single cell sequencing

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36104328	Telomere-to-telomere genome sequence of the model mould pathogen Aspergillus fumigatus	Paul Bowyer Andrew Currin Daniela Delneri Marcin G Fraczek	The pathogenic fungus Aspergillus fumigatus is a major etiological agent of fungal invasive and chronic diseases affecting tens of millions of individuals worldwide. Draft genome sequences of two clinical isolates (Af293 and A1163) are commonly used as reference genomes for analyses of clinical and environmental strains. However, the reference sequences lack coverage of centromeres, an accurate sequence for ribosomal repeats, and a comprehensive annotation of chromosomal rearrangements such as...	pmid:36104328 doi:10.1038/s41467-022-32924-7	Wed, 14 Sep 2022 06:00:00 -0400
2	pubmed:36105815	Detrimental *NFKB1* missense variants affecting the Rel-homology domain of p105/p50	Manfred Fliegauf Matias Kinnunen Sara Posadas-Cantera Nadezhda Camacho-Ordonez Hassan Abolhassani Laia Alsina Faranaz Atschekzei Delfien J Bogaert Siobhan O Burns Joseph A Church Gregor Dückers Alexandra F Freeman Lennart Hammarström Leif Gunnar Hanitsch Tessa Kerre Robin Kobbe Svetlana O Sharapova Kathrin Siepermann Carsten Speckmann Sophie Steiner Nisha Verma Jolan E Walter Emma Westermann-Clark Sigune Goldacker Klaus Warnatz Markku Varjosalo Bodo Grimbacher	Most of the currently known heterozygous pathogenic NFKB1 (Nuclear factor kappa B subunit 1) variants comprise deleterious defects such as severe truncations, internal deletions, and frameshift variants. Collectively, these represent the most frequent monogenic cause of common variable immunodeficiency (CVID) identified so far. NFKB1 encodes the transcription factor precursor p105 which undergoes limited proteasomal processing of its C-terminal half to generate the mature NF-B subunit p50....	pmid:36105815 pmc:PMC9465457 doi:10.3389/fimmu.2022.965326	Thu, 15 Sep 2022 06:00:00 -0400
3	pubmed:36108528	Inhibition of APOC1 promotes the transformation of M2 into M1 macrophages via the ferroptosis pathway and enhances anti-PD1 immunotherapy in hepatocellular carcinoma based on single-cell RNA sequencing	Xiaopei Hao Zhiying Zheng Hanyuan Liu Yao Zhang Junwei Kang Xiangyi Kong Dawei Rong Guangshun Sun Guoqiang Sun Li Liu Haibo Yu Weiwei Tang Xuehao Wang	Single-cell RNA-sequencing (scRNA-seq) presents better insights into cell behavior in the context of a complex tumor microenvironment by profiling single-cell populations. However, the mechanisms underlying treatment failure in hepatocellular carcinoma (HCC) are poorly understood. In this study, we performed deep scRNA-seq on immune cells under the isolation in peripheral blood, cancer tissues, and nearby common tissues of four HCC cases and two non-cancer controls, and 212,494 cells were...	pmid:36108528 doi:10.1016/j.redox.2022.102463	Thu, 15 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
4	pubmed:36108685	Whole-genome sequence association study identifies CDK8 as a key gene for the number of mummified piglets	Pingxian Wu Dejuan Chen Kai Wang Shujie Wang Yihui Liu Anan Jiang Weihang Xiao Yanzhi Jiang Li Zhu Xu Xu Xiaotian Qiu Xuewei Li Guoqing Tang	CONCLUSION: A powerful imputation-based association study was performed to identify genes associated with NM in pigs. CDK8 was suggested as a functional gene for the proliferation of porcine ovarian granulosa cells, but further studies are required to determine causative mutations and the effect of loci on NM in pigs.	pmid:36108685 doi:10.5713/ab.22.0115	Thu, 15 Sep 2022 06:00:00 -0400
5	pubmed:36108770	Systems genomics in age-related macular degeneration	Anneke I den Hollander Robert F Mullins Luz D Orozco Andrew P Voigt Hsu-Hsin Chen Tobias Strunz Felix Grassmann Jonathan L Haines Jonas J W Kuiper Santa J Tumminia Rando Allikmets Gregory S Hageman Dwight Stambolian Caroline C W Klaver Jef D Boeke Hao Chen Lee Honigberg Suresh Katti Kelly A Frazer Bernhard H F Weber Michael B Gorin	Genomic studies in age-related macular degeneration (AMD) have identified genetic variants that account for the majority of AMD risk. An important next step is to understand the functional consequences and downstream effects of the identified AMD-associated genetic variants. Instrumental for this next step are 'omics' technologies, which enable high-throughput characterization and quantification of biological molecules, and subsequent integration of genomics with these omics datasets, a field...	pmid:36108770 doi:10.1016/j.exer.2022.109248	Thu, 15 Sep 2022 06:00:00 -0400
6	pubmed:36108806	The single-cell landscape of kidney immune cells reveals transcriptional heterogeneity in early diabetic kidney disease	Jia Fu Zeguo Sun Xuan Wang Tuo Zhang Weijie Yuan Fadi Salem Samuel Mon-Wei Yu Weijia Zhang Kyung Lee John Cijiang He	The pathogenesis of diabetic kidney disease (DKD) involves multifactorial processes that converge to initiate and advance the disease. Although DKD is not typically classified as an inflammatory glomerular disease, mounting evidence supports the involvement of kidney inflammation as a key contributor in DKD pathogenesis, particularly through macrophages. However, detailed identification and corresponding phenotypic changes of macrophages in DKD remain poorly understood. To capture the gene...	pmid:36108806 doi:10.1016/j.kint.2022.08.026	Thu, 15 Sep 2022 06:00:00 -0400
7	pubmed:36109504	Dendritic cell-derived IL-27 p28 regulates T cell program in pathogenicity and alleviates acute graft-versus-host disease	Huanle Gong Shoubao Ma Jia Chen Bingyu Yang Shuangzhu Liu Xin Liu Jingjing Han Xiaojin Wu Lei Lei Zhinan Yin Hongjian Sun Di Yu Haiyan Liu Yang Xu Depei Wu	Interleukin 27 (IL-27), a heterodimeric cytokine composed of Epstein-Barr virus-induced 3 and p28, is a pleiotropic cytokine with both pro-and anti-inflammatory properties. However, the precise role of IL-27 in acute graft-versus-host disease is not yet fully understood. In this study, utilizing mice with IL-27 p28 deficiency in dendritic cells (DCs), we demonstrated that IL-27 p28 deficiency resulted in impaired Treg cell function and enhanced effector T cell responses, corresponding to...	pmid:36109504 doi:10.1038/s41392-022-01147-z	Thu, 15 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
8	pubmed:36109592	Tmsb10 triggers fetal Leydig differentiation by suppressing the RAS/ERK pathway	Miki Inoue Takashi Baba Fumiya Takahashi Miho Terao Shogo Yanai Yuichi Shima Daisuke Saito Kei Sugihara Takashi Miura Shuji Takada Mikita Suyama Yasuyuki Ohkawa Ken-Ichirou Morohashi	Leydig cells in fetal testes play crucial roles in masculinizing fetuses through androgen production. Gene knockout studies have revealed that growth factors are implicated in fetal Leydig cell (FLC) differentiation, but little is known about the mechanisms regulating this process. We investigate this issue by characterizing FLC progenitor cells using single-cell RNA sequencing. The sequence datasets suggest that thymosin 10 (Tmsb10) is transiently upregulated in the progenitors. While studying...	pmid:36109592 doi:10.1038/s42003-022-03941-5	Thu, 15 Sep 2022 06:00:00 -0400
9	pubmed:36109650	Genome assembly and chemogenomic profiling of National Flower of Singapore Papilionanthe Miss Joaquim 'Agnes' reveals metabolic pathways regulating floral traits	Abner Herbert Lim Zhen Jie Low Prashant Narendra Shingate Jing Han Hong Shu Chen Chong Cedric Chuan Young Ng Wei Liu Robert Vaser Mile Šiki Wing-Kin Ken Sung Niranjan Nagarajan Patrick Tan Bin Tean Teh	Singapore's National Flower, Papilionanthe (Ple.) Miss Joaquim 'Agnes' (PMJ) is highly prized as a horticultural flower from the Orchidaceae family. A combination of short-read sequencing, single-molecule long-read sequencing and chromatin contact mapping was used to assemble the PMJ genome, spanning 2.5 Gb and 19 pseudo-chromosomal scaffolds. Genomic resources and chemical profiling provided insights towards identifying, understanding and elucidating various classes of secondary metabolite...	pmid:36109650 doi:10.1038/s42003-022-03940-6	Thu, 15 Sep 2022 06:00:00 -0400
10	pubmed:36109677	ISSAAC-seq enables sensitive and flexible multimodal profiling of chromatin accessibility and gene expression in single cells	Wei Xu Weilong Yang Yunlong Zhang Yawen Chen Ni Hong Qian Zhang Xuefei Wang Yukun Hu Kun Song Wenfei Jin Xi Chen	Joint profiling of chromatin accessibility and gene expression from the same single cell provides critical information about cell types in a tissue and cell states during a dynamic process. Here, we develop in situ sequencing hetero RNA-DNA-hybrid after assay for transposase-accessible chromatin-sequencing (ISSAAC-seq), a highly sensitive and flexible single-cell multi-omics method to interrogate chromatin accessibility and gene expression from the same single nucleus. We demonstrated that...	pmid:36109677 doi:10.1038/s41592-022-01601-4	Thu, 15 Sep 2022 06:00:00 -0400
11	pubmed:36109685	Mostly natural sequencing-by-synthesis for scRNA-seq using Ultima sequencing	Sean K Simmons Gila Lithwick-Yanai Xian Adiconis Florian Oberstrass Nika Iremadze Kathryn Geiger-Schuller Pratiksha I Thakore Chris J Frangieh Omer Barad Gilad Almogy Orit Rozenblatt-Rosen Aviv Regev Doron Lipson Joshua Z Levin	Here we introduce a mostly natural sequencing-by-synthesis (mnSBS) method for single-cell RNA sequencing (scRNA-seq), adapted to the Ultima genomics platform, and systematically benchmark it against current scRNA-seq technology. mnSBS uses mostly natural, unmodified nucleotides and only a low fraction of fluorescently labeled nucleotides, which allows for high polymerase processivity and lower costs. We demonstrate successful application in four scRNA-seq case studies of different technical and...	pmid:36109685 doi:10.1038/s41587-022-01452-6	Thu, 15 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
12	pubmed:36110010	Weight of single and recurrent scattering in the reflection matrix of complex media	Cécile Brütt Alexandre Aubry Benoît Gérardin Arnaud Derode Claire Prada	In a heterogeneous medium, the wave field can be decomposed as an infinite series known as the Born expansion. Each term of the Born expansion corresponds to a scattering order, it is thus theoretically possible to discriminate single and multiple scattering contribution to the field. Experimentally, what is actually measured is the total field in which all scattering orders interfere. Conventional imaging methods usually rely on the assumption that the multiple scattering contribution can be...	pmid:36110010 doi:10.1103/PhysRevE.106.025001	Fri, 16 Sep 2022 06:00:00 -0400
13	pubmed:36110213	Pan-cancer analysis of the prognosis and immunological role of AKAP12: A potential biomarker for resistance to anti-VEGF inhibitors	Qiuju Liang Jinwu Peng Zhijie Xu Zhilan Li Feng Jiang Lingzi Ouyang Shangjun Wu Chencheng Fu Ying Liu Yuanhong Liu Yuanliang Yan	The primary or acquired resistance to anti-VEGF inhibitors remains a common problem in cancer treatment. Therefore, identifying potential biomarkers enables a better understanding of the precise mechanism. Through the GEO database, three profiles associated with bevacizumab (BV) resistance to ovarian cancer, glioma, and non-small-cell lung carcinoma, respectively, were collected for the screening process, and two genes were found. A-kinase anchor protein 12 (AKAP12), one of these two genes,...	pmid:36110213 pmc:PMC9468827 doi:10.3389/fgene.2022.943006	Fri, 16 Sep 2022 06:00:00 -0400
14	pubmed:36110854	The imbalance between Type 17 T-cells and regulatory immune cell subsets in psoriasis vulgaris	Jaehwan Kim Ariana Moreno James G Krueger	Psoriasis vulgaris is a common inflammatory disease affecting 7.5 million adults just in the US. Previously, psoriasis immunopathogenesis has been viewed as the imbalance between CD4^(+) T-helper 17 (Th17) cells and regulatory T-cells (Tregs). However, current paradigms are rapidly evolving as new technologies to study immune cell subsets in the skin have been advanced. For example, recently minted single-cell RNA sequencing technology has provided the opportunity to compare highly differing...	pmid:36110854 pmc:PMC9468415 doi:10.3389/fimmu.2022.1005115	Fri, 16 Sep 2022 06:00:00 -0400
15	pubmed:36110997	Landscape of *RB1* alterations in 22,432 Chinese solid tumor patients	Guanghui Xu Jiyang Zheng Shu Wang Yuhao Wang Guixiang Li Nan Wang Xueke She Weiming Duan Hushan Zhang Depei Huang Ting Bei Dan Fu Jianjun Yang	CONCLUSIONS: Our findings indicate that RB1 alterations are widely distributed in solid cancers of many different histotypes in China, with specific mutations differing largely among different tumor types. The present study provides a comprehensive landscape of RB1 mutations in Chinese solid tumor patient and suggests a novel therapeutic target for cancer treatment.	pmid:36110997 pmc:PMC9469137 doi:10.21037/atm-22-3162	Fri, 16 Sep 2022 06:00:00 -0400
16	pubmed:36111018	Genome-wide analysis of Chinese keloid patients identifies novel causative genes	Yue-Qian Zhu Nai-Hui Zhou Ya-Wen Xu Ke Liu Wei Li Li-Yan Shi Yin-Xi Hu Yu-Feng Xie Jing Lan Zheng-Yuan Yu	CONCLUSIONS: Whole-exome sequencing was performed in the Chinese keloid patients and some potential candidate genes related to keloid occurrence and development were identified, which may provide new molecular targets for the clinical diagnosis and treatment of keloid patients.	pmid:36111018 pmc:PMC9469174 doi:10.21037/atm-22-1303	Fri, 16 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
17	pubmed:36111046	Exploration of new therapeutic targets for viral hepatic fibrosis, alcoholic hepatic fibrosis, and non-alcoholic hepatic fibrosis	Xiaoling Wang Ying Wang Xuewei Li Shuo Qin Jun Xu Jun Xie	CONCLUSIONS: KCNN2, CD4, CD24, BCL6, KCNMA1, and other molecules obtained by the bioinformatics analysis of the RNA-sequencing data can be used as new research targets for hepatic fibrosis induced by different causes. Our findings could provide novel ideas for the treatment of hepatic fibrosis.	pmid:36111046 pmc:PMC9469126 doi:10.21037/atm-22-3593	Fri, 16 Sep 2022 06:00:00 -0400
18	pubmed:36111134	A novel necroptosis-related gene signature for predict prognosis of glioma based on single-cell and bulk RNA sequencing	Kai Guo Xinxin Duan Jiahui Zhao Boyu Sun Xiaoming Liu Zongmao Zhao	Background: Glioma is the most fatal neoplasm among the primary intracranial cancers. Necroptosis, a form of programmed cell death, is correlated with tumor progression and immune response. But, the role of necroptosis-related genes (NRGs) in glioma has not been well-uncovered. Methods: Single-cell and bulk RNA sequencing data, obtained from publicly accessed databases, were used to establish a necroptosis-related gene signature for predicting the prognosis of glioma patients. Multiple...	pmid:36111134 pmc:PMC9469195 doi:10.3389/fmolb.2022.984712	Fri, 16 Sep 2022 06:00:00 -0400
19	pubmed:36111135	A novel method to purify small RNAs from human tissues for methylation analysis by LC-MS/MS	Rong Yang Jianfeng Li Yifan Wu Xinli Jiang Shuang Qu Qiang Wang Hongwei Liang Ke Zen	Methylation modification of small RNAs, including miRNA, piRNA, and tsRNA, is critical for small RNA biogenesis and biological function. Methylation of individual small RNA can be defined by liquid chromatography-coupled with mass spectrometry (LC-MS/MS). However, LC-MS/MS analysis requires a high purity of individual small RNA. Due to the difficulty of purifying specific small RNA from tissues or cells, the progress in characterizing small RNA methylation by LC-MS/MS is limited. Here, we report...	pmid:36111135 pmc:PMC9468635 doi:10.3389/fmolb.2022.949181	Fri, 16 Sep 2022 06:00:00 -0400
20	pubmed:36111491	Comparison of singlenucleus and singlecell transcriptomes in hepatocellular carcinoma tissue	Fei Wen Xiaojie Tang Lin Xu Haixia Qu	Singlenucleus RNA sequencing (snRNAseq) is a method used to analyze gene expression in cells for which isolation is complex, such as those in hepatocellular carcinoma (HCC) tissues. It constitutes an alternative to singlecell RNA sequencing (scRNAseq) by analyzing the nucleus rather than the whole cell; however, whether it can completely replace scRNAseq in HCC remains to be clarified. In the present study, scRNAseq was compared with snRNAseq in tumor tissue obtained from patients with...	pmid:36111491 doi:10.3892/mmr.2022.12855	Fri, 16 Sep 2022 06:00:00 -0400
21	pubmed:36111504	A multiomics study of diagnostic markers and the unique inflammatory tumor microenvironment involved in tuberous sclerosis complexrelated renal angiomyolipoma	Zhan Wang Xiaoyan Liu Wenda Wang Jing Wei Samuel Seery Jiyu Xu Haidan Sun Yuncui Yu Yang Zhao Xu Wang Zhangcheng Liao Yanan Li Wei Sun Lulu Jia Yushi Zhang	Tuberous sclerosis complex (TSC) is a rare disease that threatens multiple organs in the human body. TSCassociated renal angiomyolipoma (TSCRAML) has potentially lifethreatening complications and a generally poor prognosis. The present study aimed to find plasma proteomic diagnostics and diseaseassociated markers, and explore the tumor microenvironment using multiomics. To achieve this goal, the plasma proteomics as well as tissue proteomics, bulk and singlecell RNA transcriptome from...	pmid:36111504 doi:10.3892/ijo.2022.5422	Fri, 16 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
22	pubmed:36111505	Characterisation of CYP2D6 pharmacogenetic variation in sub-Saharan African populations	David Twesigomwe Britt I Drögemöller Galen E B Wright Clement Adebamowo Godfred Agongo Palwendé R Boua Mogomotsi Matshaba Maria Paximadis Michèle Ramsay Gustave Simo Martin C Simuunza Caroline T Tiemessen Zané Lombard Scott Hazelhurst	CYP2D6 is a key enzyme in drug response owing to its involvement in the metabolism of approximately 25% of clinically prescribed medications. The encoding CYP2D6 gene is highly polymorphic and many pharmacogenetics studies have been performed worldwide to investigate the distribution of CYP2D6 star alleles (haplotypes); however, African populations have been relatively understudied to date. In this study, the distributions of CYP2D6 star alleles and predicted drug metaboliser phenotypes-derived...	pmid:36111505 doi:10.1002/cpt.2749	Fri, 16 Sep 2022 06:00:00 -0400
23	pubmed:36111531	Transcriptional and Immune Landscape of Cardiac Sarcoidosis	Jing Liu Pan Ma Lulu Lai Ana Villanueva Andrew Koenig Gregory R Bean Dawn E Bowles Carolyn Glass Michael Watson Kory J Lavine Chieh-Yu Lin	CONCLUSIONS: In this study, we identified diverse populations of immune cells with distinct molecular signatures that comprise the sarcoid granuloma. These findings provide new insights into the pathology of cardiac sarcoidosis and highlight opportunities to improve diagnostic testing.	pmid:36111531 doi:10.1161/CIRCRESAHA.121.320449	Fri, 16 Sep 2022 06:00:00 -0400
24	pubmed:36111571	Reduced cell invasion may be a characteristic of placental defects in pregnant women of advanced maternal age at single-cell level	Bin Zhang Feng Zhang Fengying Lu Jing Wang Wenbai Zhou Huihui Wang Bin Yu	The mechanisms underlying pregnancy complications caused by advanced maternal age (AMA) remain unclear. We analyzed the cellular signature and transcriptomes of human placentas in AMA women to elucidate these mechanisms. Placental tissues from two AMA women and two controls were used for single-cell RNA-sequencing (scRNA-seq). Controls consisted of AMA women who did not experience any pregnancy complications and pregnant women below the age of 35 years without pregnancy complications....	pmid:36111571 doi:10.1631/jzus.B2101024	Fri, 16 Sep 2022 06:00:00 -0400
25	pubmed:36111648	Cell type markers indicate distinct contributions of decidual stromal cells and natural killer cells in preeclampsia	Kalle T Rytkönen Nigatu Adossa Mehrad Mahmoudian Tapio Lönnberg Matti Poutanen Laura L Elo	Preeclampsia is a devastating pregnancy disorder and a major cause of maternal and perinatal mortality. By combining previous transcriptomic results on preeclampsia with single-cell sequencing (scRNA-seq) data, we here predict distinct and partly unanticipated contributions of decidual stromal cells and uterine natural killer cells in early- and late-onset preeclampsia.	pmid:36111648 doi:10.1530/REP-22-0079	Fri, 16 Sep 2022 06:00:00 -0400
26	pubmed:36111754	Characteristics of BAY 2599023 in the Current Treatment Landscape of Hemophilia A Gene Therapy	Steven W Pipe Valder R Arruda Claudia Lange Stephen Kitchen Hermann Eichler Samuel Wadsworth	Hemophilia A, a single gene disorder leading to deficient Factor VIII (FVIII), is a suitable candidate for gene therapy. The aspiration is for single administration of a genetic therapy that would allow production of endogenous FVIII sufficient to restore hemostasis and other biological processes. This would potentially result in reliable protection from bleeding, and its associated physical and emotional impacts. Gene therapy offers the possibility of a clinically relevant improvement in...	pmid:36111754 doi:10.2174/1566523222666220914105729	Fri, 16 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
27	pubmed:36111847	Macrophage-mediated PDGF Activation Correlates with Regenerative Outcomes Following Musculoskeletal Trauma	Ashish R Chowdary Tristan Maertz Dominic Henn Kurt D Hankenson Chase A Pagani Simone Marini Katherine Gallagher Carlos A Aguilar Robert J Tower Benjamin Levi	CONCLUSION: Characterization of macrophage subtypes could be used to predict fibrotic responses following injury and provide a therapeutic target to tune the healing microenvironment towards more regenerative conditions.	pmid:36111847 doi:10.1097/SLA.0000000000005704	Fri, 16 Sep 2022 06:00:00 -0400
28	pubmed:36112140	Mitochondria transfer mediates stress erythropoiesis by altering the bioenergetic profiles of early erythroblasts through CD47	Chong Yang Rui Yokomori Lee Hui Chua Shi Hao Tan Darren Qiancheng Tan Kenichi Miharada Takaomi Sanda Toshio Suda	Intercellular mitochondria transfer is a biological phenomenon implicated in diverse biological processes. However, the physiological role of this phenomenon remains understudied between erythroblasts and their erythroblastic island (EBI) macrophage niche. To gain further insights into the mitochondria transfer functions, we infused EBI macrophages in vivo into mice subjected to different modes of anemic stresses. Interestingly, we observed the occurrence of mitochondria transfer events from the...	pmid:36112140 doi:10.1084/jem.20220685	Fri, 16 Sep 2022 06:00:00 -0400
29	pubmed:36112223	Cross-regional homeostatic and reactive glial signatures in multiple sclerosis	Tim Trobisch Amel Zulji Nikolas A Stevens Sophia Schwarz Sven Wischnewski Mikail Öztürk Javier Perales-Patón Maximilian Haeussler Julio Saez-Rodriguez Dmitry Velmeshev Lucas Schirmer	Multiple sclerosis (MS) is a multifocal and progressive inflammatory disease of the central nervous system (CNS). However, the compartmentalized pathology of the disease affecting various anatomical regions including gray and white matter and lack of appropriate disease models impede understanding of the disease. Utilizing single-nucleus RNA-sequencing and multiplex spatial RNA mapping, we generated an integrated transcriptomic map comprising leukocortical, cerebellar and spinal cord areas in...	pmid:36112223 doi:10.1007/s00401-022-02497-2	Fri, 16 Sep 2022 06:00:00 -0400
30	pubmed:36112611	Mendelian segregation for parthenogenetic embryo development at the diploid level in the flowering plant Erigeron	Richard D Noyes	CONCLUSIONS: This work shows that parthenogenesis can be transmitted simply at the diploid level. This advance is key in the development of a tractable system in Erigeron aimed at the identification of the parthenogenesis locus using genetic mapping strategies. This article is protected by copyright. All rights reserved.	pmid:36112611 doi:10.1002/ajb2.16071	Fri, 16 Sep 2022 06:00:00 -0400