## single cell sequencing

| | NCT Number | Title | Authors | Description | Identifier | Dates |
|---|---|---|---|---|---|---|
| 1 | pubmed:36054938 | Integrated single-cell transcriptomic analyses reveal that GPNMB-high macrophages promote PN-MES transition and impede T cell activation in GBM | Aizhen Xiong<br>Jiwei Zhang<br>Yan Chen<br>Yi Zhang<br>Fan Yang | BACKGROUND: Glioblastoma (GBM) is the most aggressive type of primary brain tumor and is often resistant to current therapies. Tumor microenvironment-centered therapies may unleash new hope for GBM treatment. Therefore, an in-depth understanding of tumor-stroma communication is urgently needed to identify promising therapeutic targets. | pmid:36054938<br>doi:10.1016/j.ebiom.2022.104239 | Fri, 02 Sep 2022 06:00:00 -0400 |
| 2 | pubmed:36055193 | Modeling human multi-lineage heart field development with pluripotent stem cells | Donghe Yang<br>Juliana Gomez-Garcia<br>Shunsuke Funakoshi<br>Thinh Tran<br>Ian Fernandes<br>Gary D Bader<br>Michael A Laflamme<br>Gordon M Keller | The cardiomyocyte (CM) subtypes in the mammalian heart derive from distinct lineages known as the first heart field (FHF), the anterior second heart field (aSHF), and the posterior second heart field (pSHF) lineages that are specified during gastrulation. We modeled human heart field development from human pluripotent stem cells (hPSCs) by using single-cell RNA-sequencing to delineate lineage specification and progression. Analyses of hPSC-derived and mouse mesoderm transcriptomes enabled the... | pmid:36055193<br>doi:10.1016/j.stem.2022.08.007 | Fri, 02 Sep 2022 06:00:00 -0400 |
| 3 | pubmed:36055201 | High-coverage whole-genome sequencing of the expanded 1000 Genomes Project cohort including 602 trios | Marta Byrska-Bishop<br>Uday S Evani<br>Xuefang Zhao<br>Anna O Basile<br>Haley J Abel<br>Allison A Regier<br>André Corvelo<br>Wayne E Clarke<br>Rajeeva Musunuri<br>Kshithija Nagulapalli<br>Susan Fairley<br>Alexi Runnels<br>Lara Winterkorn<br>Ernesto Lowy<br>Human Genome Structural Variation Consortium<br>None Paul Flicek<br>Soren Germer<br>Harrison Brand<br>Ira M Hall<br>Michael E Talkowski<br>Giuseppe Narzisi<br>Michael C Zody | The 1000 Genomes Project (1kGP) is the largest fully open resource of whole-genome sequencing (WGS) data consented for public distribution without access or use restrictions. The final, phase 3 release of the 1kGP included 2,504 unrelated samples from 26 populations and was based primarily on low-coverage WGS. Here, we present a high-coverage 3,202-sample WGS 1kGP resource, which now includes 602 complete trios, sequenced to a depth of 30X using Illumina. We performed single-nucleotide variant... | pmid:36055201<br>doi:10.1016/j.cell.2022.08.004 | Fri, 02 Sep 2022 06:00:00 -0400 |
| 4 | pubmed:36055241 | Whole-genome CRISPR screening identifies genetic manipulations to reduce immune rejection of stem cell-derived islets | Elad Sintov<br>Igor Nikolskiy<br>Victor Barrera<br>Jennifer Hyoje-Ryu Kenty<br>Alexander S Atkin<br>Dario Gerace<br>Shannan J Ho Sui<br>Kyle Boulanger<br>Douglas A Melton | Human embryonic stem cells (hESCs) provide opportunities for cell replacement therapy of insulin-dependent diabetes. Therapeutic quantities of human stem cell-derived islets (SC-islets) can be produced by directed differentiation. However, preventing allo-rejection and recurring autoimmunity, without the use of encapsulation or systemic immunosuppressants, remains a challenge. An attractive approach is to transplant SC-islets, genetically modified to reduce the impact of immune rejection. To... | pmid:36055241<br>doi:10.1016/j.stemcr.2022.08.002 | Fri, 02 Sep 2022 06:00:00 -0400 |

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|---|---|---|---|---|---|---|
| 5 | pubmed:36055412 | Novel skewed usage of B-cell receptors in COVID-19 patients with various clinical presentations | Junpeng Ma<br>Han Bai<br>Tian Gong<br>Weikang Mao<br>Yijun Nie<br>Xuan Zhang<br>Yanyan Da<br>Xiaorui Wang<br>Hongyu Qin<br>Qiqi Zeng<br>Fang Hu<br>Xin Qi<br>Bingyin Shi<br>Chengsheng Zhang | B cell-mediated immune responses play important roles in controlling SARS-CoV infection. Here, we performed the single-cell B cell receptor sequencing (scBCR-seq) of the PBMC samples from eleven healthy controls, five asymptomatic subjects and 33 symptomatic COVID-19 patients with various clinical presentations, and subsequently analyzed the abundance and diversity of the BCR repertoires in different groups, respectively. We revealed the skewed usage of the IGHV, IGLV and IGKV genes and... | pmid:36055412<br>doi:10.1016/j.imlet.2022.08.006 | Fri, 02 Sep 2022 06:00:00 -0400 |
| 6 | pubmed:36055600 | A comparative study of cellular diversity between the Xenopus pronephric and mouse metanephric nephron | Mark E Corkins<br>MaryAnne Achieng<br>Bridget D De Lay<br>Vanja Krneta-Stankic<br>Margo P Cain<br>Brandy L Walker<br>Jichao Chen<br>Nils O Lindström<br>Rachel K Miller | The kidney is an essential organ that ensures bodily fluid homeostasis and removes soluble waste products from the organism. Nephrons, the functional units of the kidney, comprise a blood filter, the glomerulus or glomus, and an epithelial tubule that processes the filtrate from the blood or coelom and selectively reabsorbs solutes, such as sugars, proteins, ions, and water, leaving waste products to be eliminated in the urine. Genes coding for transporters are segmentally expressed, enabling... | pmid:36055600<br>doi:10.1016/j.kint.2022.07.027 | Fri, 02 Sep 2022 06:00:00 -0400 |
| 7 | pubmed:36056412 | scMTD: a statistical multidimensional imputation method for single-cell RNA-seq data leveraging transcriptome dynamic information | Jing Qi<br>Qiongyu Sheng<br>Yang Zhou<br>Jiao Hua<br>Shutong Xiao<br>Shuilin Jin | CONCLUSIONS: scMTD maintains the gene expression characteristics, enhances the clustering of cell subpopulations, assists the study of gene expression dynamics, contributes to the discovery of rare cell types, and applies to both UMI-based and non-UMI-based data. Overall, scMTD's reliability, applicability, and scalability make it a promising imputation approach for scRNA-seq data. | pmid:36056412<br>doi:10.1186/s13578-022-00886-4 | Fri, 02 Sep 2022 06:00:00 -0400 |
| 8 | pubmed:36056685 | TNFAIP3 mutation is an independent poor overall survival factor for patients with T-cell acute lymphoblastic leukemia | Cunte Chen<br>Lingling Zhou<br>Lihua Zhu<br>Gengxin Luo<br>Liang Wang<br>Chengwu Zeng<br>Hongsheng Zhou<br>Yangqiu Li | CONCLUSION: TNFAIP3 mutation mainly occurs in adult T-ALL patients, and it was associated with adverse clinical outcomes for T-ALL patients; thus, it might be a biomarker for prognostic stratification. | pmid:36056685<br>doi:10.1002/cam4.5196 | Sat, 03 Sep 2022 06:00:00 -0400 |
| 9 | pubmed:36056872 | Exploring plausible therapeutic targets for Alzheimer's disease using multi-omics approach, machine learning and docking | S Akila Parvathy Dharshini<br>Nela Pragathi Sneha<br>Dhanusha Yesudhas<br>A Kulandaisamy<br>Uday Rangaswamy<br>Anusuya Shanmugam<br>Y-H Taguchi<br>M Michael Gromiha | The progressive deterioration of neurons leads to Alzheimer's disease (AD), and developing a drug for this disorder is challenging. Substantial gene/transcriptome variability from multiple cell types leads to downstream pathophysiologic consequences that represent the heterogeneity of this disease. Identifying potential biomarkers for promising therapeutics is strenuous due to the fact that the transcriptome, epigenetic, or proteome changes detected in patients are not clear whether they are the... | pmid:36056872<br>doi:10.2174/1568026622666220902110115 | Sat, 03 Sep 2022 06:00:00 -0400 |

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| 10 | pubmed:36056959 | Genome-wide analysis reveals allelic variation and chromosome copy number variation in paromomycin-resistant Leishmania donovani | Sushmita Ghosh<br>Vinay Kumar<br>Aditya Verma<br>Tanya Sharma<br>Dibyabhaba Pradhan<br>Angamuthu Selvapandiyan<br>Poonam Salotra<br>Ruchi Singh | In the absence of adequate diagnosis and treatment, leishmaniasis remains a major public health concern on a global scale. Drug resistance remains a key obstacle in controlling and eliminating visceral leishmaniasis. The therapeutic gap due to lack of target-specific medicine and vaccine can be minimized by obtaining parasite's genomic information. This study compared whole-genome sequence of paromomycin-resistant parasite (K133PMM) developed through in vitro adaptation and selection with... | pmid:36056959<br>doi:10.1007/s00436-022-07645-x | Sat, 03 Sep 2022 06:00:00 -0400 |