metabolomics

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36103741	Profiling and spatial distribution of phenolic compounds in rapeseed by two-step extraction strategy and targeted metabolomics combined with chemometrics	Yao Zhang Huaming Xiao Xin Lv Chang Zheng Zongyuan Wu Nian Wang Jie Wang Hong Chen Fang Wei	In this study, a two-step extraction strategy (TSES) and targeted metabolomics combined with chemometrics was successfully applied for profiling of phenolic compounds in different colored rapeseeds. To this end, organic solvent extraction followed by deep eutectic solvent extraction made up the TSES with improved extraction coverage of free phenolics and enhanced extraction yield of conjugated phenolics, which combined with liquid chromatography tandem mass spectrometry (LC-MS/MS) for further	pmid:36103741 doi:10.1016/j.foodchem.2022.134151	Wed, 14 Sep 2022 06:00:00 -0400
2	pubmed:36104152	Food Metabolomics: Latest hardware - developments for non-targeted food authenticity and food safety testing	Marina Creydt Markus Fischer	The analytical requirements for food testing have increased significantly in recent years. On the one hand, because food fraud is becoming an ever-greater challenge worldwide, and on the other hand because food safety is often difficult to monitor due to the far-reaching trade chains. In addition, the expectations of consumers on the quality of food have increased, and they are demanding extensive information. Cuttingedge analytical methods are required to meet these demands. In this context,	pmid:36104152 doi:10.1002/elps.202200126	Wed, 14 Sep 2022 06:00:00 -0400
3	pubmed:36104186	Screening and identification of differential metabolites in serum and urine of bamaxiang pigs bitten by trimeresurus stejnegeri based on UPLC-Q-TOF/MS metabolomics technology	ZheZhe Guan YaLan Li ShaoCong Hu CaiFeng Mo DongLing He Zhi Huang Ming Liao	Trimeresurus stejnegeri is one of the top ten venomous snakes in China, and its bite causes acute and severe diseases. Elucidating the metabolic changes of the body caused by Trimeresurus stejnegeri bite will be beneficial to the diagnosis and treatment of snakebite. Thus, an animal pig model of Trimeresurus stejnegeri bite was established, and then the metabolites of serum and urine were subsequently screened and identified in both ESI+ and ESI- modes identified by ultraperformance liquid	pmid:36104186 doi:10.2131/jts.47.389	Wed, 14 Sep 2022 06:00:00 -0400
4	pubmed:36104635	Metabolites derived from fungi and bacteria suppress in vitro growth of Gnomoniopsis smithogilvyi, a major threat to the global chestnut industry	Matias Silva-Campos Damien L Callahan David M Cahill	CONCLUSION: The results show that G. smithogilvyi can be effectively controlled by the BCAs tested and that their use may provide a more ecological alternative for managing chestnut rot. The in vitro analysis should now be expanded to the field to assess the effectiveness of these alternatives for chestnut rot management.	pmid:36104635 doi:10.1007/s11306-022-01933-4	Wed, 14 Sep 2022 06:00:00 -0400
5	pubmed:36104729	SGLT2 inhibitors improve kidney function and morphology by regulating renal metabolic reprogramming in mice with diabetic kidney disease	Yong-Ping Lu Ze-Yu Zhang Hong-Wei Wu Li-Jing Fang Bo Hu Chun Tang Yi-Qing Zhang Lianghong Yin Dong-E Tang Zhi-Hua Zheng Ting Zhu Yong Dai	Diabetic kidney disease (DKD) is the leading cause of end-stage renal disease (ESRD) worldwide. SGLT2 inhibitors are clinically effective in halting DKD progression. However, the underlying mechanisms remain unclear. The serum and kidneys of mice with DKD were analyzed using liquid chromatography with tandem mass spectrometry (LC-MS/MS)-based metabolomic and proteomic analyses. Three groups were established: placebo-treated littermate db/m mice, placebo-treated db/db mice and EMPA-treated db/db	pmid:36104729 doi:10.1186/s12967-022-03629-8	Wed, 14 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
6	pubmed:36104763	Application of metabolomics in intrahepatic cholestasis of pregnancy: a systematic review	Zhuoqiao Yang Mengxin Yao Chunhua Zhang Xuan Hu Yi Zhong Xiangxiang Xu Jieyun Yin	CONCLUSIONS: This study provides a systematic review of metabolomics of ICP and deepens our understanding of the etiology of ICP.	pmid:36104763 doi:10.1186/s40001-022-00802-z	Wed, 14 Sep 2022 06:00:00 -0400
7	pubmed:36104776	Novel technologies to characterize and engineer the microbiome in inflammatory bowel disease	Alba Boix-Amorós Hilary Monaco Elisa Sambataro Jose C Clemente	We present an overview of recent experimental and computational advances in technology used to characterize the microbiome, with a focus on how these developments improve our understanding of inflammatory bowel disease (IBD). Specifically, we present studies that make use of flow cytometry and metabolomics assays to provide a functional characterization of microbial communities. We also describe computational methods for strain-level resolution, temporal series, mycobiome and virome data,	pmid:36104776 doi:10.1080/19490976.2022.2107866	Wed, 14 Sep 2022 06:00:00 -0400
8	pubmed:36104908	Immunotoxicity of pentachlorophenol to a marine bivalve species and potential toxification mechanisms underpinning	Weixia Zhang Yu Tang Yu Han Lin Huang Weishang Zhou Chaosheng Zhou Yuan Hu Rongmao Lu Fang Wang Wei Shi Guangxu Liu	The ubiquitous presence of pentachlorophenol (PCP) in ocean environments threatens marine organisms. However, its effects on immunity of marine invertebrates at environmentally realistic levels are still largely unknown. In this study, the immunotoxicity of PCP to a representative bivalve species was evaluated. In addition, its impacts on metabolism, energy supply, detoxification, and oxidative stress status were also analysed by physiological examination as well as comparative transcriptomic	pmid:36104908 doi:10.1016/j.jhazmat.2022.129681	Thu, 15 Sep 2022 06:00:00 -0400
9	pubmed:36105003	Integration of transcriptomic and metabolomic analysis of the mechanism of dietary N-carbamoylglutamate in promoting follicle development in yaks	Jia Zhou Shuangming Yue Jingjing Du Benchu Xue Lizhi Wang Quanhui Peng Huawei Zou Rui Hu Yahui Jiang Zhisheng Wang Bai Xue	Yak is the main livestock in the highlands of China. The low reproductive rate of yaks is a serious constraint on their production and utility. N-carbamylglutamate (NCG) can increase arginine synthesis in mammals and has been shown to improve reproductive performance. Twelve multiparous and simutaneous anoestrous female yaks were randomly divided into two groups, one of which was fed the basal diet (Control, $n=6$), and the other was fed the basal diet supplemented with NCG at 6 g/day/yak (NCG,	pmid:36105003 pme:PMC9464987 doi:10.3389/fvets.2022.946893	Thu, 15 Sep 2022 06:00:00 -0400
10	pubmed:36105024	Candidate metabolite markers of peripheral neuropathy in Chinese patients with type 2 diabetes	Ming-Mei Shao Hong-Jiao Xiang Hao Lu Pei-Hao Yin Guo-Wen Li Yun-Man Wang Lin Chen Qing-Guang Chen Cheng Zhao Qun Lu Tao Wu Guang Ji	CONCLUSION: There were serum and urine spectrum metabolomic differences in patients with DPN, which could serve as biomarkers for T2DM and DPN patients.	pmid:36105024 pmc:PMC9452362	Thu, 15 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
11	pubmed:36105149	Multi-omics insights reveal the remodeling of gut mycobiome with <i>P. gingivalis</i>	Si Chen ChenGuang Niu WanQi Lv	As a keystone periodontal pathogen, Porphyromonas gingivalis (P. gingivalis) was suggested to be involved in the progression of systemic diseases by altering the intestinal microecology. However, studies concerning gut microbiome have focused entirely on the bacterial component, while the fungal community (gut mycobiome) has been overlooked. In this study, we aimed to characterize the alteration of gut mycobiome profile with P. gingivalis administration using mice fecal samples. Metagenomic	pmid:36105149 pmc:PMC9465408 doi:10.3389/fcimb.2022.937725	Thu, 15 Sep 2022 06:00:00 -0400
12	pubmed:36105160	Multi-factor combined biomarker screening strategy to rapidly diagnose Alzheimer's disease and evaluate drug effect based on a rat model	Yanmeng Liu Xinyue Zhang Weiwei Lin Nurmuhammat Kehriman Wen Kuang Xiaomei Ling	Alzheimer's disease (AD) represents the main form of dementia; however, valid diagnosis and treatment measures are lacking. The discovery of valuable biomarkers through omics technologies can help solve this problem. For this reason, metabolomic analysis using ultraperformance liquid chromatography coupled with quadrupole time-of-flight tandem mass spectrometry (UPLC-Q-TOF-MS) was carried out on plasma, hippocampus, and cortex samples of an AD rat model. Based on the metabolomic data, we report	pmid:36105160 pmc:PMC9463486 doi:10.1016/j.jpha.2022.04.003	Thu, 15 Sep 2022 06:00:00 -0400
13	pubmed:36105172	Metabolomic fingerprinting of porcine lung tissue during pre-clinical prolonged ex vivo lung perfusion using in vivo SPME coupled with LC-HRMS	Nikita Looby Anna Roszkowska Aadil Ali Barbara Bojko Marcelo Cypel Janusz Pawliszyn	Normothermic ex vivo lung perfusion (NEVLP) has emerged as a modernized organ preservation technique that allows for detailed assessment of donor lung function prior to transplantation. The main goal of this study was to identify potential biomarkers of lung function and/or injury during a prolonged (19 h) NEVLP procedure using in vivo solid-phase microextraction (SPME) technology followed by liquid chromatography-high resolution mass spectrometry (LC-HRMS). The use of minimally invasive in vivo	pmid:36105172 pmc:PMC9463496 doi:10.1016/j.jpha.2022.06.002	Thu, 15 Sep 2022 06:00:00 -0400
14	pubmed:36105186	Study on plasma metabolomics for HIV/AIDS patients treated by HAART based on LC/MS-MS	Donghui Lao Rong Liu Jianying Liang	Background: Metabolomics can be applied to the clinical diagnosis and treatment evaluation of acquired immune deficiency syndrome (AIDS). AIDS biomarkers have become a new direction of AIDS research providing clinical guidance for diagnosis. Objective: We sought to apply both untargeted and targeted metabolomic profiling to identify potential biomarkers for AIDS patients. Methods: A liquid chromatography-tandem mass spectrometry (LC-MS/MS) based untargeted metabolomic profiling was performed on	pmid:36105186 pmc:PMC9465010 doi:10.3389/fphar.2022.885386	Thu, 15 Sep 2022 06:00:00 -0400
15	pubmed:36105197	Improved pharmacokinetics of tenofovir ester prodrugs strengthened the inhibition of HBV replication and the rebalance of hepatocellular metabolism in preclinical models	Xiaodan Hong Zuhuan Cai Fang Zhou Xiaoliang Jin Guangji Wang Bingchen Ouyang Jingwei Zhang	Tenofovir (TFV) ester prodrugs, a class of nucleotide analogs (NAs), are the first-line clinical anti-hepatitis B virus (HBV) drugs with potent antiviral efficacy, low resistance rate and high safety. In this work, three marketed TFV ester drugs, tenofovir disoproxil fumarate (TDF), tenofovir alafenamide fumarate (TAF) and tenofovir amibufenamide fumarate (TMF), were used as probes to investigate the relationships among prodrug structures, pharmacokinetic characteristics, metabolic activations,	pmid:36105197 pmc:PMC9465247 doi:10.3389/fphar.2022.932934	Thu, 15 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
16	pubmed:36105265	Acceptability and feasibility of fecal microBIOME and serum metabolite sample collection in people with end-stage kidney disease and pain being treated with HemoDialysis: A pilot study (BIOME-HDp)	Mark B Lockwood Michael J Fischer Kimberly Silva Blanca N Contreras Guillermo Zamora Amanda Goldstein Monya Meinel Christopher Holden James Lash Alana Steffens Ardith Doorenbos	Pain is known to reduce hemodialysis treatment adherence, reduce quality of life, and increase mortality. The absence of effective strategies to treat pain without medications has contributed to poor health outcomes for people with end-stage kidney disease (ESKD) on hemodialysis. It is now recognized that symbiotic microbiota in the gut play a critical role in health and disease, and new evidence sheds light on the role of the microbiome in chronic pain. The pilot study protocol presented here	pmid:36105265 pmc:PMC9464895 doi:10.1016/j.conctc.2022.100995	Thu, 15 Sep 2022 06:00:00 -0400
17	pubmed:36105361	The phenotype of the gut region is more stably retained than developmental stage in piglet intestinal organoids	Eloïse Mussard Corinne Lencina Lise Gallo Céline Barilly Maryse Poli Katia Feve Mikael Albin Laurent Cauquil Christelle Knudsen Caroline Achard Guillaume Devailly Laura Soler Sylvie Combes Martin Beaumont	Intestinal organoids are innovative in vitro tools to study the digestive epithelium. The objective of this study was to generate jejunum and colon organoids from suckling and weaned piglets in order to determine the extent to which organoids retain a location-specific and a developmental stage-specific phenotype. Organoids were studied at three time points by gene expression profiling for comparison with the transcriptomic patterns observed in crypts in vivo. In addition, the gut microbiota and	pmid:36105361 pmc:PMC9465596 doi:10.3389/fcell.2022.983031	Thu, 15 Sep 2022 06:00:00 -0400
18	pubmed:36105573	Molecular mechanisms of flavonoid accumulation in germinating common bean (Phaseolus vulgaris) under salt stress	Qi Zhang Guangyue Zheng Qi Wang Jixing Zhu Zhiheng Zhou Wenshuo Zhou Junjie Xu Haoyue Sun Jingwen Zhong Yanhua Gu Zhengong Yin Yan-Li Du Ji-Dao Du	Flavonoids are important secondary metabolites, active biomolecules in germinating beans, and have prominent applications in food and medicine due to their antioxidant effects. Rutin is a plant flavonoid with a wide biological activity range. In this study, flavonoid (rutin) accumulation and its related molecular mechanisms in germinating common bean (Phaseolus vulgaris) were observed at different time points (0-120 h) under salt stress (NaCl). The rutin content increased from germination onset	pmid:36105573 pme:PMC9465018 doi:10.3389/fnut.2022.928805	Thu, 15 Sep 2022 06:00:00 -0400
19	pubmed:36105862	Improved seed germination and plant growth mediated by compounds synthesized by endophytic Aspergillus niger (isolate 29) isolated from Albizia lebbeck (L.) Benth	Parikshana Mathur Payal Chaturvedi Charu Sharma Pradeep Bhatnagar	Plant-microbe interactions are remarkably diverse and dynamic. These interactions can be in the form of endophytic association. Colonization of endophytic microflora in crop plants improves crop health leading to crop enhancement. They stimulate the overall growth of plants by facilitating nutrient uptake and regulating various hormones. This eventually improves the plant biomass and grain yield. Owing to the assistance of the endophytes to the host plants, augmentation of crop plants with	pmid:36105862 pme:PMC9464679 doi:10.1007/s13205-022-03332-x	Thu, 15 Sep 2022 06:00:00 -0400
20	pubmed:36105942	Molecular phenotyping approaches for the detection and monitoring of carbapenem-resistant Enterobacteriaceae by mass spectrometry	Breanna Dixon Waqar M Ahmed Tim Felton Stephen J Fowler	Antimicrobial resistance is increasing in prevalence and there is a clear need for the development of rapid detection methods in clinical diagnostics. This review explores - omics studies utilising mass spectrometry to investigate the molecular phenotype associated with carbapenem resistance. Whilst the specific mechanisms of carbapenem resistance are well characterised, the resistant phenotype is poorly understood. Understanding how the acquisition of resistance affects cellular physiology and	pmid:36105942 pmc:PMC9464899 doi:10.1016/j.jmsacl.2022.09.001	Thu, 15 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
21	pubmed:36106708	Serum metabolomics analysis reveals amelioration effects of sea cucumber ether phospholipids on oxidative stress and inflammation in high-fat diet-fed mice	Xincen Wang Haohui Lan Tong Sun Peixu Cong Changhu Xue Jie Xu	Emerging evidence suggests that sea cucumber ether phospholipids (ether-PLs) can modulate high-fat diet (HFD)-induced metabolic disorders. However, whether this modulation is associated with metabolic pathways related to oxidative stress and inflammation remains unclear. This study aimed to investigate the antioxidative and anti-inflammatory effects on HFD-fed mice and the associated metabolism pathways in response to administration with sea cucumber ether-PLs using integrated biochemistry and a	pmid:36106708 doi:10.1039/d2fo00918h	Thu, 15 Sep 2022 06:00:00 -0400
22	pubmed:36106841	An integrative cellular metabolomic study reveals downregulated tricarboxylic acid cycle and potential biomarkers induced by tetrabromobisphenol A in human lung A549 cells	Hailang He Tingyu Pan Xiaojian Shi Shuang Yang Paniz Jasbi Yan Jin Julia Yue Cui Haiwei Gu	Tetrabromobisphenol A (TBBPA) is extensively utilized as a brominated flame retardant in numerous chemical products. As an environmental contaminant, the potential human toxicity of TBBPA has been attracting increasing attention. Nonetheless, the exact underlying mechanisms of toxicological effects caused by TBBPA remain uncertain. In this study, we investigated the potential mechanisms of TBBPA toxicity in vitro in the A549 cell line, one of the widely used type II pulmonary epithelial cell	pmid:36106841 doi:10.1002/tox.23657	Thu, 15 Sep 2022 06:00:00 -0400
23	pubmed:36106996	Multi-Omic Integration by Machine Learning (MIMaL)	Quinn Dickinson Andreas Aufschnaiter Martin Ott Jesse G Meyer	MOTIVATION: Cells respond to environments by regulating gene expression to exploit resources optimally. Recent advances in technologies allow measuring the abundances of transcripts, proteins, lipids and metabolites. These highly complex datasets reflect the state of the different layers in a biological system. Multi-omics is the integration of these disparate methods and data to gain a clearer picture of the biological state. Multi-omic studies of the proteome and metabolome are becoming more	pmid:36106996 doi:10.1093/bioinformatics/btac631	Thu, 15 Sep 2022 06:00:00 -0400
24	pubmed:36107703	The Maternal Prenatal and Offspring Early-Life Gut Microbiome of Childhood Asthma Phenotypes	Kathleen A Lee-Sarwar Yih-Chieh Chen Yuan Yao Chen Anita L Kozyrskyj Piush J Mandhane Stuart E Turvey Padmaja Subbarao Hans Bisgaard Jakob Stokholm Bo Chawes Søren J Sørensen Rachel S Kelly Jessica Lasky-Su Robert S Zeiger George T O'Connor Megan T Sandel Leonard B Bacharier Avraham Beigelman Vincent J Carey Benjamin J Harshfield Nancy Laranjo Diane R Gold Scott T Weiss Augusto A Litonjua	CONCLUSION: Overall, our results suggest that the early-life, including prenatal, fecal microbiome modifies risk of asthma, especially asthma with onset by age 3 years.	pmid:36107703 doi:10.1111/all.15516	Thu, 15 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
25	pubmed:36107781	Metabolome and transcriptome analysis on muscle of sporadic inclusion body myositis	Ayuka Murakami Seiya Noda Tomoyuki Kazuta Satoko Hirano Seigo Kimura Hirotaka Nakanishi Koji Matsuo Koyo Tsujikawa Madoka Iida Haruki Koike Kazuma Sakamoto Yuichiro Hara Satoshi Kuru Kenji Kadomatsu Teppei Shimamura Tomoo Ogi Masahisa Katsuno	OBJECTIVE: Sporadic inclusion body myositis (sIBM) is the most common acquired myopathy in patients older than 50 years of age. sIBM is hardly responds to any immunosuppressing theraphies, and its pathophysiology remains elusive. This study aims to explore pathogenic pathways underlying sIBM and identify novel therapeutic targets using metabolomic and transcriptomic analyses.	pmid:36107781 doi:10.1002/acn3.51657	Thu, 15 Sep 2022 06:00:00 -0400
26	pubmed:36107830	Stimulating the sir2-pgc-1 axis rescues exercise capacity and mitochondrial respiration in Drosophila tafazzin mutants	Deena Damschroder Rubén Zapata-Pérez Kristin Richardson Frédéric M Vaz Riekelt H Houtkooper Robert Wessells	Cardiolipin (CL) is a phospholipid required for proper mitochondrial function. Tafazzin remodels CL to create highly unsaturated fatty acid chains. However, when tafazzin is mutated, CL remodeling is impeded, leading to mitochondrial dysfunction and the disease Barth syndrome. Patients with Barth syndrome often have severe exercise intolerance, which negatively impacts their overall quality of life. Boosting NAD+ levels can improve symptoms of other mitochondrial diseases, but its effect in the	pmid:36107830 doi:10.1242/dmm.049279	Thu, 15 Sep 2022 06:00:00 -0400
27	pubmed:36107885	The metabolomic profile associated with clustering of cardiovascular risk factors-A multi-sample evaluation	Lars Lind Johan Sundström Sölve Elmståhl Koen F Dekkers J Gustav Smith Gunnar Engström Tove Fall Johan Ärnlöv	CONCLUSION: A complex metabolic profile was related to all cardiovascular risk factors included in MetS independently of BMI. This profile was also related to insulin sensitivity, which provide further support for the importance of insulin sensitivity as an important underlying mechanism in the clustering of cardiovascular risk factors.	pmid:36107885 doi:10.1371/journal.pone.0274701	Thu, 15 Sep 2022 06:00:00 -0400
28	pubmed:36107950	Beyond the Ground State: Predicting Electron Ionization Mass Spectra Using Excited-State Molecular Dynamics	Shunyang Wang Tobias Kind Parker Ladd Bremer Dean J Tantillo Oliver Fiehn	Here, we provide an algorithm that introduces excited states into the molecular dynamics prediction of the 70 eV electron ionization mass spectra. To decide the contributions of different electronic states, the ionization cross section associated with relevant molecular orbitals was calculated by the binary-encounter-Bethe (BEB) model. We used a fast orthogonalization model/single and double state configuration interaction (OM2/CISD) method to implement excited states calculations and combined	pmid:36107950 doi:10.1021/acs.jcim.2c00597	Thu, 15 Sep 2022 06:00:00 -0400
29	pubmed:36108037	Microbiome and Metabolome Contributions to Coral Health and Disease	Monica Schul Andrea Mason Blake Ushijima Jennifer M Sneed	AbstractCoral populations are declining worldwide as a result of increased environmental stressors, including disease. Coral health is greatly dependent on complex interactions between the host animal and its associated microbial symbionts. While relatively understudied, there is growing evidence that the coral microbiome contributes to the health and resilience of corals in a variety of ways, similar to more well-studied systems, such as the human microbiome. Many of these interactions are	pmid:36108037 doi:10.1086/720971	Thu, 15 Sep 2022 06:00:00 -0400

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30	pubmed:36108054	Leveraging the Metabolome: Translating Social Risk Into Biological Pathways	Rupal Mehta Sadiya S Khan	No abstract	pmid:36108054 doi:10.1161/CIRCRESAHA.122.321700	Thu, 15 Sep 2022 06:00:00 -0400
31	pubmed:36108149	Extracellular vesicle secretion by leukemia cells in vivo promotes CLL progression by hampering antitumor T-cell responses	Ernesto Gargiulo Elodie Viry Pablo Elias Morande Anne Largeot Susanne Gonder Feng Xian Nikolaos Ioannou Mohaned Benzarti Felix Bruno Kleine Borgmann Michel Mittelbronn Gunnar Dittmar Petr V Nazarov Johannes Meiser Basile Stamatopoulos Alan G Ramsay Etienne Moussay Jerome Paggetti	Small extracellular vesicles (sEV, or exosomes) communication among cells in the tumor microenvironment has been modeled mainly in cell culture, while their relevance in cancer pathogenesis and progression in vivo is less characterized. Here we investigated cancermicroenvironment interactions in vivo using mouse models of chronic lymphocytic leukemia (CLL). sEV isolated directly from CLL tissue were enriched in specific miRNA and immune checkpoint ligands. Distinct molecular components of	pmid:36108149 doi:10.1158/2643-3230.BCD-22-0029	Thu, 15 Sep 2022 06:00:00 -0400