single cell sequencing

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36084431	A new microsporidian pathogen, Vairimorpha gastrophysae sp. nov., isolated from Gastrophysa viridula (Coleoptera: Chrysomelidae)	Mustafa Yaman Çiçek Aydin Andreas Linde Renate Radek	Gastrophysa viridula DeGeer 1775, the green dock leaf beetle, belongs to a group of beneficial insects, which can be used as a classical biological control agent against sorrels (Rumex sp., Polygonaceae). Therefore, any infection by pathogenic organisms in this beetle is undesirable. In the present study, a new microsporidian pathogen isolated from G. viridula was identified based on morphological and ultrastructural characteristics, supported with a molecular phylogenetic analysis. Light and...	pmid:36084431 doi:10.1016/j.ejop.2022.125913	Fri, 09 Sep 2022 06:00:00 -0400
2	pubmed:36084657	Mouse embryo model derived exclusively from embryonic stem cells undergoes neurulation and heart development	Kasey Y C Lau Hernan Rubinstein Carlos W Gantner Ron Hadas Gianluca Amadei Yonatan Stelzer Magdalena Zernicka-Goetz	Several in vitro models have been developed to recapitulate mouse embryogenesis solely from embryonic stem cells (ESCs). Despite mimicking many aspects of early development, they fail to capture the interactions between embryonic and extraembryonic tissues. To overcome this difficulty, we have developed a mouse ESC-based in vitro model that reconstitutes the pluripotent ESC lineage and the two extraembryonic lineages of the post-implantation embryo by transcription-factor-mediated induction....	pmid:36084657 doi:10.1016/j.stem.2022.08.013	Fri, 09 Sep 2022 06:00:00 -0400
3	pubmed:36085050	Single-cell transcriptomics reveals common epithelial response patterns in human acute kidney injury	Christian Hinze Christine Kocks Janna Leiz Nikos Karaiskos Anastasiya Boltengagen Shuang Cao Christopher Mark Skopnik Jan Klocke Jan-Hendrik Hardenberg Helena Stockmann Inka Gotthardt Benedikt Obermayer Laleh Haghverdi Emanuel Wyler Markus Landthaler Sebastian Bachmann Andreas C Hocke Victor Corman Jonas Busch Wolfgang Schneider Nina Himmerkus Markus Bleich Kai-Uwe Eckardt Philipp Enghard Nikolaus Rajewsky Kai M Schmidt-Ott	CONCLUSIONS: The study provides an extensive resource of the cell type-specific transcriptomic responses associated with critical illness-associated AKI in humans, highlighting recurrent disease-associated signatures and inter-individual heterogeneity. Personalized molecular disease assessment in human AKI may foster the development of tailored therapies.	pmid:36085050 doi:10.1186/s13073-022-01108-9	Fri, 09 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
4	pubmed:36085325	Myogenesis defects in a patient-derived iPSC model of hereditary GNE myopathy	Rebecca E Schmitt Douglas Y Smith Dong Seong Cho Lindsey A Kirkeby Zachary T Resch Teerin Liewluck Zhiyv Niu Margherita Milone Jason D Doles	Hereditary muscle diseases are disabling disorders lacking effective treatments. UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase (GNE) myopathy (GNEM) is an autosomal recessive distal myopathy with rimmed vacuoles typically manifesting in late adolescence/early adulthood. GNE encodes the rate-limiting enzyme in sialic acid biosynthesis, which is necessary for the proper function of numerous biological processes. Outside of the causative gene, very little is known about the...	pmid:36085325 doi:10.1038/s41536-022-00238-3	Fri, 09 Sep 2022 06:00:00 -0400
5	pubmed:36085357	Integrative and comparative single-cell analysis reveals transcriptomic difference between human tumefactive demyelinating lesion and glioma	Xiao-Yong Chen Yue Chen Wen-Hua Fang Zan-Yi Wu Deng-Liang Wang Ya-Wen Xu Liang-Hong Yu Yuan-Xiang Lin De-Zhi Kang Chen-Yu Ding	Tumefactive demyelinating lesion (TDL) is an immune-mediated disease which can be misdiagnosed as glioma. At present, there is no study comparing difference between the two disorders at the cellular level. Here, we perform integrative and comparative single-cell RNA sequencing (ScRNA-seq) transcriptomic analysis on TDL and glioma lesions. At single-cell resolution, TDL is comprised primarily of immune cells, which is completely different from glioma. The integrated analysis reveals a...	pmid:36085357 doi:10.1038/s42003-022-03900-0	Sat, 10 Sep 2022 06:00:00 -0400
6	pubmed:36085927	Identifying Transient Cells During Reprogramming via Persistent Homology	Aydolun Petenkaya Farid Manuchehrfar Constantinos Chronis Jie Liang	Single-cell RNA sequencing is a powerful method that helps delineate the regulatory mechanisms shaping the diverse cellular populations. Heterogeneous cell populations consist of individual cells, and the expression of distinct sets of genes can differentiate one sub-population of cells from another, as they are responsible for the emergence of distinct cellular phenotypes. Of particular importance are cells at transition states that bridge these different cellular phenotypes. In this study, we...	pmid:36085927 doi:10.1109/EMBC48229.2022.9871358	Sat, 10 Sep 2022 06:00:00 -0400
7	pubmed:36086064	Analytics Pipeline for Visualization of Single Cell RNA Sequencing Data from Brochoaveolar Fluid in COVID-19 Patients: Assessment of Neuro Fuzzy-C-Means and HDBSCAN	Suman Gare Soumita Chel Priyanka D Pantula Abha Saxena Kishalay Mitra Rahuldeb Sarkar Lopamudra Giri	Since the mutation in SARS-COV2 poses new challenges in designing vaccines, it is imperative to develop advanced tools for visualizing the genetic information. Specially, it remains challenging to address the patient-to-patient variability and identify the signature for severe/critical conditions. In this endeavor we analyze the large-scale RNA-sequencing data collected from broncho-alveolar fluid. In this work, we have used PCA and tSNE for the dimension-reduction. The novelty of the current...	pmid:36086064 doi:10.1109/EMBC48229.2022.9871686	Sat, 10 Sep 2022 06:00:00 -0400
8	pubmed:36087152	Comparative Methylome Analysis Reveals Epigenetic Signatures Associated with Growth and Shell Color in the Pacific Oyster, Crassostrea gigas	Chao Tan Chenyu Shi Yin Li Wen Teng Yongjing Li Huiru Fu Liting Ren Hong Yu Qi Li Shikai Liu	Fast growth is one of the most important breeding goals for all economic species such as the Pacific oyster (Crassostrea gigas), an aquaculture mollusk with top global production. Although the genetic basis and molecular mechanisms of growth-related traits have been widely investigated in the oyster, the role of DNA methylation involved in growth regulation remains largely unexplored. In this study, we performed a comparative DNA methylome analysis of two selectively bred C. gigas strains with...	pmid:36087152 doi:10.1007/s10126-022-10154-8	Sat, 10 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
9	pubmed:36087198	Characterization of KIR^{+}CD8^{+} Regulatory T Cells in Humans by scRNA- and TCR-seq	Jing Li Julie Wilhelmy Mark M Davis	Previous studies have demonstrated the regulatory functions of Ly49^(+)CD8^(+) T cells toward self-reactive CD4^(+) T cells in mice. Recently, we found KIR^(+)CD8^(+) T cells are the equivalent of mouse Ly49^(+)CD8^(+) T cells in humans. They are increased in patients with autoimmune or infectious diseases as a negative feedback mechanism to suppress the arising pathogenic cells and maintain peripheral tolerance. Here, we describe the methods on how we characterize the KIR^(+)CD8^(+) T cells...	pmid:36087198 doi:10.1007/978-1-0716-2712-9_4	Sat, 10 Sep 2022 06:00:00 -0400
10	pubmed:36087200	The Intra-Tumoral T Cell Receptor Repertoire: Steps Towards a Useful Clinical Biomarker	Gayathri Nageswaran Suzanne Byrne Selvaraju Veeriah Benny Chain	Adaptive immunity recognizes and responds to tumors, although they are part of the immunological "self." T cells, both CD4+ and CD8+, play a key role in the process, and the specific set of receptors which recognize tumor antigens therefore has the potential to provide prognostic biomarkers for tracking tumor growth after cancer therapy, including immunotherapy. Most published data on the T cell repertoire continue to rely on commercial proprietary methods, which often do not allow access to the...	pmid:36087200 doi:10.1007/978-1-0716-2712-9_6	Sat, 10 Sep 2022 06:00:00 -0400
11	pubmed:36087201	Enriching and Characterizing T Cell Repertoires from 3' Barcoded Single-Cell Whole Transcriptome Amplification Products	Tasneem Jivanjee Samira Ibrahim Sarah K Nyquist G James Gatter Joshua D Bromley Swati Jaiswal Bonnie Berger Samuel M Behar J Christopher Love Alex K Shalek	Antigen-specific T cells play an essential role in immunoregulation and many diseases such as cancer. Characterizing the T cell receptor (TCR) sequences that encode T cell specificity is critical for elucidating the antigenic determinants of immunological diseases and designing therapeutic remedies. However, methods of obtaining single-cell TCR sequencing data are labor and cost intensive, typically requiring both cell sorting and full-length single-cell RNA-sequencing (scRNA-seq). New...	pmid:36087201 doi:10.1007/978-1-0716-2712-9_7	Sat, 10 Sep 2022 06:00:00 -0400
12	pubmed:36087202	Tetramer-Associated T Cell Receptor Sequencing	Michael Malone Ke-Yue Ma Shu-Qi Zhang Ning Jiang	Linking antigen specificity to T cell receptor (TCR) sequences is critical, albeit challenging, to both understanding T cell biology and developing T cell-based therapeutics. Here, we describe in detail tetramer-associated TCR sequencing (TetTCR-Seq), a novel approach to tackling this challenge. TetTCR-Seq is accomplished by multiplexing DNA-barcoded peptide-MHC (pMHC) tetramers, allowing for simultaneous recall of antigen specificity and TCR sequences after single cell sequencing. Additionally,...	pmid:36087202 doi:10.1007/978-1-0716-2712-9_8	Sat, 10 Sep 2022 06:00:00 -0400
13	pubmed:36087203	T-Cell Repertoire Characterization	Anna Pasetto Marcus Buggert	T-cell repertoire characterization is a methodology that enables the identification of T-cell receptor (TCR) gene sequences in a T-cell population. TCR genes are composed of modular gene segments V (D) J that undergo somatic recombination, resulting in unique and unpredictable sequences that can be utilized to identify each T-cell clone. The analysis of the TCR composition in a T-cell population can give information on the biological phenomenon such as antigen-driven expansion and heterogeneity...	pmid:36087203 doi:10.1007/978-1-0716-2712-9_9	Sat, 10 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
14	pubmed:36087208	A Bioinformatic Framework for Dissecting the Dynamics of T Cells from Single-Cell Transcriptome	Lei Zhang Jiesheng Li	The quantitative tracking of the dynamics of T cells is challenging in human immunology. Although bulk sequencing of T cell receptor (TCR) - and -chains has been widely used for determining the clonality of T cells, such methods are limited in unveiling the phenotypic differences of T cells with the same clonotypes. Here, we describe a bioinformatics framework, STARTRAC, that integrates the single-cell transcriptome and TCR sequences as lineage-specific markers to quantitatively assess the...	pmid:36087208 doi:10.1007/978-1-0716-2712-9_14	Sat, 10 Sep 2022 06:00:00 -0400
15	pubmed:36087210	Flexible Distance-Based TCR Analysis in Python with tcrdist3	Koshlan Mayer-Blackwell Andrew Fiore-Gartland Paul G Thomas	Paired- and single-chain T cell receptor (TCR) sequencing are now commonly used techniques for interrogating adaptive immune responses. TCRs targeting the same epitope frequently share motifs consisting of critical contact residues. Here we illustrate the key features of tcrdist3, a new Python package for distance-based TCR analysis through a series of three interactive examples. In the first example, we illustrate how tcrdist3 can integrate sequence similarity networks, gene-usage plots, and...	pmid:36087210 doi:10.1007/978-1-0716-2712-9_16	Sat, 10 Sep 2022 06:00:00 -0400
16	pubmed:36087211	Multimodal T Cell Analysis with CoNGA	Stefan A Schattgen William D Hazelton Paul G Thomas Philip Bradley	Advances in single-cell technologies have made it possible to simultaneously quantify gene expression and immune receptor sequence across thousands of individual T or B cells in a single experiment. Data from such experiments are advancing our understanding of the relationship between adaptive immune receptor sequence and transcriptional profile. We recently reported a software tool, CoNGA, specifically developed to detect correlation between receptor sequence and transcriptional profile. Here...	pmid:36087211 doi:10.1007/978-1-0716-2712-9_17	Sat, 10 Sep 2022 06:00:00 -0400