

single cell sequencing

NCT Number		Title	Authors	Description	Identifier	Dates
1	pubmed:36075220	<a href="#">S1-END-seq reveals DNA secondary structures in human cells</a>	Gabriel Matos-Rodrigues Niek van Wietmarschen Wei Wu Veenu Tripathi Natasha C Koussa Raphael Pavani William J Nathan Elsa Callen Frida Belinky Ashraf Mohammed Marek Napierala Karen Usdin Aseem Z Ansari Sergei M Mirkin André Nussenzweig	DNA becomes single stranded (ssDNA) during replication, transcription, and repair. Transiently formed ssDNA segments can adopt alternative conformations, including cruciforms, triplexes, and quadruplexes. To determine whether there are stable regions of ssDNA in the human genome, we utilized S1-END-seq to convert ssDNA regions to DNA double-strand breaks, which were then processed for high-throughput sequencing. This approach revealed two predominant non-B DNA structures: cruciform DNA formed by...	pmid:36075220 doi:10.1016/j.molcel.2022.08.007	Thu, 08 Sep 2022 06:00:00 -0400
2	pubmed:36075888	<a href="#">Single nucleus transcriptomic analysis of rat nucleus accumbens reveals cell type-specific patterns of gene expression associated with volitional morphine intake</a>	Benjamin C Reiner Yafang Zhang Lauren M Stein Emilie Dávila Perea Gabriella Arauco-Shapiro Jennifer Ben Nathan Kael Ragnini Matthew R Hayes Thomas N Ferraro Wade H Berrettini Heath D Schmidt Richard C Crist	Opioid exposure is known to cause transcriptomic changes in the nucleus accumbens (NAc). However, no studies to date have investigated cell type-specific transcriptomic changes associated with volitional opioid taking. Here, we use single nucleus RNA sequencing (snRNAseq) to comprehensively characterize cell type-specific alterations of the NAc transcriptome in rats self-administering morphine. One cohort of male Brown Norway rats was injected with acute morphine (10 mg/kg, i.p.) or saline. A...	pmid:36075888 doi:10.1038/s41398-022-02135-1	Thu, 08 Sep 2022 06:00:00 -0400
3	pubmed:36075976	<a href="#">Comparative roadmaps of reprogramming and oncogenic transformation identify Bcl11b and Atoh8 as broad regulators of cellular plasticity</a>	A Huyghe G Furlan J Schroeder E Cascales A Trajkova M Ruel F Stüder M Larcombe Y Bo Yang Sun F Mugnier L De Matteo A Baygin J Wang Y Yu N Rama B Gibert J Kielbassa L Tonon P Wajda N Gadot M Brevet M Siouda P Mulligan R Dante P Liu H Gronemeyer M Mendoza-Parra J M Polo F Lavial	Coordinated changes of cellular plasticity and identity are critical for pluripotent reprogramming and oncogenic transformation. However, the sequences of events that orchestrate these intermingled modifications have never been comparatively dissected. Here, we deconvolute the cellular trajectories of reprogramming (via Oct4/Sox2/Klf4/c-Myc) and transformation (via Ras/c-Myc) at the single-cell resolution and reveal how the two processes intersect before they bifurcate. This approach led us to...	pmid:36075976 doi:10.1038/s41556-022-00986-w	Thu, 08 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
4	pubmed:36076083	<a href="#">Multiplexed, single-molecule, epigenetic analysis of plasma-isolated nucleosomes for cancer diagnostics</a>	Vadim Fedjuk Nir Erez Noa Furth Olga Beresh Ekaterina Andreishcheva Abhijeet Shinde Daniel Jones Barak Bar Zakai Yael Mavor Tamar Peretz Ayala Hubert Jonathan E Cohen Azzam Salah Mark Temper Albert Grinshpun Myriam Maoz Aviad Zick Guy Ron Efrat Shema	The analysis of cell-free DNA (cfDNA) in plasma provides information on pathological processes in the body. Blood cfDNA is in the form of nucleosomes, which maintain their tissue- and cancer-specific epigenetic state. We developed a single-molecule multiparametric assay to comprehensively profile the epigenetics of plasma-isolated nucleosomes (EPINUC), DNA methylation and cancer-specific protein biomarkers. Our system allows for high-resolution detection of six active and repressive histone...	pmid:36076083 doi:10.1038/s41587-022-01447-3	Thu, 08 Sep 2022 06:00:00 -0400
5	pubmed:36076084	<a href="#">High-throughput continuous evolution of compact Cas9 variants targeting single-nucleotide-pyrimidine PAMs</a>	Tony P Huang Zachary J Heins Shannon M Miller Brandon G Wong Pallavi A Balivada Tina Wang Ahmad S Khalil David R Liu	Despite the availability of Cas9 variants with varied protospacer-adjacent motif (PAM) compatibilities, some genomic loci-especially those with pyrimidine-rich PAM sequences-remain inaccessible by high-activity Cas9 proteins. Moreover, broadening PAM sequence compatibility through engineering can increase off-target activity. With directed evolution, we generated four Cas9 variants that together enable targeting of most pyrimidine-rich PAM sequences in the human genome. Using phage-assisted...	pmid:36076084 doi:10.1038/s41587-022-01410-2	Thu, 08 Sep 2022 06:00:00 -0400
6	pubmed:36076202	<a href="#">Dissection of transcriptome dysregulation and immune characterization in women with germline BRCA1 mutation at single-cell resolution</a>	Xuexin Yu Wanrun Lin Alexandra Spirtos Yan Wang Hao Chen Jianfeng Ye Jessica Parker Ci Ci Liu Yiying Wang Gabriella Quinn Feng Zhou Setsuko K Chambers Cheryl Lewis Jayanthi Lea Bo Li Wenxin Zheng	CONCLUSION: These results indicate that EMT and immune evasion in normal-looking tubal mucosae may represent early events leading to the development of HGSC in women with BRCA1 germline mutation. Our findings provide a probable molecular mechanism explaining why some, but not all, women with BRCA1 germline mutation present with early development and rapid dissemination of HGSC.	pmid:36076202 doi:10.1186/s12916-022-02489-9	Thu, 08 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
7	pubmed:36076232	<a href="#">A transcriptomic map of EGFR-induced epithelial-to-mesenchymal transition identifies prognostic and therapeutic targets for head and neck cancer</a>	Henrik Schinke Enxian Shi Zhongyang Lin Tanja Quadt Gisela Kranz Jiefu Zhou Hongxia Wang Julia Hess Steffen Heuer Claus Belka Horst Zitzelsberger Udo Schumacher Sandra Genduso Kristoffer Riecken Yujing Gao Zhengquan Wu Christoph A Reichel Christoph Walz Martin Canis Kristian Unger Philipp Baumeister Min Pan Olivier Gires	CONCLUSIONS: EGFR-mediated EMT conveyed through MAPK activation contributes to HNSCC progression upon induction of migration and invasion. A 5-gene risk score based on a novel EGFR-mediated EMT signature prognosticated survival of HNSCC patients and determined ITGB4 as potential therapeutic and predictive target in patients with strong EGFR-mediated EMT.	pmid:36076232 doi:10.1186/s12943-022-01646-1	Thu, 08 Sep 2022 06:00:00 -0400
8	pubmed:36076283	<a href="#">Regulating microglial miR-155 transcriptional phenotype alleviates Alzheimer's-induced retinal vasculopathy by limiting Clec7a/Galectin-3<sup>±</sup> neurodegenerative microglia</a>	Haoshen Shi Zhuoran Yin Yosef Koronyo Dieu-Trang Fuchs Julia Sheyn Miyah R Davis Jered W Wilson Milica A Margeta Kristen M Pitts Shawn Herron Seiko Ikezu Tsuneya Ikezu Stuart L Graham Vivek K Gupta Keith L Black Mehdi Mirzaei Oleg Butovsky Maya Koronyo-Hamaoui	Single cell RNA sequencing studies identified novel neurodegeneration-associated microglial (MGnD/DAM) subtypes activated around cerebral amyloid plaques. Micro-RNA (miR)-155 of the TREM2-APOE pathway was shown to be a key transcriptional regulator of MGnD microglial phenotype. Despite growing interest in studying manifestations of Alzheimer's disease (AD) in the retina, a CNS organ accessible to noninvasive high-resolution imaging, to date MGnD microglia have not been studied in the AD retina....	pmid:36076283 doi:10.1186/s40478-022-01439-z	Thu, 08 Sep 2022 06:00:00 -0400
9	pubmed:36076571	<a href="#">PARP inhibitors in small cell lung cancer: The underlying mechanisms and clinical implications</a>	Xueting Wang Xianhu Zeng Dan Li Chunrong Zhu Xusheng Guo Lingxin Feng Zhuang Yu	Since the concept, DNA damage repair has been stated as a natural biological event, and research has increasingly revealed its strong association to tumors, aging, immunity, biochemical detection, and other factors. The discovery of abnormal DNA repair in cancers has been heralded as a paradigm shift in the treatment of malignancies. A poly (ADP-ribose) polymerase (PARP) activates poly (ADP-ribosylation) to repair single-strand DNA breaks after DNA damage. In some cancers, such as breast cancer...	pmid:36076571 doi:10.1016/j.biopha.2022.113458	Fri, 09 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
10	pubmed:36076620	<a href="#">Targeting autophagy in aortic aneurysm and dissection</a>	Ze-Min Fang Xin Feng Yue Chen Hanshen Luo Ding-Sheng Jiang Xin Yi	Autophagy is a well-conserved biological process that maintains homeostasis. Accumulating evidence has revealed that autophagy plays an important role in various cardiovascular diseases, such as aneurysm, aortic dissection, atherosclerosis, and myocardial ischemia-reperfusion injury. Here, we summarize the current experimental evidence on the function of autophagy and autophagy proteins in aortic aneurysm and dissection (AAD). AAD is a very serious aortic disease, and there are currently no...	pmid:36076620 doi:10.1016/j.biopha.2022.113547	Fri, 09 Sep 2022 06:00:00 -0400
11	pubmed:36077273	<a href="#">Sex Differences in Coronary Artery Disease and Diabetes Revealed by scRNA-Seq and CITE-Seq of Human CD4+ T Cells</a>	Ryosuke Saigusa Jenifer Vallejo Rishab Gulati Sujit Silas Armstrong Suthahar Vasantika Suryawanshi Ahmad Alimadadi Jeffrey Makings Christopher P Durant Antoine Freuchet Payel Roy Yanal Ghosheh William Pandori Tanyaporn Pattarabanjird Fabrizio Drago Angela Taylor Coleen A McNamara Avishai Shemesh Lewis L Lanier Catherine C Hedrick Klaus Ley	Despite the decades-old knowledge that males and people with diabetes mellitus (DM) are at increased risk for coronary artery disease (CAD), the reasons for this association are only partially understood. Among the immune cells involved, recent evidence supports a critical role of T cells as drivers and modifiers of CAD. CD4+ T cells are commonly found in atherosclerotic plaques. We aimed to understand the relationship of CAD with sex and DM by single-cell RNA (scRNA-Seq) and antibody sequencing...	pmid:36077273 doi:10.3390/ijms23179875	Fri, 09 Sep 2022 06:00:00 -0400
12	pubmed:36077342	<a href="#">Transcription Factor MAFB as a Prognostic Biomarker for the Lung Adenocarcinoma</a>	Omar Samir Naohiro Kobayashi Teppei Nishino Mennatullah Siyam Manoj Kumar Yadav Yuri Inoue Satoru Takahashi Michito Hamada	MAFB is a basic leucine zipper (bZIP) transcription factor specifically expressed in macrophages. We have previously identified MAFB as a candidate marker for tumor-associated macrophages (TAMs) in human and mouse models. Here, we analyzed single-cell sequencing data of patients with lung adenocarcinoma obtained from the GEO database (GSE131907). Analyzed data showed that general macrophage marker CD68 and macrophage scavenger receptor 1 (CD204) were expressed in TAM and lung tissue macrophage...	pmid:36077342 doi:10.3390/ijms23179945	Fri, 09 Sep 2022 06:00:00 -0400
13	pubmed:36077692	<a href="#">Identification of Fusion Genes and Targets for Genetically Matched Therapies in a Large Cohort of Salivary Gland Cancer Patients</a>	Gerben Lassche Sjoerd van Helvert Astrid Eijkelenboom Martijn J H Tjan Erik A M Jansen Patricia H J van Cleef Gerald W Verhaegh Eveline J Kamping Katrien Grünberg Adriana C H van Engen-van Grunsven Marjolijn J L Ligtenberg Carla M L van Herpen	Introduction: Salivary gland cancer (SGC) is a rare cancer for which systemic treatment options are limited. Therefore, it is important to characterize its genetic landscape in search for actionable aberrations, such as NTRK gene fusions. This research aimed to identify these actionable aberrations by combining NGS-based analysis of RNA (gene fusions) and DNA (single and multiple nucleotide variants, copy number variants, microsatellite instability and tumor mutational burden) in a large cohort...	pmid:36077692 doi:10.3390/cancers14174156	Fri, 09 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
14	pubmed:36077846	<a href="#">Single-Cell Profiling of the Immune Atlas of Tumor-Infiltrating Lymphocytes in Endometrial Carcinoma</a>	Fang Jiang Yuhao Jiao Kun Yang Mingyi Mao Mei Yu Dongyan Cao Yang Xiang	Endometrial carcinoma (EC) is a gynecological malignancy with a high incidence; however, thorough studies on tumor-infiltrating lymphocyte (TIL) populations in EC are lacking. We aimed to map the immune atlas of TILs in type I EC via single-cell RNA sequencing (scRNA-seq), mass cytometry and flow cytometry analysis. We found that natural killer (NK) cells and CD8+ T lymphocytes were the major components of TILs in EC patients. We first identified three transcriptionally distinct NK cell subsets,...	pmid:36077846 doi:10.3390/cancers14174311	Fri, 09 Sep 2022 06:00:00 -0400
15	pubmed:36077890	<a href="#">Dosage Compensation of the X Chromosome during Sheep Testis Development Revealed by Single-Cell RNA Sequencing</a>	Jie Su Yue Zhang Hong Su Caiyun Wang Daqing Wang Yanyan Yang Xiunan Li Wangmei Qi Haijun Li Xihe Li Yongli Song Guifang Cao	Dosage compensation is a mechanism first proposed by Susumu Ohno, whereby X inactivation balances X gene output between males (XY) and females (XX), while X upregulation balances X genes with autosomal gene output. These mechanisms have been actively studied in Drosophila and mice, but research regarding them lags behind in domestic species. It is unclear how the X chromosome is regulated in the sheep male germline. To address this, using single-cell RNA sequencing, we analyzed testes in three...	pmid:36077890 doi:10.3390/ani12172169	Fri, 09 Sep 2022 06:00:00 -0400
16	pubmed:36078044	<a href="#">Paracrine ADP Ribosyl Cyclase-Mediated Regulation of Biological Processes</a>	Cecilia Astigiano Andrea Benzi Maria Elena Laugier Francesco Piacente Laura Sturla Lucrezia Guida Santina Bruzzone Antonio De Flora	ADP-ribosyl cyclases (ADPRCs) catalyze the synthesis of the Ca <sup>2+</sup> -active second messengers Cyclic ADP-ribose (cADPR) and ADP-ribose (ADPR) from NAD <sup>+</sup> as well as nicotinic acid adenine dinucleotide phosphate (NAADP <sup>+</sup> ) from NADP <sup>+</sup> . The best characterized ADPRC in mammals is CD38, a single-pass transmembrane protein with two opposite membrane orientations. The first identified form, type II CD38, is a glycosylated ectoenzyme, while type III CD38 has its active site in the cytosol. The...	pmid:36078044 doi:10.3390/cells11172637	Fri, 09 Sep 2022 06:00:00 -0400
17	pubmed:36078111	<a href="#">Inhibition of Gap Junctional Intercellular Communication Upregulates Pluripotency Gene Expression in Endogenous Pluripotent Muse Cells</a>	Khaled Hatabi Yukari Hirohara Yoshihiro Kushida Yasumasa Kuroda Shohei Wakao James Trosko Mari Dezawa	Gap junctions (GJ) are suggested to support stem cell differentiation. The Muse cells that are applied in clinical trials are non-tumorigenic pluripotent-like endogenous stem cells, can be collected as stage-specific embryonic antigen 3 (SSEA-3+) positive cells from multiple tissues, and show triploblastic differentiation and self-renewability at a single cell level. They were reported to up-regulate pluripotency gene expression in suspension. We examined how GJ inhibition affected pluripotency...	pmid:36078111 doi:10.3390/cells11172701	Fri, 09 Sep 2022 06:00:00 -0400
18	pubmed:36078120	<a href="#">A Single-Cell Survey of Cellular Heterogeneity in Human Great Saphenous Veins</a>	Yiping Sun Xueqing Hu Kui Zhang Man Rao Pengbin Yin Ran Dong	CONCLUSIONS: Our results identified critical cell-specific responses and cellular interactions in GSVs. Beyond serving as a repertoire, this work illustrates multifactorial likelihood of VGF.	pmid:36078120 doi:10.3390/cells11172711	Fri, 09 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
19	pubmed:36079096	<a href="#">Snail Track Lesion with Flat Keratometry in Anterior Segment Dysgenesis Caused by a Novel <i>FOXC1</i> Variant</a>	Pavlina Skalicka Jana Jedlickova Ales Horinek Marie Trkova Alice E Davidson Stephen J Tuft Lubica Dudakova Petra Liskova	We report the phenotype of a 15-year-old female patient with anterior segment dysgenesis (ASD) caused by a novel heterozygous loss-of-function FOXC1 variant. The proband underwent an ophthalmic examination as well as a molecular genetic investigation comprising exome sequencing, a single nucleotide polymorphism array to access copy number and Sanger sequencing to exclude non-coding causal variants. There was bilateral mild iris hypoplasia with pupil deformation and iridocorneal adhesions. In...	pmid:36079096 doi:10.3390/jcm11175166	Fri, 09 Sep 2022 06:00:00 -0400
20	pubmed:36079970	<a href="#">Recent Advances in Monitoring Stem Cell Status and Differentiation Using Nano-Biosensing Technologies</a>	Wijin Kim Eungyeong Park Hyuk Sang Yoo Jongmin Park Young Mee Jung Ju Hyun Park	In regenerative medicine, cell therapies using various stem cells have received attention as an alternative to overcome the limitations of existing therapeutic methods. Clinical applications of stem cells require the identification of characteristics at the single-cell level and continuous monitoring during expansion and differentiation. In this review, we recapitulate the application of various stem cells used in regenerative medicine and the latest technological advances in monitoring the...	pmid:36079970 doi:10.3390/nano12172934	Fri, 09 Sep 2022 06:00:00 -0400
21	pubmed:36081501	<a href="#">Potential role of HTLV-1 Tax-specific cytotoxic t lymphocytes expressing a unique t-cell receptor to promote inflammation of the central nervous system in myelopathy associated with HTLV-1</a>	Yukie Tanaka Tomoo Sato Naoko Yagishita Junji Yamauchi Natsumi Araya Satoko Aratani Katsunori Takahashi Yasuo Kunitomo Misako Nagasaka Yoshinobu Kanda Kaoru Uchimaru Tomohiro Morio Yoshihisa Yamano	Human T-lymphotropic virus 1 (HTLV-1) infection causes two serious diseases: adult T-cell leukemia/lymphoma (ATL) and HTLV-1-associated myelopathy (HAM). Immunological studies have revealed that HTLV-1 Tax-specific CD8^(+) cytotoxic T-cells (Tax-CTLs) in asymptomatic carriers (ACs) and ATL patients play an important role in the elimination of HTLV-1-infected host cells, whereas Tax-CTLs in HAM patients trigger an excessive immune response against HTLV-1-infected host cells infiltrating the...	pmid:36081501 pmc:PMC9446235 doi:10.3389/fimmu.2022.993025	Fri, 09 Sep 2022 06:00:00 -0400
22	pubmed:36081907	<a href="#">Novel prognostic matrisome-related gene signature of head and neck squamous cell carcinoma</a>	Chao Huang Yun Liang Yi Dong Li Huang Anlei Li Ran Du Hao Huang	Background: Head and neck squamous cell carcinoma (HNSCC) is a common malignancy of the mucosal epithelium of the oral cavity, pharynx, and larynx. Laryngeal squamous cell carcinoma (LSCC) and oral squamous cell carcinoma are common HNSCC subtypes. Patients with metastatic HNSCC have a poor prognosis. Therefore, identifying molecular markers for the development and progression of HNSCC is essential for improving early diagnosis and predicting patient outcomes. Methods: Gene expression RNA-Seq...	pmid:36081907 pmc:PMC9445128 doi:10.3389/fcell.2022.884590	Fri, 09 Sep 2022 06:00:00 -0400
23	pubmed:36081985	<a href="#">Knowledge structure and emerging trends in the application of deep learning in genetics research: A bibliometric analysis [2000-2021]</a>	Bijun Zhang Ting Fan	Introduction: Deep learning technology has been widely used in genetic research because of its characteristics of computability, statistical analysis, and predictability. Herein, we aimed to summarize standardized knowledge and potentially innovative approaches for deep learning applications of genetics by evaluating publications to encourage more research. Methods: The Science Citation Index Expanded ^TM) (SCIE) database was searched for deep learning applications for genomics-related...	pmid:36081985 pmc:PMC9445221 doi:10.3389/fgene.2022.951939	Fri, 09 Sep 2022 06:00:00 -0400



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24	pubmed:36081988	<a href="#">Early-Life Exposure of Pigs to Topsoil Alters miRNA and mRNA Expression in Peripheral Blood Mononuclear Cells</a>	M M De Souza D A Koltes H Beiki M A Sales T Tsai C V Maxwell J Zhao J E Koltes	Exposure to less-hygienic conditions during early childhood has been associated with stimulation and development of the immune system. A recent study indicated that exposure of piglets to soil-borne microbes during lactation was related with modulation of gut microbiota and immune function. To identify the potential molecular mechanisms and pathways impacted by early-life topsoil exposure, we analyzed the messenger RNA (mRNA) and micro-RNA (miRNA) expression in peripheral blood mononuclear cells...	pmid:36081988 pmc:PMC9445269 doi:10.3389/fgene.2022.886875	Fri, 09 Sep 2022 06:00:00 -0400
25	pubmed:36081991	<a href="#">Editorial: Reproductive genomics</a>	Rong Liu Yan Yun Wenjie Shu Xi Wang Mengcheng Luo	No abstract	pmid:36081991 pmc:PMC9445836 doi:10.3389/fgene.2022.1002458	Fri, 09 Sep 2022 06:00:00 -0400
26	pubmed:36082002	<a href="#">Construction of a prognostic model related to copper dependence in breast cancer by single-cell sequencing analysis</a>	Xiao Guan Na Lu Jianping Zhang	Purpose: To explore the clinical significance of copper-dependent-related genes (CDRG) in female breast cancer (BC). Methods: CDRG were obtained by single-cell analysis of the GSE168410 dataset in the Gene Expression Omnibus (GEO) database. According to a 1:1 ratio, the Cancer Genome Atlas (TCGA) cohort was separated into a training and a test cohort randomly. Based on the training cohort, the prognostic model was built using COX and Lasso regression. The test cohort was used to validate the...	pmid:36082002 pmc:PMC9445252 doi:10.3389/fgene.2022.949852	Fri, 09 Sep 2022 06:00:00 -0400
27	pubmed:36082279	<a href="#">Characterization of <i>MET</i> Exon 14 Skipping Alterations (in NSCLC) and Identification of Potential Therapeutic Targets Using Whole Transcriptome Sequencing</a>	So Yeon Kim Jun Yin Stephen Bohlman Phillip Walker Sanja Dacic Chul Kim Hina Khan Stephen V Liu Patrick C Ma Misako Nagasaka Karen L Reckamp Jim Abraham Dipesh Uprety Feng Wang Joanne Xiu Jian Zhang Haiying Cheng Balazs Halmos	CONCLUSIONS: METex14 splicing alterations and MET co-amplification translated to higher and synergistic MET expression at the transcriptomic level. High frequencies of MDM2 and CDK4 co-amplifications and association with multiple immunosuppressive checkpoints and angiogenic pathways provide insight into potential actionable targets for combination strategies in METex14 NSCLC.	pmid:36082279 pmc:PMC9445394 doi:10.1016/j.jto.2022.100381	Fri, 09 Sep 2022 06:00:00 -0400
28	pubmed:36082430	<a href="#">Single-cell landscape and clinical outcomes of infiltrating B cells in colorectal cancer</a>	Jie Xia Zhangjuan Xie Gengming Niu Zhou Lu Zhiqiang Wang Yun Xing Jun Ren Zhiqing Hu Runqi Hong ZhiPeng Cao Shanliang Han Yiwei Chu Ronghua Liu Chongwei Ke	B cells constitute a major component of infiltrating immune cells in colorectal cancer (CRC). However, the characteristics of B cells and their clinical significance remain unclear. In this study, using single-cell RNA sequencing and multicolour immunofluorescence staining experiments, we identified five distinct subtypes of B cells with their marker genes, distribution patterns and functional properties in the CRC tumour microenvironment. Meanwhile, we found a higher proportion of IgG plasma...	pmid:36082430 doi:10.1111/imm.13568	Fri, 09 Sep 2022 06:00:00 -0400

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29	pubmed:36082968	<a href="#">A Gain of Function Ryanodine Receptor 2 Mutation (R1760W-RyR2) in Catecholaminergic Polymorphic Ventricular Tachycardia</a>	Siyuan Li Tingting Lv Jing Yang Kun Li Ying Yang Ping Zhang	Catecholaminergic polymorphic ventricular tachycardia (CPVT) is an inherited arrhythmia syndrome associated with Ca <sup>2+</sup> leak predominantly caused by ryanodine receptor 2 (RyR2) mutations. We identified a R1760W-RyR2 mutation located between the N-terminal domain and the central domain of RyR2 in a CPVT patient by DNA sequencing. Recombinant mutant RyR2(-2801mcherry) plasmid generated by the overlap extension polymerase chain reaction and seamless cloning was transfected in HEK293 cells for the...	pmid:36082968 doi:10.1111/1440-1681.13722	Fri, 09 Sep 2022 06:00:00 -0400
30	pubmed:36082978	<a href="#">Multi-species meta-analysis identifies transcriptional signatures associated with cardiac endothelial responses in the ischaemic heart</a>	Ziwen Li Emmanouil G Solomonidis Bronwyn Berkeley Michelle Nga Huen Tang Katherine Ross Stewart Daniel Perez-Vicencio Ian R McCracken Ana Mishel Spiroski Gillian A Gray Anna K Barton Stephanie L Sellers Paul R Riley Andrew H Baker Mairi Brittan	CONCLUSION: We present a high-resolution single cell meta-atlas of healthy and injured coronary endothelial cells in the mouse and human heart, revealing a suite of novel targets with great potential to promote vascular regeneration, and providing a rich resource for therapeutic development.	pmid:36082978 doi:10.1093/cvr/cvac151	Fri, 09 Sep 2022 06:00:00 -0400
31	pubmed:36083008	<a href="#">A machine learning-based method for automatically identifying novel cells in annotating single cell RNA-seq data</a>	Ziyi Li Yizhuo Wang Irene Ganan-Gomez Simona Colla Kim-Anh Do	MOTIVATION: Single cell RNA sequencing (scRNA-seq) has been widely used to decompose complex tissues into functionally distinct cell types. The first and usually the most important step of scRNA-seq data analysis is to accurately annotate the cell labels. In recent years, many supervised annotation methods have been developed and shown to be more convenient and accurate than unsupervised cell clustering. One challenge faced by all the supervised annotation methods is the identification of the...	pmid:36083008 doi:10.1093/bioinformatics/btac617	Fri, 09 Sep 2022 06:00:00 -0400
32	pubmed:36083529	<a href="#">Phylogenomic characterization and pangenomic insights into the surfactin-producing bacteria Bacillus subtilis strain RI4914</a>	Julie Kenya de Lima Ferreira Alessandro de Mello Varani Marcos Rogério Tótola Michelle Fernandes Almeida Dirceu de Sousa Melo Cristina Ferreira Silva E Batista Antonio Chalfun-Junior Kellen Kauanne Pimenta de Oliveira Luiz Fernando Wurdig Roesch Victor Satler Pylro	Bacillus subtilis is a versatile bacterial species able to produce surfactin, a lipopeptide biosurfactant. We carried out the phylogenomic characterization and pangenomic analyses using available B. subtilis complete genomes. Also, we report the whole genome of the biosurfactant-producing B. subtilis strain RI4914 that was isolated from effluent water from an oil exploration field. We applied a hybrid sequencing approach using both long- and short-read sequencing technologies to generate a...	pmid:36083529 doi:10.1007/s42770-022-00815-0	Fri, 09 Sep 2022 06:00:00 -0400



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33	pubmed:36083564	<a href="#">Single-cell transcriptome study in forensic medicine: prospective applications</a>	Qiuyun Yang Yuhang Wu Manrui Li Shuqiang Cao Yadong Guo Lin Zhang Xiameng Chen Weibo Liang	Next-generation sequencing and single-cell RNA sequencing (scRNA-seq) technologies have advanced rapidly in recent years. scRNA-seq reveals the unique gene expression of each cell type, providing directions for exploring cell heterogeneity, cell type-specific responses to injury/disease, and the mechanisms underlying these processes. The development of sequencing technology and improved sequencing throughput have brought about a revolution in single-cell transcriptome study, bringing great...	pmid:36083564 doi:10.1007/s00414-022-02889-9	Fri, 09 Sep 2022 06:00:00 -0400
34	pubmed:36083797	<a href="#">Cell therapy attenuates endothelial dysfunction in hypertensive rats with heart failure and preserved ejection fraction</a>	Geoffrey de Couto Thassio Mesquita Xiaokang Wu Alex Rajewski Feng Huang Akbarshakh Akhmerov Na Na Di Wu Yizhou Wang Liang Li My Tran Peter Kilfoil Eugenio Cingolani Eduardo Marbán	Heart failure with preserved ejection fraction (HFpEF) is defined by increased left ventricular (LV) stiffness, impaired vascular compliance and fibrosis. Although systemic inflammation, driven by comorbidities, has been proposed to play a key role, the precise pathogenesis remains elusive. To test the hypothesis that inflammation drives endothelial dysfunction in HFpEF, we used cardiosphere-derived cells (CDCs), which reduce inflammation and fibrosis, improving function, structure and survival...	pmid:36083797 doi:10.1152/ajpheart.00287.2022	Fri, 09 Sep 2022 06:00:00 -0400
35	pubmed:36084081	<a href="#">TMExplorer: A tumour microenvironment single-cell RNAseq database and search tool</a>	Erik Christensen Alaine Naidas David Chen Mia Husic Parisa Shooshtari	MOTIVATION: The tumour microenvironment (TME) contains various cells including stromal fibroblasts, immune and malignant cells, and its composition can be elucidated using single-cell RNA sequencing (scRNA-seq). scRNA-seq datasets from several cancer types are available, yet we lack a comprehensive database to collect and present related TME data in an easily accessible format.	pmid:36084081 doi:10.1371/journal.pone.0272302	Fri, 09 Sep 2022 06:00:00 -0400