metabolomics

	NCT Number	Title	Authors	Description	Identifier	Dates
1	pubmed:36088713	Endogenous hydrocortisone caused metabolic perturbation and nutritional deterioration of animal-derived food in a dose-dependent manner	Wei Jia Xin Wang Lin Shi	Endogenous hydrocortisone causes detrimental effects on public health and domestic animal products, but the potential mechanisms remain elusive. Hydrocortisone was detected from seventy-two Guanzhong-Black pigs in three replicates (216 samples) (0.00 ± 46.38 g kg^(-1)), indicating the existence of endogenous hydrocortisone. Herein, we investigated the effects of hydrocortisone on the metabolic signatures in pork via integrative metabolomics and proteomics by UHPLC-Q-Orbitrap HRMS	pmid:36088713 doi:10.1016/j.foodchem.2022.134145	Sun, 11 Sep 2022 06:00:00 -0400
2	pubmed:36088784	Transcriptomic and metabolomic analyses reveal the main metabolites in Dendrobium officinale leaves during the harvesting period	Can Si Danqi Zeng Zhenming Yu Jaime A Teixeira da Silva Jun Duan Chunmei He Jianxia Zhang	Dendrobium officinale, which is a medicine food homology plant, contains many metabolites, especially polysaccharides and flavonoids. Unlike flowers and stems, which are the most frequently harvested organs for a variety of uses, leaves tend to be discarded. This study assessed main metabolites in leaves to identify the most appropriate timing of collection during harvest, which was divided into three stages (S1-S3: 8, 10, and 11 months after sprouting, respectively). Metabolomic and	pmid:36088784 doi:10.1016/j.plaphy.2022.08.026	Sun, 11 Sep 2022 06:00:00 -0400
3	pubmed:36088848	Direct introduction MALDI FTICR MS based on dried droplet deposition applied to non-targeted metabolomics on Pisum Sativum root exudates	Valentina Calabrese Isabelle Schmitz-Afonso Wassila Riah-Anglet Isabelle Trinsoutrot-Gattin Barbara Pawlak Carlos Afonso	Non-targeted metabolomic approaches based on direct introduction (DI) through a soft ionization source are nowadays used for large-scale analysis and wide cover-up of metabolites in complex matrices. When coupled with ultra-high-resolution Fourier-Transform ion cyclotron resonance (FTICR MS), DI is generally performed through electrospray (ESI), which, despite the great analytical throughput, can suffer of matrix effects due to residual salts or charge competitors. In alternative, matrix	pmid:36088848 doi:10.1016/j.talanta.2022.123901	Sun, 11 Sep 2022 06:00:00 -0400
4	pubmed:36088854	Detection of acute ischemic stroke and backtracking stroke onset time via machine learning analysis of metabolomics	Yiheng Zhang Dayu Zhu Tao Li Xiaoya Wang Lili Zhao Xiaofei Yang Meijuan Dang Ye Li Yulun Wu Ziwei Lu Jialiang Lu Yating Jian Heying Wang Lei Zhang Xiaoyun Lu Ziyu Shen Hong Fan Wenshan Cai Guilian Zhang	The time window from stroke onset is critical for the treatment decision. However, in unknown onset stroke, it is often difficult to determine the exact onset time because of the lack of assessment methods, which can result in controversial and random treatment decisions. Previous studies have shown that serum biomarkers, in addition to imaging assessment, are useful for determining the stroke onset time. However, as yet there are no specific biomarkers or corresponding methodologies that are	pmid:36088854 doi:10.1016/j.biopha.2022.113641	Sun, 11 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
5	pubmed:36089117	Folate enzyme MTHFD2 links one-carbon metabolism to unfolded protein response in glioblastoma	Zhiyuan Zhu Karrie Mei-Yee Kiang Ning Li Jiaxin Liu Pingde Zhang Lei Jin Xiaozheng He Shizhong Zhang Gilberto Ka-Kit Leung	The mitochondrial folate enzyme methylenetetrahydrofolate dehydrogenase/cyclohydrolase (MTHFD2) has shown oncogenic roles in various cancers and may have non-metabolic functions. This study investigated the role of MTHFD2 in glioblastoma pathogenesis. We find that MTHFD2 expression is enriched in gliomas by analysing public databases and clinical specimens. RNA interference (RNAi) and inhibitor of MTHFD2 hamper the proliferation of glioblastoma and induce apoptosis in cell lines, glioma	pmid:36089117 doi:10.1016/j.canlet.2022.215903	Sun, 11 Sep 2022 06:00:00 -0400
6	pubmed:36089660	Berberine ameliorates depression-like behavior in CUMS mice by activating TPH1 and inhibiting IDO1-associated with tryptophan metabolism	Ping-Yuan Ge Shu-Yue Qu Sai-Jia Ni Zeng-Ying Yao Yi-Yu Qi Xin Zhao Rui Guo Nian-Yun Yang Qi-Chun Zhang Hua-Xu Zhu	Berberine, which is a potential antidepressant, exhibits definite efficiency in modulating the gut microbiota. Depressive behaviors in mice induced using chronic unpredictable mild stress (CUMS) stimulation were evaluated by behavioral experiments. The markers of neurons and synapses were measured using immunohistochemical staining. An enzymelinked immunosorbent assay was adopted to analyze serum inflammatory cytokines levels and neurotransmitters were evaluated by LC-MS/MS. Untargeted	pmid:36089660 doi:10.1002/ptr.7616	Sun, 11 Sep 2022 06:00:00 -0400
7	pubmed:36089851	Tao-Hong-Si-Wu decoction improves depressive symptoms in model rats via amelioration of BDNF-CREB-arginase I axis disorders	Xiaoping Zhang Zeng Li Chuanpu Shen Jinzhi He Longfei Wang Lei Di Bin Rui Ning Li Zhicheng Liu	CONTEXT: The traditional Chinese medicine formula Tao-Hong-Si-Wu decoction (TSD), used for treating ischaemic stroke, has the potential to treat depressive disorder (DD).	pmid:36089851 doi:10.1080/13880209.2022.2116460	Mon, 12 Sep 2022 06:00:00 -0400
8	pubmed:36090025	Comparison of extraction methods for intracellular metabolomics of human tissues	Carolin Andresen Tobias Boch Hagen M Gegner Nils Mechtel Andreas Narr Emrullah Birgin Erik Rasbach Nuh Rahbari Andreas Trumpp Gernot Poschet Daniel Hübschmann	Analyses of metabolic compounds inside cells or tissues provide high information content since they represent the endpoint of biological information flow and are a snapshot of the integration of many regulatory processes. However, quantification of the abundance of metabolites requires their careful extraction. We present a comprehensive study comparing ten extraction protocols in four human sample types (liver tissue, bone marrow, HL60, and HEK cells) aiming to detect and quantify up to 630	pmid:36090025 pmc:PMC9461704 doi:10.3389/fmolb.2022.932261	Mon, 12 Sep 2022 06:00:00 -0400
9	pubmed:36090035	Metabolomics reveals mouse plasma metabolite responses to acute exercise and effects of disrupting AMPK-glycogen interactions	Mehdi R Belhaj Nathan G Lawler John A Hawley David I Broadhurst Nolan J Hoffman Stacey N Reinke	Introduction: The AMP-activated protein kinase (AMPK) is a master regulator of energy homeostasis that becomes activated by exercise and binds glycogen, an important energy store required to meet exercise-induced energy demands. Disruption of AMPK-glycogen interactions in mice reduces exercise capacity and impairs whole-body metabolism. However, the mechanisms underlying these phenotypic effects at rest and following exercise are unknown. Furthermore, the plasma metabolite responses to an acute	pmid:36090035 pmc:PMC9449498 doi:10.3389/fmolb.2022.957549	Mon, 12 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
10	pubmed:36090044	Influence of seasonal and geographic variation on the anti-HSV-1 properties and chlorogenic acids content of <i>Helichrysum aureonitens</i> Sch. Bip	Wilson Bamise Adeosun Garland K More Paul Steenkamp Gerhard Prinsloo	Pharmacological studies conducted in the past revealed the potential source of medicinal plants in the development of novel medicines. The phenolic contents of medicinal plants containing chlorogenic acids (CGA) have been linked to a variety of therapeutic effects, especially antiviral activity. Helichrysum aureonitens is a medicinal plant which has been reported to contain chlorogenic acids compounds and has also shown antiviral activities against a number of virus species including Herpes	pmid:36090044 pmc:PMC9452954 doi:10.3389/fmolb.2022.961859	Mon, 12 Sep 2022 06:00:00 -0400
11	pubmed:36090050	Metabolic profiling of induced acute pancreatitis and pancreatic cancer progression in a mutant Kras mouse model	Tatiana J Carneiro Joana Pinto Eva M Serrao António S Barros Kevin M Brindle Ana M Gil	Untargeted Nuclear Magnetic Resonance (NMR) metabolomics of polar extracts from the pancreata of a caerulin-induced mouse model of pancreatitis (Pt) and of a transgenic mouse model of pancreatic cancer (PCa) were used to find metabolic markers of Pt and to characterize the metabolic changes accompanying PCa progression. Using multivariate analysis a 10-metabolite metabolic signature specific to Pt tissue was found to distinguish the benign condition from both normal tissue and precancerous	pmid:36090050 pmc:PMC9452780 doi:10.3389/fmolb.2022.937865	Mon, 12 Sep 2022 06:00:00 -0400
12	pubmed:36090056	Revealing the pharmacological effect and mechanism of darutoside on gouty arthritis by liquid chromatography/mass spectrometry and metabolomics	Jing Wang Yan-Chun Sun	Darutoside is a diterpenoids compound with significant anti-inflammatory activity, however the pharmacological action and mechanism are still unclear. Metabolomics strategy was used to uncovering the pharmacological action and effective mechanism of darutoside against acute gouty arthritis rats. Liquid chromatography coupled with mass spectrometry technique was performed to explore the serum metabolites and potential pathways. We found that darutoside can up-regulate the level of glutamate,	pmid:36090056 pmc:PMC9448993 doi:10.3389/fmolb.2022.942303	Mon, 12 Sep 2022 06:00:00 -0400
13	pubmed:36090115	Untargeted metabolite profiling to elucidate rhizosphere and leaf metabolome changes of wheat cultivars (<i>Triticum aestivum</i> L.) treated with the plant growth-promoting rhizobacteria <i>Paenibacillus alvei</i> (T22) and <i>Bacillus subtilis</i>	Manamele D Mashabela Fidele Tugizimana Paul A Steenkamp Lizelle A Piater Ian A Dubery Msizi I Mhlongo	The rhizosphere is a highly complex and biochemically diverse environment that facilitates plant-microbe and microbemicrobe interactions, and this region is found between plant roots and the bulk soil. Several studies have reported plant root exudation and metabolite secretion by rhizosphere-inhabiting microbes, suggesting that these metabolites play a vital role in plant-microbe interactions. However, the biochemical constellation of the rhizosphere soil is yet to be fully elucidated and thus	pmid:36090115 pmc:PMC9453603 doi:10.3389/fmicb.2022.971836	Mon, 12 Sep 2022 06:00:00 -0400
14	pubmed:36090174	Effects of lipoteichoic and arachidonic acids on the immune-regulatory mechanism of bovine mammary epithelial cells using multiomics analysis	Weitao Dong Yan Chen Quanwei Zhang Xiaoxuan Zhao Peiwen Liu Haijian He Ting Lu Yuxuan He Xianghong Du Junjie Hu Xingxu Zhao Yong Zhang	Staphylococcus aureus is one of the most important pathogens causing mastitis in dairy cows. It mainly utilizes the properties of its pathogenic factor, lipoteichoic acid (LTA), to elicit a host-cell inflammatory response and evade the host-cell immune response. Arachidonic acid (AA) has a regulatory role in the inflammatory response, cell metabolism, and apoptosis. The study aimed to establish a cell model by determining the optimal concentration of LTA and AA for cell induction using the Cell	pmid:36090174 pmc:PMC9450935 doi:10.3389/fvets.2022.984607	Mon, 12 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
15	pubmed:36090329	Metabolomic profiling identifies biomarkers and metabolic impacts of surgery for colorectal cancer	Feng Zhuang Xuesong Bai Yang Shi Le Chang Wanchao Ai Juan Du Wei Liu Humin Liu Xukun Zhou Zhong Wang Tao Hong	CONCLUSION: Through serum-based metabolomics, our study demonstrated the differential metabolic characteristics in CRC patients after surgery compared with those before surgery. Our results suggested that metabonomic analysis may be a powerful method for exploring physiological alterations in CRC patients after surgery as well as a useful tool for identifying candidate biomarkers and monitoring disease recurrence.	pmid:36090329 pmc:PMC9453208 doi:10.3389/fsurg.2022.913967	Mon, 12 Sep 2022 06:00:00 -0400
16	pubmed:36090365	Does urinary metabolite signature act as a biomarker of post-stroke depression?	Wa Cai Xia-Fei Wang Xi-Fang Wei Jing-Ruo Zhang Chen Hu Wen Ma Wei-Dong Shen	CONCLUSION: The systematic review provided evidence that differential urinary metabolites analyzed by the GC-MS-based approach might be used as a biomarker for the diagnosis and prognosis of PSD.	pmid:36090365 pmc:PMC9448878 doi:10.3389/fpsyt.2022.928076	Mon, 12 Sep 2022 06:00:00 -0400
17	pubmed:36090468	Metabolomics based inferences to unravel phenolic compound diversity in cereals and its implications for human gut health	Rhowell Jr N Tiozon Kristel June D Sartagoda Luster May N Serrano Alisdair R Fernie Nese Sreenivasulu	BACKGROUND: Whole grain cereals are a good source of nutrients. Several cutting-edge metabolomic platforms have been deployed to identify various phenolic compounds and enhance cereal bioactive bioavailability. A diet rich in cereal phenolics may modify the microbial composition, support gut homeostasis, and increase gut health, thereby lowering the risk of non-communicable illness.	pmid:36090468 pmc:PMC9449372 doi:10.1016/j.tifs.2022.06.011	Mon, 12 Sep 2022 06:00:00 -0400
18	pubmed:36091013	Multi-omics analysis reveals the metabolic regulators of duodenal low-grade inflammation in a functional dyspepsia model	Shuai Ji Yanting You Baizhao Peng Tianyu Zhong Yuxiang Kuang Shasha Li Lijing Du Liqian Chen Xiaomin Sun Jiaojiao Dai Suiping Huang Yuyao Wu Yanyan Liu	Several gastrointestinal phenotypes and impairment of duodenal mucosal barrier have been reported in clinical studies in patients with functional dyspepsia (FD). Due to the preferential colonization of the mucosa, intestinal microbes and their metabolites are commonly involved in host metabolism and immune responses. However, there are no studies on the intertwined correlation among multi-level data. For more comprehensive illustrating, a multi-omics analysis focusing on the duodenum was	pmid:36091013 pmc:PMC9453867 doi:10.3389/fimmu.2022.944591	Mon, 12 Sep 2022 06:00:00 -0400
19	pubmed:36091252	Analysis of serum fatty acid, amino acid, and organic acid profiles in gestational hypertension and gestational diabetes mellitus via targeted metabolomics	Xiangju Kong Qiushuang Zhu Yuanjie Dong Yuqiao Li Jinxiao Liu Qingna Yan Mingli Huang Yucun Niu	This study aimed to characterize metabolite differences and correlations between hypertensive disorders of pregnancy (HP) and gestational diabetes mellitus (GDM) using univariate, multivariate analyses, RF, and pathway analyses in a cross-sectional study. Dietary surveys were collected and targeted metabolomics was applied to measure levels of serum fatty acids, amino acids, and organic acids in 90 pregnant women at 24-28 weeks gestation at the First Affiliated Hospital of Harbin Medical	pmid:36091252 pmc:PMC9458889 doi:10.3389/fnut.2022.974902	Mon, 12 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
20	pubmed:36091491	Multi-omic analyses identify mucosa bacteria and fecal metabolites associated with weight loss after fecal microbiota transplantation	Fen Zhang Tao Zuo Yating Wan Zhilu Xu Chunpan Cheung Amy Y Li Wenyi Zhu Whitney Tang Paul K S Chan Francis K L Chan Siew C Ng	Fecal microbiota transplantation (FMT) has shown promising results in animal models of obesity, while results in human studies are inconsistent. We aimed to determine factors associated with weight loss after FMT in nine obese subjects using serial multi-omics analysis of the fecal and mucosal microbiome. The mucosal microbiome, fecal microbiome, and fecal metabolome showed individual clustering in each subject after FMT. The colonic microbiome in patients showed more marked variance after FMT	pmid:36091491 pmc:PMC9460156 doi:10.1016/j.xinn.2022.100304	Mon, 12 Sep 2022 06:00:00 -0400
21	pubmed:36091512	Variability of body mass index and risks of prostate, lung, colon, and ovarian cancers	Yangyang Sun Lingling Zhou Tao Shan Qiong Ouyang Xu Li Yuanming Fan Ying Li Hang Gong Raphael N Alolga Gaoxiang Ma Yuqiu Ge Heng Zhang	CONCLUSION: The findings imply that maintaining a stable weight across adulthood is associated with a decreased incidence of lung cancer.	pmid:36091512 pmc:PMC9452651 doi:10.3389/fpubh.2022.937877	Mon, 12 Sep 2022 06:00:00 -0400
22	pubmed:36091591	Validation of the Anticolitis Efficacy of the Jian-Wei-Yu-Yang Formula	Jing Yan Yan Tang Wei Yu Lu Jiang Chen Liu Qi Li Zhiqiang Zhang Changlei Shao Yang Zheng Xihao Liu Xincheng Liu	CONCLUSION: The JW capsule attenuated the progression of murine colitis by a prompt resolution of inflammation and bloody stool and by re-establishing a microbiome profile that favors re-epithelization and prevents carcinogenesis.	pmid:36091591 pmc:PMC9451982 doi:10.1155/2022/9110704	Mon, 12 Sep 2022 06:00:00 -0400
23	pubmed:36091722	Exploration of metabolic responses towards hypoxia mimetic DMOG in cancer cells by using untargeted metabolomics	Mohammad Imran Khan	Hypoxia is considered as one of the most crucial elements of tumor microenvironment. The hypoxia inducible transcription factors (HIF-1/2) are used by the cancer cells to adapt hypoxic microenvironment through regulating the expression of various target genes, including metabolic enzymes. Dimethyloxalylglycine (DMOG), a hypoxic mimetic used for HIF stabilisation in cell and animal models, also demonstrates multiple metabolic effects. In past, it was shown that in cancer cells, DMOG treatment	pmid:36091722 pmc:PMC9460158 doi:10.1016/j.sjbs.2022.103426	Mon, 12 Sep 2022 06:00:00 -0400
24	pubmed:36091780	Tremella fuciformis polysaccharides alleviate induced atopic dermatitis in mice by regulating immune response and gut microbiota	Lingna Xie Kaiye Yang Yiheng Liang Zhenyuan Zhu Zhengqiang Yuan Zhiyun Du	Atopic dermatitis (AD), characterized by severe pruritus, immune imbalance, and skin barrier dysfunction, has a high incidence worldwide. Recent evidence has shown that the modulation of gut microbiota is crucial for alleviating clinical symptoms of AD. Tremella fuciformis polysaccharides (TFPS) have been demonstrated to have a variety of biological activities such as immunomodulatory, anti-tumor, antioxidant, anti-inflammatory, neuroprotective, hypoglycemic and hypolipidemic effects. However,	pmid:36091780 pmc:PMC9452665 doi:10.3389/fphar.2022.944801	Mon, 12 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
25	pubmed:36091783	Application of metabolomics and network analysis to reveal the ameliorating effect of four typical "hot" property herbs on hypothyroidism rats	Yang-Yang Wang Yan-Ping Sun Bing-You Yang Qiu-Hong Wang Hai-Xue Kuang	Herbs with a "hot" properties are frequently used to treat cold symptoms in TCM. However, the underlying mechanisms of the herbs with "hot" properties on hypothyroidism have not been investigated. This study aimed to explore four typical "hot" and "cold" property herb on hypothyroidism. Firstly, the difference efficacy between the four typical "hot" property herbs and the four typical "cold" property herbs was assessed by physical signs, thyroid function, and the metabolic profile using	pmid:36091783 pmc:PMC9452843 doi:10.3389/fphar.2022.955905	Mon, 12 Sep 2022 06:00:00 -0400
26	pubmed:36091795	A stepwise strategy integrating metabolomics and pseudotargeted spectrum-effect relationship to elucidate the potential hepatotoxic components in <i>Polygonum multiflorum</i>	Yunfei Song Jianbo Yang Xiaowen Hu Huiyu Gao Pengfei Wang Xueting Wang Yue Liu Xianlong Cheng Feng Wei Shuangcheng Ma	Polygonum multiflorum (PM) Thunb., a typical Chinese herbal medicine with different therapeutic effect in raw and processed forms, has been used worldwide for thousands of years. However, hepatotoxicity caused by PM has raised considerable concern in recent decades. The exploration of toxic components in PM has been a great challenge for a long time. In this study, we developed a stepwise strategy integrating metabolomics and pseudotargeted spectrum-effect relationship to illuminate the	pmid:36091795 pmc:PMC9459084 doi:10.3389/fphar.2022.935336	Mon, 12 Sep 2022 06:00:00 -0400
27	pubmed:36091827	Application of metabolomics in the diagnosis of non-alcoholic fatty liver disease and the treatment of traditional Chinese medicine	Mingmei Shao Yifei Lu Hongjiao Xiang Junmin Wang Guang Ji Tao Wu	Non-alcoholic fatty liver disease (NAFLD) is the most common chronic liver disease around the world, and it often coexists with insulin resistance-related diseases including obesity, diabetes, hyperlipidemia, and hypertension, which seriously threatens human health. Better prevention and treatment strategies are required to improve the impact of NAFLD. Although needle biopsy is an effective tool for diagnosing NAFLD, this method is invasive and difficult to perform. Therefore, it is very	pmid:36091827 pmc:PMC9453477 doi:10.3389/fphar.2022.971561	Mon, 12 Sep 2022 06:00:00 -0400
28	pubmed:36091834	Using an untargeted metabolomics approach to analyze serum metabolites in COVID-19 patients with nucleic acid turning negative	Wenyu Chen Ming Yao Miaomiao Chen Zhao Ou Qi Yang Yanbin He Ning Zhang Min Deng Yuqi Wu Rongchang Chen Xiaoli Tan Ziqing Kong	Background: The coronavirus disease of 2019 (COVID-19) is a severe public health issue that has infected millions of people. The effective prevention and control of COVID-19 has resulted in a considerable increase in the number of cured cases. However, little research has been done on a complete metabonomic examination of metabolic alterations in COVID-19 patients following treatment. The current project pursues rigorously to characterize the variation of serum metabolites between healthy	pmid:36091834 pmc:PMC9449332 doi:10.3389/fphar.2022.964037	Mon, 12 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
29	pubmed:36092021	Intestinal microbiomics and liver metabolomics insights into the preventive effects of chromium (III)-enriched yeast on hyperlipidemia and hyperglycemia induced by high-fat and high-fructose diet	Mei-Ting Wang Wei-Ling Guo Zi-Yi Yang Feng Chen Tian-Tian Lin Wen-Long Li Xu-Cong Lv Ping-Fan Rao Lian-Zhong Ai Li Ni	In recent years, organic chromium (III) supplements have received increasing attentions for their low toxicity, high bioavailability and wide range of health-promoting benefits. This study aimed to investigate the preventive effects of chromium (III)-enriched yeast (YCr) on high-fat and high-fructose diet (HFHFD)-induced hyperlipidemia and hyperglycemia in mice, and further clarify its mechanism of action from the perspective of intestinal microbiomics and liver metabolomics. The results	pmid:36092021 pmc:PMC9449561 doi:10.1016/j.crfs.2022.08.015	Mon, 12 Sep 2022 06:00:00 -0400
30	pubmed:36092416	Metabolome and RNA-seq Analysis of Responses to Nitrogen Deprivation and Resupply in Tea Plant (Camellia sinensis) Roots	Wenluan Xu Jing Li Luyu Zhang Xuyang Zhang Hua Zhao Fei Guo Yu Wang Pu Wang Yuqiong Chen Dejiang Ni Mingle Wang	Nitrogen (N) is an important contributor in regulating plant growth and development as well as secondary metabolites synthesis, so as to promote the formation of tea quality and flavor. Theanine, polyphenols, and caffeine are important secondary metabolites in tea plant. In this study, the responses of Camellia sinensis roots to N deprivation and resupply were investigated by metabolome and RNA-seq analysis. N deficiency induced content increase for most amino acids (AAs) and reduction for the	pmid:36092416 pmc:PMC9459018 doi:10.3389/fpls.2022.932720	Mon, 12 Sep 2022 06:00:00 -0400
31	pubmed:36092435	BoGDB: An integrative genomic database for Brassica oleracea L	Yong Wang Jialei Ji Zhiyuan Fang Limei Yang Mu Zhuang Yangyong Zhang Honghao Lv	Brassica oleracea is an important species due to its high economic and nutritional value. Moreover, it is an ideal model for studies of morphology and genome evolution. In the genomic era, with massive "omics" data being generated, a high-efficiency platform is crucial to deepen our understanding of this important species. In this study, we developed the B. oleracea Genome Database (BoGDB) to consolidate genome, transcriptome, and metabolome data of B. oleracea cultivars, providing the first	pmid:36092435 pmc:PMC9449717 doi:10.3389/fpls.2022.852291	Mon, 12 Sep 2022 06:00:00 -0400
32	pubmed:36092633	Integrated Network Pharmacology Analysis and Serum Metabolomics to Reveal the Antimalaria Mechanism of Artesunate	Feiran Wang Jian Song Yingying Yan Qian Zhou Xiaojing Li Ping Wang Zongtong Yang Qiuhong Zhang Huimin Zhang	Artesunate is a widely used drug in clinical treatment of malaria. The aim of this study was to investigate the therapeutic mechanism of artesunate on malaria using an integrated strategy of network pharmacology and serum metabolomics. The mice models of malaria were established using 2 × 10 red blood cells infected with Plasmodium berghei ANKA injection. Giemsa and hematoxylin-eosin (HE) staining were used to evaluate the efficacy of artesunate on malaria. Next, network pharmacology analysis	pmid:36092633 pmc:PMC9453802 doi:10.1021/acsomega.2c04157	Mon, 12 Sep 2022 06:00:00 -0400
33	pubmed:36092704	The metabolic fate of oxaliplatin in the biological milieu investigated during in vivo lung perfusion using a unique miniaturized sampling approach based on solid-phase microextraction coupled with liquid chromatography-mass spectrometry	Mariola Olkowicz Hernando Rosales-Solano Khaled Ramadan Aizhou Wang Marcelo Cypel Janusz Pawliszyn	Adjuvant chemotherapy after pulmonary metastasectomy for colorectal cancer may reduce recurrence and improve survival rates; however, the benefits of this treatment are limited by the significant side effects that accompany it. The development of a novel in vivo lung perfusion (IVLP) platform would permit the localized delivery of high doses of chemotherapeutic drugs to target residual micrometastatic disease. Nonetheless, it is critical to continuously monitor the levels of such drugs during	pmid:36092704 pmc:PMC9453651 doi:10.3389/fcell.2022.928152	Mon, 12 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
34	pubmed:36093113	Acupuncture ameliorates breast cancer- related fatigue by regulating the gut microbiota-gut-brain axis	Zhuan Lv Ruidong Liu Kaiqi Su Yiming Gu Lu Fang Yongfu Fan Jing Gao Xiaodi Ruan Xiaodong Feng	Cancer-related fatigue (CRF) is the most common side effect of chemotherapy for breast cancer (BC). Acupuncture treatment has an anti-fatigue effect and can regulate gut microbiota disturbance in fatigue patients. Related studies have shown that the gut microbiota-gut-brain axis is closely related to the occurrence of CRF. In this study, we first investigated the alterations of acupuncture on fatigue-like behavior, gut microbiota, gut inflammation and neuroinflammation response, gut barriers,	pmid:36093113 pmc:PMC9449876 doi:10.3389/fendo.2022.921119	Mon, 12 Sep 2022 06:00:00 -0400
35	pubmed:36093201	Integrated microbiome and metabolome analysis reveals the potential therapeutic mechanism of <i>Qing-Fei-Pai-Du</i> decoction in mice with coronavirus-induced pneumonia	Gaosong Wu Wendan Zhang Ningning Zheng Xianpeng Zu Saisai Tian Jing Zhong Yuhao Zhang Jingyu Liao Lili Sheng Guanbo Ge Houkai Li Weidong Zhang	Current studies have shown that gut microbiota may be closely related to the severity of coronavirus disease 2019 (COVID-19) by regulating the host immune response. Qing-Fei-Pai-Du decoction (QFPDD) is the recommended drug for clinical treatment of patients with COVID-19 in China, but whether it exerts a therapeutic effect by modulating the immune response through gut microbiota remains unclear. In this study, we evaluated the therapeutic effects of QFPDD in pneumonia model mice and performed	pmid:36093201 pmc:PMC9461713 doi:10.3389/fcimb.2022.950983	Mon, 12 Sep 2022 06:00:00 -0400
36	pubmed:36093215	Metabolic alterations in alga Chlamydomonas reinhardtii exposed to nTiO amaterials	Wei Liu Mengting Li Weiwei Li Arturo A Keller Vera I Slaveykova	Nano-sized titanium dioxide (nTiO(2)) is one of the most commonly used materials, however the knowledge about the molecular basis for metabolic and physiological changes in phytoplankton is yet to be explored. In the present study we use a combination of targeted metabolomics, transcriptomics and physiological response studies to decipher the metabolic perturbation in green alga Chlamydomonas reinhardtii exposed for 72 h to increasing concentrations (2, 20, 100 and 200 mg L^(-1)) of nTiO(2) with	pmid:36093215 pmc:PMC9367718 doi:10.1039/d2en00260d	Mon, 12 Sep 2022 06:00:00 -0400
37	pubmed:36093571	Analysis of Serum Metabolism in Premature Infants before and after Feeding Based on Gas Chromatography-Mass Spectrometry and the Relationship with Necrotizing Enterocolitis	Fusheng Wang Guanghuan Wang Weizhong Li Chenbin Xu Zailin Zeng Yongcui Zhou	Preterm birth and enteral feeding are two main factors leading to necrotizing enterocolitis (NEC). The metabolomics of preterm infants before and after feeding can provide a basis for the prediction of NEC. Using the method of cross-sectional study, the mode was established with 19 prematures' serumal samples at birth and after feeding as the control group. The serum was analyzed by gas chromatography-mass spectrometry (GC-MS). Chemometric analysis includes the principal component analysis	pmid:36093571 doi:10.1002/bmc.5505	Mon, 12 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
38	pubmed:36093868	The combination of microbiome and metabolome to analyze the cross-cooperation mechanism of <i>Echinacea purpurea</i> polysaccharide with the gut microbiota <i>in vitro</i> and <i>in vivo</i>	Chang Liu Wenhao Jiang Fangwei Yang Yuliang Cheng Yahui Guo Weirong Yao Yong Zhao He Qian	Echinacea purpurea polysaccharide (EPP) is a functional compound in Echinacea purpurea. At present, it is generally recognized that plant polysaccharides can regulate the intestinal microecology, but there are few studies on EPP. In this study, we used the digestive model (stomach-small intestine-colon) and a mouse model to study the effect of EPP on intestinal microecology and the mechanism. Also, combined with the microbiome and metabolome analysis methods, the interaction network mechanism of	pmid:36093868 doi:10.1039/d2fo02336a	Mon, 12 Sep 2022 06:00:00 -0400
39	pubmed:36094015	Sorting-free metabolic profiling uncovers the vulnerability of fatty acid -oxidation in in vitro quiescence models	Karin Ortmayr Mattia Zampieri	Quiescent cancer cells are rare nondiving cells with the unique ability to evade chemotherapies and resume cell division after treatment. Despite the associated risk of cancer recurrence, how cells can reversibly switch between rapid proliferation and quiescence remains a long-standing open question. By developing a unique methodology for the cell sorting-free separation of metabolic profiles in cell subpopulations in vitro, we unraveled metabolic characteristics of quiescent cells that are	pmid:36094015 doi:10.15252/msb.202110716	Mon, 12 Sep 2022 06:00:00 -0400
40	pubmed:36094096	Integrating multi-omics summary data using a Mendelian randomization framework	Chong Jin Brian Lee Li Shen Qi Long Alzheimer's Disease Neuroimaging Initiative Alzheimer's Disease Metabolomics Consortium	Mendelian randomization is a versatile tool to identify the possible causal relationship between an omics biomarker and disease outcome using genetic variants as instrumental variables. A key theme is the prioritization of genes whose omics readouts can be used as predictors of the disease outcome through analyzing GWAS and QTL summary data. However, there is a dearth of study of the best practice in probing the effects of multiple -omics biomarkers annotated to the same gene of interest. To	pmid:36094096 doi:10.1093/bib/bbac376	Mon, 12 Sep 2022 06:00:00 -0400
41	pubmed:36094342	Nutritional Modulation of Sleep Latency, Duration, and Efficiency: A Randomised, Repeated-Measures, Double-Blind Deception Study	Carl Langan-Evans Mark A Hearris Chloe Gallagher Stephen Long Craig Thomas Andrew D Moss William Cheung Glyn Howatson James P Morton	CONCLUSIONS: Data demonstrate that employing the proposed blend of novel nutritional ingredients during free living conditions reduced sleep onset latency, increased total sleep duration and increased sleep efficiency, leading to reduced perceptions of morning sleepiness. These effects may be mediated by the upregulation of key metabolites involved in the neurophysiological modulation of the sleep/wake cycle.	pmid:36094342 doi:10.1249/MSS.0000000000003040	Mon, 12 Sep 2022 06:00:00 -0400
42	pubmed:36094355	JUMPptm: Integrated software for sensitive identification of post-translational modifications and its application in Alzheimer's disease study	Suresh Poudel David Vanderwall Zuo-Fei Yuan Zhiping Wu Junmin Peng Yuxin Li	Mass spectrometry (MS)-based proteomic analysis of posttranslational modifications (PTMs) usually requires the pre-enrichment of modified proteins or peptides. However, recent ultra-deep whole proteome profiling generates millions of spectra in a single experiment, leaving many unassigned spectra, some of which may be derived from PTM peptides. Here we present JUMPptm, an integrative computational pipeline, to extract PTMs from unenriched whole proteome. JUMPptm combines the advantages of JUMP,	pmid:36094355 doi:10.1002/pmic.202100369	Mon, 12 Sep 2022 06:00:00 -0400

	NCT Number	Title	Authors	Description	Identifier	Dates
43	pubmed:36094592	Influence of Extracellular Vesicles from the Follicular Fluid of Young Women and Women of Advanced Maternal Age with Different miRNA Profiles on Sperm Functional Properties	A P Sysoeva O S Nepsha N P Makarova D N Silachev N N Lobanova A V Timofeeva Yu A Shevtsova E E Bragina E A Kalinina	We studied the effect of co-culturing of extracellular vesicles in the follicular fluid of young women and women of advanced maternal age on sperm motility. Vesicles were obtained by differential centrifugation. The sperm fraction was isolated from the seminal fluid of 18 patients (age 28-36 years). The spermatozoa were incubated with vesicles (1:2 ratio) for 60 or 120 min at 37°C in a CO2 incubator. A fraction of spermatozoa incubated without vesicles served as the control. After the	pmid:36094592 doi:10.1007/s10517-022-05589-x	Mon, 12 Sep 2022 06:00:00 -0400
44	pubmed:36094945	Transcriptomic analysis reveals Aspergillus oryzae responds to temperature stress by regulating sugar metabolism and lipid metabolism	Chunmiao Jiang Jinxin Ge Bin He Zhe Zhang Zhihong Hu Yongkai Li Bin Zeng	Aspergillus oryzae is widely used in industrial applications, which always encounter changes within multiple environmental conditions during fermentation, such as temperature stress. However, the molecular mechanisms by which A. oryzae protects against temperature stress have not been elucidated. Therefore, this study aimed to characterize the fermentative behavior, transcriptomic profiles, and metabolic changes of A. oryzae in response to temperature stress. Both low and high temperatures	pmid:36094945 doi:10.1371/journal.pone.0274394	Mon, 12 Sep 2022 06:00:00 -0400
45	pubmed:36094960	Plasma metabolome predicts trained immunity responses after antituberculosis BCG vaccination	Valerie A C M Koeken Cancan Qi Vera P Mourits L Charlotte J de Bree Simone J C F M Moorlag Vidhisha Sonawane Heidi Lemmers Helga Dijkstra Leo A B Joosten Arjan van Laarhoven Cheng-Jian Xu Reinout van Crevel Mihai G Netea Yang Li	The antituberculosis vaccine Bacillus Calmette-Guérin (BCG) induces nonspecific protection against heterologous infections, at least partly through induction of innate immune memory (trained immunity). The amplitude of the response to BCG is variable, but the factors that influence this response are poorly understood. Metabolites, either released by cells or absorbed from the gut, are known to influence immune responses, but whether they impact BCG responses is not known. We vaccinated 325	pmid:36094960 doi:10.1371/journal.pbio.3001765	Mon, 12 Sep 2022 06:00:00 -0400
46	pubmed:36095062	SGLT2 Inhibitors in Heart Failure: Targeted Metabolomics and Energetic Metabolism	Carlos G Santos-Gallego Manuel Mayr Juan Badimon	No abstract	pmid:36095062 doi:10.1161/CIRCULATIONAHA.122.06080 5	Mon, 12 Sep 2022 06:00:00 -0400
47	pubmed:36095068	Correction to: Metabolomic Profiling of the Effects of Dapagliflozin in Heart Failure with Reduced Ejection Fraction: DEFINE-HF		No abstract	pmid:36095068 doi:10.1161/CIR.000000000001099	Mon, 12 Sep 2022 06:00:00 -0400
48	pubmed:36095209	The TOR complex controls ATP levels to regulate actin cytoskeleton dynamics in Arabidopsis	Liufeng Dai Baojie Wang Ting Wang Etienne H Meyer Valentin Kettel Natalie Hoffmann Heather E McFarlane Shalan Li Xuna Wu Kelsey L Picard Patrick Giavalisco Staffan Persson Yi Zhang	Energy is essential for all cellular functions in a living organism. How cells coordinate their physiological processes with energy status and availability is thus an important question. The turnover of actin cytoskeleton between its monomeric and filamentous forms is a major energy drain in eukaryotic cells. However, how actin dynamics are regulated by ATP levels remain largely unknown in plant cells. Here, we observed that seedlings with impaired functions of target of rapamycin complex 1	pmid:36095209 doi:10.1073/pnas.2122969119	Mon, 12 Sep 2022 06:00:00 -0400