

single cell sequencing

NCT Number		Title	Authors	Description	Identifier	Dates
1	pubmed:36048084	Structure of the hypothetical protein TTHA1873 from Thermus thermophilus	I Yuvaraj Santosh Kumar Chaudhary J Jeyakanthan K Sekar	The crystal structure of an uncharacterized hypothetical protein, TTHA1873 from Thermus thermophilus, has been determined by X-ray crystallography to a resolution of 1.78 Å using the single-wavelength anomalous dispersion method. The protein crystallized as a dimer in two space groups: P4(3)2(1)2 and P6(1)22. Structural analysis of the hypothetical protein revealed that the overall fold of TTHA1873 has a -sandwich jelly-roll topology with nine -strands. TTHA1873 is a dimeric metal-binding...	pmid:36048084 doi:10.1107/S2053230X22008457	Thu, 01 Sep 2022 06:00:00 -0400
2	pubmed:36060667	Identification and Validation of Immune Markers in Coronary Heart Disease	Yuxiong Pan Jian Zhang Jin Li Wei Zhao	CONCLUSION: In conclusion, we identified different immune and m6A patterns in CHD. Thus, it could be speculated that the immune system plays a crucial role in CHD, and m6A is correlated with immune genes.	pmid:36060667 pmc:PMC9439891 doi:10.1155/2022/2877679	Mon, 05 Sep 2022 06:00:00 -0400
3	pubmed:36067577	Research Note: Transcriptomic analysis of LMH cells in response to the overexpression of a hypothetical protein identified in Eimeria tenella SD-01 strain	Bing-Jin Mu Yi-Jing Meng Xiao-Xin Liu Lin-Mei Yu Wen-Bin Zheng Shi-Chen Xie Xing-Quan Zhu Qing Liu Wen-Wei Gao	Though genome sequencing of Eimeria tenella predicts more than 8,000 genes, the molecular functions of many proteins remain unknown. In this study, the coding region corresponding to the mature peptide of a hypothetical protein of E. tenella (ETH_00023950) was amplified and expressed in a bacterial system. Following preparation of polyclonal antibody that recognizes ETH_00023950, the expression of ETH_00023950 in merozoites was examined. Meanwhile, we determined the transcriptomic responses of...	pmid:36067577 doi:10.1016/j.psj.2022.102109	Tue, 06 Sep 2022 06:00:00 -0400
4	pubmed:36068142	Single cell RNA-sequencing: A powerful yet still challenging technology to study cellular heterogeneity	May Ke Badran Elshenawy Helen Sheldon Anjali Arora Francesca M Buffa	Almost all biomedical research to date has relied upon mean measurements from cell populations, however it is well established that what it is observed at this macroscopic level can be the result of many interactions of several different single cells. Thus, the observable macroscopic 'average' cannot outright be used as representative of the 'average cell'. Rather, it is the resulting emerging behaviour of the actions and interactions of many different cells. Single-cell RNA sequencing...	pmid:36068142 doi:10.1002/bies.202200084	Tue, 06 Sep 2022 06:00:00 -0400
5	pubmed:36068167	Transcriptomic Features in a Single Extracellular Vesicle via Single-Cell RNA Sequencing	Tao Luo Si-Yi Chen Zhi-Xin Qiu Ya-Ru Miao Yue Ding Xiang-Yu Pan Yirong Li Qian Lei An-Yuan Guo	Although many studies have investigated functional molecules in extracellular vesicles (EVs), the exact number of ribonucleic acid molecules in a single-EV is unknown. Therefore, it is critical to explore the transcriptomic features and heterogeneity at the level of a single-EV. Here, using the 10x Genomics platform, the RNA cargos are profiled in single EVs derived from human K562 and mesenchymal stem cells. The key steps are labeling intact EVs using calcein-AM, detecting the EV concentration...	pmid:36068167 doi:10.1002/smt.202200881	Tue, 06 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
6	pubmed:36068211	Long read genome assemblies complemented by single cell RNA-sequencing reveal genetic and cellular mechanisms underlying the adaptive evolution of yak	Xue Gao Sheng Wang Yan-Fen Wang Shuang Li Shi-Xin Wu Rong-Ge Yan Yi-Wen Zhang Rui-Dong Wan Zhen He Ren-De Song Xin-Quan Zhao Dong-Dong Wu Qi-En Yang	Wild yak (Bos mutus) and domestic yak (Bos grunniens) are adapted to high altitude environment and have ecological, economic, and cultural significances on the Qinghai-Tibetan Plateau (QTP). Currently, the genetic and cellular bases underlying adaptations of yak to extreme conditions remains elusive. In the present study, we assembled two chromosome-level genomes, one each for wild yak and domestic yak, and screened structural variants (SVs) through the long-read data of yak and taurine cattle....	pmid:36068211 doi:10.1038/s41467-022-32164-9	Tue, 06 Sep 2022 06:00:00 -0400
7	pubmed:36068241	Multimodal single cell sequencing implicates chromatin accessibility and genetic background in diabetic kidney disease progression	Parker C Wilson Yoshiharu Muto Haojia Wu Anil Karihaloo Sushrut S Waikar Benjamin D Humphreys	The proximal tubule is a key regulator of kidney function and glucose metabolism. Diabetic kidney disease leads to proximal tubule injury and changes in chromatin accessibility that modify the activity of transcription factors involved in glucose metabolism and inflammation. Here we use single nucleus RNA and ATAC sequencing to show that diabetic kidney disease leads to reduced accessibility of glucocorticoid receptor binding sites and an injury-associated expression signature in the proximal...	pmid:36068241 doi:10.1038/s41467-022-32972-z	Tue, 06 Sep 2022 06:00:00 -0400
8	pubmed:36068607	Identification of HBEGF+ fibroblasts in the remission of rheumatoid arthritis by integrating single-cell RNA sequencing datasets and bulk RNA sequencing datasets	Nachun Chen Baoying Fan Zhiyong He Xinping Yu Jinjun Wang	CONCLUSIONS: HBEGF+ fibroblasts play a role in the remission of rheumatoid arthritis, and HBEGF has potential to become a novel biomarker for prediction of RA progress.	pmid:36068607 doi:10.1186/s13075-022-02902-x	Tue, 06 Sep 2022 06:00:00 -0400
9	pubmed:36068728	Women's responses to prenatal genetic diagnosis and attitudes to termination of pregnancy after non-invasive prenatal testing: An online survey of Western Australian women	Sarah Long Peter O'Leary Jan E Dickinson	CONCLUSION: Women expressed clear preferences for termination of pregnancy for severe conditions and as early in gestation as feasible. Information and support from genetic counsellors are a highly valued resource in decision-making following a prenatal diagnosis of a fetal genetic abnormality.	pmid:36068728 doi:10.1111/ajo.13608	Wed, 07 Sep 2022 06:00:00 -0400
10	pubmed:36069222	Serum levels of iCAF-derived Osteoglycin predict favorable outcome in pancreatic cancer	Mark P G Dings Paul Manoukian Cynthia Waasdorp Judith S E Quik Marin Strijker Sophie C Lodestijn Sanne M van Neerven Leandro F Moreno Rodrigo Leite de Oliveira Bert A Bonsing Marco J Bruno Olivier R Busch Michael Doukas Casper H van Eijck Nadia Haj Mohammad Ignace H de Hingh I Quintus Molenaar Marc G Besselink Louis Vermeulen Jan Paul Medema Hanneke W M van Laarhoven Maarten F Bijlsma	Pancreatic ductal adenocarcinoma (PDAC) is characterized by abundant stroma, the main cellular constituents of which are cancer-associated fibroblasts (CAFs). Stroma-targeting agents have been proposed to improve the poor outcome of current treatments. However, clinical trials using these agents showed disappointing results. Heterogeneity in the PDAC CAF population was recently delineated demonstrating that both tumor-promoting and -suppressive activities co-exist in the stroma. Here, we aimed...	pmid:36069222 doi:10.1002/ijc.34276	Wed, 07 Sep 2022 06:00:00 -0400

NCT Number		Title	Authors	Description	Identifier	Dates
11	pubmed:36069349	Changes in chromatin accessibility are not concordant with transcriptional changes for single-factor perturbations	Karun Kiani Eric M Sanford Yogesh Goyal Arjun Raj	A major goal in the field of transcriptional regulation is the mapping of changes in the binding of transcription factors to the resultant changes in gene expression. Recently, methods for measuring chromatin accessibility have enabled us to measure changes in accessibility across the genome, which are thought to correspond to transcription factor-binding events. In concert with RNA-sequencing, these data in principle enable such mappings; however, few studies have looked at their concordance...	pmid:36069349 doi:10.15252/msb.202210979	Wed, 07 Sep 2022 06:00:00 -0400
12	pubmed:36069549	Enhanced <i>In Vitro</i> and <i>In Vivo</i> Potency of a T Cell Epitope in the Ebola Virus Glycoprotein Following Amino Acid Replacement at HLA-A*02:01 Binding Positions	Sylvie Chabot Yusra Gimie Karam Obeid Jackwan Kim Clement A Meseda Krishnamurthy Konduru Gerardo Kaplan Li Sheng Fowler Jerry P Weir Keith Peden Marian E Major	Studies on Ebola virus disease (EVD) survivors and clinical studies on Ebola virus (EBOV) vaccine candidates have pinpointed the importance of a strong antibody response in protection and survival from EBOV infection. However, little is known about the T cell responses to EBOV or EBOV vaccines. We used HLA-A*02:01 (HLA-A2) transgenic mice to study HLA-A2-specific T cell responses elicited following vaccination with EBOV glycoprotein (EBOV-GP) presented with three different systems: (i)...	pmid:36069549 doi:10.1128/jvi.01166-21	Wed, 07 Sep 2022 06:00:00 -0400
13	pubmed:36070019	Molecular study on recombinant cold-adapted, detergent- and alkali stable esterase (EstRag) from Lysinibacillus sp.: a member of family VI	Amira A Matrawy Ahmed I Khalil Amira M Embaby	Cold-adapted esterases have potential industrial applications. To fulfil the global continuous demand for these enzymes, a cold-adapted esterase member of family VI from Lysinibacillus sp. YS11 was cloned on pET-28b (+) vector and expressed in E. coli BL21(DE3) Rosetta cells for the first time. The open reading frame (654 bp; GenBank MT120818.1) encodes a polypeptide (designated EstRag: 217 amino acid residues). EstRag amino acid sequence has conserved esterase signature motifs: pentapeptide...	pmid:36070019 doi:10.1007/s11274-022-03402-5	Wed, 07 Sep 2022 06:00:00 -0400
14	pubmed:36070083	Epithelial cell-expressed type II IL-4 receptor mediates eosinophilic esophagitis	Shmulik Avlas Guy Shani Natalie Rhone Michal Itan Avishay Dolitzky Hazut Inbal Sharon Grisaru-Tal Gordon Yaara Tetsuo Shoda Adina Ballaban Netali Morgenstern Ben-Baruch Mark Rochman Yael Diesendruck Limor Nahary Almog Bitton Zamir Halpern Itai Benhar Chen Varol Marc E Rothenberg Ariel Munitz	CONCLUSIONS: We demonstrate a definitive role for IL-13 signaling via IL-13R1 in EoE. These data provide mechanistic insights into the mode of action of current therapies in EoE and highlight the type II IL-4R as a future therapeutic target.	pmid:36070083 doi:10.1111/all.15510	Wed, 07 Sep 2022 06:00:00 -0400

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15	pubmed:36070228	Glioma stem cell signature predicts the prognosis and the response to tumor treating fields treatment	Bo Chen Xiaoxi Zhou Liting Yang Hongshu Zhou Ming Meng Hao Wu Zhixiong Liu Liyang Zhang Chuntao Li	CONCLUSION: Our study constructed a GSC signature consisting of 11 GSC-specific genes and identified its prognostic value in gliomas. TTF is a promising therapeutic approach for patients with GSC-enriched glioma.	pmid:36070228 doi:10.1111/cns.13956	Wed, 07 Sep 2022 06:00:00 -0400
16	pubmed:36070519	Different T-cell and B-cell repertoire elicited by the SARS-CoV-2 inactivated vaccine and S1 subunit vaccine in rhesus macaques	Li Qin Yuanyuan Zuo Shuying Liu Bingxiang Li Hongye Wang Heng Li Jing Li Yanli Chen Ming Sun Huiwen Zheng	Multiple types of SARS-CoV-2 vaccines have been used worldwide, but summarizing their immunologic efficacy post-vaccination remains challenging. The BCR and TCR sequencing based on single-cell sorting makes it possible to evaluate the vaccine-induced immune responses of B or T cells. In this study, we compared the repertoire diversities of B cells and T cells between a whole-virus inactivated vaccine and an S1 protein subunit vaccine in rhesus macaques. We found that the inactivated vaccine...	pmid:36070519 doi:10.1080/21645515.2022.2118477	Wed, 07 Sep 2022 06:00:00 -0400
17	pubmed:36070560	Decoding the Spermatogenesis Program: New Insights from Transcriptomic Analyses	Mashiat Rabbani Xianing Zheng Gabe L Manske Alexander Vargo Adrienne N Shami Jun Z Li Saher Sue Hammoud	Spermatogenesis is a complex differentiation process coordinated spatiotemporally across and along seminiferous tubules. Cellular heterogeneity has made it challenging to obtain stage-specific molecular profiles of germ and somatic cells using bulk transcriptomic analyses. This has limited our ability to understand regulation of spermatogenesis and to integrate knowledge from model organisms to humans. The recent advancement of single-cell RNA-sequencing (scRNA-seq) technologies provides...	pmid:36070560 doi:10.1146/annurev-genet-080320-040045	Wed, 07 Sep 2022 06:00:00 -0400