single cell sequencing

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36113773	A transcriptional cross species map of pancreatic islet cells	Sophie Tritschler Moritz Thomas Anika Böttcher Barbara Ludwig Janine Schmid Undine Schubert Elisabeth Kemter Eckhard Wolf Heiko Lickert Fabian J Theis	CONCLUSIONS: Here, we provide a high- resolution transcriptional map of healthy human islet cells and their murine and porcine counterparts, which is easily queryable via an online interface. This comprehensive resource informs future efforts that focus on pancreatic endocrine function, failure and regeneration, and enables to assess molecular conservation in islet biology across species for translational purposes.	pmid:36113773 doi:10.1016/j.molmet.2022.101595	Fri, 16 Sep 2022 06:00:00 -0400
2	pubmed:36113894	Personalized neoantigen vaccine combined with PD-1 blockade increases CD8 [±] tissueresident memory T-cell infiltration in preclinical hepatocellular carcinoma models	Hengkai Chen Zhenli Li Liman Qiu Xiuqing Dong Geng Chen Yingjun Shi Linsheng Cai Wenhan Liu Honghao Ye Yang Zhou Jiahe Ouyang Zhixiong Cai Xiaolong Liu	CONCLUSIONS: This study showed that NeoVAC plus -PD-1 could induce a strong antitumor response and long-term tumor-specific immune memory in HCC by increasing CD8^(+) T(RMs) infiltration, which might serve as a potential immune-therapeutic target for HCC.	pmid:36113894 doi:10.1136/jitc-2021-004389	Fri, 16 Sep 2022 06:00:00 -0400
3	pubmed:36114029	Cancer-associated fibroblasts-derived FMO2 as a biomarker of macrophage infiltration and prognosis in epithelial ovarian cancer	Sihui Yu Rui Yang Tianhan Xu Xi Li Sufang Wu Jiawen Zhang	CONCLUSION: Our results address the tumor-supporting role of FMO2 in EOC and its association with immune components, and it might be a prospective target for stroma-oriented therapies against EOC.	pmid:36114029 doi:10.1016/j.ygyno.2022.09.003	Fri, 16 Sep 2022 06:00:00 -0400
4	pubmed:36114209	Clustering by measuring local direction centrality for data with heterogeneous density and weak connectivity	Dehua Peng Zhipeng Gui Dehe Wang Yuncheng Ma Zichen Huang Yu Zhou Huayi Wu	Clustering is a powerful machine learning method for discovering similar patterns according to the proximity of elements in feature space. It is widely used in computer science, bioscience, geoscience, and economics. Although the state-of-the-art partition-based and connectivity-based clustering methods have been developed, weak connectivity and heterogeneous density in data impede their effectiveness. In this work, we propose a boundary-seeking Clustering algorithm using the local Direction	pmid:36114209 doi:10.1038/s41467-022-33136-9	Fri, 16 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
5	pubmed:36114245	B-cell receptor physical properties affect relative IgG1 and IgE responses in mouse egg allergy	Christopher C Udoye Christina N Rau Sarah M Freye Larissa N Almeida Sarah Vera-Cruz Kai Othmer Rabia Ü Korkmaz Ann-Katrin Clauder Timo Lindemann Markus Niebuhr Fabian Ott Kathrin Kalies Andreas Recke Hauke Busch Anke Fähnrich Fred D Finkelman Rudolf A Manz	Mutated and unmutated IgE and IgG play different and partly opposing roles in allergy development, but the mechanisms controlling their relative production are incompletely understood. Here, we analyzed the IgE-response in murine food allergy. Deep sequencing of the complementary-determining region (CDR) repertoires indicated that an ongoing unmutated extrafollicular IgE response coexists with a germinal center response, even after long-lasting allergen challenges. Despite overall	pmid:36114245 doi:10.1038/s41385-022-00567-y	Fri, 16 Sep 2022 06:00:00 -0400
6	pubmed:36114266	Quantitative analysis of CRISPR/Cas9- mediated provirus deletion in blue egg layer chicken PGCs by digital PCR	Stefanie Altgilbers Claudia Dierks Sabine Klein Steffen Weigend Wilfried A Kues	Primordial germ cells (PGCs), the precursors of sperm and oocytes, pass on the genetic material to the next generation. The previously established culture system of chicken PGCs holds many possibilities for functional genomics studies and the rapid introduction of desired traits. Here, we established a CRISPR/Cas9-mediated genome editing protocol for the genetic modification of PGCs derived from chickens with blue eggshell color. The sequence targeted in the present report is a provirus (EAV-HP)	pmid:36114266 doi:10.1038/s41598-022-19861-7	Fri, 16 Sep 2022 06:00:00 -0400
7	pubmed:36114457	Boolean implication analysis of single-cell data predicts retinal cell type markers	Rohan Subramanian Debashis Sahoo	CONCLUSIONS: The results of this study demonstrate the benefits of a Boolean approach that considers asymmetric relationships. We have shown a statistically significant improvement from correlational, symmetric methods in the prediction accuracy of retinal cell-type specific genes. Furthermore, our method contains no cell or tissue-specific tuning and hence could impact other areas of gene expression analyses in cancer and other human diseases.	pmid:36114457 doi:10.1186/s12859-022-04915-4	Fri, 16 Sep 2022 06:00:00 -0400
8	pubmed:36114517	Determination of double- and single-stranded DNA breaks in bovine sperm is predictive of their fertilizing capacity	Jordi Ribas-Maynou Ariadna Delgado-Bermúdez Yentel Mateo-Otero Estel Viñolas Carlos O Hidalgo W Steven Ward Marc Yeste	CONCLUSION: The statistically significant correlations found between intracellular ROS, sperm viability, sperm motility, DNA damage and chromatin deprotamination suggested a sequence of events all driven by oxidative stress, where viability and motility would be affected first and sperm chromatin would be altered at a later stage, thus suggesting that bovine sperm should be used for fertilization within 2 h post-thaw. Fertility correlations supported that the assessment of global DNA damage	pmid:36114517 doi:10.1186/s40104-022-00754-8	Fri, 16 Sep 2022 06:00:00 -0400

1	NCT Number	Title	Authors	Description	Identifier	Dates
9	pubmed:36114956	Single-cell transcriptomic analysis reveals the adverse effects of cadmium on the trajectory of neuronal maturation	Bo Song Yuwei Zhang Guiya Xiong Huan Luo Bing Zhang Yixi Li Zhibin Wang Zhijun Zhou Xiuli Chang	Cadmium (Cd) is an extensively existing environmental pollutant that has neurotoxic effects. However, the molecular mechanism of Cd on neuronal maturation is unveiled. Single-cell RNA sequencing (scRNA-seq) has been widely used to uncover cellular heterogeneity and is a powerful tool to reconstruct the developmental trajectory of neurons. In this study, neural stem cells (NSCs) from subventricular zone (SVZ) of newborn mice were treated with CdCl(2) for 24 h and differentiated for 7 days to	pmid:36114956 doi:10.1007/s10565-022-09775-5	Sat, 17 Sep 2022 06:00:00 -0400