. We performed single-cell sequencing in bronchoalveolar lavage fluid (BALF) from mine workers with silicosis and their co-workers who did not develop silicosis, and found that the RAB20 deficiency in monocytes/macrophages was strongly linked to the development of silicosis. In the silicosis murine model, RAB20 knockout...	pmid:36131930 pmc:PMC9484360 doi:10.3389/fimmu.2022.967299	Thu, 22 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
13	pubmed:36131936	Single cell RNA sequencing reveals hemocyte heterogeneity in <i>Biomphalaria glabrata</i>: Plasticity over diversity	Rémi Pichon Silvain Pinaud Emmanuel Vignal Cristian Chaparro Marine Pratlong Anaïs Portet David Duval Richard Galinier Benjamin Gourbal	The freshwater snail <i>Biomphalaria glabrata</i> is an intermediate host of <i>Schistosoma mansoni</i> , the agent of human intestinal schistosomiasis. However, much is to be discovered about its innate immune system that appears as a complex black box, in which the immune cells (called hemocytes) play a major role in both cellular and humoral response towards pathogens. Until now, hemocyte classification has been based exclusively on cell morphology and ultrastructural description and depending on the...	pmid:36131936 pmc:PMC9484523 doi:10.3389/fimmu.2022.956871	Thu, 22 Sep 2022 06:00:00 -0400
14	pubmed:36132681	Multifunctional self-assembled peptide nanoparticles for multimodal imaging-guided enhanced theranostic applications against glioblastoma multiforme	Syed Faheem Askari Rizvi Azam Ali Munir Ahmad Shuai Mu Haixia Zhang	The synthesis of self-assembled peptide nanoparticles using a facile one-pot synthesis approach is gaining increasing attention, allowing therapy in combination with diagnosis. Their drawback is limited diagnostic potential, which can be improved after necessary modifications and efficacious functionalization. Herein, a cyclic heptapeptide having the Arg-Gly-Asp-Lys-Leu-Ala-Lys sequence was modified by conjugation of the -amino group of the terminal lysine residue with diethylenetriamine...	pmid:36132681 pmc:PMC9419261 doi:10.1039/d1na00597a	Thu, 22 Sep 2022 06:00:00 -0400
15	pubmed:36133906	Systematic analysis of MCM3 in pediatric medulloblastoma via multi-omics analysis	Liangliang Cao Yang Zhao Zhuangzhuag Liang Jian Yang Jiajia Wang Shuangwei Tian Qinhua Wang Baocheng Wang Heng Zhao Feng Jiang Jie Ma	Minichromosome maintenance proteins are DNA-dependent ATPases that bind to replication origins and allow a single round of DNA replication. One member of this family, MCM3, is reportedly active in most cancers. To systematically elucidate the mechanisms affected by aberrant MCM3 expression and evaluate its clinical significance, we analyzed multi-omics data from the GEO database and validated them in cell lines and tumor samples. First, we showed the upregulation of MCM3 in medulloblastoma (MB)...	pmid:36133906 pmc:PMC9483186 doi:10.3389/fmolb.2022.815260	Thu, 22 Sep 2022 06:00:00 -0400
16	pubmed:36134527	Tuning the Dynamics of Viral Factories- Inspired Compartments Formed by Peptide-RNA Liquid-Liquid Phase Separation	Itai Katzir Elvira Haimov Ayala Lampel	Viral factories are intracellular microcompartments formed by mammalian viruses in their host cells, and contain necessary machinery for viral genome replication, capsid assembly and maturation, thus serve as "factories" for formation of new viral particles. Recent evidence suggest that these compartments are formed by liquid-liquid phase separation (LLPS) of viral proteins and nucleic acids and present dynamic properties. Inspired by the remarkable functionalities of viral factories we designed...	pmid:36134527 doi:10.1002/adma.202206371	Thu, 22 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
17	pubmed:36134564	Acute myeloid leukemia with myelodysplasia-related changes and blasts of the mixed T/myeloid phenotype: a case report	Xian-Fu Sheng Li-Li Hong Fei-Yan Huang Hai-Feng Zhuang	A rare but clinically important diagnostic dilemma arises when cases meet the criteria for both acute myeloid leukemia with myelodysplasia-related changes (AML-MRC) and mixed phenotype acute leukemia, especially those that evolve from myelodysplastic syndrome. We describe a 56-year-old male patient who presented with cytopenias and was initially diagnosed with myelodysplastic syndrome with single lineage dysplasia. Nearly 1 year later, this patient progressed to acute leukemia, and his blast...	pmid:36134564 doi:10.1177/03000605221122741	Thu, 22 Sep 2022 06:00:00 -0400
18	pubmed:36134665	Multiple Nf1 Schwann cell populations reprogram the plexiform neurofibroma tumor microenvironment	Leah J Kershner Kwangmin Choi Jianqiang Wu Xiyuan Zhang Melissa Perrino Nathan Salomonis Jack F Shern Nancy Ratner	To define alterations early in tumor formation, we studied nerve tumors in neurofibromatosis 1 (NF1), a tumor predisposition syndrome. Affected individuals develop neurofibromas, benign tumors driven by NF1 loss in Schwann cells (SCs). By comparing normal nerve cells to plexiform neurofibroma (PN) cells using single-cell and bulk RNA sequencing, we identified changes in 5 SC populations, including a de novo SC progenitor-like (SCP-like) population. Long after Nf1 loss, SC populations developed...	pmid:36134665 doi:10.1172/jci.insight.154513	Thu, 22 Sep 2022 06:00:00 -0400
19	pubmed:36134697	Hyaluronic acids mediate the infiltration, migration, and M2 polarization of macrophages: evaluating metabolic molecular phenotypes in gliomas	Hao Zhang Nan Zhang Ziyu Dai Zeyu Wang Xun Zhang Xisong Liang Liyang Zhang Songsan Feng Wantao Wu Weijie Ye Jian Zhang Peng Luo Zaoqu Liu Quan Cheng Zhixiong Liu	Gliomas cause high mortality around the world. The metabolic pattern of the tumor was previously suggested to be associated with the patient's survival outcome and immune activity. Yet, this relationship in glioma remains unknown. This study systematically evaluated the immune landscape in different phenotypes classified by metabolic-related pathways of 3068 glioma samples and 33 glioblastoma single-cell sequencing samples. Machine learning prediction analysis of microarray with R (pamr) was...	pmid:36134697 doi:10.1002/1878-0261.13315	Thu, 22 Sep 2022 06:00:00 -0400
20	pubmed:36134995	Polymorphisms of the IL-17A Gene Influence Milk Production Traits and Somatic Cell Score in Chinese Holstein Cows	Sahar Ghulam Mohyuddin Yan Liang Wei Ni Abdelaziz Adam Idriss Arbab Huiming Zhang Mingxun Li Zhangping Yang Niel A Karrow Yongjiang Mao	The cow's milk production characteristics are a significant economic indicator in the livestock industry. Serum cytokines such as interleukin-17 (IL-17) may be potential indicators for bovine mastitis concerning the milk somatic cell count (SCC) and somatic cell score (SCS). The current study aims to find previously undiscovered single nucleotide polymorphisms in the bovine (IL-17A) gene and further investigates their associations with milk production traits in Chinese Holstein cows. Twenty...	pmid:36134995 doi:10.3390/bioengineering9090448	Thu, 22 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
21	pubmed:36135446	The Landscape of Cell Death Processes with Associated Immunogenic and Fibrogenic Effects in Arrhythmogenic Cardiomyopathy	Wenzhao Lu Yanfang Rao Yao Li Yan Dai Keping Chen	Arrhythmogenic cardiomyopathy (ACM) is a heritable myocardial disease characterized by life-threatening ventricular arrhythmias and sudden cardiac death. Cardiomyocyte death is an essential pathogenic mechanism in ACM, but the cell death landscape has never been elucidated. Our study aimed to address this problem based on RNA-sequencing (RNA-seq) data. Myocardial RNA-seq data from arrhythmogenic right ventricular cardiomyopathy (ARVC) patients and normal controls were obtained from the Gene...	pmid:36135446 doi:10.3390/jcdd9090301	Thu, 22 Sep 2022 06:00:00 -0400
22	pubmed:36136268	Colorectal cancer organoid models uncover oxaliplatin-resistant mechanisms at single cell resolution	Guanglong Chen Ting Gong Zhe Wang Zeyu Wang Xiaolin Lin Sunrui Chen Chu Sun Weijie Zhao Ye Kong Huihan Ai Hang Yang Yusheng Liu Fangyan Wu Jiawei Kang Shasha Zhao Xiuying Xiao Jing Sun Aina He Zhi Li	CONCLUSION: We generated an oxaliplatin-resistant CRC organoid model that was employed to provide potential therapeutic targets for treating CRC patients exhibiting oxaliplatin-resistance.	pmid:36136268 doi:10.1007/s13402-022-00705-5	Thu, 22 Sep 2022 06:00:00 -0400
23	pubmed:36136514	Mesenchymal cell replacement corrects thymus hypoplasia in murine models of 22q11.2 deletion syndrome	Pratibha Bhalla Qiumei Du Ashwani Kumar Chao Xing Angela Moses Igor Dozmorov Christian A Wysocki Ondine B Cleaver Timothy J Pirolli Mary Louise Markert M Teresa de la Morena Antonio Baldini Nicolai Sc van Oers	22q11.2 deletion syndrome (22q11.2DS) is the most common human chromosomal microdeletion, causing developmentally linked congenital malformations; thymus hypoplasia, hypoparathyroidism and/or cardiac defects. Thymus hypoplasia leads to T cell lymphopenia, which most often results in mild SCID. Despite decades of research, the molecular underpinnings leading to thymus hypoplasia in 22q11.2DS remain unknown. Comparing embryonic thymuses from mouse models of 22q11.2DS (Tbx1neo2/neo2) revealed...	pmid:36136514 doi:10.1172/JCI160101	Thu, 22 Sep 2022 06:00:00 -0400
24	pubmed:36136607	A human STAT3 gain-of-function variant confers T cell dysregulation without predominant Treg dysfunction in mice	Erica G Schmitt Kelsey A Toth Samuel I Risma Ana Kolicheski Nermina Saucier Rafael J Feliciano Berríos Zev J Greenberg Jennifer W Leiding Jack J Bleesing Akaluck Thatayatikom Laura G Schuettpelez John R Edwards Tiphanie P Vogel Megan A Cooper	Primary immune regulatory disorders (PIRD) are a group of disorders characterized by immune dysregulation, presenting with a wide range of clinical disease including autoimmunity, autoinflammation, or lymphoproliferation. Autosomal dominant germline gain-of-function (GOF) variants in STAT3 result in a PIRD with a broad clinical spectrum. Studies in patients have documented a decreased frequency of FOXP3+ regulatory T (Treg) cells and an increased frequency of Th17 cells in some patients with...	pmid:36136607 doi:10.1172/jci.insight.162695	Thu, 22 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
25	pubmed:36137068	Comparative single-cell transcriptional atlases of Babesia species reveal conserved and species-specific expression profiles	Yasaman Rezvani Caroline D Keroack Brendan Elsworth Argenis Arriolas Marc-Jan Gubbels Manoj T Duraisingh Kourosh Zarringhalam	Babesia is a genus of apicomplexan parasites that infect red blood cells in vertebrate hosts. Pathology occurs during rapid replication cycles in the asexual blood stage of infection. Current knowledge of Babesia replication cycle progression and regulation is limited and relies mostly on comparative studies with related parasites. Due to limitations in synchronizing Babesia parasites, fine-scale time-course transcriptomic resources are not readily available. Single-cell transcriptomics provides...	pmid:36137068 doi:10.1371/journal.pbio.3001816	Thu, 22 Sep 2022 06:00:00 -0400