

single cell sequencing

NCT Number		Title	Authors	Description	Identifier	Dates
1	pubmed:36085725	Segmentation with Residual Attention U-Net and an Edge-Enhancement Approach Preserves Cell Shape Features	Nanyan Zhu Chen Liu Britney Forsyth Zakary S Singer Andrew F Laine Tal Danino Jia Guo	The ability to extrapolate gene expression dynamics in living single cells requires robust cell segmentation, and one of the challenges is the amorphous or irregularly shaped cell boundaries. To address this issue, we modified the U-Net architecture to segment cells in fluorescence widefield microscopy images and quantitatively evaluated its performance. We also proposed a novel loss function approach that emphasizes the segmentation accuracy on cell boundaries and encourages shape feature...	pmid:36085725 doi:10.1109/EMBC48229.2022.9871026	Sat, 10 Sep 2022 06:00:00 -0400
2	pubmed:36086608	Detecting anatomical characteristics of single motor units by combining high density electromyography and ultrafast ultrasound: a simulation study	Marco Carbonaro Silvia Zaccardi Silvia Seoni Kristen M Meiburger Alberto Botter	Muscle force production is the result of a sequence of electromechanical events that translate the neural drive issued to the motor units (MUs) into tensile forces on the tendon. Current technology allows this phenomenon to be investigated non-invasively. Single MU excitation and its mechanical response can be studied through high-density surface electromyography (HDsEMG) and ultrafast ultrasound (US) imaging respectively. In this study, we propose a method to integrate these two techniques to...	pmid:36086608 doi:10.1109/EMBC48229.2022.9871578	Sat, 10 Sep 2022 06:00:00 -0400
3	pubmed:36089620	sciCAN: single-cell chromatin accessibility and gene expression data integration via cycle-consistent adversarial network	Yang Xu Edmon Begoli Rachel Patton McCord	The boom in single-cell technologies has brought a surge of high dimensional data that come from different sources and represent cellular systems from different views. With advances in these single-cell technologies, integrating single-cell data across modalities arises as a new computational challenge. Here, we present an adversarial approach, sciCAN, to integrate single-cell chromatin accessibility and gene expression data in an unsupervised manner. We benchmarked sciCAN with 5 existing...	pmid:36089620 doi:10.1038/s41540-022-00245-6	Sun, 11 Sep 2022 06:00:00 -0400
4	pubmed:36091020	Association between frontal fibrosing Alopecia and Rosacea: Results from clinical observational studies and gene expression profiles	Lin Liu Yangmei Chen Jiayi Chen Yuzhou Xue Tingqiao Chen Yuxin Li Xinyi Shao Jin Chen	CONCLUSION: This study contributes to the understanding of the relationship between FFA and rosacea, and based on the hub genes, we reveal the potential pathologies shared by the two diseases. This finding provides new insights of underlying molecular mechanisms and it may inspire future research on this comorbidity.	pmid:36091020 pmc:PMC9448884 doi:10.3389/fimmu.2022.985081	Mon, 12 Sep 2022 06:00:00 -0400
5	pubmed:36098511	A Glu-Glu-Tyr Sequence in the Cytoplasmic Tail of the M2 Protein Renders Influenza A Virus Susceptible to Restriction of the Hemagglutinin-M2 Association in Primary Human Macrophages	Sukhmani Bedi Rajat Mudgal Amanda Haag Akira Ono	Influenza A virus (IAV) assembly at the plasma membrane is orchestrated by at least five viral components, including hemagglutinin (HA), neuraminidase (NA), matrix (M1), the ion channel M2, and viral ribonucleoprotein (vRNP) complexes, although particle formation is observed with expression of only HA and/or NA. While these five viral components are expressed efficiently in primary human monocyte-derived macrophages (MDMs) upon IAV infection, this cell type does not support efficient HA-M2...	pmid:36098511 doi:10.1128/jvi.00716-22	Tue, 13 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
6	pubmed:36098652	The Single-Cell Immunogenomic Landscape of B and Plasma Cells in Early-Stage Lung Adenocarcinoma	Dapeng Hao Guangchun Han Ansam Sinjab Lorena Isabel Gomez-Bolanos Rossana Lazcano Alejandra Serrano Sharia D Hernandez Enyu Dai Xuanye Cao Jian Hu Minghao Dang Ruiping Wang Yanshuo Chu Xingzhi Song Jianhua Zhang Edwin R Parra Jennifer A Wargo Stephen G Swisher Tina Cascone Boris Sepesi Andrew P Futreal Mingyao Li Steven M Dubinett Junya Fujimoto Luisa M Solis Soto Ignacio I Wistuba Christopher S Stevenson Avrum Spira Shabnam Shalapour Humam Kadara Linghua Wang	Tumor-infiltrating B and plasma cells (TIBs) are prevalent in lung adenocarcinoma (LUAD), however they are poorly characterized. We performed paired single-cell RNA and B cell receptor (BCR) sequencing of 16 early-stage LUADs and 47 matching multi-region normal tissues. By integrative analysis of ~50,000 TIBs, we define 12 TIB subsets in the LUAD and adjacent normal ecosystems and demonstrate extensive remodeling of TIBs in LUADs. Memory B cells and plasma cells (PCs) were highly enriched in...	pmid:36098652 doi:10.1158/2159-8290.CD-21-1658	Tue, 13 Sep 2022 06:00:00 -0400
7	pubmed:36098743	Zbtb34 promotes embryonic stem cell proliferation by elongating telomere length	Zheng Liu Xinran Wei Yue Gao Xiaodie Gao Xia Li Yujuan Zhong Xiujuan Wang Chong Liu Tianle Shi Jiabin Lv Tao Liu	Zbtb34 is a novel zinc finger protein, which is revealed by biological software analysis to have 3 zinc fingers, but its functions remain unknown. In this study, mouse Zbtb34 cDNA was amplified by PCR and inserted into the plasmid pEGFP-N1 to generate Zbtb34-EGFP fusion protein. The upregulation of Zbtb34 in mouse embryonic stem cells promoted telomere elongation and increased cell proliferation. In order to understand the above phenomena, the telomere co-immunoprecipitation technique was...	pmid:36098743 doi:10.18632/aging.204285	Tue, 13 Sep 2022 06:00:00 -0400
8	pubmed:36098765	Web-based gene expression analysis-paving the way to decode healthy and diseased ocular tissue	Julian Wolf Thabo Lapp Thomas Reinhard Hansjürgen Agostini Günther Schlunck Clemens Lange	CONCLUSION: Ocular transcriptome databases provide comprehensive and intuitive insights into the transcriptional profiles of a variety of healthy and diseased ocular tissues. Thus, they improve our understanding of the underlying molecular mediators, support hypothesis generation and help in the search for new diagnostic and therapeutic targets for various ocular diseases.	pmid:36098765 doi:10.1007/s00347-022-01721-4	Tue, 13 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
9	pubmed:36098925	Next-generation sequencing in the biodiversity conservation of endangered medicinal plants	Ruchika Sharma Chandragouda Patil Jaseela Majeed Subodh Kumar Geeta Aggarwal	Medicinal plants have been used as traditional herbal medicines in the treatment of various types of diseases. However, the increased demand for these plants highlights the importance of conservation specifically for endangered species. Significant advancements in next-generation sequencing (NGS) technologies have accelerated medicinal plant research while reducing costs and time demands. NGS systems enable high-throughput whole genome sequencing as well as direct RNA sequencing and...	pmid:36098925 doi:10.1007/s11356-022-22842-y	Tue, 13 Sep 2022 06:00:00 -0400
10	pubmed:36099047	Single cell transcriptomics reveals skewed cellular communication and phenotypic shift in pulmonary artery remodeling	Slaven Crnkovic Francesco Valzano Elisabeth Fließner Juergen Gindlhuber Helene Thekkekara Puthenparampil Maria C Basil Michael P Morley Jeremy Katzen Elisabeth Gschwandtner Walter Klepetko Edward Cantu Heimo Wolinski Horst Olschewski Jorg Lindenmann You-Yang Zhao Edward E Morrissey Leigh M Marsh Grazyna Kwapiszewska	A central feature of progressive vascular remodeling is altered smooth muscle cell (SMC) homeostasis; however, the understanding of how different cell populations contribute to this process is limited. Here, we utilized single cell RNA sequencing to provide insight into cellular composition changes within isolated pulmonary arteries (PA) from pulmonary arterial hypertension (PAH) and donor lungs. Our results revealed that remodeling skewed the balanced communication network between immune and...	pmid:36099047 doi:10.1172/jci.insight.153471	Tue, 13 Sep 2022 06:00:00 -0400
11	pubmed:36099421	EGFR Mutations and PD-L1 Expression in Early-Stage Non-Small Cell Lung Cancer: A Real-World Data From a Single Center in Brazil	Icaro Alves Pinto Rodrigo de Oliveira Cavagna Aline Larissa Virginio da Silva Josiane Mourão Dias Iara Vidigal Santana Laísa Caroline Souza Flávio Augusto Ferreira da Silva Maria Fernanda Biazotto Fernandes Gustavo Dix Junqueira Pinto Izabella Santos Negreiros Maria Fernanda Santiago Gonçalves Flávia Escremim de Paula Gustavo Nóriz Berardinelli Giovanna Maria Stanfoca Casagrande Marcela Oliveira da Silva Eduardo Caetano Albino da Silva Marco Antonio de Oliveira Alexandre Arthur Jacinto Vinicius Duval da Silva Rui Manuel Reis Pedro De Marchi Letícia Ferro Leal	CONCLUSION: The frequencies of EGFR mutations and PD-L1 positivity were described for early-stage non-squamous patients with NSCLC. These results will be essential for guiding treatment strategies with the recent approvals of osimertinib and immunotherapy in the adjuvant setting.	pmid:36099421 doi:10.1093/oncolo/oyac167	Tue, 13 Sep 2022 06:00:00 -0400
12	pubmed:36100084	Developmental regulation of epithelial cell cuboidal-to-squamous transition in Drosophila follicle cells	Dongyu Jia Allison Jevitt Yi-Chun Huang Belen Ramos Wu-Min Deng	Epithelial cells form continuous membranous structures for organ formation, and these cells are classified into three major morphological categories: cuboidal, columnar, and squamous. It is crucial that cells transition between these shapes during the morphogenetic events of organogenesis, yet this process remains poorly understood. All three epithelial cell shapes can be found in the follicular epithelium of Drosophila egg chamber during oogenesis. Squamous cells (SCs), are initially restricted...	pmid:36100084 doi:10.1016/j.ydbio.2022.09.001	Tue, 13 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
13	pubmed:36100256	Clinical application of comprehensive genomic profiling panel to thoracic malignancies: A single-center retrospective study	Kei Kunimasa Naotoshi Sugimoto Takahisa Kawamura Tomoyuki Yamasaki Keiichiro Honma Shigenori Nagata Yoji Kukita Fumie Fujisawa Tazuko Inoue Yuko Yamaguchi Mitsuko Kitasaka Toru Wakamatsu Takuo Yamai Sachiko Yamamoto Takuji Hayashi Takako Inoue Motohiro Tamiya Fumio Imamura Kazuo Nishimura Kazumi Nishino	CONCLUSIONS: CGP panels are useful in thoracic malignancies, especially lung cancer, because they can detect overlooked driver mutations and genetic alterations. We believe that the significance of conducting a CGP panel prior to treatment may also exist, as it may lead to the prediction of ICI treatment efficacy.	pmid:36100256 doi:10.1111/1759-7714.14643	Tue, 13 Sep 2022 06:00:00 -0400
14	pubmed:36100597	Diverse cell-specific patterns of alternative polyadenylation in Drosophila	Seungjae Lee Yen-Chung Chen FCA Consortium Austin E Gillen J Matthew Taliaferro Bart Deplancke Hongjie Li Eric C Lai	Most genes in higher eukaryotes express isoforms with distinct 3' untranslated regions (3' UTRs), generated by alternative polyadenylation (APA). Since 3' UTRs are predominant locations of post-transcriptional regulation, APA can render such programs conditional, and can also alter protein sequences via alternative last exon (ALE) isoforms. We previously used 3'-sequencing from diverse Drosophila samples to define multiple tissue-specific APA landscapes. Here, we exploit comprehensive single...	pmid:36100597 doi:10.1038/s41467-022-32305-0	Tue, 13 Sep 2022 06:00:00 -0400
15	pubmed:36103259	Assessment of a Simplified Cell-Free DNA Method for Prenatal Down Syndrome Screening	Glenn E Palomaki Elizabeth E Eklund Edward M Kloza Geralyn M Lambert-Messerlian	CONCLUSIONS: Our assessment of this simplified cfDNA-based system for prenatal screening for common trisomies performed in a prenatal screening laboratory is encouraging. Improved detection, low failure rates and rapid reporting can be achieved by collecting 2 samples. Future priorities should include achieving higher run precision using a single collection tube. Clinicaltrials.gov Registration Number: NCT03087357.	pmid:36103259 doi:10.1093/clinchem/hvac131	Wed, 14 Sep 2022 06:00:00 -0400
16	pubmed:36103539	Transcription and splicing regulation by NLRC5 shape the interferon response in human pancreatic cells	Florian Szymczak Maria Inês Alvelos Sandra Marín-Cañas Ângela Castela Stéphane Demine Maikel Luis Colli Anne Op de Beeck Sofia Thomaidou Lorella Marselli Arnaud Zaldumbide Piero Marchetti Décio L Eizirik	IFN is a key regulator of the dialogue between pancreatic cells and the immune system in early type 1 diabetes (T1D). IFN up-regulates HLA class I expression in human cells, fostering autoantigen presentation to the immune system. We observed by bulk and single-cell RNA sequencing that exposure of human induced pluripotent-derived islet-like cells to IFN induces expression of HLA class I and of other genes involved in antigen presentation, including the transcriptional activator NLRC5. We...	pmid:36103539 doi:10.1126/sciadv.abn5732	Wed, 14 Sep 2022 06:00:00 -0400