single cell sequencing

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36122567	A New Understanding, Guided by Single-Cell Sequencing, of the Establishment and Maintenance of the Ovarian Reserve in Mammals	Emily R Frost Emmalee A Ford Alexandra E Peters Robin Lovell-Badge Güne Taylor Eileen A McLaughlin Jessie M Sutherland	BACKGROUND: Oocytes are a finite and non-renewable resource that are maintained in primordial follicle structures. The ovarian reserve is the totality of primordial follicles, present from birth, within the ovary and its establishment, size, and maintenance dictates the duration of the female reproductive lifespan. Understanding the cellular and molecular dynamics relevant to the establishment and maintenance of the reserve provides the first steps necessary for modulating both individual human...	pmid:36122567 doi:10.1159/000526426	Mon, 19 Sep 2022 06:00:00 -0400
2	pubmed:36122800	Transcriptomic heterogeneity of skin across different anatomic sites	Yicen Yan Jie Tian Yang Wang Yurong Li Chong Zhang Shenxi Zhang Pingping Lin Rui Peng Chunxia Zhao Le Zhuang Binbin Lai Liang Zhou Guohong Zhang Hang Li	Multi-omic studies including RNA-Sequencing, single-cell RNA-Sequencing, and epigenomics can provide insight into the connection between anatomically heterogeneous gene expression profile of skin and dermatoses-predisposed sites, in which RNA-Sequencing is essential. Therefore, herein, 159 skin samples collected mainly from discarded normal skin tissue during surgical treatment for benign skin tumors were used for RNA-sequencing. Based on cluster analysis, the skin was divided into four regions,...	pmid:36122800 doi:10.1016/j.jid.2022.08.053	Mon, 19 Sep 2022 06:00:00 -0400
3	pubmed:36123219	Analysis of BRCA2 Copy Number Loss and Genomic Instability in Circulating Tumor Cells from Patients with Metastatic Castration-resistant Prostate Cancer	Ethan S Barnett Nikolaus Schultz Konrad H Stopsack Ernest T Lam Andrea Arfe Jerry Lee Jimmy L Zhao Joseph D Schonhoft Emily A Carbone Niamh M Keegan Andreas Wibmer Yipeng Wang David B Solit Wassim Abida Richard Wenstrup Howard I Scher	CONCLUSIONS: Copy number profiles can reliably be generated using CTC sWGS, which detected a majority of tissue-confirmed BRCA2 loss and "CTC-only" losses. BRCA2 losses were supported by increases in genomic instability.	pmid:36123219 doi:10.1016/j.eururo.2022.08.010	Mon, 19 Sep 2022 06:00:00 -0400
4	pubmed:36123393	Single nuclei transcriptomics of muscle reveals intra-muscular cell dynamics linked to dystrophin loss and rescue	Deirdre D Scripture-Adams Kevin N Chesmore Florian Barthélémy Richard T Wang Shirley Nieves-Rodriguez Derek W Wang Ekaterina I Mokhonova Emilie D Douine Jijun Wan Isaiah Little Laura N Rabichow Stanley F Nelson M Carrie Miceli	In Duchenne muscular dystrophy, dystrophin loss leads to chronic muscle damage, dysregulation of repair, fibro-fatty replacement, and weakness. We develop methodology to efficiently isolate individual nuclei from minute quantities of frozen skeletal muscle, allowing single nuclei sequencing of irreplaceable archival samples and from very small samples. We apply this method to identify cell and gene expression dynamics within human DMD and mdx mouse muscle, characterizing effects of dystrophin...	pmid:36123393 doi:10.1038/s42003-022-03938-0	Mon, 19 Sep 2022 06:00:00 -0400

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5	pubmed:36123598	Elucidating the diversity of malignant mesenchymal states in glioblastoma by integrative analysis	Rony Chanoch-Myers Adi Wider Mario L Suva Itay Tirosh	CONCLUSIONS: Diverse MES states occur in glioblastoma. These states share a subset of core genes but differ primarily in their association with hypoxia vs. astrocytic expression programs, and with immune suppression vs. activation, respectively.	pmid:36123598 doi:10.1186/s13073-022-01109-8	Mon, 19 Sep 2022 06:00:00 -0400
6	pubmed:36123835	Robust neuronal differentiation of human embryonic stem cells for neurotoxicology	Athina Samara Martin Falck Mari Spildrejorde Magnus Leithaug Ganesh Acharya Robert Lyle Ragnhild Eskeland	Here, we describe a protocol for rapid neuronal differentiation from human embryonic stem cells (hESCs) toward a heterogenous population of telencephalic progenitors, immature and mature neurons, for drug-screening and early-brain differentiation studies. hESC neuronal differentiation depends on adhesion and minimal cell-passaging to avert monolayer cross-connectivity rupture. In this protocol, we detail optimized cell-seeding densities and coating conditions with high cell viability suitable...	pmid:36123835 doi:10.1016/j.xpro.2022.101533	Tue, 20 Sep 2022 06:00:00 -0400
7	pubmed:36124068	Systematic Characterization of Expression Patterns and Immunocorrelations of Formin-Like Genes in Breast Cancer	Erli Gao Xuehai Wang Fengxu Wang Siyuan Deng Weiyi Xia Rui Wang Xiangdong Wang Xinyuan Zhao Haixin Qian	CONCLUSIONS: The fact and result which we analyzed demonstrate FMNL1 as a diagnostic marker for TIICs by comprehensively elucidating the expression patterns and changeable prognostic implications of FMNLs in BrCa clinical applications.	pmid:36124068 pmc:PMC9482526 doi:10.1155/2022/8577821	Tue, 20 Sep 2022 06:00:00 -0400
8	pubmed:36124658	Comparison of scRNA-seq data analysis method combinations	Li Xu Tong Xue Weiyue Ding Linshan Shen	Single-cell ribonucleic acid (RNA)-sequencing (scRNA-seq) data analysis refers to the use of appropriate methods to analyze the dataset generated by RNA-sequencing performed on the single-cell transcriptome. It usually contains three steps: normalization to eliminate the technical noise, dimensionality reduction to facilitate visual understanding and data compression and clustering to divide the data into several similarity-based clusters. In addition, the gene expression data contain a large...	pmid:36124658 doi:10.1093/bfgp/elac027	Tue, 20 Sep 2022 06:00:00 -0400
9	pubmed:36124665	Density-based detection of cell transition states to construct disparate and bifurcating trajectories	Tian Lan Gyorgy Hutvagner Xuan Zhang Tao Liu Limsoon Wong Jinyan Li	Tree- and linear-shaped cell differentiation trajectories have been widely observed in developmental biologies and can be also inferred through computational methods from single-cell RNA-sequencing datasets. However, trajectories with complicated topologies such as loops, disparate lineages and bifurcating hierarchy remain difficult to infer accurately. Here, we introduce a density-based trajectory inference method capable of constructing diverse shapes of topological patterns including the most...	pmid:36124665 doi:10.1093/nar/gkac785	Tue, 20 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
10	pubmed:36124685	Integrated longitudinal analysis of adult grade 4 diffuse gliomas with long-term relapse interval revealed upregulation of TGF- signaling in recurrent tumors	Elham Kashani Désirée Schnidrig Ali Hashemi Gheinani Martina Selina Ninck Philipp Zens Theoni Maragkou Ulrich Baumgartner Philippe Schucht Gunnar Rätsch Mark A Rubin Sabina Berezowska Charlotte K Y Ng Erik Vassella SOCIBP consortium	CONCLUSIONS: Our results suggest an important role of TGF- signaling in recurrent gliomas. This may have clinical implication, since TGF- inhibitors have entered clinical phase studies and may potentially be used in combination therapy to interfere with chemoradiation resistance. Recurrent gliomas show high incidence of early branching evolution. High tumor plasticity is confirmed at the level of microRNA and mRNA expression profiles.	pmid:36124685 doi:10.1093/neuonc/noac220	Tue, 20 Sep 2022 06:00:00 -0400
11	pubmed:36124798	Discovering significant evolutionary trajectories in cancer phylogenies	Leonardo Pellegrina Fabio Vandin	MOTIVATION: Tumors are the result of a somatic evolutionary process leading to substantial intra-tumor heterogeneity. Single-cell and multi-region sequencing enable the detailed characterization of the clonal architecture of tumors and have highlighted its extensive diversity across tumors. While several computational methods have been developed to characterize the clonal composition and the evolutionary history of tumors, the identification of significantly conserved evolutionary trajectories...	pmid:36124798 doi:10.1093/bioinformatics/btac467	Tue, 20 Sep 2022 06:00:00 -0400
12	pubmed:36124800	SimBu: bias-aware simulation of bulk RNA-seq data with variable cell-type composition	Alexander Dietrich Gregor Sturm Lorenzo Merotto Federico Marini Francesca Finotello Markus List	MOTIVATION: As complex tissues are typically composed of various cell types, deconvolution tools have been developed to computationally infer their cellular composition from bulk RNA sequencing (RNA-seq) data. To comprehensively assess deconvolution performance, gold-standard datasets are indispensable. Gold-standard, experimental techniques like flow cytometry or immunohistochemistry are resource-intensive and cannot be systematically applied to the numerous cell types and tissues profiled with...	pmid:36124800 doi:10.1093/bioinformatics/btac499	Tue, 20 Sep 2022 06:00:00 -0400
13	pubmed:36124841	Dynamic cancer drivers: a causal approach for cancer driver discovery based on bio-pathological trajectories	Andres M Cifuentes-Bernal Vu V H Pham Xiaomei Li Lin Liu Jiuyong Li Thuc Duy Le	The traditional way for discovering genes which drive cancer (namely cancer drivers) neglects the dynamic information of cancer development, even though it is well known that cancer progresses dynamically. To enhance cancer driver discovery, we expand cancer driver concept to dynamic cancer driver as a gene driving one or more bio-pathological transitions during cancer progression. Our method refers to the fact that cancer should not be considered as a single process but a compendium of altered...	pmid:36124841 doi:10.1093/bfgp/elac030	Tue, 20 Sep 2022 06:00:00 -0400
14	pubmed:36125273	Uncovering Lasonolide A Biosynthesis Using Genome-Resolved Metagenomics	Siddharth Uppal Jackie L Metz René K M Xavier Keshav Kumar Nepal Dongbo Xu Guojun Wang Jason C Kwan	Invertebrates, particularly sponges, have been a dominant source of new marine natural products. For example, lasonolide A (LSA) is a potential anticancer molecule isolated from the marine sponge Forcepia sp., with nanomolar growth inhibitory activity and a unique cytotoxicity profile against the National Cancer Institute 60-cell-line screen. Here, we identified the putative biosynthetic pathway for LSA. Genomic binning of the Forcepia sponge metagenome revealed a Gram-negative bacterium...	pmid:36125273 doi:10.1128/mbio.01524-22	Tue, 20 Sep 2022 06:00:00 -0400

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15	pubmed:36125329	[Thymosin 4 and prothymosin promote cardiac regeneration post-ischemic injury in mice](#)	Monika M Gladka Anne Katrine Z Johansen Sebastiaan J van Kampen Marijn M C Peters Bas Molenaar Danielle Versteeg Lieneke Kooijman Lorena Zentilin Mauro Giacca Eva van Rooij	The adult mammalian heart is a post-mitotic organ. Even in response to necrotic injuries, where regeneration would be essential to reinstate cardiac structure and function, only a minor percentage of cardiomyocytes undergo cytokinesis. The gene program that promotes cell division within this population is not fully understood. Here, we demonstrate increased EdU incorporation in cardiomyocytes at 3 days post-myocardial infarction (MI) in mice. By applying multi-color lineage tracing, we show that...	pmid:36125329 doi:10.1093/cvr/cvac155	Tue, 20 Sep 2022 06:00:00 -0400
16	pubmed:36125951	[Single-cell genomics reveals population structures from *in vitro* evolutionary studies of *Salmonella*](#)	Matt Bawn Johana Hernandez Eleftheria Trampari Gaetan Thilliez Christopher Quince Mark A Webber Robert A Kingsley Neil Hall Iain C Macaulay	Single-cell DNA sequencing has the potential to reveal detailed hierarchical structures in evolving populations of cells. Single cell approaches are increasingly used to study clonal evolution in human ageing and cancer but have not yet been deployed to study evolving clonal microbial populations. Here, we present an approach for single bacterial genomic analysis for in vitro evolution experiments using FACS isolation of individual bacteria followed by whole-genome amplification and sequencing....	pmid:36125951 doi:10.1099/mgen.0.000871	Tue, 20 Sep 2022 06:00:00 -0400
17	pubmed:36126183	[A Versatile in Vivo DNA Assembly Toolbox for Fungal Strain Engineering](#)	Zofia Dorota Jarczynska Katherina Garcia Vanegas Marcus Deichmann Christina Nørskov Jensen Marouschka Jasmijn Scheeper Malgorzata Ewa Futyma Tomas Strucko Fabiano Jares Contesini Tue Sparholt Jørgensen Jakob Blæsbjerg Hoof Uffe Hasbro Mortensen	Efficient homologous recombination in baker's yeast allows accurate fusion of DNA fragments via short identical sequence tags in vivo. Eliminating the need for an Escherichia coli cloning step speeds up genetic engineering of this yeast and sets the stage for large high-throughput projects depending on DNA construction. With the aim of developing similar tools for filamentous fungi, we first set out to determine the genetic- and sequence-length requirements needed for efficient fusion reactions,...	pmid:36126183 doi:10.1021/acssynbio.2c00159	Tue, 20 Sep 2022 06:00:00 -0400